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Biochemistry

A small single-"finger" peptide from the erythroid transcription factor GATA-1 binds specifically to DNA as a zinc or iron complex

(zinc finger/globin gene regulation)

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ABSTRACT **Sequence-specific DNA binding has been demonstrated for a synthetic peptide comprising only one of the two "finger"-like domains of the erythroid transcription factor GATA-1 (also termed Eryf-1, NF-E1, or GF-1). Quantitative analysis of gel-retardation assays yields a specific association constant of 1.2×10^8 M, compared with values of about 10^9 M for the full-length natural GATA-1 protein. By the use of peptides of various lengths, it was possible to delineate the smallest region necessary for specific binding. A single C-terminal finger of the double-finger motif is necessary but not sufficient for sequence-specific interaction. Basic amino acids located C-terminal to the finger (some more than 20 amino acids away) are also essential for tight binding. In addition to demonstrating that zinc is important for the formation of an active binding complex, we show that other ions, notably Fe^{2+}, can fulfill this role. Our results make it clear that the GATA-1 metal binding motif is quite distinct from that found in the steroid hormone family and that GATA-1 is a member of a separate class of DNA binding proteins.**

The erythroid transcription factor GATA-1 was the first identified (1–4) member of a distinct family of "finger"-motif DNA binding proteins, which now includes regulatory proteins expressed in other cell lineages (GATA-2, -3, and -4; refs. 5 and 6 and T.E., unpublished data) and in a wide variety of organisms. The GATA-1 protein of chickens, mice, humans, and other vertebrates is found in erythroid-lineage cells (1–4) and in some other human and mouse hematopoietic lineages (7, 8). Binding sites for GATA-1 are found in the cis-regulatory elements of all globin genes (9–13) and most other erythroid-specific genes that have been examined (14–19). Chicken GATA-1 binds (1, 20) as a 35-kDa monomer to an asymmetric DNA target sequence, (A/T)GATA(A/G). The chicken α^D-globin (21), the human γ-globin (22, 23), and the mouse GATA-1 promoters (24) contain slightly higher-affinity sites consisting of two copies of the core consensus sequence, both contacted by a single molecule of GATA-1. The protein (1–4) has two related but nonidentical finger elements of the form Cys-Xaa-Xaa-Cys-$(Xaa)_{17}$-Cys-Xaa-Xaa-Cys, reminiscent of the pair of motifs found in the steroid hormone receptor superfamily (25), but quite different in amino acid sequence, in the number of residues in the motifs, and in the spacing between them. Unlike other such proteins, multiple fingers are not essential to binding; the binding properties of GATA-1 are only weakly affected by deletion or mutation of the N-terminal finger (23). Furthermore, certain fungi [*Saccharomyces cerevisiae* (26, 27), *Aspergillus nidulans* (28), *Neurospora crassa* (29)] contain trans-acting factors that have only a single finger, which is more closely related in sequence to the C-terminal finger of vertebrate GATA-1. It therefore appeared likely that this finger alone might exhibit specific binding behavior. We synthesized a 66-amino acid peptide containing the C-terminal finger domain and found that it binds tightly and specifically to the GATA target sequence. Quantitative binding studies have been carried out with this peptide and with truncated versions of the peptide that delineate the domain essential to binding. The DNA binding activity requires stoichiometric quantities of Zn^{2+}, but other heavy metals can be substituted. We find that the addition of Fe^{2+} in place of Zn^{2+} results in a peptide–metal complex that binds somewhat better than the zinc compound. This raises the tantalizing possibility that some transcription factors of the GATA-1 family may use iron to stabilize the active structure.

METHODS

Peptide Synthesis. Assembly of peptide chains was accomplished using solid-phase synthesis procedures on an Applied Biosystems model 430A automated synthesizer. The following side-chain protecting groups were used: tosyl (Arg), cyclohexyl (Glu, Asp), formyl (Trp), benzyl (Ser, Thr), 4-chlorocarbobenzoxy (Lys), 2-bromocarbobenzoxy (Tyr), *N*-benzyloxymethyl (His), and 4-methylbenzyl (Cys). Cleavage of the side-chain protecting groups and removal from the resin were accomplished by low–high HF cleavage (30). The cleaved peptide was extracted from the resin with 5% (vol/vol) aqueous acetic acid containing 1 mM dithiothreitol. The peptide solution was concentrated, applied to a Sephadex G-50 column, and eluted with the same solution. Fractions containing the peptide were pooled, concentrated, and further purified by reverse-phase HPLC on a Vydac C_8 column, with a water–acetonitrile solvent gradient in 0.05% trifluoroacetic acid. Purity of the peptides was determined by HPLC (93% or greater), amino acid analysis, and peptide sequencing.

Gel-Mobility-Shift Titrations of GATA Peptides. Peptides were dissolved in solvents containing 0.05% trifluoroacetic acid at 5–10 pmol/μl, as determined by ultraviolet absorption spectroscopy using an estimated molar extinction at 280 nm of 12,100. The solvent also contained various amounts of zinc acetate, ferrous chloride, ferric chloride, manganese chloride, cobalt chloride, or cadmium acetate, typically at molar ratios to peptide of 1.5:5. For Fe^{2+}, this solvent also contained 1 mM 2-mercaptoethanol. Although the yield of active (binding) peptide varied (see figures), there was no obvious correlation with this ratio. Samples of the peptide dissolved in 40 μl of the trifluoroacetic acid/metal ion solvent were adjusted in pH by the stepwise addition of four 5-μl aliquots of 75 mM Tris·HCl (pH 7.5). In some cases nitrogen was bubbled through the solutions before they were mixed.

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Abbreviation: GR, glucocorticoid receptor.

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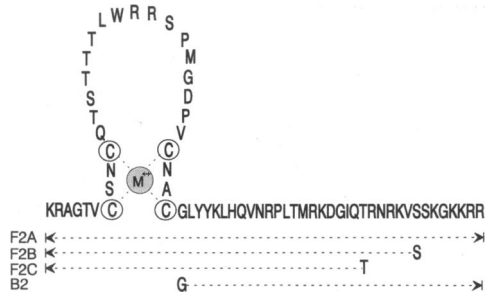

FIG. 1. Peptides used in these studies are derived from the C-terminal finger domain and adjacent basic region of the chicken GATA-1 (*Eryf1*) gene (1). M, metal.

All data including gel images shown in the figures were obtained with a Molecular Dynamics PhosphorImager; all numerical values were obtained by direct computer analysis of the stored images.

RESULTS

The properties of the C-terminal finger of GATA-1 were explored using the 66-amino acid peptide (F2A) containing the four cysteine residues and extending 35 amino acids beyond this cluster in the C-terminal direction (Fig. 1). Gel-mobility-shift assays were used to measure the interaction between this peptide and an oligonucleotide duplex containing a single GATA motif, derived from one of the GATA-1 binding sites in the chicken β/ε-globin enhancer (31). As shown in Fig. 2*A*, the peptide interacted strongly with its target DNA to produce a single complex. Quantitative analysis of the binding data revealed an apparent association constant of 1.2×10^8 M (Table 1). A typical Scatchard plot is shown in Fig. 3. In comparison, binding studies of crude nuclear extracts from 9-day embryonic erythrocytes gave values of about 10^9 M for the affinity of full-length chicken GATA-1 for this sequence (data not shown). To determine the binding affinity for DNA sequences from which the GATA motif is absent, we measured binding to the labeled GATA oligonucleotide in the presence of an excess of unlabeled nonspecific competitor carrying either the binding motif of the transcription factor Sp1 (32) or a mutated GATA-1 binding site (data not shown). We also directly measured the binding to a labeled oligomer carrying the Sp1 site. We estimate that the affinity of F2A for the nonspecific sequences is about three orders of magnitude weaker (moles of nonspecific site vs. moles of specific site) than its affinity for the GATA sequence.

Table 1. Association constants of F2A peptide with specific DNA as a function of heavy metal ion

Metal ion	Apparent association constant, M
Zn^{2+}	$1.20 \pm 0.25 \times 10^8$ (3)
Fe^{2+}	$2.18 \pm 0.48 \times 10^8$ (3)
Co^{2+}	$1.20 \pm 0.25 \times 10^8$ (2)
Cd^{2+}	$0.63 \pm 0.09 \times 10^8$ (2)
Mn^{2+}	—

Means ± standard deviations are shown for the number of titrations given in parentheses.

Provided that the peptide was prepared in the absence of Zn^{2+} and other heavy metals, it did not bind to DNA (Fig. 2*A*). Addition of Zn^{2+} resulted in formation of a peptide–metal complex that bound. CD and NMR studies (data not shown) with this peptide demonstrated that it existed as a random coil in the absence of Zn but formed a single ordered structure when one equivalent of Zn was added. Although we have reported (1) difficulty in demonstrating a similar metal ion dependence with full-length GATA-1, we have more recently been able to remove and add back (unpublished data) the metal ion in such a way (33) as to reconstitute some activity.

The gel-shift assay is easily adapted to the measurement of the Zn/peptide ratio. F2A was reconstituted in the presence of ^{65}Zn, and the labeled peptide was mixed either with unlabeled specific DNA probe or with the same concentration of probe containing ^{32}P label. Parallel gel-mobility-shift data were obtained with both probes. The results (Table 2) show that each mole of complex carries almost exactly one mole of zinc, as expected for an asymmetric site binding a single F2A molecule. This result is entirely consistent with the earlier observation (1) that GATA-1 itself binds as a monomer.

To determine whether other heavy metal ions could substitute for zinc to form a structure capable of specific binding,

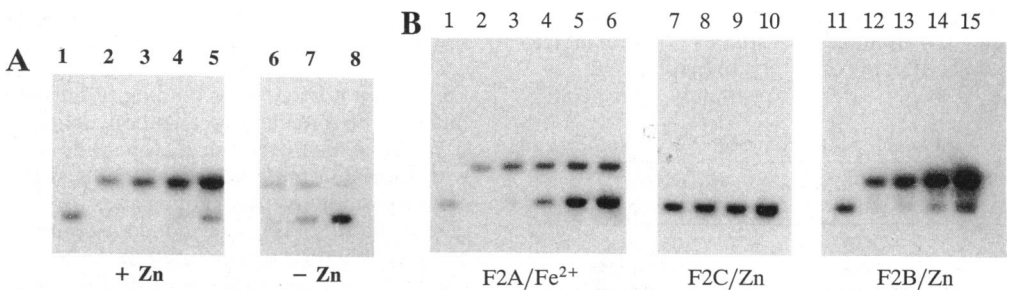

FIG. 2. Gel-mobility-shift titrations of GATA peptides. (*A*) Lanes 1–5 show titration of peptide F2A, reconstituted with Zn^{2+}, with a 5′-^{32}P-end-labeled synthetic oligonucleotide duplex containing the sequence of oligo A/B (see Fig. 4) derived from the chicken β/ε-globin enhancer. Of the two adjacent sites in the enhancer, this binds full-length GATA-1 more strongly. All titrations in this figure were carried out with this oligonucleotide. Lanes: 1, oligo A/B only; 2–5, each sample contained, in a volume of 10 μl, 2.7 pmol of peptide and 0.21, 0.42, 0.84, or 1.68 pmol of duplex, respectively. The solvent contained (final concentration) 50 mM Tris·HCl (pH 7), 10 mM NaCl, 3.7% (vol/vol) Ficoll, 0.0125% Triton X-100, and 50 ng of poly(dI-dC). This small amount of polynucleotide serves to prevent nonspecific binding to oligo A/B when peptide is in excess. It does not appear to have a significant effect on measured apparent binding constants. At this concentration, a nonspecific DNA would uniformly reduce apparent binding constants about 2-fold. Lanes 6–8 show peptide F2A treated identically to sample used in lanes 1–5, except that no metal ion was added; 2.7 pmol of peptide and 0.21, 0.42, or 0.84 pmol of DNA were present in lanes 6–8, respectively. The small amount of complex observed probably arises from unavoidable contamination with metal ions during preparation of peptide. (*B*) Gel-shift assays. Conditions were similar to those described in *A*. Lanes: 1, oligo A/B DNA only; 2–6, 2.7 pmol of F2A/Fe^{2+} with 0.22, 0.44, 0.87, 1.31, or 1.74 pmol, respectively, of oligo A/B; 7–10, peptide F2C/Zn, showing absence of binding for this truncated peptide; 7–9, 0.87 pmol of oligo A/B DNA and 2.7, 5.4, or 16.2 pmol, respectively, of F2C/Zn; 10, 1.74 pmol of oligo A/B and 5.4 pmol of F2C/Zn; 11, oligo A/B only; 12–15, 3.3 pmol of peptide F2B/Zn with 0.21, 0.43, 0.86, or 1.72 pmol of oligo A/B, respectively. Metal ion/peptide ratio, 4.9; reaction volume, 10 μl in all cases.

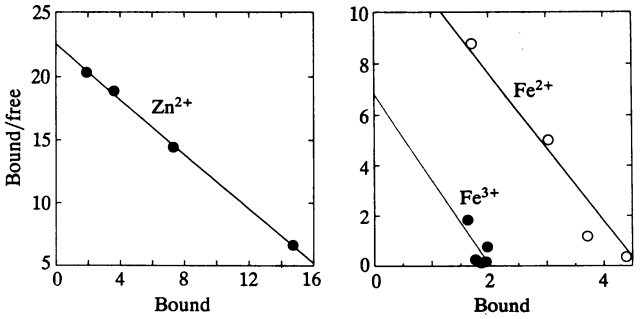

FIG. 3. Scatchard analysis of gel-shift binding data shown in Fig. 2*A*. Titrations were performed with a fixed amount of peptide and various amounts of probe. The ratio of bound to free DNA sequence A/B is plotted vs. the molar concentration of bound sequence A/B in the reaction mixture ($\times 10^8$). (*Left*) F2A/Zn peptide. (*Right*) F2A–Fe^{2+} and F2A–Fe^{3+} peptides. A summary of numerical results for several such experiments is given in Table 1. The concentration of peptide capable of binding, determined from such graphs, can be compared with the total peptide concentration measured by optical absorbance (see above). The efficiency of reconstitution was about 75% with Zn^{2+} and 17–47% with Fe^{2+}.

we introduced Co^{2+}, Cd^{2+}, Mn^{2+}, Fe^{2+}, and Fe^{3+} ions into peptide F2A with the same reconstitution methods employed to make the zinc complex. As shown in Table 1, Mn^{2+} was ineffective in generating binding activity, but addition of cobalt or cadmium ion produced actively binding peptide–metal ion complexes with affinity constants the same as or somewhat smaller than that obtained with the zinc complex. The reconstitutions with ferrous and ferric ion are of particular interest. As shown in Fig. 2*B*, addition of ferrous ion produced a peptide capable of binding to the specific DNA probe with an apparent affinity constant (Table 1) that was somewhat greater than that of the zinc or cobalt complexes and more than twice as great as that of the cadmium compound. Introduction of ferric ion also resulted in a species that bound with this affinity, but the amount of active complex formed was smaller (Fig. 3 *Right*). It is likely that the active complex binds ferrous ion. Under the acidic conditions used in the reconstitution, ferric ion solutions also contained some ferrous ion, but Fe^{3+} itself was probably inactive.

The ability of F2A to bind DNA specifically depends both upon the zinc-binding domain and on the highly basic C-terminal tail, as predicted by mutagenesis studies (34) with intact GATA-1. A peptide containing only the tail (peptide B2, Fig. 1) bound to the GATA-1 site to form only nonspecific

Table 2. Zn/DNA ratio in gel-shifted complexes

Zn, pmol	DNA duplex, pmol	Zn/DNA molar ratio
2.65	2.50	1.06
2.86	3.00	0.95

Gel-shift experiments like those in Fig. 2 were carried out as follows. Lanes: 1 and 2, 3.37 pmol of unlabeled oligo A/B DNA and 0.13 pmol of 5′-^{32}P-end-labeled oligo A/B; 3 and 4, DNA as in lanes 1 and 2, but 10.9 and 16.4 pmol of F2A/^{65}Zn peptide was added, respectively; 5 and 6, 3.5 pmol of unlabeled DNA in each and 10.9 and 16.4 pmol, respectively, of F2A/^{65}Zn. Peptide samples were prepared as in Fig. 2*A*, except that the zinc chloride/trifluoroacetic acid solution used to dissolve the peptide sample contained 9×10^{-4} mCi of ^{65}Zn (Amersham) lyophilized from a 0.1 M HCl solution. Conditions were similar to those in Fig. 2*A*, except that 200 ng of poly(dI·dC) was added to each reaction mixture. Zinc ion concentrations in the complex were obtained by comparison with standards. DNA concentration in the complex was determined from the fraction of all ^{32}P found in the complex and the known concentration of DNA. (In samples containing high ^{32}P and ^{65}Zn, the contribution of ^{65}Zn to the radioactive signal is only 2% of the total.)

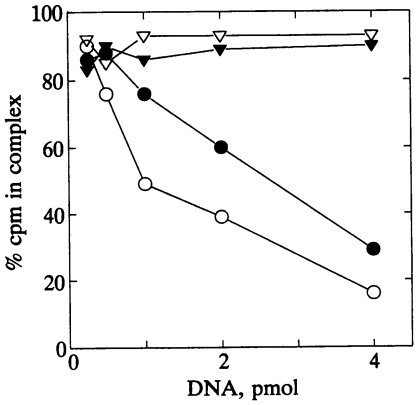

FIG. 4. Competition of oligo A/B with other oligomers for binding to F2A/Zn. ^{32}P-labeled oligo A/B was mixed with a 40-fold molar excess of unlabeled oligomer. Aliquots containing 0.5 pmol of peptide F2A/Zn (measured as binding activity rather than total concentration) were titrated with increasing amounts of the oligomer mixture. The percentage of labeled (specific) DNA in complex is plotted vs. total pmol of DNA present in a volume of 10 μl. The unlabeled oligomers used were as follows: ○, oligo A/B; ●, oligo C/D, containing the more weakly binding GATA sequence from the chicken β/ε-globin enhancer (see text); ▼, possible GATA-family binding site for the yeast Dal80 protein (36); ▽, oligo ABM, which is A/B that has been mutated at the GATA binding site. Oligomer duplexes used in these studies were as follows: the binding site motif is underlined and mutated bases are in lowercase type: A/B, 5′-AGCTTCGGTTGCAGATAAACATTGAATTCA; C/D, 5′-AGCTTCGAGTCTTGATAGCAAAAGAATTCA; ABM, 5′-AGCTTCGGTTGCActgAAACATTGAATTCA; Dal80, 5′-ATTTAAACTGAAAATGATAGTCTGCGCGGCA.

aggregates, as expected for electrostatic interactions at low ionic strength (data not shown). A second peptide, F2C (residues 1–53), from which 13 amino acids in the C-terminal tail were deleted (Fig. 1) showed no evidence of any binding (Fig. 2*B*), despite the fact that NMR and CD studies revealed that F2C was able to bind zinc and form a structure closely related to that observed with the F2A peptide (data not shown). However, a peptide slightly longer than F2C [F2B (residues 1–59)] bound to GATA sequences with an affinity comparable to that of the full-length peptide (Fig. 2*B*). These results suggest that the six additional residues (residues 54–59 of F2A) either contact DNA or are important for stabilization of residues nearby that contact DNA. The exceedingly basic region (KGKKRR) at the C terminus of F2A was not needed for binding; it has been suggested that this may be a nuclear localization signal (35).

We have also used the F2A peptide to study interactions with variant or mutated DNA binding sites. The chicken β/ε enhancer contains two binding sites for GATA-1, of unequal binding affinity (31). The sequence contained in the stronger of these (oligo A/B) was used in the experiments described above. Experiments that measure the competition of the two sites for binding to peptide F2A are shown in Fig. 4. The peptide retained the binding preference observed in the full-length protein; analysis of the data revealed that the stronger site (oligo A/B) bound somewhat more tightly than the weaker one (oligo C/D). We have used two other DNA sequences as competitors (Fig. 4). One of these (ABM) was a mutated version of the strong GATA-1 binding site. Under these conditions, as expected, no significant competition was detected. The second sequence was a possible binding site (36) for the yeast GATA-family protein Dal80. Both chicken GATA-1 and the F2A peptide bound to this sequence only weakly. The F2B peptide showed similar binding specificity to these oligonucleotides but appeared to have a relatively higher affinity than did F2A for nonspecific sequences (data

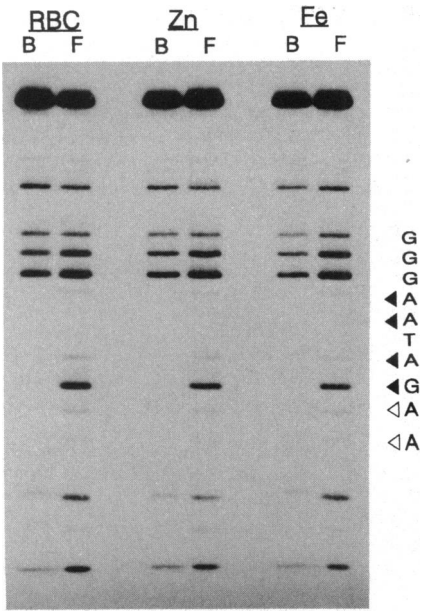

FIG. 5. Duplex probe (E/F) 5'-AGCTTCGCAGCAA-GATAAGGGCTGAATTCA was partially methylated with dimethyl sulfate (41) and used in a gel-mobility assay exactly as described above, except that the reaction was scaled up 5-fold. At the 50% titration point, bound (B) and free (F) complexes were eluted from the gel, and the DNA in each sample was purified and cleaved with piperidine (37) prior to electrophoresis on a 15% polyacrylamide gel. Arrows indicate strong (solid) and weaker (open) sites of interference. RBC, eryrothcytes.

not shown). Thus much of the information for sequence discrimination is retained in the 59-amino acid F2B peptide.

To examine further the specificity of the interaction between the GATA peptides and their binding site, we studied the effect of DNA methylation on binding. The methylation interference patterns of the complexes are shown in Fig. 5. The patterns are identical whether full-length GATA-1 or peptide F2A complexed with either zinc or iron was used. This shows that either metal ion is capable of organizing the peptide structure to give a DNA binding domain that makes the same contacts with DNA as the native erythroid protein.

DISCUSSION

It is instructive to compare the known properties of the glucocorticoid receptor (GR) (38) with those of the GATA peptides and GATA-1 itself. Marked differences are obvious. In the GR, both the regions containing the zinc fingers are required to stabilize and orient the DNA-binding α-helical region, permitting specific contacts within the recognition half-sites. Thus the two finger motifs of the GR are part of a single structural domain that binds DNA. High binding specificity is further achieved by dimerization of the protein, which brings each monomer into the proper orientation for recognition of its half-site on the DNA. The region containing the C-terminal finger of the GR has a predominant role in establishing the protein–protein contacts that stabilize the dimer.

In contrast (Figs. 2–4), the single-finger GATA-1 peptide F2B alone contains the information necessary for strong specific binding; our data suggest that this peptide is close to the minimum size necessary for the binding function. Mutagenesis of full-length mouse or chicken GATA-1, which contains two finger regions, has shown that the region containing the C-terminal finger is of central importance for strong binding to a single asymmetric GATA site. When appropriate double sites are present, methylation interference assays reveal that the N-terminal finger protects one of the binding motifs (23) but makes only a small contribution to binding properties detected by the effect of its deletion on the dissociation rate constant (23, 34). The data presented here show that both the metal-binding region and basic portions of the peptide are required for strong selective binding; we note that five of the six amino acids at the C terminus of peptide F2B are conserved in all vertebrate GATA proteins. As shown by our data (Fig. 2*B*), these residues (amino acids 54–59) distant from the metal binding motif are also crucial for DNA binding. The metal complex region of F2A or F2B may serve to stabilize and orient a domain that also carries residues that interact specifically with DNA.

The properties of Zn^{2+} complexes and the known structure of such proteins as the GR make it probable that the cysteine sulfhydryl groups of GATA-1 are arranged tetrahedrally about the central metal ion. The ability of GATA-1 and the single-finger peptide F2A to form an active complex in the presence of Fe^{2+} is consistent with the known physical properties of that ion. Fe^{2+} is able to form both octahedral low-spin, and tetrahedral high-spin complexes. It is reasonable to suppose that in this case the four sulfur atoms of the finger are disposed tetrahedrally around Fe^{2+}. An example of such a configuration is found in rubredoxin, an iron protein with the sequence Cys-Xaa-Xaa-Cys-$(Xaa)_{29}$-Cys-Xaa-Xaa-Cys; the cysteine residues are placed tetrahedrally around iron (39–41). Rubredoxin is not a DNA binding protein but is thought to function in bacterial electron transport. We do not yet know whether the members of the vertebrate GATA-1 family are zinc or iron proteins *in vivo*; definitive determination of the state of mouse, human, or chicken GATA-1 *in vivo* awaits the availability of large quantities of quite pure GATA-1. These proteins function in the iron-rich erythroid intracellular environment, which by itself is not necessarily an argument for the presence of iron in the vertebrate factors. On the other hand, it is quite possible that the GATA-1 family of proteins may have evolved from early iron binding factors. Some support for this proposal can be derived from the observation that globin-like genes of primitive organisms are often involved in electron transport functions, and it may be that the early regulatory factors controlling the expression of such proteins also contained iron. A vestige of this system might remain in the GATA-family regulatory factor URBS-1, found in *Ustilago*. URBS-1 is involved in the regulation of synthesis of siderophores (S. Leong, personal communication), compounds that tightly complex Fe^{3+} and are involved in iron transport and homeostasis. Whether these and other GATA-family proteins of primitive organisms ever form functional iron complexes must now be determined.

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1. Evans, T. & Felsenfeld, G. (1989) *Cell* **58**, 877–885.
2. Tsai, S.-F., Martin, D. I. K., Zon, L. I., D'Andrea, A. D., Wong, G. G. & Orkin, S. H. (1989) *Nature (London)* **339**, 446–451.
3. Trainor, C. D., Evans, T., Felsenfeld, G. & Boguski, M. S. (1990) *Nature (London)* **343**, 92–96.
4. Zon, L. I., Tsai, S.-F., Burgess, S., Matsudaira, P., Bruns, G. A. P. & Orkin, S. H. (1990) *Proc. Natl. Acad. Sci. USA* **87**, 668–672.
5. Yamamoto, M., Ko, L. J., Leonard, M. W., Beug, H., Orkin, S. H. & Engel, J. D. (1990) *Genes Dev.* **4**, 1650–1662.
6. Ho, I. C., Vorhees, P., Marin, N., Oakley, B. K., Tsai, S.-F., Orkin, S. H. & Leiden, J. M. (1991) *EMBO J.* **10**, 1187–1192.
7. Martin, D. I. K., Zon, L. I., Mutter, G. & Orkin, S. H. (1990) *Nature (London)* **344**, 444–447.
8. Romeo, P. H., Prandini, M. H., Joulin, V., Mignotte, V., Prenant, M., Vainchenker, W., Marguerie, G. & Uzan, G. (1990) *Nature (London)* **344**, 447–449.

9. Galson, D. L. & Housman, D. E. (1988) *Mol. Cell. Biol.* **8,** 381–392.
10. deBoer, E., Antoniou, M., Mignotte, V., Wall, L. & Grosveld, F. (1988) *EMBO J.* **7,** 4203–4212.
11. Catala, F., deBoer, E., Habets, G. & Grosveld, F. (1989) *Nucleic Acids Res.* **17,** 3811–3827.
12. Barnhart, K. M., Kim, C. G. & Sheffery, M. (1989) *Mol. Cell. Biol.* **9,** 2606–2614.
13. Perkins, N. D., Nicolas, R. H., Plumb, M. A. & Goodwin, G. H. (1989) *Nucleic Acids Res.* **17,** 1299–1314.
14. Plumb, M., Franpton, J., Wainwright, H., Walker, M., Macleod, K., Goodwin, G. & Harrison, P. (1989) *Nucleic Acids Res.* **17,** 73–91.
15. Mignotte, V., Wall, L., deBoer, E., Grosveld, F. & Romeo, P.-H. (1989) *Nucleic Acids Res.* **17,** 37–54.
16. Rousseau, S., Renaud, J. & Ruiz-Carrillo, A. (1989) *Nucleic Acids Res.* **17,** 7495–7511.
17. Chiba, T., Ikawa, Y. & Kazuo, T. (1991) *Nucleic Acids Res.* **19,** 3843–3848.
18. Zon, L. I., Youssoufian, H., Mather, C., Lodish, H. F. & Orkin, S. H. (1991) *Proc. Natl. Acad. Sci. USA* **88,** 10638–10641.
19. Brady, H. J. M., Sowden, J. C., Edwards, M. & Butterworth, P. H. W. (1989) *FEBS Lett.* **257,** 451–456.
20. Reitman, M. & Felsenfeld, G. (1988) *Proc. Natl. Acad. Sci. USA* **85,** 6267–6271.
21. Evans, T. & Felsenfeld, G. (1991) *Mol. Cell. Biol.* **11,** 843–853.
22. Martin, D. I. K., Tsai, S.-F. & Orkin, S. H. (1989) *Nature (London)* **338,** 435–438.
23. Martin, D. & Orkin, S. H. (1990) *Genes Dev.* **4,** 1886–1898.
24. Tsai, S., Strauss, E. & Orkin, S. H. (1991) *Genes Dev.* **5,** 919–931.
25. Evans, R. M. (1988) *Science* **240,** 889–895.
26. Minehart, P. & Magasanik, B. (1991) *Mol. Cell. Biol.* **11,** 6216–6228.
27. Cunningham, T. S. & Cooper, T. G. (1991) *Mol. Cell. Biol.* **11,** 6205–6215.
28. Kudla, B., Caddick, M. X., Langdon, T., Martinez-Rossi, N. M., Bennett, C. F., Sibley, S., Davies, R. W. & Arst, H. N., Jr. (1990) *EMBO J.* **9,** 1355–1364.
29. Fu, Y.-H. & Marzluf, G. A. (1990) *Mol. Cell. Biol.* **10,** 1056–1065.
30. Tam, J. P., Heath, W. F. & Merrifield, R. B. (1983) *J. Am. Chem. Soc.* **105,** 6442–6455.
31. Evans, T., Reitman, M. & Felsenfeld, G. (1988) *Proc. Natl. Acad. Sci. USA* **85,** 5976–5980.
32. Kadonaga, J. T., Carner, K. R., Masiary, F. R. & Tjian, R. (1987) *Cell* **51,** 1079–1080.
33. Freedman, L. P., Luisi, B. F., Korezun, Z. R., Basavappa, R., Sigler, P. B. & Yamamoto, K. R. (1988) *Nature (London)* **334,** 543–546.
34. Yang, H.-Y. & Evans, T. (1992) *Mol. Cell. Biol.* **12,** 4562–4570.
35. Dingwall, C. & Laskey, R. A. (1991) *Trends Biochem. Sci.* **16,** 478–481.
36. Zhu, H. & Riggs, A. F. (1992) *Proc. Natl. Acad. Sci. USA* **89,** 5015–5019.
37. Maxam, A. & Gilbert, W. (1980) *Methods Enzymol.* **65,** 499–560.
38. Luisi, B. F., Xu, W. X., Otwinowski, Z., Freedman, L. P., Yamamoto, K. R. & Sigler, P. B. (1991) *Nature (London)* **352,** 497–505.
39. Watenpaugh, K. D., Sieker, L. C. & Jensen, L. H. (1979) *J. Mol. Biol.* **131,** 509–522.
40. Watenpaugh, K. D., Sieker, L. C. & Jensen, L. H. (1980) *J. Mol. Biol.* **138,** 615–633.
41. Adman, E. T., Sieker, L. C. & Jensen, L. H. (1991) *J. Mol. Biol.* **217,** 337–352.

From: Isabelle Coche
To: Zachary Adelman
CC: Benjamin Robinson
Date: 6/26/2017 11:46:02 AM
Subject: Re: CBD online forum - schedule announced - starting July 3

Hi Zach

Great, we'll make sure to include you.

Isabelle

From: Zachary Adelman <zachadel@tamu.edu>
Date: Monday, 26 June 2017 15:38
To: Isabelle Coche <
Cc: Benjamin Robinson <
Subject: Re: CBD online forum - schedule announced - starting July 3

Isabelle,
Thanks for the update. I am still planning on participating, and I would certainly welcome your assistance in following the discussions.
best,
zach

On Fri, Jun 23, 2017 at 10:52 AM, Isabelle Coche > wrote:

> Dear Zach
>
> I hope you are well. I wanted to let you know that the schedule of the online forum for CBD has been announced. It will start on July 3rd and it will be divided in 4 sessions to cover the 5 topics outlined in the decision text adopted at CBD. I have copied the relevant text from the decision below, although it is likely that it will be reformulated and broken down by the moderators to make it more suitable for the online forum. Gene drive is likely to come up in the very first weeks as well as under the third set (topics 3 and 4) but could pop up throughout.
>
> I hope you are able to participate. My team will be monitoring the conversation and will send regular updates and signal when it would be useful to see more engagement. This is meant to help everyone not spend hours on the sites figuring out what's happening, but of course doesn't preclude anyone from doing so. My team can also relay any concerns, warnings or call for engagement that you wish to share.
>
> If you would prefer not the be included in our mailing list, please let us know.
>
> Best,
>
> Isabelle
>
> **TOPICS & SCHEDULE**
>
> **3-17 July** Topic 1: **Review recent technological developments within the field of synthetic biology** to assess if the

developments could lead to impacts on biodiversity and the three objectives of the Convention, including unexpected and significant impacts

17-31 July Topic 2: Identify any living organisms already developed or currently under research and development through techniques of synthetic biology which do not fall under the definition of living modified organisms under the Cartagena Protocol;

4-18 Sept Topic 3: Further **analyse evidence of benefits and adverse effects of organisms**, components and products of synthetic biology vis-à-vis the three objectives of the Convention, and **gather information on risk management measures, safe use and best practices for safe handling** of organisms, components and products of synthetic biology
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18 Sept-2 Oct Topic 5: provide recommendations on the basis of its deliberations to facilitate future discussions and actions on synthetic biology under the Convention, as well as an analysis against the criteria set out in paragraph 12 of decision IX/29 to contribute to the completion of the assessment requested in paragraph 2 of decision XII/24 by the Subsidiary Body on Scientific, Technical and Technological Advice;

From: Isabelle Coche
To:
Date: 6/26/2017 11:29:25 AM
Subject: CBD online forum on synthetic biology

Apologies for any cross-posting

Dear all

We have been working for the past few months with an informal group of organisations interested in gene drive, which includes Target Malaria, GBIRd, TIGS, FNIH, the Danforth Center and others. They have reached out to you about registering as experts for the online forum on synthetic biology organised by the CBD. The dates for the online forum have just been announced (see below) so we are helping organise briefing calls for those interested in learning more about how the online forum will be organised and how it will work and to introduce this expert group to each other.

As **the online forum begins July 3rd**, we have a short window of opportunity to do the briefing calls. I have listed below a few different times in the hope that it enables most of you to join if you wish. The calls should last about half an hour and we will cover the context and purpose of the online forum, where the topic of gene drive might come up and share some insights about what maybe the most productive way to participate. If some of you have joined online forum in the past and you are willing to share your views, that would be welcome too.

BRIEFING CALLS

If possible, let me know if you wish to join any of these calls by responding to the doodle poll: *I*

- Tuesday 27 June: 10 am UK
- Tuesday 27 June: 5 pm UK
- Wednesday 28 June: 1pm UK
- Wednesday 28 June: 10 pm UK
- Friday 30 June: 5pm UK

CALL IN DETAILS

Please join the meeting from your computer, tablet or smartphone.

You can also dial in using your phone.

Access Code:

Australia (Long distance): +61 2 8355 1031
Belgium (Long distance): +32 (0) 28 93 7001
Canada +1 (647) 497-9371
France (Long distance): +33 (0) 170 950 585
Germany (Long distance): +49 (0) 692 5736 7208
Ireland (Long distance): +353 (0) 19 030 050
Italy (Long distance): +39 0 693 38 75 50
Netherlands (Long distance): +31 (0) 208 080 208
New Zealand (Long distance): +64 9 925 0481
Spain (Long distance): +34 911 82 9890
Switzerland (Long distance): +41 (0) 435 0167 65
United Kingdom (Long distance): +44 (0) 20 3713 5010
United States (Long distance): +1 (312) 757-3117

TOPICS & SCHEDULE of the online forum

3-17 July Topic 1: **Review recent technological developments within the field of synthetic biology** to assess if the developments could lead to impacts on biodiversity and the three objectives of the Convention, including unexpected and significant impacts

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Best

Isabelle

Isabelle Coche
Vice President Strategy

www.emergingag.com
Follow Emerging ag on LinkedIn

CBD Online Forum on Synthetic Biology will take place soon! Experts should **register online** to participate.
Contact us if you require assistance.
Supporter of the Manyinga orphan schools project – find out more at www.manyinga.org

From: Zachary Adelman <zachadel@tamu.edu>
To: Isabelle Coche
CC: Benjamin Robinson
Date: 6/26/2017 8:38:54 AM
Subject: Re: CBD online forum - schedule announced - starting July 3

Isabelle,
Thanks for the update. I am still planning on participating, and I would certainly welcome your assistance in following the discussions.
best,
zach

On Fri, Jun 23, 2017 at 10:52 AM, Isabelle Coche > wrote:

> Dear Zach
>
> I hope you are well. I wanted to let you know that the schedule of the online forum for CBD has been announced. It will start on July 3rd and it will be divided in 4 sessions to cover the 5 topics outlined in the decision text adopted at CBD. I have copied the relevant text from the decision below, although it is likely that it will be reformulated and broken down by the moderators to make it more suitable for the online forum. Gene drive is likely to come up in the very first weeks as well as under the third set (topics 3 and 4) but could pop up throughout.
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>
> Best,
>
> Isabelle
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From: GenScript <services@genscriptmail.com>
To: zachadel@tamu.edu
Date: 6/25/2017 9:22:42 PM
Subject: Researchers discover that blind people have a "visual" brain

From: Isabelle Coche
To: Zachary Adelman
CC: Benjamin Robinson
Date: 6/23/2017 10:52:33 AM
Subject: CBD online forum - schedule announced - starting July 3

Dear Zach

I hope you are well. I wanted to let you know that the schedule of the online forum for CBD has been announced. It will start on July 3rd and it will be divided in 4 sessions to cover the 5 topics outlined in the decision text adopted at CBD. I have copied the relevant text from the decision below, although it is likely that it will be reformulated and broken down by the moderators to make it more suitable for the online forum. Gene drive is likely to come up in the very first weeks as well as under the third set (topics 3 and 4) but could pop up throughout.

I hope you are able to participate. My team will be monitoring the conversation and will send regular updates and signal when it would be useful to see more engagement. This is meant to help everyone not spend hours on the sites figuring out what's happening, but of course doesn't preclude anyone from doing so. My team can also relay any concerns, warnings or call for engagement that you wish to share.

If you would prefer not the be included in our mailing list, please let us know.

Best,

Isabelle

TOPICS & SCHEDULE

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This version of Total Outlook Converter Pro is not registered.

From:	Raul Medina <rfmedina@tamu.edu>
To:	Zach Adelman Gregory Sword
CC:	Portney, Kent E Goldsmith, Carol Elizabeth Heitman Edward Vargo Kevin Myles Micky Eubanks David Kerns Sakiko Okumoto
Date:	6/20/2017 8:17:19 AM
Subject:	AFRI gene drive: Interesting Paper
Attachments:	Courtier-Orgogozo_et_al-2017-EMBO_reports.pdf

An interesting paper attached.

Cheers

Dr. Raul F. Medina
Associate Professor
Department of Entomology
Texas A&M University
TAMU 2475
College Station, TX 77843
USA
Phone: +1-301-335-4464

From: Zachary Adelman <zachadel@tamu.edu>
Sent: Friday, June 16, 2017 9:32 PM
To: Gregory Sword
Cc: Portney, Kent E; Goldsmith, Carol; Elizabeth Heitman; Edward Vargo; Kevin Myles; Micky Eubanks; Raul Medina; David Kerns; Sakiko Okumoto
Subject: Re: AFRI gene drive

Greg,
No worries. The meeting went well. The bike take-homes are that we are asking for descriptions of the individual case studies by the end of this month. Nothing fancy, about a half a page each. We can probably work off the material that was prepared for the letter of intent and grow it a little. The case studies should describe the problem and the unique issues that make gene drive a potential solution, as well as identify stakeholders who we would potentially interact/survey. The four case studies are pigweed-cotton (gene drive in an invasive weed), boll weevil (gene drive in an insect pest of agriculture), indian meal moth (gene drive in a stored grain/urban environment), mosquito spp (potential vectors of a dangerous agent that is not yet present in the US).

In addition to the case studies, we also need to identify meetings/workshops/events that are already scheduled to occur in the region in 2018 that we can piggyback on, as we will likely not have the budget to organize our own large scale events.

zach

On Fri, Jun 16, 2017 at 4:04 PM, Greg Sword <gasword@tamu.edu > wrote:

> Hi folks.

Sorry. I blew it on the time zone conversion. Thought it was only a one hour difference, but it's two!

Hope the meeting went well.

Take care,
Greg

Sent from my iPhone
Please excuse any more typos than usual.

> On Jun 7, 2017, at 2:43 PM, Zachary Adelman <zachadel@tamu.edu > wrote:
>
> All,
> Let's meet next Friday June 16th at 3pm. Kent, if you would like us to come to your building that will be fine, otherwise we can meet in the Heep Center again (329; call in number 979-458-0302)
> thanks everyone,
> zach

From: James, Stephanie (FNIH) [T]
To: 'Zachary Adelman'
'Zhijian Tu'
'aajames@uci.edu'
'Friedman, Robert
'gclanzaro@ucdavis.edu'
'omar.akbari@ucr.edu'
'Cinnamon Bloss'
'sentelle@uci.edu'
'john.marshall@berkeley.edu'
'Kevin Esvelt'
'fcatter@hsph.harvard.edu'
'Fred Gould'
'dfwirth@hsph.harvard.edu'
'pagre@jhu.edu'
'a.burt@i
'Nolan, Tony F J'
'George Dimopoulos (gdimopo1@jhu.edu)'
'Ethan Bier (ebier@ucsd.edu)'
'ljacob13@
'luke.alphe
'kykanesh@hawaii.edu'
'Heath Packard'
'J Royden Saah'
'Isabelle Coche'
'ssubramani@ucsd.edu'
'Scott Miller'
'Jeff Chertack'
'Wegrzyn, Renee'
'Cheever, Anne (contr-bto)'
'Sarah Carter'
'Ryan Phelan'
'Anna Buchman'
'Fred Gould'
'Crisanti, Andrea'
'Christophides, George K'
'Windbichler, Nikolai'
a.burt@imperial.ac.uk
Fredros Okumu
'Emerson, Claudia'
Brindley, Paul (pbrindley@email.gwu.edu)
Costero-Saint Denis, Adriana (NIH/NIAID) [E]
Rao, Malla (NIH/NIAID) [E]
Hall, Lee (NIH/NIAID) [E]
'mcapurro@icb.usp.br'
CC: Tountas, Karen (FNIH) [T]
'Claudia Emerson
'Claudia Emerson'
Date: 6/16/2017 4:10:18 PM

Dear colleagues,

Subject: RE: Talking about Gene Drive

Dear colleagues,

FNIH is now ready to begin serious preparations for the proposed communications workshop “Talking about Gene Drive,” to be held on November 4, 2017, in Baltimore, MD. At this time, we request that you go to our online registration site at fnih.org/TalkingAboutGeneDrive and confirm your intention to participate. We need the information on number of people we can expect to attend in order to reserve a room for the meeting. Therefore, **we respectfully request that you confirm your attendance no later than July 31.**

Since we still have plenty of flexibility about room size right now, you are welcome to forward this invitation to other researchers working on gene drive whom you think would be interested in attending the workshop. However, please make sure they also know that they must respond by July 31. After that time, we can’t guarantee we will be able to accommodate any additional participants.

Again, we hope that you will join us for some interesting and useful discussions on this timely subject.

Best regards,
Stephanie

From: James, Stephanie (FNIH) [T]
Sent: Monday, May 08, 2017 6:12 PM
To: 'Zachary Adelman' <zachadel@tamu.edu>; 'Zhijian Tu' <jaketu@vt.edu>; 'aajames@uci.edu' <aajames@uci.edu>; 'Friedman, Robert 'gclanzaro@ucdavis.edu' <gclanzaro@ucdavis.edu>; 'omar.akbari@ucr.edu' <omar.akbari@ucr.edu>; 'Cinnamon Bloss' <cbloss@eng.ucsd.edu>; 'sentelle@uci.edu' <sentelle@uci.edu>; 'john.marshall@berkeley.edu' <john.marshall@berkeley.edu>; 'Kevin Esvelt' <esvelt@mit.edu>; 'fcatter@hsph.harvard.edu' <fcatter@hsph.harvard.edu>; Fred Gould <fred_gould@ncsu.edu>; 'dfwirth@hsph.harvard.edu' <dfwirth@hsph.harvard.edu>; 'pagre@jhu.edu' <pagre@jhu.edu>; Nolan, Tony F J >; George Dimopoulos (gdimopo1@jhu.edu) <gdimopo1@jhu.edu>; Ethan Bier (ebier@ucsd.edu) <ebier@ucsd.edu>; 'ljacob13@jhu.edu' <ljacob13@jhu.edu>; 'luke.alphey ' <luke.alphey 'kykanesh@hawaii.edu' <kykanesh@hawaii.edu>; 'Heath Packard' <heath.packard >; 'J Royden Saah' <royden.saah >; Isabelle Coche >; 'ssubramani@ucsd.edu' <ssubramani@ucsd.edu>; 'Scott Miller' < ; 'Jeff Chertack' >; 'Wegrzyn, Renee' <renee.wegrzyn@darpa.mil>; 'Cheever, Anne (contr-bto)' <anne.cheever.ctr@darpa.mil>; 'Sarah Carter' >; 'Ryan Phelan' < >; Anna Buchman <annabuch@ucr.edu>; Fred Gould <fgould@ncsu.edu>; Crisanti, Andrea < Christophides, George K Windbichler, Nikolai >; Fredros Okumu ; 'Emerson, Claudia' ; Brindley, Paul (pbrindley@email.gwu.edu) <pbrindley@email.gwu.edu>; Costero-Saint Denis, Adriana (NIH/NIAID) [E] <acostero@niaid.nih.gov>; Rao, Malla (NIH/NIAID) [E] <MRao@niaid.nih.gov>; Hall, Lee (NIH/NIAID) [E] <LHALL@niaid.nih.gov>; aajames@uci.edu
Cc: Tountas, Karen (FNIH) [T] Claudia Emerson (; Claudia Emerson
Subject: RE: Talking about Gene Drive

Dear colleagues,

Based on demonstration of interest, the Foundation for the National Institutes of Health (FNIH) will sponsor a one day workshop on the topic of “Talking about Gene Drive” – to be held just before the annual American Society of Tropical Medicine and Hygiene (ASTMH) meeting on November 4, 2017, in Baltimore, MD.

The intent of the workshop will be to:

- discuss how gene drive technology is being described in the media and at venues such as the Convention on Biological Diversity;
- consider ways to work together to enhance communication and clarify public perception about gene drive technology;
- share some basic communications skills that might come in handy in the future

A revised draft agenda responding to various initial comments is attached.

The workshop is open to those working on gene drive technology for public health and conservation goals. We believe this will provide an important venue for bringing both groups together to discuss plans for communicating about the technology with the public. Please let me know if there are others not included on this list who might be interested in attending. FNIH will open a registration page closer to the time in order to judge logistics requirements.

FNIH will support the cost of the meeting space, food (breakfast and lunch) and speaker travel. We are holding this workshop in conjunction with the ASTMH meeting because many interested parties are already planning to attend that meeting. We regret that FNIH cannot support the participation of all attendees. We assume that most of you have some travel support from other sources, but please let me know if that is not the case. We hope that you will add this to your calendar and plan to join us for some lively conversation!

Best regards,
Stephanie

Stephanie James, PhD, FASTMH
Director, Science Division
Foundation for the National Institutes of Health
9650 Rockville Pike | Bethesda, MD 20814 | www.fnih.org
Direct (301) 451-2810 | Fax (301) 480-1661 | Email

For 13 consecutive years, Charity Navigator has rated the FNIH as an organization that *exceeds industry standards.*

From:	Lee, Andrew [USA]
Required:	Wegrzyn, Renee Parr, Lianne (contr-bto) Cheever, Anne (contr-bto) Escalon, Lynn L ERD-MS Christopher.M.Warner@usace.army.mil Kevin Myles (mylesk@tamu.edu) Pledger, David W Sakiko Okumoto Okumoto, Sakiko Zachary Adelman April.Godlewski.ctr@darpa.mil
Subject:	TAMU/DARPA Monthly Tech Update
Location:	Dial-in: 866-692-4541\; Participant: 34756564#
When:	6/30/2017 10:30:00 AM - 11:30:00 AM
Attachments:	e1601910.full.pdf

TAMU/DARPA Tech Update

Please send update slides to DARPA at least 2 business days prior to the scheduled meeting.

Dial-in: 866-692-4541
Participant:

Additional topic to be discussed
-Tribolium gene drive modeling paper Drury et al. “CRISPR/Cas9 gene drives in genetically variable and nonrandomly mating wild populations” from Science Advances 2017.

-Discuss potential future LEEDR meeting

From:	Raul Medina <rfmedina@tamu.edu>
To:	Elizabeth Heitman Goldsmith, Carol Zach Adelman
CC:	Portney, Kent E Edward Vargo Gregory Sword Kevin Myles Micky Eubanks Elizabeth Heitman
Date:	6/15/2017 3:09:39 PM
Subject:	Re: AFRI gene drive
Attachments:	biotech_national_strategy_final.pdf

Dear Colleagues,

I have attached a release by the 2016 White House proposing a National Strategy for Modernizing the Regulatory System for Biotechnology Products (a.k.a. The Coordinated Framework for Regulation of Biotechnology). This may be useful to browse before our discussion tomorrow. It is unclear how much the current administration would like to implement the strategy, I guess time will tell.

See you tomorrow

Dr. Raul F. Medina
Associate Professor
Department of Entomology
Texas A&M University
TAMU 2475
College Station, TX 77843
USA
Phone: +1-301-335-4464

From: Elizabeth Heitman <Elizabeth.Heitman@UTSouthwestern.edu>
Sent: Wednesday, June 14, 2017 5:45 PM
To: Goldsmith, Carol; Zach Adelman
Cc: Portney, Kent E; Edward Vargo; Gregory Sword; Kevin Myles; Micky Eubanks; Raul Medina; Elizabeth Heitman
Subject: RE: AFRI gene drive

Dear Carol,

Thank you very much for coordinating all of this. My office phone is 214-648-5379 and my cell phone is My Skype address is eheitman1

There is some likelihood that I will be on my cell phone because my husband and I plan to drive from Dallas to Houston for the weekend. He'll be driving, but it is not clear that he will be able to leave work before 5. (We had originally planned to drive to College Station in the morning for me to be there in person for the meeting, but he got called to cover someone else's shift on Friday, so our departure time is uncertain.)

And Colleagues,

I have attached here a couple of documents that I hope will be useful for our discussion. The first is a copy of a modified set of briefing slides from the National Academies' gene drive report, which emphasize our conclusions and recommendations about ethics, public engagement, and governance. The full report, together with a 4 page summary, is at http://nas-sites.org/gene-drives/

The second is an article from 2015 on "the ethical challenges created by CRISPR", including section on gene drives. This article has a bit more alarmist tone than it might if it were written today, and concerns about gene drives make up only a column of the 4 pages (see bottom of the middle column of page 1422 to just below the italicized quote in the right column on that page.) I find if a very useful article, however, because it summarizes the regulatory processes and gaps in both the US and international systems, together with consideration for fostering/protecting the public's trust and raises a lot of the points that keep showing up in magazine articles and blog posts for the general public.

Finally, if you didn't hear the NPR news story about a shooting among farmers over the use of illegal herbicides to deal with pigweed in cotton fields, take a look at http://www.npr.org/2017/06/14/532879755/a-pesticide-a-pigweed-and-a-farmers-murder The story seems told in a way to elicit an emotional response as much as rational consideration, but – assuming that we want to use case studies to frame our pubic engagement -- the problems it illustrates are ones that we would probably like to present for discussion.

I look forward to talking with everyone on Friday.

Liz Heitman

Elizabeth Heitman, PhD
Program in Ethics in Science and Medicine
University of Texas Southwestern Medical Center
5323 Harry Hines Boulevard, NC5.832
Dallas, TX 75390-9070
(214)-648-5379
(214)-648-4967 fax
Email: Elizabeth.Heitman@UTSouthwestern.edu
www.utsouthwestern.edu/ethics

From: Goldsmith, Carol [mailto:clgoldsmith@tamu.edu]
Sent: Wednesday, June 14, 2017 8:28 AM
To: Zach Adelman <zachadel@tamu.edu>
Cc: Portney, Kent E <kportney@tamu.edu>; Elizabeth Heitman <Elizabeth.Heitman@UTSouthwestern.edu>; Edward Vargo <ed.vargo@tamu.edu>; Gregory Sword <gasword@tamu.edu>; Kevin Myles <mylesk@tamu.edu>; Micky Eubanks <m-eubanks@tamu.edu>; Raul Medina <rfmedina@tamu.edu>
Subject: RE: AFRI gene drive

As a call in number, you can use 979-862-1098. The conference phone can patch in up to six people. I suggest you share your number with me in case we have challenges connecting.

You can also connect with us via Skype; just send me your Skype address.

Carol L. Goldsmith, MPA
Senior Research Associate and Institute Manager
Institute for Science, Technology and Public Policy

From: Zachary Adelman [mailto:zachadel@tamu.edu]
Sent: Tuesday, June 13, 2017 10:09 AM
To: Goldsmith, Carol <clgoldsmith@tamu.edu >
Cc: Portney, Kent E <kportney@tamu.edu >; Elizabeth Heitman <Elizabeth.Heitman@utsouthwestern.edu >; Edward Vargo <ed.vargo@tamu.edu >; Gregory Sword <gasword@tamu.edu >; Kevin Myles <mylesk@tamu.edu >; Micky Eubanks <m-eubanks@tamu.edu>; Raul Medina <rfmedina@tamu.edu >
Subject: Re: AFRI gene drive

Thanks Carol. See you on Friday. Can you provide a teleconference number for those that may not be able to make it in person?
zach

On Tue, Jun 13, 2017 at 10:01 AM, Goldsmith, Carol <clgoldsmith@tamu.edu > wrote:

> Hello All,
>
> Kent and I would like to host you in the ITSPP Conference Room (1121) for our meeting this Friday at 3:00. We're in the Allen

Building. You can park in lot 111 with a business permit or in lot 43 with any valid TAMU permit.

Carol L. Goldsmith, MPA
Senior Research Associate and Institute Manager
Institute for Science, Technology and Public Policy

From: Zachary Adelman [mailto:zachadel@tamu.edu]
Sent: Wednesday, June 07, 2017 4:43 PM
To: Portney, Kent E <kportney@tamu.edu >; Goldsmith, Carol <clgoldsmith@tamu.edu >; Elizabeth Heitman <Elizabeth.Heitman@utsouthwestern.edu >; Edward Vargo <ed.vargo@tamu.edu >; Gregory Sword <gasword@tamu.edu >; Kevin Myles <mylesk@tamu.edu >; Micky Eubanks <m-eubanks@tamu.edu >; Raul Medina <rfmedina@tamu.edu >
Subject: AFRI gene drive

All,
Let's meet next Friday June 16th at 3pm. Kent, if you would like us to come to your building that will be fine, otherwise we can meet in the Heep Center again (329; call in number 979-458-0302)
thanks everyone,
zach

National Strategy for Modernizing the Regulatory System for Biotechnology Products

Product of the Emerging Technologies Interagency Policy Coordination Committee's Biotechnology Working Group

September 2016

About the Emerging Technologies Interagency Policy Coordination Committee

Assembled under the auspices of the National Science and Technology Council (NSTC), the purpose of the Emerging Technologies Interagency Policy Coordination Committee is to serve as a point of coordination for identifying and, where appropriate, addressing cross-cutting policy issues, such as regulatory approaches, associated with areas that affect multiple agencies and would benefit from a clear, consistently applied U.S. Government position. The group was established to help agencies develop, coordinate, and apply the broad range of policies associated with emerging technologies to further government interests and oversight, and to foster leadership and consistency internationally.

About the Office of Science and Technology Policy

The White House Office of Science and Technology Policy (OSTP) was established by the National Science and Technology Policy, Organization, and Priorities Act of 1976. OSTP's responsibilities include advising the President in policy formulation and budget development on questions in which science and technology are important elements; articulating the President's science and technology policy and programs; and fostering strong partnerships among Federal, State, and local governments, and the scientific communities in industry and academia. The Director of OSTP also serves as Assistant to the President for Science and Technology and manages the NSTC. More information is available at www.whitehouse.gov/ostp.

About the Emerging Technologies Interagency Policy Coordination Committee Biotechnology Working Group

The Emerging Technologies Interagency Policy Coordination Committee Biotechnology Working Group (Biotechnology WG), an interagency group organized under the NSTC, was established in response to a 2015 Executive Office of the President Memorandum for Heads of Food and Drug Administration, Environmental Protection Agency, and Department of Agriculture entitled *Modernizing the Regulatory System for Biotechnology Products*. That memorandum established the Biotechnology WG to take steps to increase the transparency, coordination, predictability, and efficiency of the regulatory system for the products of biotechnology.

Acknowledgements

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Executive Summary

The policy of the United States Government is to seek regulatory approaches that protect health and the environment while reducing regulatory burdens and avoiding unjustifiably inhibiting innovation, stigmatizing new technologies, or creating trade barriers.[1,2,3] These principles also apply to the update of the regulatory framework and systems that regulate the products of biotechnology put forward in this National Strategy for Modernizing the Regulatory Framework for such products. Federal agencies that regulate biotechnology products should strive continually to improve predictability, increase efficiency, and reduce uncertainty in their regulatory processes and requirements. It is critical that these improvements:

- maintain high standards that are based on the best available science and that deliver appropriate health and environmental protection;
- establish transparent, coordinated, predictable, and efficient regulatory practices across agencies with overlapping jurisdiction; and
- promote public confidence in the oversight of the products of biotechnology through clear and transparent public engagement.

While the current regulatory system for the products of biotechnology effectively protects health and the environment, in some cases, uncertainty about agency jurisdiction, lack of predictability of timeframes for review, and other processes have imposed unnecessary costs and burdens on small and mid-sized companies and academics. In response, in July 2015, the Executive Office of the President (EOP) issued a memorandum[4] (July 2015 EOP memorandum) directing the primary agencies that regulate the products of biotechnology—the U.S. Environmental Protection Agency (EPA), the U.S. Food and Drug Administration (FDA), and the U.S. Department of Agriculture (USDA)—to accomplish three tasks:

- update the Coordinated Framework for the Regulation of Biotechnology (Coordinated Framework) by clarifying current roles and responsibilities;
- develop a long-term strategy to ensure that the Federal regulatory system is equipped to efficiently assess the risks, if any, of the future products of biotechnology; and
- commission an expert analysis of the future landscape of biotechnology products to support this effort.

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[1] "Improving Regulation and Regulatory Review", Executive Order 13563, January 18, 2011.
[2] "Identifying and Reducing Regulatory Barriers", Executive Order 13610, May 10, 2012.
[3] "Principles for Regulation and Oversight of Emerging Technologies", Memorandum for the Heads of Departments and Agencies, March 11, 2011.
[4] Memorandum for Heads of Food and Drug Administration, Environmental Protection Agency, and Department of Agriculture, "Modernizing the Regulatory System for Biotechnology Products", Executive Office of the President, July 2, 2015. The memorandum can be found at https://www.whitehouse.gov/sites/default/files/microsites/ostp/modernizing_the_reg_system_for_biotech_products_memo_final.pdf

In directing the agencies to accomplish these three tasks, the Administration's goal is to ensure public confidence in the regulatory system and improve the transparency, predictability, coordination, and, ultimately, efficiency of the biotechnology regulatory system. This *National Strategy for Modernizing the Regulatory System for Biotechnology Products* was developed in order to satisfy the second of the three tasks identified in the July 2015 EOP memorandum and the accompanying proposed Update to the Coordinated Framework was developed to satisfy the first of the three tasks. EPA, FDA, and USDA have commissioned an independent study by the National Academy of Sciences (NAS) to satisfy the third of the three tasks.

Background

The discovery of the three-dimensional structure of DNA in 1953 by Rosalind Franklin, James Watson, and Francis Crick laid the groundwork for an era of innovation in the life sciences. Twenty years later, Stanley Cohen and colleagues described recombinant-DNA techniques that could be used to cut gene sequences from the DNA of one organism and splice them into the DNA of another organism.[5]

In response to concerns as to whether the "regulatory framework that pertained to products developed by traditional genetic manipulation techniques was adequate for products obtained with the new techniques,"[6] such as recombinant DNA, the Coordinated Framework for the Regulation of Biotechnology was published in 1986. It outlined a comprehensive Federal regulatory policy for ensuring the safety of biotechnology products and described oversight responsibilities under existing statutes and among the relevant Federal agencies. While the Coordinated Framework addressed which agency(ies) have oversight authority for biotechnology products, it "did not address how that authority should be exercised in the frequent situations in which a statute leaves the implementing agency latitude for discretion."[7] Thus, in 1992, the Coordinated Framework was updated to describe the "proper basis for agencies' exercise of oversight authority within the scope of discretion afforded by statute."[7]

In part, the oversight system established by the Coordinated Framework led to decades of development and commercialization of biotechnology products with applications in medicine, agriculture, energy, biomanufacturing, and environmental protection, and to the growth of a large and competitive biotechnology sector in the United States and worldwide.

Advances in science and technology have, however, dramatically altered the biotechnology landscape since the issuance of the 1986 Coordinated Framework and associated 1992 update, enabling the development of products that were not envisioned when the 1986 and 1992 documents were published. Consequently, a further update of the Coordinated Framework was needed to facilitate the appropriate Federal oversight by the regulatory system and increase transparency, while continuing to provide a framework for advancing innovation.

In July 2015, the Administration released a memorandum[4] (July 2015 EOP memorandum) noting that while "the current regulatory system for the products of biotechnology effectively protects health and the environment, in some cases, unnecessary costs and burdens associated with uncertainty about agency jurisdiction, lack of predictability of timeframes for review, and other processes have arisen. These costs and burdens have limited the ability of small and mid-sized

[5] Cohen, S.N., A.C.Y. Chang, H, Boyer, and R.B Helling. 1973. Construction of biologically functional bacterial plasmids in vitro. Proceedings of the National Academy of Sciences of the United States of America 70:3240–3244.
[6] https://www.aphis.usda.gov/brs/fedregister/coordinated_framework.pdf
[7] https://www.whitehouse.gov/sites/default/files/microsites/ostp/57_fed_reg_6753__1992.pdf

companies to navigate the regulatory process and of the public to understand easily how the safety of these products is assured."

That memorandum reiterated that the Federal regulatory system must protect health and the environment while reducing regulatory burdens and avoiding unjustifiably inhibiting innovation, stigmatizing new technologies, or creating trade barriers. It also initiated a process to modernize the Federal regulatory system for biotechnology products[8] and to establish mechanisms for periodic updates of that system.[4]

The objectives of the tasks described in the July 2015 EOP memorandum are to ensure public confidence in the regulatory system and to prevent unnecessary barriers to future innovation and competitiveness by improving the transparency, predictability, and efficiency of the regulation of biotechnology products and the coordination among regulatory agencies, while continuing to protect health and the environment.

This *National Strategy for Modernizing the Regulatory System for Biotechnology Products* (*Strategy*) sets forth a vision for ensuring that the Federal regulatory system is prepared to efficiently assess the risks, if any, of the future products of biotechnology. The *Strategy* and the accompanying proposed Update to the Coordinated Framework, which *inter alia* clarifies agency jurisdiction for biotechnology products, were developed by the Biotechnology WG. The Biotechnology WG was established by the July 2015 EOP memorandum under the Emerging Technologies Interagency Policy Coordination (ETIPC) Committee.

To inform the development of these documents and other activities described in the July 2015 EOP memorandum, the National Science and Technology Council (NSTC) published a notice of request for information (RFI) in the *Federal Register* to seek relevant data and information from stakeholders. In addition, the White House Office of Science and Technology Policy (OSTP), EPA, FDA, and USDA jointly held three public meetings, under the auspices of the NSTC, in different regions of the country to inform the public about their activities and seek public comments.[9,10,11] Transcripts of the public meetings, including oral comments received at the meetings, were placed in the public docket.[12] The third public meeting also included breakout listening sessions, and a summary of individual input received during those sessions is available in the public docket.[12] The Biotechnology WG reviewed all written comments submitted in response to the RFI, oral comments made at the three public meetings, and input from the breakout listening sessions, in preparing this *Strategy*. A general summary of the issues raised in

[8] "Biotechnology products" refers to products developed through genetic engineering or the targeted or in vitro manipulation of genetic information of organisms, including plants, animals, and microbes. It also covers some of the products produced by such plants, animals, and microbes or their derived products as determined by existing statutes and regulations. Products such as human drugs and medical devices are not the focus of the activities described in the memorandum (July 2015 EOP memorandum).

[9] http://www.fda.gov/NewsEvents/MeetingsConferencesWorkshops/ucm463783.htm

[10] https://www.epa.gov/regulation-biotechnology-under-tsca-and-fifra/modernizing-regulatory-system-biotechnology-products

[11] https://www.aphis.usda.gov/aphis/ourfocus/biotechnology/stakeholder-meetings/cf_meeting/

[12] http://www.regulations.gov/docket?D=FDA-2015-N-3403

public responses and a review of these responses is provided in Appendix 1 of the proposed Update to the Coordinated Framework. EPA, FDA, and USDA will continue to consider relevant public responses as part of future work related to the implementation of this *Strategy*.

In addition, as these agencies continue their work in pursuit of the objectives in the July 2015 EOP memorandum, consideration will be given to additional actions to clarify further their regulatory processes and procedures, as appropriate. In this regard, agencies will consider the results of the forthcoming National Academy of Sciences report on the *Future Biotechnology Products and Opportunities to Enhance Capabilities of the Biotechnology Regulatory System*.

Goals and Objectives

The goal of this *Strategy* is to ensure that the Federal regulatory system is equipped to efficiently assess the risks, if any, associated with future products of biotechnology while supporting innovation, protecting health and the environment, promoting public confidence in the regulatory process, increasing transparency and predictability, and reducing unnecessary costs and burdens. EPA, FDA, and USDA intend to fulfill this goal, including by addressing the following priorities identified in the July 2015 EOP memorandum.

Increasing Transparency

- Establish a timetable and mechanisms to work with stakeholders to identify impediments to innovation, focusing on building new, and augmenting existing, stakeholder collaborations to inform efforts, increase transparency, streamline processes, reduce costs and response times, and ensure the protection of health and the environment
- Coordinate the development of tools and mechanisms for assisting small businesses developing biotechnology products to navigate the regulatory system
- Develop a modernized, user-friendly set of tools for presenting to the public the regulatory agencies' authorities, practices, and bases for decision making for the regulation of biotechnology products, including digital services, to improve the interactions among FDA, EPA, USDA, the general public, and product developers, as well as updating these tools and practices regularly to ensure optimal transparency
- Engage with the public to discuss how the Federal Government uses a risk-based, scientifically sound approach to regulating the products of biotechnology, and clearly communicating to the public which types of products are regulated, which types of products are not regulated, and why

Increasing Predictability and Efficiency

- Develop a plan for periodic, formal horizon-scanning assessments of new biotechnology products to ensure that regulatory agencies are prepared for future products well before they reach the regulatory system

- Ensure product evaluations are risk-based and grounded in the best science available, including regularly adjusting regulatory activities based on experience with specific products and the environments into which those products have been introduced
- Identify changes to authorities, regulations, and policies that could improve agencies' abilities to assess expeditiously the potential impacts and risks arising from future products of biotechnology and to ensure the transparency, predictability, and efficiency of regulatory oversight for such products

Supporting the Science that Underpins the Regulatory System

- Develop a coordinated and goal-oriented plan for supporting the science that informs regulatory activities with regard to the assessment of biotechnology products, and to reflect these priorities in agency budget submissions

Increasing Transparency

EPA, FDA, and USDA have developed processes to communicate with the public and stakeholders, including consumers and small businesses. For example, all three of these agencies have mechanisms for soliciting and utilizing public input related to regulatory decisions. Examples include advisory committees of experts in key disciplines relevant to specific products or product areas;[13] opportunities for public input on regulations and guidance documents, through petitions on certain environmental assessments and impact statements, and through public meetings; webinars and workshops on the regulatory framework for interested stakeholders, including industry and consumers; and information on regulatory activities and updates for consumers posted on agency websites. The agencies' websites provide information to the public on agencies' activities, including guidance for developers of products subject to regulatory oversight, and consumer and public-oriented brochures and factsheets, many of which are available several different languages.

The proposed Update to the Coordinated Framework that accompanies this *Strategy* contains a table that summarizes the current responsibilities and the relevant coordination across EPA, FDA, and USDA for the regulatory oversight of biotechnology products, based on the scope of each agency's current authorities. Product developers who are uncertain regarding the relevant regulatory requirements, particularly small businesses, are encouraged to contact the agencies early in the product development process to obtain information from the agencies on potential safety and regulatory requirements that may be associated with their intended products.

[13] For example, EPA regularly holds meetings of its Federal Insecticide, Fungicide, and Rodenticide Act Scientific Advisory Panel (SAP) to solicit technical advice from recognized experts in their respective scientific disciplines on specific topics relevant to EPA's regulation of pesticides. These meetings generally are open to the public, and pertinent materials are made available to the public through EPA's website for the SAP (https://www.epa.gov/sap). The public also is given an opportunity to comment on the questions being posed to the SAP at each meeting.

Discussions with regulatory officials can provide information on the regulatory process most relevant to their product and how best to navigate the regulatory system.

Examples of existing mechanisms and activities are listed below

- **EPA, FDA, USDA, and OSTP hosted three public meetings to clarify current roles and responsibilities in different regions of the country at which, in total, over 800 people participated in person or by webcast.** The first meeting was held on October 30, 2015, at the FDA's White Oak Campus in Silver Spring, Maryland to inform the public about the activities described in the July 2015 EOP memorandum, invite oral comments from interested parties, and provide information about where and how to submit written comments, data, or other information. The second public meeting was held on March 9, 2016 at EPA's Region 6 Office in Dallas, Texas. The primary purpose of this meeting was to illustrate current Federal roles and responsibilities regarding biotechnology products by reviewing case studies of hypothetical products. The third public meeting was held on March 30, 2016, at the University of California's Davis Conference Center in Davis, California. At this public meeting, representatives from the EPA, FDA, and USDA illustrated the current roles and responsibilities of the EPA, FDA, and USDA regarding biotechnology products by discussing case studies of hypothetical products. In addition, breakout listening sessions were conducted that focused on three general thematic areas relevant to the tasks assigned to the EPA, FDA, and USDA in the July 2015 EOP memorandum – Governance; Education, Communication, and Outreach; and Improving Regulatory Certainty. Additional materials for all of these meetings, including agendas and presentations, are available on the meeting websites and in the corresponding docket on regulations.gov.
- **EPA, FDA, and USDA periodically host workshops to help small businesses developing biotechnology products navigate the regulatory system.** For example, in 2011 EPA, FDA, and USDA hosted a workshop during which case studies were presented by product developers and each of the three regulatory agencies described how they would engage with the developer as the product went through each of the three regulatory systems. USDA provides enhanced education, coordination, and outreach through its Specialty Regulatory Crop Assistance program and provides a detailed User's Guide to assist companies in preparing petitions for nonregulated status. FDA holds workshops on topics of emerging relevance to FDA to engage all stakeholders and obtain expert input into future directions and policy development. EPA, FDA, and USDA will continue to organize such workshops and to announce these through their respective stakeholder announcements, web portals, and *Federal Register* notices as appropriate.
- **EPA, FDA, and USDA provide information to developers and to the general public via their websites and through email systems**. These websites and email systems allow developers to pose specific questions related to those agencies' programs, including USDA's BiotechQuery, EPA's BPPDQuestions, and FDA's links for industry and consumer inquiries.

FDA also issues Constituent Updates to inform stakeholders of regulatory activities, such as public meetings or the availability of regulatory documents for public comment; as well as Consumer Updates and other information for consumers on a variety of topics. EPA provides guidance on its website regarding reduced Pesticide Registration Improvement Act (PRIA) fees for small businesses, and fee waivers for IR-4 submissions and Federal and state governments. EPA also keeps the public informed about biotechnology issues via its webpages and updates distributed to interested parties via email and the Federal Register. For example, EPA involves the public in regulatory decisions for significant new biotechnology pesticide products and for biotechnology microorganism products.

- **EPA, FDA, and USDA will continue to provide leadership in international fora to promote scientific competency, understanding of the U.S. regulatory approach, and regulatory compatibility worldwide for biotechnology products.** The U.S. agencies actively work to strengthen engagement between countries through coordinated and collaborative international initiatives. Through these efforts the United States shares technical and scientific expertise and supports the adoption of transparent, risk-based regulatory approaches grounded in the best science available, including with respect to the application of the most recent technical and scientific advances to the biotechnology products. These initiatives support attainment of shared global health and environmental protection goals while supporting greater regulatory predictability and reducing impediments to U.S. innovation and products worldwide. For example, experts from two U.S. regulatory agencies currently chair, and all three agencies actively contribute to, working groups in the Organization for Economic Cooperation and Development (OECD) on scientific and technical issues underpinning regulatory approaches for the products of agricultural and industrial biotechnology.

- **EPA Office of Pollution Prevention and Toxics (OPPT) is currently updating the *Points to Consider in the Preparation of Toxic Substances Control Act (TSCA) Biotechnology Submissions for Microorganisms (Points to Consider)* document.** This document identifies a broad range of risk assessment topics relevant to TSCA biotechnology submissions and provides technical support to assist those who must prepare microorganism pre-manufacturing notifications to EPA under TSCA. The *Points to Consider* do not currently provide specific support for product developers using the emerging technologies of algae production and advanced biotechnology. To keep its risk assessment process for biotechnology algae open and transparent, EPA intends to develop a separate document on the scientific and technological issues it currently understands to be key and unique for evaluating risks, if any, from the production and use of biotechnology algae. EPA will develop its *Algae Guidance for the Preparation of TSCA Biotechnology Submissions* document in parallel with updating the *Points to Consider* document. EPA held a public meeting on this effort on September 30, 2015. There will be a follow up meeting on October 27, 2016. See here for more information.

- **FDA has instituted a number of activities aimed at providing assistance to regulated small businesses.** These include small business assistance programs, which provide technical assistance to small companies; meetings to hear the views and perspectives of small businesses; educational workshops; informational materials; and an accessible, efficient channel through which small businesses can acquire information from the FDA. FDA publishes the Small Business Guide to FDA to help make small businesses' contacts with FDA as efficient and productive as possible. This guide is presented as a blueprint that small firms can follow to achieve their business aims consistent with FDA's mission on public health. FDA created openFDA in June 2014, to make FDA's public information more accessible and useful to developers. FDA has made a continuous effort to better understand the needs of the developer community and build on existing resources.
- **USDA organizes workshops with specialty crops groups to discuss the regulatory system and how best to navigate it.** FDA and EPA participate with USDA in these workshops, such as those hosted periodically by Specialty Regulatory Crop Assistance program and at periodic USDA annual Stakeholder Meetings, so that attendees understand how to navigate the regulatory system at all three agencies. In September, 2016, the agencies are hosting a workshop to provide regulatory assistance for public sector scientists and public and private sector crop developers on putting together a regulatory dossier for genetically engineered specialty crops.

Future activities

- **EPA, FDA, and USDA are exploring new opportunities to conduct sessions with industry, consumers, and other stakeholders, including at scientific conferences and at agency-hosted workshops, much like the annual USDA Biotechnology Regulatory Service stakeholder meeting.**
- **EPA, FDA, and USDA will review existing communication tools and, as appropriate, may revise existing or develop new user-friendly sources of regulatory information for product developers and the general public.** For example, FDA has information for consumers on its website about food from genetically engineered plants and about FDA's consultation process for developers of such foods. See "Consumer Info About Food from Genetically Engineered Plants," "How FDA Regulates Food from Genetically Engineered Plants," and "Questions & Answers on Food From Genetically Engineered Plants". FDA also regularly updates its Genetically Engineered Animals web page, including a current listing of all animals with related FDA-approved applications. In addition, FDA has developed a Strategic Plan for Risk Communication, which describes FDA's strategy for improving how the agency communicates with patients and consumers about regulated products. USDA maintains a variety of information on its website about how it protects plant health including a video overview of its biotechnology regulatory program. EPA and USDA

also regularly update their web page listings for registered and deregulated biotech products, respectively.

In addition, the agencies are reviewing the feedback received during the three public meetings and the fall 2015 Request for Information to better understand the specific areas of interest to the public regarding the regulation of biotechnology products and preferred mechanisms for conveying regulatory information. For example, the agencies are examining the feasibility of providing a single source for regulatory information so that developers can easily determine the appropriate regulatory pathway for their product. In addition, the agencies are examining the feasibility of expanding various types of training programs where product developers, particularly small companies, and the public would have opportunity to learn about the roles of the three regulatory agencies.

- **EPA Office of Pesticide Programs (OPP) will hold a "Plant-Incorporated Protectant (PIP) Data Requirements Symposium" on September 29, 2016 to describe for stakeholders and the public its thoughts on the types of data appropriate for evaluating a PIP product in the registration process.** This symposium is intended to be an opportunity for EPA scientists to describe the various types of information and data they would normally review when evaluating various types of PIPs, and to clarify expectations by describing procedures, new efficiency initiatives, and the regulatory approach that underpins EPA OPP's approach to PIPs. This meeting is also intended to help small businesses better understand EPA's requirements and thus to better navigate the regulatory system. USDA and FDA will also be participating in the Symposium to provide information on their respective regulatory systems. Learn more here.

Increasing Predictability and Efficiency

Consistent with the 1986 Coordinated Framework, the 1992 Update to the Coordinated Framework, Executive Order 13563, Executive Order 13610, the 2011 "Principles for Regulation and Oversight of Emerging Technologies" memorandum (2011 memorandum), and the July 2015 EOP memorandum, EPA, FDA, and USDA strive to develop and implement regulatory approaches to protect health and the environment while reducing regulatory burdens and avoiding unjustifiably inhibiting innovation, stigmatizing new technologies, or creating trade barriers. The 1992 Update to the Coordinated Framework describes a risk-based, science-based regulatory approach "to ensure that limited federal oversight resources are applied where they will accomplish the greatest net beneficial protection of public health and the environment."[7] The United States Government reiterated that this risk- and science-based approach to regulation applied to oversight of products of emerging technologies, such as synthetic biology and genetic engineering, in the 2011 memorandum.[3] This National Strategy reaffirms the centrality of this approach in the United States Government.

EPA, FDA, and USDA rely on horizon scanning techniques to detect early signs of important developments in biotechnology. The three regulatory agencies maintain staffs of experts, trained

in a variety of scientific disciplines, who keep up with knowledge in the various sciences important to understanding and evaluating biotechnology products. These agencies learn about new technologies and new products in development through a combination of activities, including participation in scientific and trade forums and discussions with national and international counterparts; monitoring scientific and trade literature; participating on technical advisory panels; maintaining membership in interagency, national, and international scientific organizations dedicated to state-of-the-art science and technology; and convening scientific advisory committees and public meetings. On occasion, EPA, FDA, and USDA have also sought advice on cutting-edge issues from groups of independent technical experts including, for example, the National Academies of Science, Engineering and Medicine.

Examples of existing mechanisms and activities are listed below

- **EPA, FDA, and USDA have commissioned an independent study by the National Academy of Sciences (NAS)** "Future Biotechnology Products and Opportunities to Enhance Capabilities of the Biotechnology Regulatory System." The study will identify (1) major advances and potential new types of biotechnology products over the next five to ten years, (2) potential future products that might pose a different type of risk relative to existing products and organisms, (3) areas in which the risks or lack of risk relating to biotechnology are well understood, and (4) the scientific capabilities, tools, and expertise that may be useful to the regulatory agencies as they oversee potential future products of biotechnology. NAS initiated the study in early 2016. Consistent with the July 2015 EOP memorandum, products such as human drugs and medical devices are not a focus of the study. The NAS committee held three public meetings in the spring and summer of 2016 to gather information for the study. The findings by NAS will be considered by the agencies in order to inform ongoing and future agency activities, including the implementation of the *Strategy*. EPA, FDA, and USDA will use the report to (1) gain a better understanding of future products and how they fit within the U.S. regulatory system; (2) consider any necessary updates to scientific assessments; (3) consider any necessary updates to regulatory processes or procedures; and (4) help enhance communication with stakeholders. The July 2015 EOP memorandum also notes that, due to the rapid pace of change in this arena, such independent external analysis should be completed at least every five years.
- **EPA, FDA, and USDA's frequent interactions with product developers.** All three agencies encourage product developers to begin discussions with the regulatory agencies early in the development process, as advance notice and information about products being contemplated enable the agencies to provide input to developers about the safety and regulatory issues relevant to their product. Staff from each of the three agencies routinely have discussions with their counterparts at the other agencies to share information (as appropriate) about products on the horizon or in the regulatory pipeline.
- **EPA, FDA, and USDA strive to use the best available science to address the protection**

goals established by their respective statutes. For example, USDA's authority under the Plant Protection Act identifies the aspects of plant health that need to be protected from harm (what to protect, where, over what period).[14] These aspects of plant health drive the collection of relevant information for a plant health risk assessment. USDA's environmental risk assessment is an iterative process that uses a scientific approach in which specific hypotheses are formulated and then either proven or refuted through the use of appropriate testing methods.

- **EPA OPP is modifying its approach to PIPs in breeding line intermediates (BLIs).** A BLI is used in plant breeding to bring together or "stack" several individual PIPs into seed. EPA's current approach requires a unique registration for each combination of two or more PIPs combined in BLIs. As companies combine multiple PIPs together, the number of BLI registrations needed to develop one combination PIP product increases. In light of this, EPA is proposing to modify its approach so that a unique registration for each combination of PIPs in BLIs would no longer be required. Rather, EPA will regulate PIPs in BLIs through conditions placed on the registrations of the individual PIPs to be combined in BLIs. This will result in a reduction in the number of registrations needed to produce a combination PIP product. Learn more here.

- **FDA's continuous efforts to expand regulatory science and the use of "smart regulation."** FDA's Strategic Priorities, 2014-2018, identified several cross-cutting strategic priorities and FDA's core mission goals and objectives, which are relevant to ensuring science- and risk-based product evaluations. For example, regulatory science and "smart regulation" are among the focus of FDA's programs. In addition, FDA's core mission goals and objectives include: (1) increasing the use of regulatory science to inform standards development, analysis, and decision-making; (2) increasing regulatory science capacity to effectively evaluate products; and (3) reducing risks in the manufacturing, production, and distribution of FDA-regulated products. For example, with respect to the safety of foods derived from genetically engineered plants, FDA's voluntary consultation process focuses on the characteristics of the plant species and the introduced trait. This process is consistent with international standards established by *Codex Alimentarius*.

- **USDA's encouragement of product development through its *Am I Regulated* process and its permit and notification system.** USDA developed the *Am I Regulated* process by which developers, including small private- and public-sector entities, will ask whether a proposed product would be subject to USDA regulations prior to requesting an authorization for a regulated activity. This allows USDA to have some early notification of products that may be about to enter the regulatory system and provides an additional window into emerging technologies. Also, through the USDA authorization system, which provides permits and notifications for regulated import, interstate movement, and field testing of

[14] Plant Protection Act of 2000; (PPA, 7 U.S.C. 7701 et seq.).

biotech products, the agency is able to learn about potential commercial products three or more years before they are commercialized.

- **USDA's efforts underway to revise its regulations at 7 CFR part 340.** On February 5, 2016, USDA published a notice in the *Federal Register* announcing that it is developing a draft programmatic environmental impact statement (EIS), required under the National Environmental Policy Act, that will evaluate a range of risk-based approaches to regulation that the Agency can take as it works to update its biotechnology regulations. The notice also invites the public to comment on the range of alternatives that USDA will study in the draft EIS, along with definitions that USDA plans to use in the draft EIS. Learn more here.
- **USDA developed an international product horizon scanning assessment.** Recognizing that future biotechnology products are currently being developed in other countries, USDA has developed, and shares with EPA and FDA, annual Vulnerability Assessments that scan information about plant, animal, and microorganism biotechnology research and development activities in other countries for biotechnology products that are in development pipelines and could be imported into the United States. These assessments identify products already in commercial production in other countries, but not yet authorized in the United States.

Future activities

During development of the proposed Update to the Coordinated Framework, the agencies identified a number of actions intended to improve predictability and efficiency. To this end, EPA, FDA, and USDA are committing to the following:

- **EPA, FDA, and USDA commit to interagency communication that helps with timely decisions on regulatory jurisdiction for biotechnology products, in order to help clarify for developers which of the regulatory agency(ies) might have oversight responsibility for a novel biotechnology product for a specific application.**
- **EPA, FDA, and USDA will continue to explore ways to enhance collaborations for the oversight of biotechnology products in an effort to optimize the review and use of scientific data or regulatory assessments**. Greater collaborations between agencies have the potential to reduce the cost, complexity, and time needed to bring safe, new products to market, which is especially important to small and mid-sized companies and academics. Enhanced collaboration and, where feasible, coordination, can also benefit developers and the public by ensuring that the best possible science, standards, and practice drive the regulatory process.
- **EPA, FDA and USDA will continue to examine their regulatory structures with the goal of clarifying how the U.S. Federal Government will regulate genetically engineered insects in an integrated and coordinated fashion to cover the full range of potential products.** The agencies are working to better align their responsibilities over genetically

engineered insects with their traditional oversight roles, for example, considering mechanisms that would enable EPA to regulate genetically engineered mosquitos under FIFRA when the developer claims they are intended to control population levels, and FDA to regulate them under FD&C Act when the developer makes a disease claim. USDA will continue to exercise its authorities for control of certain plant or animal pest insects.

- **EPA OPP is undertaking a reorganization of the EPA staff assigned to the regulation of biopesticides**, **including genetically engineered microorganisms and plant-incorporated protectants**. The reorganization is to facilitate interaction among the various experts needed to address novel products of modern biotechnology, and, thus, to facilitate EPA's ability to more efficiently address such products. The reorganization will also create efficiencies by centralizing review and regulation of plant-incorporated protectants (PIPs) into one group.
- **EPA OPP is modifying its approach to transformation event in product identification.** The "transformation event" is generally part of the identity of a PIP. EPA has historically assumed that a different transformation event means a different PIP even if the same vector is used in the engineering. Advances in techniques for the sequencing of genetic information now give EPA the ability to determine whether PIPs associated with different transformation events might be properly considered as "identical or substantially similar". Such a consideration could, for example, affect how the PIP is registered. The modified approach to transformation event would apply to PIPs in seed propagated and in clonally propagated plants, but would likely be most useful for companies developing PIPs in clonally propagated plants. More details will be made available to interested stakeholders at EPA OPP's September 29, 2016 "Plant-Incorporated Protectant (PIP) Data Requirements Symposium."
- **EPA OPP intends to clarify its approach to pesticidal products derived from genome editing techniques.** This clarification will be consistent with the principles for the regulation of biotechnology products articulated in the Coordinated Framework and the goals and objectives of the July 2015 EOP memorandum.
- **FDA intends to clarify its policy for the regulation of products derived from genome editing techniques, including, as appropriate, identifying and/or updating relevant existing guidance documents.** For example, FDA intends to update its Guidance for Industry 187, *Regulation of Genetically Engineered Animals Containing Heritable Recombinant DNA Constructs*, to clarify how developers of animals produced using emerging technologies (e.g., genome editing) may meet applicable statutory and regulatory requirements. This update will be consistent with the principles for the regulation of biotechnology products articulated in the proposed Update to the Coordinated Framework and the goals and objectives of the July 2015 EOP memorandum.
- **FDA intends to explore updating guidance regarding the consultation procedures for food derived from new plant varieties.** An update to these procedures, which date back to 1996, will help developers have a clearer understanding of what FDA expects during a

consultation. Any update to these procedures will be consistent with the principles for the regulation of biotechnology products articulated in the proposed Update to the Coordinated Framework and the goals and objectives of the July 2015 EOP memorandum.

- **FDA's Emerging Sciences Working Group will be used to identify science and technology trends of relevance to FDA's regulatory responsibilities, including those for biotechnology products.** For FDA to achieve its mission of protecting and promoting public health, it must be prepared for emerging issues and scientific advances that will affect regulated products, and it must be so prepared well in advance of formal FDA regulatory submissions. To help it realize this goal, FDA formed the Emerging Sciences Working Group. The group will provide an FDA-wide science-based forum to identify and communicate scientific regulatory approaches to anticipated high-impact emerging science and technology.

Supporting the Science that Underpins the Regulatory System

One of the key principles of the U.S. Federal regulatory system for biotechnology products is that regulatory reviews and decisions should be based on the best available science. EPA, FDA, and USDA/APHIS support such science through collaborations with Federal research agencies and through intramural and extramural research portfolios, when appropriate.

Examples of existing mechanisms and activities are listed below

- **FDA leverages its intramural and extramural research portfolios to support regulatory science.** Regulatory science, for FDA, is the science of developing new tools, standards, and approaches to assess the safety, effectiveness, quality, toxicity, public health impact, or performance of FDA-regulated products. FDA identified regulatory science as a cross-cutting strategic priority in its most recent Strategic Priorities document, issued in 2014. In addition, FDA developed a Strategic Plan for Regulatory Science that identified plans to close critical gaps in scientific knowledge required to support regulatory decision-making. As discussed in this plan, a science priority area is to ensure FDA readiness to evaluate innovative emerging technologies, including by coordinating regulatory science for emerging technology product areas. In addition, the Global Coalition of Regulatory Science Research, for example, is building a foundation of collaborative research, scientific exchange, and training as a basis for regulatory decision-making. As needed, FDA also engages in various extramural and intramural research activities to address scientific gaps and develop new methods, models, and approaches required to inform regulatory policy development and decision-making. For example, FDA has relationships with several academic institutions through its Centers of Excellence in Regulatory Science and Innovation (CERSI) as well as through several subject-specific Centers of Excellence. FDA regulatory science activities seek to employ or develop tools that are relevant to biotechnology products (e.g., with respect to food safety, research to

improve the understanding of allergens to help inform the assessment of the potential allergenicity of proteins; and research related to whole genome sequencing).

- **USDA leverages expertise and resources from USDA's research agencies, the Agricultural Research Service (ARS) and the National Institute of Food and Agriculture**. In cases where there is mutual interest, USDA funds can be directed towards research to inform regulatory activities. One mechanism for such coordination is the Biotechnology Risk Assessment Grants (BRAG) program, which supports the generation of new information that will assist Federal regulatory agencies in making science-based decisions about the effects of introducing biotechnology products into the environment. Investigations of effects on both managed and natural environments are relevant. Also, APHIS discusses research needs with ARS which, when mutual interests arise, uses intramural funds for projects that inform regulatory activities.

Future activities

- **EPA, FDA, and USDA will continue to explore mechanisms to enhance coordination with Federal research agencies to help support agencies' regulatory science needs.**

Implementation of the Strategy

As instructed in the July 2015 EOP memorandum, for at least five years, starting one year after the release of the S*trategy*, EPA, FDA, and USDA are expected to produce an annual report on the specific steps the agencies are taking to implement this *Strategy*. In their first annual report, the agencies may, if appropriate, provide a concrete list of regulatory and other activities and expected timeframes. The agencies will also include in that report any additional actions taken by the agencies to improve the transparency, predictability, and efficiency of biotechnology regulation and the coordination among the regulatory agencies. This report will be made available to the public by the Executive Office of the President.

From:	Elizabeth Heitman <Elizabeth.Heitman@UTSouthwestern.edu>
To:	Goldsmith, Carol Zach Adelman
CC:	Portney, Kent E Edward Vargo Gregory Sword Kevin Myles Micky Eubanks Raul Medina Elizabeth Heitman
Date:	6/14/2017 5:45:11 PM
Subject:	RE: AFRI gene drive
Attachments:	Heitman - Gene Drives on the Horizon_Ethics, Engagement, & Governance_6-14-17.xps Caplan et al. The ethical challenges created by CRISPR - EMBO Reports 2015.pdf

Dear Carol,

Thank you very much for coordinating all of this. My office phone is 214-648-5379 and my cell phone is 615-481-0638. My Skype address is eheitman1

There is some likelihood that I will be on my cell phone because my husband and I plan to drive from Dallas to Houston for the weekend. He'll be driving, but it is not clear that he will be able to leave work before 5. (We had originally planned to drive to College Station in the morning for me to be there in person for the meeting, but he got called to cover someone else's shift on Friday, so our departure time is uncertain.)

And Colleagues,

I have attached here a couple of documents that I hope will be useful for our discussion. The first is a copy of a modified set of briefing slides from the National Academies' gene drive report, which emphasize our conclusions and recommendations about ethics, public engagement, and governance. The full report, together with a 4 page summary, is at http://nas-sites.org/gene-drives/

The second is an article from 2015 on "the ethical challenges created by CRISPR", including section on gene drives. This article has a bit more alarmist tone than it might if it were written today, and concerns about gene drives make up only a column of the 4 pages (see bottom of the middle column of page 1422 to just below the italicized quote in the right column on that page.) I find if a very useful article, however, because it summarizes the regulatory processes and gaps in both the US and international systems, together with consideration for fostering/protecting the public's trust and raises a lot of the points that keep showing up in magazine articles and blog posts for the general public.

Finally, if you didn't hear the NPR news story about a shooting among farmers over the use of illegal herbicides to deal with pigweed in cotton fields, take a look at http://www.npr.org/2017/06/14/532879755/a-pesticide-a-pigweed-and-a-farmers-murder The story seems told in a way to elicit an emotional response as much as rational consideration, but – assuming that we want to use case studies to frame our pubic engagement -- the problems it illustrates are ones that we would probably like to present for discussion.

I look forward to talking with everyone on Friday.

Liz Heitman

Elizabeth Heitman, PhD
Program in Ethics in Science and Medicine
University of Texas Southwestern Medical Center
5323 Harry Hines Boulevard, NC5.832
Dallas, TX 75390-9070
(214)-648-5379
(214)-648-4967 fax

Email: Elizabeth.Heitman@UTSouthwestern.edu
www.utsouthwestern.edu/ethics

From: Goldsmith, Carol [mailto:clgoldsmith@tamu.edu]
Sent: Wednesday, June 14, 2017 8:28 AM
To: Zach Adelman <zachadel@tamu.edu>
Cc: Portney, Kent E <kportney@tamu.edu>; Elizabeth Heitman <Elizabeth.Heitman@UTSouthwestern.edu>; Edward Vargo <ed.vargo@tamu.edu>; Gregory Sword <gasword@tamu.edu>; Kevin Myles <mylesk@tamu.edu>; Micky Eubanks <m-eubanks@tamu.edu>; Raul Medina <rfmedina@tamu.edu>
Subject: RE: AFRI gene drive

As a call in number, you can use 979-862-1098. The conference phone can patch in up to six people. I suggest you share your number with me in case we have challenges connecting.

You can also connect with us via Skype; just send me your Skype address.

Carol L. Goldsmith, MPA
Senior Research Associate and Institute Manager
Institute for Science, Technology and Public Policy

From: Zachary Adelman [mailto:zachadel@tamu.edu]
Sent: Tuesday, June 13, 2017 10:09 AM
To: Goldsmith, Carol <clgoldsmith@tamu.edu >
Cc: Portney, Kent E <kportney@tamu.edu >; Elizabeth Heitman <Elizabeth.Heitman@utsouthwestern.edu >; Edward Vargo <ed.vargo@tamu.edu >; Gregory Sword <gasword@tamu.edu >; Kevin Myles <mylesk@tamu.edu >; Micky Eubanks <m-eubanks@tamu.edu>; Raul Medina <rfmedina@tamu.edu >
Subject: Re: AFRI gene drive

Thanks Carol. See you on Friday. Can you provide a teleconference number for those that may not be able to make it in person?
zach

On Tue, Jun 13, 2017 at 10:01 AM, Goldsmith, Carol <clgoldsmith@tamu.edu > wrote:

> Hello All,
>
> Kent and I would like to host you in the ITSPP Conference Room (1121) for our meeting this Friday at 3:00. We're in the Allen Building. You can park in lot 111 with a business permit or in lot 43 with any valid TAMU permit.
>
> **Carol L. Goldsmith**, MPA
> Senior Research Associate and Institute Manager
> *Institute for Science, Technology and Public Policy*
>
> **From:** Zachary Adelman [mailto:zachadel@tamu.edu]
> **Sent:** Wednesday, June 07, 2017 4:43 PM
> **To:** Portney, Kent E <kportney@tamu.edu >; Goldsmith, Carol <clgoldsmith@tamu.edu >; Elizabeth Heitman <Elizabeth.Heitman@utsouthwestern.edu >; Edward Vargo <ed.vargo@tamu.edu >; Gregory Sword <gasword@tamu.edu >; Kevin Myles <mylesk@tamu.edu >; Micky Eubanks <m-eubanks@tamu.edu >; Raul Medina <rfmedina@tamu.edu >
> **Subject:** AFRI gene drive
>
> All,
> Let's meet next Friday June 16th at 3pm. Kent, if you would like us to come to your building that will be fine, otherwise we can meet in the Heep Center again (329; call in number 979-458-0302)
> thanks everyone,
> zach

UT Southwestern

Medical Center

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From:	Susan Brown <sjbrown@ksu.edu>
To:	Brockhouse, Charles L Denis Tagu Mary Ann McDowell g.christophides@imperial.ac.uk grthomas@umail.iu.edu b.evans@yale.edu mfritz13@umd.edu alistair.miles@well.ox.ac.uk cherrys@mail.med.upenn.edu jcchiu@ucdavis.edu zachadel@tamu.edu lbartholomay@wisc.edu Rita.Rio@mail.wvu.edu kuhnr@purdue.edu anupama.dahanukar@ucr.edu
CC:	Katie (Merz) Cybulski Sarah Craig Ashley Scott Molly Scheel Kristin Michel Michael Pfrender semrich@nd.edu hughrobe@uiuc.edu
Date:	6/12/2017 3:39:39 PM
Subject:	Re: Arthropod Genomics Symposium Speaker Information

It was a GREAT meeting. Thanks to all of the speakers for making it so special. Thanks to the local organizing committee for a smoothly run meeting.
Sue

Susan J Brown
University Distinguished Professor of Biology
Ackert Hall
Kansas State University
Manhattan KS 66506
Office: 785 532 3935

From: Brockhouse, Charles L <CharlesBrockhouse@creighton.edu>
Sent: Sunday, June 11, 2017 5:46 PM
To: Denis Tagu; Mary Ann McDowell; g.christophides@imperial.ac.uk; grthomas@umail.iu.edu; Brockhouse, Charles L; b.evans@yale.edu; mfritz13@umd.edu; alistair.miles@well.ox.ac.uk; cherrys@mail.med.upenn.edu; jcchiu@ucdavis.edu; zachadel@tamu.edu; lbartholomay@wisc.edu; Rita.Rio@mail.wvu.edu; kuhnr@purdue.edu; anupama.dahanukar@ucr.edu
Cc: Katie (Merz) Cybulski; Sarah Craig; Ashley Scott; Molly Scheel; Kristin Michel; Susan Brown; Michael Pfrender; semrich@nd.edu; hughrobe@uiuc.edu
Subject: Re: Arthropod Genomics Symposium Speaker Information

I d like to second Denis thanks. It was a great and valuable symposium. I learned a lot, met old friends again and made some

new ones.
Thanks for inviting me to participate.

Charles

C. Brockhouse, PhD
Associate Professor, Genetics
Biology Department
Creighton University

From: Denis Tagu <denis.tagu@inra.fr >
Date: Sunday, June 11, 2017 at 5:40 PM
To: Mary Ann McDowell <mmcdowe1@nd.edu >, "g.christophides " <g.christophides >, "grthomas@umail.iu.edu " <grthomas@umail.iu.edu >, "Brockhouse, Charles L" <CharlesBrockhouse@creighton.edu >, "b.evans@yale.edu" <b.evans@yale.edu >, "mfritz13@umd.edu " <mfritz13@umd.edu >, "alistair. <alistair.miles@well.ox.ac.uk >, "cherrys@mail.med.upenn.edu " <cherrys@mail.med.upenn.edu >, "jcchiu@ucdavis.edu " <jcchiu@ucdavis.edu >, "zachadel@tamu.edu " <zachadel@tamu.edu >, "lbartholomay@wisc.edu " <lbartholomay@wisc.edu >, "Rita.Rio@mail.wvu.edu " <Rita.Rio@mail.wvu.edu >, "kuhnr@purdue.edu " <kuhnr@purdue.edu >, "anupama.dahanukar@ucr.edu " <anupama.dahanukar@ucr.edu >
Cc: "Katie (Merz) Cybulski" <kmerz@nd.edu >, Sarah Craig <craig.20@nd.edu >, Ashley Scott <ascott12@nd.edu >, Molly Scheel <Molly.A.Scheel.2@nd.edu >, Kristin Michel <kmichel@k-state.edu >, Susan Brown <sjbrown@ksu.edu >, Michael Pfrender <Michael.Pfrender.1@nd.edu >, Scott Emrich <semrich@nd.edu >, "hughrobe@uiuc.edu " <hughrobe@uiuc.edu >
Subject: RE: Arthropod Genomics Symposium Speaker Information

Dea Mary Ann (and colleagues),

Thank you again for this terrific meeting. A very good opportunity to listen to good science, to meet nice people, start new collaboration.

So thanks very much for the invitation

Have a nice sunday!

Denis

denis.tagu@inra.fr

Denis Tagu INRA Rennes UMR 1349 IGEPP INRA Agrocampus Ouest Rennes - Universit Rennes 1 B P35327 35653 Le Rheu cedex France Tel: 33(0) 223 48 51 65 Tel: 33(0) 676 35 67 93 Fax: 33(0) 223 48 51 50 denis.tagu@inra.fr https://www6.rennes.inra.fr/igepp_eng/Personnel/T/Tagu-Denis https://www6.rennes.inra.fr/igepp_eng/ https://www.rennes.inra.fr/igepp

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De : Mary Ann McDowell <mmcdowe1@nd.edu >
Envoy : vendredi 10 f vrier 2017 03:15
: g.christophides@ ; Denis Tagu; grthomas@umail.iu.edu ; CharlesBrockhouse@creighton.edu ; b.evans@yale.edu ; mfritz13@umd.edu ; alistair.miles@ ; cherrys@mail.med.upenn.edu ; jcchiu@ucdavis.edu ; zachadel@tamu.edu ; lbartholomay@wisc.edu ; Rita.Rio@mail.wvu.edu ; kuhnr@purdue.edu ; anupama.dahanukar@ucr.edu
Cc : Katie (Merz) Cybulski; Sarah Craig; Ashley Scott; Molly Scheel; Kristin Michel; Susan Brown; Michael Pfrender; semrich@nd.edu ; hughrobe@uiuc.edu
Objet : Arthropod Genomics Symposium Speaker Information

Dear Arthropod Genomics Speakers,
On behalf of the organizing committee, I thank you for agreeing to speak at the 10th Arthropod Genomics Symposium (AGS) hosted by the Eck Institute for Global Health at the University of Notre Dame (UND). The symposium will begin Thursday evening, June 8 and will conclude with a banquet on Saturday evening, June 10, 2017. The meeting in 2017 will be preceded by an Arthropod Database Workshop starting June 7th.
We will provide your transportation expenses, registration fee and housing costs at UND for three nights. **You will be receiving an email from Ms. Katie Cybulski (**kmerz@nd.edu **) from our Institute to arrange your travel.** We have reserved a block of rooms on campus near the conference center, but encourage you to take a walk down memory lane and choose the dormitory option. The University of Notre Dame has a strong residency hall tradition. The rooms are air-conditioned, located near the conference center, and linens are provided; however, lavatories and showers are shared with separate men s and women s facilities on each floor.
We have an exciting agenda planned this year (https://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/), with sessions ranging from Emerging Genomes to Metagenomics (see list of speakers below). **Please send me a title for your presentation as soon as possible so that we can begin advertising your specific session.**
In addition to Katie Cybulski, you may receive additional correspondence from Conference Center contact, Lauri Roberts, or Ashley Scott. Feel free to contact me at any time should you have questions. I look forward to our interactions at Arthropod Genomics 2017!

Keynote Speaker-Thursday, June 8 pm
George Christophides, Imperial College, London

I5K Session-Friday, June 8 am
Denis Tagu, Universite de Rennes
Gregg Thomas, Indiana University
Charles Brockhouse, Creighton University
Benjamin Evans, Yale University

Ecological/Population Genomics-Friday, June 9 am
Megan Fritz, University of Maryland
Alistair Miles, The Wellcome Trust Centre for Human Genetics

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JoAnna Chiu, UC-Davis

Vector Genomics- Saturday, June 10 am
Zach Adelman, Texas A&M University
Lyric Bartholomay, University of Wisconsin-Madison

Metagenomics- Saturday, June 10 am
Rita Rio, Western Virginia University
Richard Kuhn, Purdue University

Sensory Genomics- Saturday, June 10 pm
Zain Syed, University of Notre Dame
Anupama Dahanukar, UC-Riverside

Regards,
Mary Ann McDowell

(AGC Symposium Committee: Mary Ann McDowell, Molly Duman-Scheel, Michael Pfrender, Scott Emrich, Sue Brown, Kristin Michel, Hugh Robertson)

From:	Brockhouse, Charles L <CharlesBrockhouse@creighton.edu>
To:	Denis Tagu Mary Ann McDowell g.christophides grthomas@umail.iu.edu Brockhouse, Charles L b.evans@yale.edu mfritz13@umd.edu alistair.miles cherrys@mail.med.upenn.edu jcchiu@ucdavis.edu zachadel@tamu.edu lbartholomay@wisc.edu Rita.Rio@mail.wvu.edu kuhnr@purdue.edu anupama.dahanukar@ucr.edu
CC:	Katie (Merz) Cybulski Sarah Craig Ashley Scott Molly Scheel Kristin Michel Susan Brown Michael Pfrender semrich@nd.edu hughrobe@uiuc.edu
Date:	6/11/2017 5:46:49 PM
Subject:	Re: Arthropod Genomics Symposium Speaker Information

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C. Brockhouse, PhD
Associate Professor, Genetics
Biology Department
Creighton University

From: Denis Tagu < >
Date: Sunday, June 11, 2017 at 5:40 PM
To: Mary Ann McDowell <mmcdowe1@nd.edu >, " <
"grthomas@umail.iu.edu " <grthomas@umail.iu.edu >, "Brockhouse, Charles L" <CharlesBrockhouse@creighton.edu >, "b.evans@yale.edu " <b.evans@yale.edu >, "mfritz13@umd.edu " <mfritz13@umd.edu >, "
<alistair.miles@well.ox.ac.uk >, "cherrys@mail.med.upenn.edu " <cherrys@mail.med.upenn.edu >, "jcchiu@ucdavis.edu "
<jcchiu@ucdavis.edu >, "zachadel@tamu.edu " <zachadel@tamu.edu >, "lbartholomay@wisc.edu "
<lbartholomay@wisc.edu >, "Rita.Rio@mail.wvu.edu " <Rita.Rio@mail.wvu.edu >, "kuhnr@purdue.edu "
<kuhnr@purdue.edu >, "anupama.dahanukar@ucr.edu " <anupama.dahanukar@ucr.edu >
Cc: "Katie (Merz) Cybulski" <kmerz@nd.edu >, Sarah Craig <craig.20@nd.edu >, Ashley Scott <ascott12@nd.edu >, Molly Scheel <Molly.A.Scheel.2@nd.edu >, Kristin Michel <kmichel@k-state.edu >, Susan Brown <sjbrown@ksu.edu >, Michael Pfrender <Michael.Pfrender.1@nd.edu >, Scott Emrich <semrich@nd.edu >, "hughrobe@uiuc.edu " <hughrobe@uiuc.edu >

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Have a nice sunday!

Denis

denis.tagu@inra.fr

Denis Tagu INRA Rennes UMR 1349 IGEPP INRA Agrocampus Ouest Rennes - Universit Rennes 1 BP35327 35653 Le Rheu cedex France Tel: 33(0) 223 48 51 65 Tel: 33(0) 676 35 67 93 Fax: 33(0) 223 48 51 50 denis.tagu@inra.fr https://www6.rennes.inra.fr/igepp_eng/Personnel/T/Tagu-Denis https://www6.rennes.inra.fr/igepp_eng/ https://www.rennes.inra.fr/igepp

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: ; Denis Tagu; grthomas@umail.iu.edu ; CharlesBrockhouse@creighton.edu ; b.evans@yale.edu ; mfritz13@umd.edu ; alistair.miles@well.ox.ac.uk ; cherrys@mail.med.upenn.edu ; jcchiu@ucdavis.edu ; zachadel@tamu.edu ; lbartholomay@wisc.edu ; Rita.Rio@mail.wvu.edu ; kuhnr@purdue.edu ; anupama.dahanukar@ucr.edu
Cc : Katie (Merz) Cybulski; Sarah Craig; Ashley Scott; Molly Scheel; Kristin Michel; Susan Brown; Michael Pfrender; semrich@nd.edu ; hughrobe@uiuc.edu
Objet : Arthropod Genomics Symposium Speaker Information

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Regards,
Mary Ann McDowell

(AGC Symposium Committee: Mary Ann McDowell, Molly Duman-Scheel, Michael Pfrender, Scott Emrich, Sue Brown, Kristin Michel, Hugh Robertson)

From:	Denis Tagu <d
To:	Mary Ann McDowell grthomas@umail.iu.edu CharlesBrockhouse@creighton.edu b.evans@yale.edu mfritz13@umd.edu cherrys@mail.med.upenn.edu jcchiu@ucdavis.edu zachadel@tamu.edu lbartholomay@wisc.edu Rita.Rio@mail.wvu.edu kuhnr@purdue.edu anupama.dahanukar@ucr.edu
CC:	Katie (Merz) Cybulski Sarah Craig Ashley Scott Molly Scheel Kristin Michel Susan Brown Michael Pfrender semrich@nd.edu hughrobe@uiuc.edu
Date:	6/11/2017 4:40:50 PM
Subject:	RE: Arthropod Genomics Symposium Speaker Information

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Denis

ATTENTION; new email address: denis.tagu@inra.fr

Denis Tagu INRA Rennes UMR 1349 IGEPP INRA Agrocampus Ouest Rennes - Universit Rennes 1 B P35327 35653 Le Rheu cedex France Tel: 33(0) 223 48 51 65 Tel: 33(0) 676 35 67 93 Fax: 33(0) 223 48 51 50 denis.tagu@inra.fr https://www6.rennes.inra.fr/igepp_eng/Personnel/T/Tagu-Denis https://www6.rennes.inra.fr/igepp_eng/ https://www.rennes.inra.fr/igepp

De : Mary Ann McDowell <mmcdowe1@nd.edu>
Envoy : vendredi 10 f vrier 2017 03:15
: g.christophides@imperial.ac.uk; Denis Tagu; grthomas@umail.iu.edu; CharlesBrockhouse@creighton.edu; b.evans@yale.edu; mfritz13@umd.edu; alistair.miles@well.ox.ac.uk; cherrys@mail.med.upenn.edu; jcchiu@ucdavis.edu; zachadel@tamu.edu; lbartholomay@wisc.edu; Rita.Rio@mail.wvu.edu; kuhnr@purdue.edu; anupama.dahanukar@ucr.edu
Cc : Katie (Merz) Cybulski; Sarah Craig; Ashley Scott; Molly Scheel; Kristin Michel; Susan Brown; Michael Pfrender; semrich@nd.edu; hughrobe@uiuc.edu

Objet : Arthropod Genomics Symposium Speaker Information

Dear Arthropod Genomics Speakers,

On behalf of the organizing committee, I thank you for agreeing to speak at the 10th Arthropod Genomics Symposium (AGS) hosted by the Eck Institute for Global Health at the University of Notre Dame (UND). The symposium will begin Thursday evening, June 8 and will conclude with a banquet on Saturday evening, June 10, 2017. The meeting in 2017 will be preceded by an Arthropod Database Workshop starting June 7th.

We will provide your transportation expenses, registration fee and housing costs at UND for three nights. **You will be receiving an email from Ms. Katie Cybulski (**kmerz@nd.edu **) from our Institute to arrange your travel.** We have reserved a block of rooms on campus near the conference center, but encourage you to take a walk down memory lane and choose the dormitory option. The University of Notre Dame has a strong residency hall tradition. The rooms are air-conditioned, located near the conference center, and linens are provided; however, lavatories and showers are shared with separate men s and women s facilities on each floor.

We have an exciting agenda planned this year (https://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/), with sessions ranging from Emerging Genomes to Metagenomics (see list of speakers below). **Please send me a title for your presentation as soon as possible so that we can begin advertising your specific session.**

In addition to Katie Cybulski, you may receive additional correspondence from Conference Center contact, Lauri Roberts, or Ashley Scott. Feel free to contact me at any time should you have questions. I look forward to our interactions at Arthropod Genomics 2017!

Keynote Speaker-Thursday, June 8 pm
George Christophides, Imperial College, London

I5K Session-Friday, June 8 am
Denis Tagu, Universite de Rennes
Gregg Thomas, Indiana University
Charles Brockhouse, Creighton University
Benjamin Evans, Yale University

Ecological/Population Genomics-Friday, June 9 am
Megan Fritz, University of Maryland
Alistair Miles, The Wellcome Trust Centre for Human Genetics

Functional Genomics-Friday, June 9 pm
Sara Cherry, University of Pennsylania
JoAnna Chiu, UC-Davis

Vector Genomics- Saturday, June 10 am
Zach Adelman, Texas A&M University
Lyric Bartholomay, University of Wisconsin-Madison

Metagenomics- Saturday, June 10 am
Rita Rio, Western Virginia University
Richard Kuhn, Purdue University

Sensory Genomics- Saturday, June 10 pm

Zain Syed, University of Notre Dame
Anupama Dahanukar, UC-Riverside

Regards,
Mary Ann McDowell

(AGC Symposium Committee: Mary Ann McDowell, Molly Duman-Scheel, Michael Pfrender, Scott Emrich, Sue Brown, Kristin Michel, Hugh Robertson)

From:	O'Reilly, Marina (NIH/OD) [E] <OReillyM@OD.NIH.GOV>
To:	Ross, Lainie [PED] Michael B. Atkins 'Donahue, Kevin' 'Kaufman, Howard' 'Ross, Lainie' 'Lee, Dean' 'Albritton, Lorraine M' 'Zachary Adelman' 'Kathleen Boris-Lawrie'
CC:	'barne063@umn.edu' 'blickis@cinj.rutgers.edu' 'jht35@georgetown.edu' Beckham, Shayla (NIH/OD) [E] Tucker, Jessica (NIH/OD) [E]
Date:	6/9/2017 10:56:36 AM
Subject:	RE: OSP NIH Guidelines workshop teleconference

Yes. Thank you!

From: Ross, Lainie [PED] [mailto:lross@peds.bsd.uchicago.edu]
Sent: Friday, June 09, 2017 11:53 AM
To: O'Reilly, Marina (NIH/OD) [E] <OReillyM@OD.NIH.GOV>; Michael B. Atkins <mba41@georgetown.edu>; 'Donahue, Kevin' >; 'Kaufman, Howard' <Howard.kaufman@rutgers.edu>; 'Ross, Lainie' <lross@uchicago.edu>; 'Lee, Dean' ; 'Albritton, Lorraine M' <lalbritt@uthsc.edu>; 'Zachary Adelman' <zachadel@tamu.edu>; 'Kathleen Boris-Lawrie' <kbl@umn.edu>
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Assuming this is still all east standard time

Lainie Friedman Ross, MD, PhD
Carolyn and Matthew Bucksbaum Professor of Clinical Ethics
Professor, Departments of Pediatrics, Medicine, and Surgery
Associate Director, MacLean Center for Clinical Medical Ethics
University of Chicago

Phone: (773) 702-6323
Fax: (773) 834-5964
email: Lross@uchicago.edu
Office: C-128 (main corridor, old Children's (Wyler) Hospital)

mailing address:
Department of Pediatrics
University of Chicago
5841 S. Maryland Ave, MC 6082
room C-128
Chicago IL 60637

"A doctor has opportunities for studying human nature which are given to no one else, wherefore a philosopher ought to begin his life as a doctor, and a doctor should end his life by becoming a philosopher." --Ancient Greek saying.

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Sent: Friday, June 09, 2017 10:49 AM

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This version of Total Outlook Converter Pro is not registered.

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CC:	'barne063@umn.edu' 'blickis@cinj.rutgers.edu' 'jht35@georgetown.edu' Beckham, Shayla (NIH/OD) [E] Tucker, Jessica (NIH/OD) [E]
Date:	6/9/2017 10:53:12 AM
Subject:	RE: OSP NIH Guidelines workshop teleconference

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CC:	'barne063@umn.edu' 'blickis@cinj.rutgers.edu' 'jht35@georgetown.edu' Beckham, Shayla (NIH/OD) [E] Tucker, Jessica (NIH/OD) [E]
Date:	6/9/2017 10:48:42 AM
Subject:	OSP NIH Guidelines workshop teleconference
Attachments:	NIH OSP NIH Guidelines Workshop_Public_060717_for posting.docx

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NIH Guidelines: Honoring the Past, Charting the Future

Bethesda North Marriott Hotel & Conference Center
5701 Marinelli Rd
Rockville, MD 20852

DAY 1 - Tuesday 18th July 2017

8:00 am – 8:30 am	**Registration**
8:30 am – 9:00 am	**Welcoming Remarks** ***Carrie D. Wolinetz, Ph.D.*** **Associate Director for Science Policy, NIH**
9:00 am – 9:15 am	**Introduction** ***Francis S. Collins, M.D., Ph.D.*** **Director, NIH**
9:15 am – 10:00 am	**SESSION I – Keynote Presentation** *The keynote will provide insights into the historical significance of Asilomar, the 40 year history of the NIH Guidelines for Research Involving Recombinant or Synthetic Nucleic Acid Molecules, and the Recombinant DNA Advisory Committee (RAC); and explore the future of biosafety oversight in the life sciences in light of the emergence of new biotechnologies.* ***David Baltimore, Ph.D.*** **President Emeritus; Robert Andrews Millikan Professor of Biology, California Institute of Technology**
10:00 am – 10:15 am	**BREAK**
10:15 am – 11:30 am	**SESSION II – The Current NIH Framework for the Oversight of Research with Recombinant or Synthetic Nucleic Acid Molecules**

This session will explore the current framework established by the NIH Guidelines, including the roles of Institutional Biosafety Committees (IBCs) and the RAC.

Panelists:

Jessica Tucker, Ph.D.
Director, Biosafety, Biosecurity and Emerging Biotechnology Policy Division, Office of Science Policy, NIH

Stephen J. Libby, Ph.D.
IBC Chair, Research Associate Professor, University of Washington

Hans-Peter Kiem, M.D., Ph.D.
Director, Cell and Gene Therapy Program, Fred Hutchinson Cancer Research Center

11:30 am – 12:45 pm **Lunch Break**

12:45 pm – 2:15 pm **SESSION III – Role of the *NIH Guidelines*: Intersection with Other Biosafety Regulations and Guidance**

The panel will examine the essential elements of the system of oversight established in the NIH Guidelines, and how the NIH Guidelines intersect or complement other biosafety guidance.

Panelists:

Federal Representatives

2:15 pm – 2:30 pm **BREAK**

2:30 pm – 4:15 pm **SESSION IV – Emerging Biotechnologies: Issues Raised for the Current System of Biosafety Oversight**

If Asilomar were today, what emerging biotechnologies would be captured in the biosafety oversight system? An overview of various emerging biotechnologies will be presented, along with a discussion of whether there are distinct biosafety issues posed by these technologies. Can these potential challenges be managed by the current framework for risk assessment and biosafety oversight?

Panelists:

Feng Zhang, Ph.D.
Professor in Neuroscience, MIT

Drew Endy, Ph.D.
President, BioBricks Foundation
Associate Professor, Bioengineering, Stanford University

Zach Adelman, Ph.D.
Associate Professor, Department of Entomology, Texas A&M University

Kenneth Oye, Ph.D.
Professor of Political Science, and Data Systems and Society, MIT

4:15 pm – 4:30 pm **Wrap-up of Day 1**

4:30 pm **ADJOURN**

DAY 2 – Wednesday 19th July 2017

8:00 am – 8:15 am **Introduction**

8:15 am – 10:15 am **SESSION V – Roundtable Discussion - Future Role of the RAC**

This roundtable will include a discussion of the benefits of having a public forum for biosafety discussions, and the types of engagement that would best meet the needs of the scientific community and the public. Questions explored will include, how can the RAC be best used to help ensure the safe advancement of life sciences research? Are there emerging biotechnologies that would benefit from the public engagement provided by RAC discussions? What role should the RAC have in providing biosafety guidance?

Moderator:

Howard Federoff, M.D., Ph.D.
Vice Chancellor for Health Affairs and CEO UC Irvine Health System, University of California, Irvine

Lead Discussants:

Marie-Louise Hammarskjöld, M.D., Ph.D.
Professor, Microbiology, Immunology, and Cancer Biology, University of Virginia

Margaret Foster Riley, J.D.
Professor of Law, University of Virginia

Joseph Kanabrocki, Ph.D, CBSP
Associate Vice President for Research Safety, University of Chicago

Nancy King, J.D.
Professor, Social Sciences and Health Policy, Wake Forest School of Medicine

10:15 am – 10:30 am **BREAK**

10:30 am – 12:30 pm **SESSION VI – Roundtable Discussion - Future Face of Biosafety Oversight**

This roundtable will include a discussion of what the ideal Federal and local oversight systems for helping to ensure the safe conduct of life sciences research might look like. Questions explored will include, what should be the scope of the biosafety oversight system? What are the pros and cons of a biosafety oversight framework that focuses on research with recombinant or synthetic nucleic acid molecules? Are there additional types of research that pose biosafety concerns that warrant oversight, which are not captured in the current system; are there types of research that are part of the current system that no longer require such oversight? How can we help ensure adequate biosafety oversight without unduly burdening the research enterprise?

Moderator:

Joseph Kanabrocki, Ph.D, CBSP
Associate Vice President for Research Safety, University of Chicago

Lead Discussants:

Elizabeth Gilman Duane, M.S., RBP, CBSP
Director, Environment, Health, Safety and Sustainability
Amgen Inc.

Lydia Sohn, Ph.D
IBC Chair, Professor of Mechanical Engineering, University of California, Berkeley

Ara Tahmassian, Ph.D.
Chief Research Compliance Officer, Harvard University

Maureen O'Leary Ph.D., CBSP
President, American Biological Safety Association (ABSA) International

12:30 pm – 12:45 pm **SESSION VII - Open Forum for Stakeholder Input**

12:45 pm – 1:00 pm **Closing Remarks**

Carrie D. Wolinetz, Ph.D.
Associate Director for Science Policy, NIH

1:00 pm **ADJOURN**

From:	O'Reilly, Marina (NIH/OD) [E] <OReillyM@OD.NIH.GOV>
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CC:	barne063@umn.edu blickis@cinj.rutgers.edu jht35@georgetown.edu Beckham, Shayla (NIH/OD) [E] Tucker, Jessica (NIH/OD) [E]
Date:	6/7/2017 3:31:26 PM
Subject:	RE: Update on NIH Guidelines workshop and teleconference scheduling

Yes, EDT. I'm sorry we didn't note that.

Thanks,
Marina

From: Ross, Lainie [PED] [mailto:lross@peds.bsd.uchicago.edu]
Sent: Wednesday, June 07, 2017 4:29 PM
To: O'Reilly, Marina (NIH/OD) [E] <OReillyM@OD.NIH.GOV>; Michael B. Atkins <mba41@georgetown.edu>; 'Donahue, Kevin' ; 'Kaufman, Howard' <Howard.kaufman@rutgers.edu>; 'Ross, Lainie' <lross@uchicago.edu>; 'Lee, Dean' ; 'Albritton, Lorraine M' <lalbritt@uthsc.edu>; 'Zachary Adelman' <zachadel@tamu.edu>; 'Kathleen Boris-Lawrie' <kbl@umn.edu>
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Subject: RE: Update on NIH Guidelines workshop and teleconference scheduling

Are the times east coast times? I am assuming so. lsfr

Lainie Friedman Ross, MD, PhD
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Professor, Departments of Pediatrics, Medicine, and Surgery
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(301) 496-9838 (OSP office)
oreillym@od.nih.gov

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Subscribe to "Under the Poliscope " NIH OSP's new blog!

From:	O'Reilly, Marina (NIH/OD) [E] <OReillyM@OD.NIH.GOV>
To:	Michael B. Atkins 'Donahue, Kevin' 'Kaufman, Howard' 'Ross, Lainie' 'Lee, Dean' 'Albritton, Lorraine M' 'Zachary Adelman' 'Kathleen Boris-Lawrie'
CC:	barne063@umn.edu blickis@cinj.rutgers.edu jht35@georgetown.edu Beckham, Shayla (NIH/OD) [E] Tucker, Jessica (NIH/OD) [E]
Date:	6/7/2017 3:26:44 PM
Subject:	Update on NIH Guidelines workshop and teleconference scheduling
Attachments:	NIH OSP NIH Guidelines Workshop_Public_060717_for posting.docx

Dear Drs. Atkins, Adelman, Albritton, Boris-Lawrie, Donahue, Kaufman, Lee, and Ross,

I wanted to provide you with an update about the workshop *NIH Guidelines*: Honoring the Past, Charting the Future. Please find attached a recent draft agenda. Interest in the workshop has been so great that registrations exceeded the capacity of our venue, so a larger venue has been arranged. The workshop will be held at the Bethesda North Marriott hotel, which is also where you will be staying.

Session V of the workshop will focus on the future role of the RAC. We would appreciate your participation in that roundtable discussion. In order to provide you with some more information about the goals of that discussion, we'd like to set up a teleconference to discuss this with you. Shayla set up this doodle poll. Would you please fill out the poll and we'll schedule the teleconference for whatever time is most convenient for everyone?

http://doodle.com/poll/uv4nvu5rghzw9a83

Please let me know if you have any questions. We're looking forward to speaking with you soon and seeing you at the workshop.

Thank you,
Marina

Marina O'Reilly, Ph.D.
Director, Recombinant DNA Activities Program
Division of Biosafety, Biosecurity, and Emerging Biotechnologies Policy
Office of Science Policy
Office of the Director
National Institutes of Health
6705 Rockledge Dr., Suite 750
Bethesda, MD 20892
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NIH Guidelines: Honoring the Past, Charting the Future

Bethesda North Marriott Hotel & Conference Center
5701 Marinelli Rd
Rockville, MD 20852

DAY 1 - Tuesday 18th July 2017

8:00 am – 8:30 am	**Registration**
8:30 am – 9:00 am	**Welcoming Remarks** ***Carrie D. Wolinetz, Ph.D.*** **Associate Director for Science Policy, NIH**
9:00 am – 9:15 am	**Introduction** ***Francis S. Collins, M.D., Ph.D.*** **Director, NIH**
9:15 am – 10:00 am	**SESSION I – Keynote Presentation** *The keynote will provide insights into the historical significance of Asilomar, the 40 year history of the NIH Guidelines for Research Involving Recombinant or Synthetic Nucleic Acid Molecules, and the Recombinant DNA Advisory Committee (RAC); and explore the future of biosafety oversight in the life sciences in light of the emergence of new biotechnologies.* ***David Baltimore, Ph.D.*** **President Emeritus; Robert Andrews Millikan Professor of Biology, California Institute of Technology**
10:00 am – 10:15 am	**BREAK**
10:15 am – 11:30 am	**SESSION II – The Current NIH Framework for the Oversight of Research with Recombinant or Synthetic Nucleic Acid Molecules**

This session will explore the current framework established by the NIH Guidelines, including the roles of Institutional Biosafety Committees (IBCs) and the RAC.

Panelists:

Jessica Tucker, Ph.D.
Director, Biosafety, Biosecurity and Emerging Biotechnology Policy Division, Office of Science Policy, NIH

Stephen J. Libby, Ph.D.
IBC Chair, Research Associate Professor, University of Washington

Hans-Peter Kiem, M.D., Ph.D.
Director, Cell and Gene Therapy Program, Fred Hutchinson Cancer Research Center

11:30 am – 12:45 pm **Lunch Break**

12:45 pm – 2:15 pm **SESSION III – Role of the *NIH Guidelines*: Intersection with Other Biosafety Regulations and Guidance**

The panel will examine the essential elements of the system of oversight established in the NIH Guidelines, and how the NIH Guidelines intersect or complement other biosafety guidance.

Panelists:

Federal Representatives

2:15 pm – 2:30 pm **BREAK**

2:30 pm – 4:15 pm **SESSION IV – Emerging Biotechnologies: Issues Raised for the Current System of Biosafety Oversight**

If Asilomar were today, what emerging biotechnologies would be captured in the biosafety oversight system? An overview of various emerging biotechnologies will be presented, along with a discussion of whether there are distinct biosafety issues posed by these technologies. Can these potential challenges be managed by the current framework for risk assessment and biosafety oversight?

Panelists:

Feng Zhang, Ph.D.
Professor in Neuroscience, MIT

Drew Endy, Ph.D.
President, BioBricks Foundation
Associate Professor, Bioengineering, Stanford University

Zach Adelman, Ph.D.
Associate Professor, Department of Entomology, Texas A&M University

Kenneth Oye, Ph.D.
Professor of Political Science, and Data Systems and Society, MIT

4:15 pm – 4:30 pm **Wrap-up of Day 1**

4:30 pm **ADJOURN**

DAY 2 – Wednesday 19th July 2017

8:00 am – 8:15 am **Introduction**

8:15 am – 10:15 am **SESSION V – Roundtable Discussion - Future Role of the RAC**

This roundtable will include a discussion of the benefits of having a public forum for biosafety discussions, and the types of engagement that would best meet the needs of the scientific community and the public. Questions explored will include, how can the RAC be best used to help ensure the safe advancement of life sciences research? Are there emerging biotechnologies that would benefit from the public engagement provided by RAC discussions? What role should the RAC have in providing biosafety guidance?

Moderator:

Howard Federoff, M.D., Ph.D.
Vice Chancellor for Health Affairs and CEO UC Irvine Health System, University of California, Irvine

Lead Discussants:

Marie-Louise Hammarskjöld, M.D., Ph.D.
Professor, Microbiology, Immunology, and Cancer Biology, University of Virginia

Margaret Foster Riley, J.D.
Professor of Law, University of Virginia

Joseph Kanabrocki, Ph.D, CBSP
Associate Vice President for Research Safety, University of Chicago

Nancy King, J.D.
Professor, Social Sciences and Health Policy, Wake Forest School of Medicine

10:15 am – 10:30 am **BREAK**

10:30 am – 12:30 pm **SESSION VI – Roundtable Discussion - Future Face of Biosafety Oversight**

This roundtable will include a discussion of what the ideal Federal and local oversight systems for helping to ensure the safe conduct of life sciences research might look like. Questions explored will include, what should be the scope of the biosafety oversight system? What are the pros and cons of a biosafety oversight framework that focuses on research with recombinant or synthetic nucleic acid molecules? Are there additional types of research that pose biosafety concerns that warrant oversight, which are not captured in the current system; are there types of research that are part of the current system that no longer require such oversight? How can we help ensure adequate biosafety oversight without unduly burdening the research enterprise?

Moderator:

Joseph Kanabrocki, Ph.D, CBSP
Associate Vice President for Research Safety, University of Chicago

Lead Discussants:

Elizabeth Gilman Duane, M.S., RBP, CBSP
Director, Environment, Health, Safety and Sustainability
Amgen Inc.

Lydia Sohn, Ph.D
IBC Chair, Professor of Mechanical Engineering, University of California, Berkeley

Ara Tahmassian, Ph.D.
Chief Research Compliance Officer, Harvard University

Maureen O'Leary Ph.D., CBSP
President, American Biological Safety Association (ABSA) International

12:30 pm – 12:45 pm **SESSION VII - Open Forum for Stakeholder Input**

12:45 pm – 1:00 pm **Closing Remarks**

Carrie D. Wolinetz, Ph.D.
Associate Director for Science Policy, NIH

1:00 pm **ADJOURN**

From:	Ross, Lainie [PED] <lross@peds.bsd.uchicago.edu>
To:	'O'Reilly, Marina (NIH/OD) [E]' Michael B. Atkins 'Donahue, Kevin' 'Kaufman, Howard' 'Ross, Lainie' 'Lee, Dean' 'Albritton, Lorraine M' 'Zachary Adelman' 'Kathleen Boris-Lawrie'
CC:	barne063@umn.edu blickis@cinj.rutgers.edu jht35@georgetown.edu Beckham, Shayla (NIH/OD) [E] Tucker, Jessica (NIH/OD) [E]
Date:	6/7/2017 3:28:45 PM
Subject:	RE: Update on NIH Guidelines workshop and teleconference scheduling

Are the times east coast times? I am assuming so. lsfr

Lainie Friedman Ross, MD, PhD
Carolyn and Matthew Bucksbaum Professor of Clinical Ethics
Professor, Departments of Pediatrics, Medicine, and Surgery
Associate Director, MacLean Center for Clinical Medical Ethics
University of Chicago

Phone: (773) 702-6323
Fax: (773) 834-5964
email: Lross@uchicago.edu
Office: C-128 (main corridor, old Children's (Wyler) Hospital)

mailing address:
Department of Pediatrics
University of Chicago
5841 S. Maryland Ave, MC 6082
room C-128
Chicago IL 60637

"A doctor has opportunities for studying human nature which are given to no one else, wherefore a philosopher ought to begin his life as a doctor, and a doctor should end his life by becoming a philosopher." --Ancient Greek saying.

From: O'Reilly, Marina (NIH/OD) [E] [mailto:OReillyM@OD.NIH.GOV]
Sent: Wednesday, June 07, 2017 3:27 PM
To: Michael B. Atkins; 'Donahue, Kevin'; 'Kaufman, Howard'; 'Ross, Lainie'; 'Lee, Dean'; 'Albritton, Lorraine M'; 'Zachary Adelman'; 'Kathleen Boris-Lawrie'
Cc: barne063@umn.edu; blickis@cinj.rutgers.edu; jht35@georgetown.edu; Beckham, Shayla (NIH/OD) [E]; Tucker, Jessica (NIH/OD) [E]
Subject: Update on NIH Guidelines workshop and teleconference scheduling

Dear Drs. Atkins, Adelman, Albritton, Boris-Lawrie, Donahue, Kaufman, Lee, and Ross,

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Session V of the workshop will focus on the future role of the RAC. We would appreciate your participation in that roundtable discussion. In order to provide you with some more information about the goals of that discussion, we'd like to set up a teleconference to discuss this with you. Shayla set up this doodle poll. Would you please fill out the poll and we'll schedule the teleconference for whatever time is most convenient for everyone?

Please let me know if you have any questions. We're looking forward to speaking with you soon and seeing you at the workshop.

Thank you,
Marina

Marina O'Reilly, Ph.D.
Director, Recombinant DNA Activities Program
Division of Biosafety, Biosecurity, and Emerging Biotechnologies Policy
Office of Science Policy
Office of the Director
National Institutes of Health
6705 Rockledge Dr., Suite 750
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From:	Janet Thavarajah <j
To:	zachadel@tamu.edu
Date:	6/7/2017 11:51:43 AM
Subject:	RE: Invitation to record a lecture for an online series on 'Gene Drives and Active Genetics' edited by Prof. Ethan Bier
Attachments:	Gene drives and active genetics Briefing Notes June 2017.pdf

Dear Prof. Adelman,

Please find attached the briefing notes mentioned below for the series which includes information on the series objectives, target audience and details of the current and proposed talks along with current and suggested speakers. Apologies for not attaching it earlier.

Thank you and I look forward to hearing from you.

Kind Regards,

Janet

Janet Thavarajah, BSc, MSc, BDS.
Senior Producer
Henry Stewart Talks
Russell House, 28-30 Little Russell Street
London, WC1A 2HN
Tel: +44 (0)207 092 3468 (direct)
Fax: +44 (0)207 404 2081
Email: j
Website: www.hstalks.com
Working Days: Tuesday, Wednesday, Thursday, Friday

From: Janet Thavarajah [mailto]
Sent: 07 June 2017 17:44
To: 'zachadel@tamu.edu' <zachadel@tamu.edu>
Subject: Invitation to record a lecture for an online series on 'Gene Drives and Active Genetics' edited by Prof. Ethan Bier

Dear Prof Adelman,

I am a Producer for Henry Stewart Talks, a leading international provider of online seminar-style presentations in the biomedical and life sciences. We are assembling a library of talks available online for research scientists, postgraduate students and senior undergraduates and I am contacting you to see if you might be interested in preparing a talk for our series titled "**Gene Drives and Active Genetics**". I would be delighted if you were able to join our faculty of speakers.

The series editor is **Prof. Ethan Bier, University of California, San Diego,** and attached is his series briefing note; this document includes information on the series objectives, target audience and details of the current and proposed talks along with current and suggested speakers. Part of Prof. Bier's role as editor is to highlight the key topics and the most prominent speakers in this field – and you have been identified as a leading expert in this area. We are therefore very keen for you to participate in the series, and in particular we hoped that you would be interested in presenting a talk titled "**Male determination factors in mosquitoes**".

The series will be comprised of approximately 18 talks presented by the world's leading experts. Each talk will be approximately 40 minutes and consist of slides with accompanying synchronised narration. Prof. Bier also previously served as an editor for a series on 'The Legacy of Drosophila Genetics' with great success. Extracts from these published talks can be viewed by clicking on the link below:

https://hstalks.com/playlist/283/the-legacy-of-drosophila-genetics/?biosci

The recording process is straightforward and presenters are sent a headset with a high-quality microphone for recording their presentations. We can record the narration via a Skype call; this is the simplest and quickest recording method as we will manage

the recording entirely from our end of the call so you won't need to install any recording software. Alternatively, we can provide software which allows you to record your narration on your own if you prefer. A technical support team is available to assist speakers in converting non-PowerPoint slides into PowerPoint and, where requested, to provide hints and tips to improve the quality of the finished presentations.

Our speakers will receive complimentary access to the series and royalties payments in remuneration for their contribution. We allocate a percentage of the revenue from our subscriptions to be divided between our speakers and editors as royalty payments; you'll receive a payment every year.

A breakdown of the next steps:

1. Confirm participation – I will send you a contract and support documents to create a presentation
2. Review and complete contract
3. Once you have completed the contract, I will dispatch headset
4. Give you ~2-3 months to work on the presentation. If you are ready before then, that's fine too.
5. Arrange a Skype session to record the audio.
6. Our technical team will work on syncing everything together, can take a few months
7. Send you the final version to review and amend before the release.
8. If you have any questions about the series, please do not hesitate to contact me. I look forward to hearing from you shortly.

Completed presentations are scheduled to be submitted by 29th September 2017, however if you are concerned about being too busy at present, our recording timelines can be flexible so please don't let this dissuade you as we always try to accommodate any schedule. I would be grateful if you could reply to this email to let me know if you would be interested in joining our speaking faculty on this timely new series and provide an approximate date by which you could complete the recording of your presentation.

Kind regards,

Janet

Janet Thavarajah, BSc, MSc, BDS.
Senior Producer
Henry Stewart Talks
Russell House, 28-30 Little Russell Street
London, WC1A 2HN
Tel: +44 (0)207 092 3468 (direct)
Fax: +44 (0)207 404 2081
Email:
Website: www.hstalks.com
Working Days: Tuesday, Wednesday, Thursday, Friday

From: Teresa Gold <t-gold@tamu.edu>
To: Aaron Tarone
Adrienne Brundage
Carla Smith
Cecilia Tamborindeguy
Craig Coates
David Ragsdale
Edward Vargo
Gabriel Hamer
Gregory Sword
Hojun Song
Jeffery Tomberlin
James Woolley
John Oswald
Juliana Rangel Posada
Bernal, Julio S
Kevin Myles
Keyan Zhu Salzman
Kevin Heinz
Michel Slotman
Micky Eubanks (m-eubanks@tamu.edu)
Patricia Pietrantonio
Pete Teel
Raul Medina
Robert N. Coulson (r-coulson@tamu.edu)
Robert Puckett
Johnston J Spencer
Spencer T Behmer (s-behmer@tamu.edu)
Zach Adelman
CC: David Ragsdale
Date: 6/2/2017 2:52:04 PM
Subject: FW: Spousal Hire Assistance - Dr. Perkin
Attachments: LOI_Lindsey_Perkin.pdf
L_Perkin_CV2017.pdf

Forward on behalf of Dr. Ragsdale
****

From: David Ragsdale
Sent: Friday, June 2, 2017 2:33 PM
Subject: FW: Spousal Hire Assistance - Dr. Perkin
Importance: High

All ENTO faculty:

The Department of Wildlife and Fisheries Science is making an offer to a faculty member who has a trailing spouse who is currently doing entomological research. See the LOI.pdf for specifics. This letter of interest states that her research experience includes utilization of insect model systems to answer molecular based questions, such as insect adaptation to climate, host-parasite interactions, pesticide resistance, and insect digestion physiology. My current position with the USDA, ARS in Manhattan, KS aims to find novel, molecular-based pest control strategies that can be integrated into pest management using the model organism and stored product pest, *Tribolium castaneum*….."

Please take a look at Dr. Perkin's CV (attached) and let me know if you have an interest in interviewing her for a position in your lab.

As an aside, I don't see a good fit for a faculty hire as part of a partner placement program in the department. I believe the best course of action is for her to try to fit into one of your labs (grant funded) positions. Non-faculty positions unfortunately do not fall under the DOF Partner Placement Program, so there isn't any institutional support for this individual that I'm aware of. There could be some modest funding available from WFSC and or the College, but I'd not count on any financial support.

David

David W. Ragsdale
Professor and Head
Department of Entomology
Texas A&M University

Phone: 979-845-2510

From: Masser, Michael P
Sent: Monday, May 15, 2017 9:10 AM
To: David Ragsdale
Cc: Miles, Dawn L
Subject: FW: Spousal Hire Assistance - Dr. Perkin
Importance: High

FYI – Thanks for the consideration.

Michael P. Masser
Professor and Head
Wildlife and Fisheries Sciences
Texas A&M University
210 Nagle Hall
2258 TAMU
College Station, TX 77843-2258
mmasser@tamu.edu
http:wfsc.tamu.edu
979-845-6295
Fax – 979-845-3786

Lindsey C. Perkin, Ph.D.
USDA, Agricultural Research Service
1515 College Ave, Manhattan, KS 66502

Dr. Michael Masser
Professor & Department Head
Department of Wildlife and Fisheries Sciences
Texas A&M University

May 3, 2017

Dear Dr. Masser,

I'm writing regarding spousal accommodation opportunities at Texas A&M University (TAMU) in concordance with the recent hire of my husband, , in the Department of Wildlife and Fisheries Sciences. I am a broadly trained molecular biologist with interest in applying molecular biology, genomics, and genetic techniques to study the underlying genetic architecture of complex phenotypes, with emphasis in pest insects. Thus, I feel I fit well into the College of Agriculture and Life Sciences, in particular the Department of Entomology. My career goals and preferences align best with research-based positions, such as research associate, research faculty, or assistant professor. I also have experience in the classroom and would be open to incorporating teaching into my duties at TAMU.

My research experience includes utilization of insect model systems to answer molecular-based questions, such as insect adaptation to climate, host-parasite interactions, pesticide resistance, and insect digestion physiology. My current position with the USDA, ARS in Manhattan, KS aims to find novel, molecular-based pest control strategies that can be integrated into pest management using the model organism and stored product pest, *Tribolium castaneum* (red flour beetle). I am also currently preparing a collaborative grant proposal to explore the genetics of pesticide resistance in stored product pests, *T. castaneum* and *Rhyzopertha dominica* (lesser grain borer). Given the opportunity to continue this work in an academic or government setting in College Station, I can make significant contributions to molecular-based pest control strategies. These contributions would require minimal additional investment from TAMU given that much of the equipment for this research is available onsite and rearing and maintaining stored product insects requires modest investment.

Through collaboration with current faculty in the Department of Entomology and the local USDA, ARS Southern Plains Agricultural Research Center, I am interested in expanding my research program into other pest insects, specifically those that impact local agriculture and crops across the Midwest and Southern Plains.

Thank you for this opportunity and I hope to hear from you soon. If you have questions or would like copies of manuscripts, feel free to call (620.243.2633) or email me (lindsey.perkin@ars.usda.gov).

Sincerely,

Lindsey Perkin

Lindsey Perkin, PhD

Lindsey C. Perkin, Ph.D.

née Lindsey C. Fallis

United States Department of Agriculture, Agricultural Research Service
1515 College Ave, Manhattan, KS 66503
PHONE: (620) 243-2633
EMAIL: lindsey.perkin@ars.usda.gov
ARS WEBSITE: https://www.ars.usda.gov/plains-area/mhk/cgahr/spieru/people/lindsey-perkin/
LINKEDIN: https://www.linkedin.com/in/lindsey-perkin-408a0bb7
RESEARCHGATE: https://www.researchgate.net/profile/Lindsey_Perkin

EDUCATION

Ph.D. Biology. Kansas State University, Manhattan, Kansas 2012

M.S. Biology. Texas Christian University, Fort Worth, Texas 2007

B.S. Biology. Texas Christian University, Fort Worth, Texas 2005

RESEARCH EXPERIENCE

2013 - present **Postdoctoral Molecular Biologist**, United States Department of Agriculture, Agricultural Research Service, Mentor: Dr. Brenda Oppert
Projects: *Identification and analysis of cysteine peptidases in Tribolium castaneum, Venom transcriptome of the parasitoid wasp, Anisopteromalus calandrae, Phosphine resistance in T. castaneum and Rhyzopertha dominica*

2012 - 2013 **Postdoctoral Research Associate**, Emory University, Mentor: Dr. Todd Schlenke
Project: *The transcriptomic response of Drosophila melanogaster immune genes in response to parasitoid wasps*

2007 - 2012 **Graduate Research Assistant**, Kansas State University, Mentor: Dr. Theodore Morgan
Dissertation title: *The genetics of adaptive thermotolerance phenotypes in Drosophila melanogaster*

2004 - 2007 **Undergraduate and Graduate Research Assistant**, Texas Christian University, Mentor: Dr. Michael Misamore
Thesis title: *Identification of gamete surface proteins in Dreissena polymorpha*

PUBLICATIONS

Peer Reviewed

1. Oppert, B., L. Perkin, A.G. Martynov, E.N. Elpidina. **2017**. Cross-species comparison of the gut: Differential gene expression sheds light on biological differences in closely related tenetrionids. *In Press.* Journal of Insect Physiology.

2. Perkin, L.C., A.R. Gerken, B. Oppert. **2017**. RNA-Seq validation of RNAi identifies additional gene connectivity in *Tribolium castaneum* (Coleoptera: Tenebrionidae). *In Press.* Journal of Insect Science.

3. Perkin, L.C., Elpidina, E.N., Oppert, B. **2017**. RNAi induces a compensation response similar to dietary inhibitors in *Tribolium castaneum* larvae. Insect Molecular Biology. **26**:35-45.

4. Perkin, L. C., Adrianos, S. L., Oppert, B. **2016**. Gene disruption technologies have the potential to transform stored product insect pest control. Insects. **7(3)**:46.

5. Perkin, L.C. Elpidina, E.N. Oppert, B. **2016**. Expression patterns of cysteine peptidase genes across the *Tribolium castaneum* life cycle provide clues to enzyme function. PeerJ **4**:e1581.

6. Perkin, L.C. Friesen, K., Flinn, P.W., Oppert, B. **2015**. Venom gland components of the ectoparasitoid wasp, *Anisopteromalus calandrae*. Journal of Venom Research **6**:19-37.

7. Oppert, B., R.N.C. Guedes, M.J. Aikins, L. Perkin, Z. Chen, T.W. Phillips, K.Y. Zhu, G.P. Opit, K. Hoon, Y. Sun, G. Meredith, K. Bramlett, N.S. Hernandez, B. Sanderson, M.W. Taylor, D. Dhingra, B. Blakey, M. Lorenzen, F. Adedipe, and F. Arthur. **2015.** Genes related to mitochondrial functions are differentially expressed in phosphine-resistant and –susceptible *Tribolium castaneum.* BMC Genomics **16**:968.

8. Martynov, A.G., E.N. Elpindina, L.C. Perkin, B. Oppert. **2015**. Functional analysis of C1 family cysteine peptidases in the larval gut of *Tenebrio molitor* and *Tribolium castaneum*. BMC Genomics **16**:75.

9. Fallis, L.C., J.J. Fanara, T.J. Morgan. **2014**. Developmental thermal plasticity among *Drosophila melanogaster* populations. Journal of Evolutionary Biology. **27**:557-564.

10. Fallis, L.C., J.J. Fanara, T.J. Morgan. **2011**. Genetic variation in heat-stress resistance among South American *Drosophila* populations. Genetica. **139**:1331-1337.

11. Fallis, L.C., K.K. Stein, J.W. Lynn, M.J. Misamore. **2010**. Identification and role of carbohydrates on the surface of gametes in the zebra mussel, *Dreissena polymorpha*. Biology Bulletin. **218**:61-74.

In Preparation

12. Perkin, L.C., K.L. Schuler, K.J. Clowers, T.J. Morgan. The genetic basis of thermotolerance phenotypes in *Drosophila melanogaster. In preparation.*

13. Perkin, L.C., K. Hardwick, T.A. Schlenke. *Drosophila melanogaster* transcriptomic response to parasitoid wasp attack. *In preparation.*

14. Perkin, L.C., J.C. Cutler, T.A. Schlenke. Trypanosome effects on larval and adult *Drosophila melanogaster* fitness. *In preparation*.

15. Perkin, L.C. and B. Oppert. Genome-wide expression across *Tribolium castaneum* life stages: a search for pest management genes. Insect Molecular Biology. *In preparation.*

16. Scully, E., A.R. Gerken, L.C. Perkin, D. Scheff, S.L. Adrianos, R. Morrison, B. Oppert, F. Arthur, J. Campbell. Exploiting sensory genomics/systems for improved monitoring and control of stored product pests. Journal of Chemical Ecology. *In preparation.*

17. R. Morrison, J. Campbell, E. Scully, L.C. Perkin, B. Oppert, F. Arthur. Key factors affecting the success of agricultural pests: Case study with the model species, *Tribolium castaneum*. Biological Reviews. *In preparation.*

18. Arthropod Genome Research Team. Arthropod RNA interference and gene editing research at the USDA-ARS: Current developments and future prospects. Trends in Entomology. *In preparation.*

UNDERGRADUATE STUDENTS MENTORED

2015 - present **Steven Reyna**: Develop economical and eco-friendly control strategies for coleopteran storage pests based on oral RNA interference (RNAi). Currently working towards a PhD in the Department of Entomology at North Caroline State University.

2012 - 2013 **Josh Cutler**: Trypanosome effects on larval and adult *Drosophila melanogaster* fitness. Developed poster for an international conference and contributed to a manuscript for publication. Currently attending University of Miami Miller School of Medicine.

2009 - 2012 **Kendra Schuler**: The genetic basis of thermotolerance phenotypes in *Drosophila melanogaster.* Presented poster at regional conference and contributed to the developed of a manuscript for publication. Currently working as a genetic counselor.

TEACHING EXPERIENCE

2010 - 2011 National Science Foundation (NSF) Evidence-based Inquiry into the Distant, Remote or Past (EIDRoP) GK-12 Fellow, Resident Scientist/Teaching Assistant, JCHS USD 475

2007 - 2011 Graduate Teaching Assistant, Division of Biology, Kansas State University
Principles of Biology (Fall 2001, Fall 2008, Fall 2009, Spring 2010, Fall 2011)
Developmental Biology Lab (Spring 2008, Spring 2009)

2005 - 2007 Graduate Teaching Assistant, Dept. of Biology, Texas Christian University
Introduction to Biological Sciences Lab (Fall 2005, Spring 2006, Fall 2006, Spring 2007)

INVITED PRESENTATIONS

2017 Perkin, L. C. "*Uncovering adaptation: Employing next-generation sequencing to reveal the genetic architecture of adaptive traits"* Department of Biology, Middle Tennessee State University, Murfreesboro, TN.

2016 Perkin, L. C. "*Beetleomics: Targeting the Tribolium gut for control"* International Congress of Entomology, Early Career Scientists Symposium. Orlando, FL.

2016 Perkin, L. C. "*Molecular approaches to solving pest control problems*" Department of Entomology, Kansas State University, Manhattan, KS.

2016 Perkin, L.C. *"All the better to eat you with: Identifying and characterizing digestive cysteine peptidases in* Tribolium castaneum" Plant and Animal Genomics, San Diego, CA.

2015 Perkin, L. C. "*Using next-generation sequencing to decipher the molecular basis of organismal adaptation"* Department of Biology, Tennessee Technological University, Cookeville, TN.

2015 Perkin, L. C. and B. Oppert. "*Thinking outside the box: Creative approaches to solving problems with insect pests"* Bayer Inc., Raleigh, NC.

2015 Perkin, L.C. *"All the better to eat you with: Identifying and characterizing digestive cysteine peptidases in* Tribolium castaneum" Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN.

2015 Perkin, L. and B. Oppert. "*Using RNAi to understand cysteine peptidase expression in the* Tribolium castaneum *gut"* North Central Branch Meeting of Entomology Society of America, RNAi Symposium. Manhattan, KS.

2014 Fallis, L.C., B. Oppert, A.G. Martynov, E. N. Elpidina. "*Changes in Cysteine Peptidase Gene Expression throughout the Tribolium Castaneum Life Cycle"* Plant and Animal Genome, San Diego, CA.

2013 Fallis, L.C., K. L. Schuler, K.J. Clowers, T. J. Morgan. "*The genetic basis of thermotolerance phenotypes in* Drosophila melanogaster.*"* Agricultural Research Service, United States Department of Agriculture, Manhattan, KS.

2011 Fallis, L.C, K.L. Schuler, K.J. Clowers, T.J. Morgan. "*The genetic basis of thermotolerance phenotypes in* Drosophila melanogaster.*"* Emory University, Atlanta, GA.

2011 Fallis, L.C, K.L. Schuler, K.J. Clowers, T.J. Morgan. "*The genetic basis of thermotolerance phenotypes in* Drosophila melanogaster.*"* Texas Tech University, Lubbock, TX

MEETINGS ATTENDED AND CONTRIBUTED PAPERS

2017 Perkin, L.C., B. Oppert. **Poster**: *"Genome-wide expression across* Tribolium castaneum *life stages: a search for pest management genes"* Plant and Animal Genome, San Diego, CA.

2016 Perkin, L.C., K. Friesen, P. Flinn, B. Oppert. **Poster**:*"Eaten alive: lessons from the venom gland transcriptome of the wasp* Anisopteromalus calandrae" Advances in Genome Biology and Technology, Orlando, FL.

2015 Perkin, L.C., K. Friesen, P. Flinn, B. Oppert. **Poster**:*"Eaten alive: lessons from the venom gland transcriptome of the wasp* Anisopteromalus calandrae" Arthropod Genomics, Manhattan, KS.

2015 Perkin, L.C., K. Friesen, P. Flinn, B. Oppert. **Poster**:"*Identifying venom gland components of the ectoparasitoid wasp,* Anisopteromalus calandrae" Plant and Animal Genome, San, Diego, CA.

2014 Perkin (Fallis), L.C., A.G. Martynov, E.N. Elpidina B. Oppert. **Poster**:"*Expression patterns of cysteine peptidase genes across the* Tribolium castaneum *life cycle provide clues to function and evolutionary history"* XIVth International Symposium on Proteinases, Inhibitors, and Biological Control meeting, Portorož, Slovenia.

2014 Fallis, L.C., B. Oppert, A.G. Martynov, E.N. Elpidina. **Poster**:"*Expansion of Cysteine Peptidase Gene Family in Tribolium castaneum"* Advances in Genome Biology and Technology, Marco Island, FL.

2013 Fallis, L.C., J.C. Cutler, T.A. Schlenke. **Poster**:"*Trypanosome effects on larval and adult* Drosophila melanogaster *fitness."* The Fly Meeting, Washington D.C.

2011 Fallis, L.C, K.L. Schuler, K.J. Clowers, T.J. Morgan. **Poster**:"*The genetic basis of thermotolerance phenotypes in* Drosophila melanogaster.*"* Evolution, Norman, OK.

2011 Fallis, L.C., N. Busch, T.J. Morgan. **Oral**:"*Artificial selection in the classroom using* Drosophila melanogaster.*"* EIDRoP GK-12 NSF Capstone Meeting, Manhattan, KS.

2010 Fallis, L.C., Fanara, J.J., and Morgan, T. J. **Poster**:"*Phenotypic Variation in Thermotolerance Phenotypes in Natural Populations of* Drosophila melanogaster." Ecological Genomics Symposium, Kansas City, MO.

2010 Fallis, L.C., Clowers, K.J., Schuler, K.L., and Morgan, T.J. **Poster**:"*The genetics of thermotolerance in* Drosophila melanogaster." Ecological Genomics Symposium, Kansas City, MO.

2010 Fallis, L.C., Clowers, K.J., Schuler, K.L., and Morgan, T.J. **Poster**:"*The genetics of thermotolerance in* Drosophila melanogaster." Evolution, Portland, OR.

2009 Fallis, L.C. and Morgan, T.J. **Oral**:"*The genetics of thermotolerance in* Drosophila melanogaster." Kansas Entomology Society, Manhattan, KS.

2009 Fallis, L., J.J. Fanarra, T.J. Morgan. **Oral:***"Geographic variation in thermal plasticity among* Drosophila *populations."* Evolution, Moscow, ID.

2009 Fallis, L., T.J. Morgan. **Oral**:"*The genetic basis of thermotolerance phenotypes in Drosophila: A high resolution complementation mapping approach."* Midwest Ecology and Evolution Conference, Lincoln, NE.

2009 Fallis, L., T.J. Morgan. **Oral**:*'The genetic basis of thermotolerance phenotypes in Drosophila melanogaster."* Molecular Cellular and Developmental Biology Seminar, Manhattan, KS.

2009 Fallis, L., T.J. Morgan. **Oral**:"*The genetic basis of thermotolerance phenotypes in Drosophila: A high resolution complementation mapping approach."* Kansas State Graduate Research Forum, Manhattan, KS.

2008 Fallis, L.C., Fanara, J.J., and Morgan, T.J. **Poster**:"*Phenotypic Variation in Thermotolerance Phenotypes in Natural Populations of* Drosophila melanogaster." Ecological Genomics Symposium, Kansas City, MO.

2007 Fallis, L., K.M. Kendro-McAnlis, M. Misamore, and J.W. Lynn. **Poster**:"*Comparison of Carbohydrates on the surface of Gametes in the Zebra Mussel* Dreissena polymorpha*, the Oyster* Crassostrea virginica*, and the Blue Mussel* Mytilus edulis." Gordon Conference, Vermont.

2006 Fallis, L., K.M. Kendro-McAnlis, M. Misamore, and J.W. Lynn. **Poster**:"*Identification and Distribution of Carbohydrates on the surface of Gametes in the Zebra Mussel* Dreissena polymorpha *and the Oyster* Crassostrea virginica." American Society of Cell Biology Annual Meeting, San Diego, CA.

FELLOWSHIPS

2013 – present Molecular Biology Postdoctoral Associate, Agricultural Research Service, United States Department of Agriculture, Manhattan, KS

2012 - 2013 Postdoctoral Associate, Emory University, Atlanta, GA

2010 - 2011 NSF EIDRoP GK12 Fellowship, Kansas State University, $30,000

2009 US Department of Education GAANN Fellowship, Kansas State University, $28,900

2008, 2007 Ecological Genomics Fellowship, Kansas State University, $25,000

2008 Summer Institute in Statistical Genetics Fellowship, University of Washington, $1,000

RESEARCH GRANTS

2016 USDA AFRI Proposal submission, not funded, $497,382.25

2016 USDA ARS Areawide Pest Management Proposal submission, not funded, $1,900,000

2010 US Department of Education GAANN research support, Kansas State University, $4,000

2006 Adkins Research Grant, Texas Christian University, $3,500

TRAVEL GRANTS AND AWARDS

2016 Agriculture Research Service, USDA, Performance Award, $1,000

2015 Agriculture Research Service, USDA, Performance Award, $700

2014 Agriculture Research Service, USDA, Performance Award, $1,000

2014 CRDF Global Russia Travel Grants Competition, $10,000 - To attend XIVth International Symposium on Proteinases, Inhibitors, and Biological Control meeting, Portorož, Slovenia

2011 NSF EIDRoP GK12 Travel Grant, $500 - To Attend Ecological Genomics Symposium, Kansas City, MO

2011 NSF EIDRoP GK12 Travel Grant, $1,400 - To Attend: Evolution, Oklahoma City, OK

2011	NSF EIDRoP GK12 Travel Grant, $500 - To Attend: National Science Teacher Association (NSTA) Meeting, Kansas City, MO
2010	Outstanding Graduate Student Presentation, H. Henley Haymaker Award, Biology Department, Kansas State University, $500
2010	US Department of Education GAANN travel stipend, Kansas State University $1,000 - To Attend: Evolution, Portland, OR
2009	Biology Graduate Student Association Travel Grant, Kansas State University, $362 - To Attend: Midwest Ecology and Evolution Conference, Lincoln, NE
2009	Best PhD Poster Presentation, Presidential Award, Kansas Entomological Society, Kansas State University
2008	Ecological Genomics Travel Grant, Kansas State University, $475 - To Attend: Summer Institute in Statistical Genetics University of Washington
2006	Graduate Student Travel Grant, Texas Christian University, $400 - To Attend: American Society of Cell Biology Annual Meeting, San Diego, CA.

TRAINING/WORKSHOPS

2016	An Introduction to Evidence-Based Undergraduate STEM teaching, edX online course
2016	The Science and Politics of the GMO, edX online course
2015	Grantsmanship Fundamentals Class, Agricultural Research Service
2014	Ion Torrent Isothermal Amplification Kit Beta testing group, R&D for new technology
2013	Perl Computer Programming Course, Kansas State University
2011	NSF EIDRoP GK-12 Summer Institute, Kansas State University
2008	Summer Institute in Statistical Genetics University of Washington

OUTREACH AND SERVICE

2017	Co-organizer for the Plant and Animal Genomics, Arthropod Genomics workshop, San Diego, CA
2016 - 2019	Friends of Angelo & Jennette Volpe Library Board Member
2016	Participant in the KU SEARCH Symposium, Lawrence, KS via Skype
2012 - 2017	Journal referee for *Heredity*, *Applied Microbiology and Biotechnology, PLoS ONE, Journal* of *Stored Product Pest, Journal of Pest Science, Journal of Comparative Physiology-B, Entomologia Experimentalis et Applicata, Journal of Insect Science*
2010 - 2011	NSF EIDRoP GK-12 Program, Junction City High school, USD 475 Junction City, KS
2009 - 2010	Biology Graduate Student Association, Travel Grant Committee Member
2009 - 2010	Division of Biology Seminar Committee, Graduate Student Representative
2009	Biology Graduate Student Association, Food and Fun Committee Chair
2009	Genetics Symposium speaker, Chaparral High School, USD 361, Anthony, KS
2009	Biology field trip day, Westmorland Elementary School, USD 323, Wamego, KS
2008	Girls Researching Our World Program, Kansas State University, Manhattan, KS
2008, 2009	Biology Graduate Student Association, T-Shirt Committee Chair
2006	Science fair judge, Everman ISD, TX and Fort Worth ISD, TX

PROFESSIONAL MEMBERSHIPS

2015 - present	Association for Women in Science
2010 - 2012	National Science Teachers of America
2007 - 2013	Society for the Study of Evolution
2007 - 2012	Ecological Genomics Institute

From:	Lee, Andrew [USA]
Required:	Wegrzyn, Renee Parr, Lianne (contr-bto) Cheever, Anne (contr-bto) Escalon, Lynn L ERD-MS Christopher.M.Warner@usace.army.mil Kevin Myles (mylesk@tamu.edu) Pledger, David W Sakiko Okumoto Okumoto, Sakiko Zachary Adelman April.Godlewski.ctr@darpa.mil
Subject:	TAMU/DARPA Monthly Tech Update
Location:	Dial-in: 866-692-4541\; Participant:
When:	6/30/2017 10:30:00 AM - 11:30:00 AM
Attachments:	e1601910.full.pdf

TAMU/DARPA Tech Update

Please send update slides to DARPA at least 2 business days prior to the scheduled meeting.

Dial-in: 866-692-4541
Participant:

Additional topic to be discussed
Tribolium gene drive modeling paper Drury et al. “CRISPR/Cas9 gene drives in genetically variable and nonrandomly mating wild populations” from Science Advances 2017.

From: Pluhar, Lauren <LPluhar@cvm.tamu.edu>
To: Kim, Tae Kwon
charlotte_hieke@tamu.edu
JCAI@TAMU.EDU
Curry, Caitlin
Rodriguez, Jessica
Williams, Diarra
Lee, Annah
paulinor_42@tamu.edu
xiongcaixing@tamu.edu
holtjocelyn@tamu.edu
Liao, Yifei
Little, Sara V.
francisco.gomez@tamu.edu
Bredemeyer, Kevin
hle15@tamu.edu
j_wulff@tamu.edu
Lozano, Jessica
Gonzalez, Selma
Ott, Jeannine
Breaux, Bre
ljcohen@ucdavis.edu
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smtodd@vt.edu
matteil@email.chop.edu
kristen.kuhn@ars.usda.gov
catoe@nist.gov
Mulenga, Albert
giri.athrey@tamu.edu
Cai, James
Derr, James
Snowden, Karen
Suva, Larry
Esteve-Gassent, Maria
mmateos@tamu.edu
p-pietrantonio@tamu.edu
rfmedina@tamu.edu

	Reddy, Sanjay Lawhon, Sara wlr@tamu.edu Murphy, William zachadel@tamu.edu gasword@tamu.edu Keri.Norman@ARS.USDA.GOV Criscitiello, Michael charlie@ag.tamu.edu Joshua.Hill@ag.tamu.edu Noushin.Ghaffari@ag.tamu.edu shichen.wang@ag.tamu.edu Emma.Howard@ag.tamu.edu Yanni.Lun@ag.tamu.edu rmetz@tamu.edu Gail.Martin@ag.tamu.edu Matt.Loose@nottingham.ac.uk jtyson@msl.ubc.ca j.quick@bham.ac.uk mick.watson@roslin.ed.ac.uk n.j.loman@bham.ac.uk craig.nessler@ag.tamu.edu Bill.McCutchen@ag.tamu.edu David.Lunt@ag.tamu.edu Bob.Avant@ag.tamu.edu Burghardt, Robert Seabury, Christopher Gustafson, Ashley a-datta@tamu.edu dragsdale@tamu.edu dbaltensperger@tamu.edu Vemulapalli, Ramesh mmasser@tamu.edu Castiglioni, Evelyn caldwell@tamu.edu jktomberlin@tamu.edu ed.vargo@tamu.edu tamlucilia@tamu.edu mylesk@tamu.edu paul_straight@tamu.edu pteel@tamu.edu ghamer@tamu.edu Hamer, Sarah
CC:	Nancye Penn Voelker, Cynthia Kovar, Yvonne
Date:	6/1/2017 8:58:09 AM

Subject: RE: Invitation: PoreCampUSA Kick-Off Dinner

Just a friendly reminder to please RSVP for the Monday, June 5, 2017 PoreCamp USA Kick-Off Dinner, if you have not done so already. You may RSVP using the link in the invitation below.

Thank you,
Lauren

Lauren Pluhar | Administrative Coordinator
Office of Research & Graduate Studies | College of Veterinary Medicine & Biomedical Sciences | Texas A&M University
Veterinary and Biomedical Education Complex, VENI 317U | 4461 TAMU | College Station, TX 77843-4461
phone: 979.845.5092 | fax: 979.845.5088 | lpluhar@cvm.tamu.edu | http://vetmed.tamu.edu/research

From: CVM Office of Research & Graduate Studies [mailto:noreply@cvm.tamu.edu]
Sent: Friday, May 26, 2017 4:41 PM
To: Pluhar, Lauren <LPluhar@cvm.tamu.edu >
Subject: [Texas A&M CVM] Join us for the PoreCampUSA Kick-Off Dinner!

We are excited to welcome PoreCampUSA to Texas A&M University!

We are excited to welcome
PoreCampUSA to Texas A&M University!

The first training opportunity offered in the United States based
on the Oxford Nanopore Technology (ONT) MinION sequencing system

Please join us for the kick-off dinner
for this week-long training

Monday, June 5, 2017
5:00–6:00pm ~ Appetizers & Cash Bar
6:00pm ~ Dinner
6:30pm ~ Panel with Drs. Nick Loman, Josh Quick,
Matt Loose, John Tyson, & Mick Watson

3rd floor, Mark Francis Foyer
VENI Bldg. (#1812)

Texas A&M College of Veterinary Medicine & Biomedical Sciences
660 Raymond Stotzer Parkway | College Station, Texas

Parking details to follow

[Please RSVP by Thursday, June 1, 2017](#)

Office of Research & Graduate Studies
Texas A&M College of Veterinary Medicine & Biomedical Sciences
4461 TAMU | College Station, TX 77843-4461
979.845.5092 | vetmed.tamu.edu/research

From:	Lee, Andrew [
Required:	Wegrzyn, Renee Parr, Lianne (contr-bto) Cheever, Anne (contr-bto) Escalon, Lynn L ERD-MS Christopher.M.Warner@usace.army.mil Kevin Myles (mylesk@tamu.edu) Pledger, David W Sakiko Okumoto Okumoto, Sakiko Zachary Adelman April.Godlewski.ctr@darpa.mil
Subject:	TAMU/DARPA Monthly Tech Update
Location:	Dial-in: 866-692-4541\; Participant:
When:	6/23/2017 1:00:00 PM - 2:00:00 PM
Attachments:	e1601910.full.pdf

TAMU/DARPA Tech Update
Recurs: the 4th Friday of every month

Please send update slides to DARPA at least 2 business days prior to the scheduled meeting.

Dial-in: 866-692-4541
Participant:

Additional topic to be discussed
Tribolium gene drive modeling paper Drury et al. “CRISPR/Cas9 gene drives in genetically variable and nonrandomly mating wild populations” from Science Advances 2017.

From:	Alvarado, Jessica <JAlvarado@cvm.tamu.edu>
To:	Jerome Menet Andrew Hillhouse Threadgill, David W Cai, James Skow, Loren Riggs, Penny Bazer, Fuller Burghardt, Robert Raudsepp, Terje junkins@tamu.edu Johnston J Spencer Katju, Vaishali Bergthorsson, Ulfar Juliana Rangel Posada Aaron Tarone Zachary Adelman karpac@tamu.edu Green, Eleanor Welsh, Jane Vemulapalli, Ramesh Suva, Larry
CC:	Pluhar, Lauren Alvarado, Jessica Scott, Amanda R Cornett, Dianne G. Voelker, Cynthia Castiglioni, Evelyn
Date:	5/26/2017 4:11:18 PM
Subject:	Dr. Trudy Mackay Visit 5/29-5/31
Attachments:	CV_Mackay_05_2017.pdf Trudy Mackay Visit 2017.pdf

Good afternoon,

Please see the attached final version of Dr. Mackay's visit along with her CV. Let me know if you have any questions.

Have a great weekend!

Thanks,
Jess

Jessica R. Alvarado
Executive Assistant | The Department of Veterinary Integrative Biosciences
College of Veterinary Medicine & Biomedical Sciences
Texas A&M University
Office 345C | TAMU 4458 | College Station, TX 77843
P: 979.845.2820 | F: 979.847.8981
jalvarado@cvm.tamu.edu
http://vetmed.tamu.edu/vibs/

VETERINARY MEDICINE
& BIOMEDICAL SCIENCES
TEXAS A&M UNIVERSITY

CURRICULUM VITAE

TRUDY FRANCES CHARLENE MACKAY

MAY 2017

BORN: September 10, 1952, Moncton, New Brunswick, Canada

NATIONALITY: U. S. A. and Canada

ADDRESS: Department of Biological Sciences, Box 7614, North Carolina State University, Raleigh, North Carolina 27695-7614

CONTACT: Email: trudy_mackay@ncsu.edu
Tel: 919-515-5810
Fax: 919-515-3355

EDUCATION

B. Sc. (Hon)	Biology	Dalhousie University, 1974
M. Sc.	Biology	Dalhousie University, 1976
Ph.D.	Genetics	University of Edinburgh, 1979
Postdoctoral	Genetics	Dalhousie University, 1979-1980

HONORS AND AWARDS

Dalhousie University Entrance Scholarship, 1970-1974
B. Sc. awarded with first class honours in Biology, Dalhousie University, 1974
Dalhousie University Medal in Biology, 1974
National Research Council of Canada Graduate Fellowship, Department of Biology, Dalhousie University, 1974-1975
Killam Graduate Scholarship, Department of Biology, Dalhousie University, 1974-1975
M. Sc. Thesis approved with distinction, Dalhousie University, 1976
Royal Commission for the Exhibition of 1851 Overseas Scholarship, Department of Genetics, University of Edinburgh, 1976-1979
McCauley Award, Department of Genetics, University of Edinburgh, 1979
Natural Sciences and Engineering Research Council of Canada Postdoctoral Fellowship, Department of Biology, Dalhousie University, 1979-1980
Killam Postdoctoral Fellowship, Department of Biology, Dalhousie University (honorary), 1979-1980.
Alumni Outstanding Research Award, College of Agriculture and Life Sciences, NC State University, 2000
Fellow, American Association for the Advancement of Science, 2003
Genetics Society of America Medal, 2004
Fellow, American Academy of Arts and Sciences, 2005
Fellow, Royal Society, 2006
Member, New York Academy of Sciences, 2007
O. Max Gardner Award, University of NC, 2007
Adjunct Professor, Department of Endodontics, School of Dentistry, University of NC, Chapel Hill, 2007
Fellow, National Academy of Sciences of the USA, 2010
North Carolina Award for Science, 2011
Honoris Causa, University of Buenos Aires, Argentina, 2013
Alexander Quarles Holladay Medal for Excellence, NC State University, 2015
Wolf Prize for Agriculture, 2016

Alumni Outstanding Research Award, College of Sciences, NC State University, 2016
NC State University Research Leadership Academy, 2016
5th International Conference on Quantitative Genetics Award for Outstanding Contributions in Research and Teaching in Quantitative Genetics, 2016
Honorary Professor, Beijing Forestry University, China, 2016

EMPLOYMENT

Lecturer, Department of Genetics, University of Edinburgh 1980-1987 (Awarded tenure, 1983)
Associate Professor, Department of Genetics, North Carolina State University, 1987-1993
Professor, Department of Genetics, North Carolina State University, 1993-1996
William Neal Reynolds Professor of Genetics, North Carolina State University, 1996-present
Distinguished University Professor of Genetics, North Carolina State University, 2006-2013
Associate faculty, Department of Entomology, North Carolina State University, 2008-present
William Neal Reynolds and Distinguished University Professor of Biological Sciences, 2013-2017
Distinguished University Professor and Goodnight Innovation Distinguished Chair of Biological Sciences, 2017-present

SOCIETY MEMBERSHIPS

Genetics Society of America
Society for the Study of Evolution
American Association for the Advancement of Science
Sigma Xi

RESEARCH INTERESTS

My general research goal is to understand the genetic and environmental factors affecting variation in quantitative (or complex) traits. This is necessary for risk modification of multifactorial human diseases, in theory for a more comprehensive view of the genetic processes underlying phenotypic evolution and in practice for improving production traits in domestic species.

A comprehensive understanding of the genetic architecture of quantitative traits requires that we know (1) at what genetic loci (Quantitative Trait Loci, or QTLs) segregating and mutational variation occurs; (2) the homozygous, heterozygous and epistatic effects, pleiotropic effects on other characters, including fitness; and environmental sensitivities of QTL alleles; and (3) the molecular genetic basis of quantitative variation in nature. This detailed characterization is only feasible in genetically tractable model organisms. Further, the nature of genetic variation for quantitative traits is expected to differ depending on the relationship of the trait to fitness. My research focuses on *Drosophila melanogaster*, which has a wealth of genetic and genomic resources, and morphological, behavioral, physiological and life history characters spanning the gamut of fitness profiles.

Drosophila sensory bristle numbers are morphological traits with high levels of naturally occurring genetic variation and which are thought to be under strong stabilizing selection in the wild. Only when we know what loci contribute to naturally segregating variation for bristle numbers and frequencies of functional allelic variants at these loci will we be able to infer what evolutionary forces lead to the maintenance of substantial genetic variation despite strong selection. Animals display rich behavioral repertoires of responses to environmental stimuli, yet almost nothing is known of the genes

underlying quantitative genetic variation in behavioral traits. We are studying olfactory responses to chemicals, mating behavior, aggression, alcohol sensitivity and adult locomotor behavior to understand the genetic architecture of complex behaviors. We also study longevity and resistance to multiple stressors (starvation, chill coma, oxidative stress) as model life history traits, whose genetic basis may be conserved across taxa, including humans.

We use two complementary approaches to identify QTLs and determine their effects for each of the traits of interest. First, we screen random *P* transposable element insert lines, derived in an inbred background, to identify candidate genes and pathways affecting quantitative trait phenotypes. Second, we map QTLs causing naturally occurring variation for quantitative traits by linkage or association with molecular markers, respectively, in linkage mapping populations and in samples of alleles from random breeding populations. We have derived a population of 205 inbred lines from the Raleigh, NC natural population with complete sequences, which we are currently expanding to 2,000 lines. These lines constitute the *Drosophila* Genetic Reference Panel (DGRP), a community resource for whole genome association mapping of quantitative traits. Because DNA polymorphisms do not directly affect variation in quantitative traits, but do so via networks of interacting transcripts, proteins, and metabolites, we are performing whole genome expression analyses on the DGRP lines to derive causal networks of genetically variable transcripts associated with quantitative traits. Since the effects of QTL alleles can be environment-specific, we incorporate ecologically relevant macro-environments in all the above studies.

RESEARCH SUPPORT

(AMOUNTS GIVEN ARE TOTAL DIRECT COSTS)

PAST SUPPORT

1. GR/C44884. Mutational variation for quantitative traits in *Drosophila melanogaster.* P.I., T. F. C. Mackay. Science and Engineering Research Council (Great Britain). 1983-1986. £65,000 (approximately $117,000).

2. GR/D76042. Population genetics of transposable elements in *Drosophila*. P.I., T. F. C. Mackay. Science and Engineering Research Council. (Great Britain). 1986-1987. £13,000 (approximately $23,400).

3. P01 GM11546. *P*-element-induced quantitative variation in *Drosophila*. Mackay component, National Institutes of Health Quantitative Genetics Research Program. P.I., C. C. Cockerham. 1987-1990. 1990 Mackay component, $117,035.

4. NC06077. *P*-element-induced quantitative variation in *Drosophila melanogaster*. P.I., T. F. C. Mackay. North Carolina State University, North Carolina Agricultural Research Service. 1988-1991. $21,000 per annum.

5. Distribution of effects of mutants on quantitative traits. P.I., T. F. C. Mackay. North Atlantic Treaty Organization, travel grant for collaborative research. co-P.I., Prof. W.G. Hill, Department of Genetics, University of Edinburgh. 1988-1993. Travel and subsistence budget for total award, $8,700.

6. P01 GM45344. Quantitative genetic variation in *Drosophila*. Mackay component, National Institutes of Health Statistical and Quantitative Genetics Research Program. P.I., B. S. Weir. 1990-1995. $735,571 Mackay component.

7. R01 GM45146. Quantitative trait loci in *Drosophila*. P.I., T. F. C. Mackay. National Institutes of Health. 1991-1995. $304,273.

8. Quantitative genetics of ovariole number in *Drosophila melanogaster*. National Institutes of Health NRSA Postdoctoral Fellowship. P.I., M. Wayne, Sponsor T. F. C. Mackay. 1994-1997. $63,900.

9. DEB-9317754. The contribution of new mutations to genotype-environment interaction for fitness. P.I., T. F. C. Mackay. National Science Foundation. co-P.I., J. D. Fry. 1994-1997. $210,000.

10. R01 DC02485. Molecular genetics of olfaction in *Drosophila* . P.I., R. R. H. Anholt; co-P.I., T. F. C. Mackay. National Institutes of Health. 1994-1998. $581,751.

11. R01 GM45146. Quantitative trait loci in *Drosophila*. P.I., T. F. C. Mackay. National Institutes of Health. 1995-1999. $554,223.

12. Quantitative genetics of *Drosophila* life history traits. National Institutes of Health NRSA Postdoctoral Fellowship. P.I., J. Leips, Sponsor T. F. C. Mackay. 1997-2000. $63,900.

13. P01 GM45344. Quantitative genetic variation in *Drosophila*. National Institutes of Health Statistical and Quantitative Genetics Research Program. P.I., B. S. Weir. 1995-2000. $834,728 Mackay component.

14. R03 TW00997. Quantitative trait loci for longevity in Drosophila. P.I., T. F. C. Mackay; Collaborator, E. G. Pasyukova. National Institutes of Health, Forgarty International Center. 1998-2001. $50,000.

15. R01 GM59469. Molecular genetics of olfaction in *Drosophila* . P.I., R. R. H. Anholt; co-P. I., T. F. C. Mackay. National Institutes of Health. 1999-2003. $1,165,718.

16. NC06274. Quantitative genetic variation in *Drosophila melanogaster*. P.I., T. F. C. Mackay. North Carolina State University, North Carolina Agricultural Research Service. $33,000 per annum.

17. R01 GM45146. Quantitative trait loci in *Drosophila.* P.I., T. F. C. Mackay. National Institutes of Health. 1999-2003. $1,666,289.

18. F32 GM20897. The genetic basis of variation in olfactory behavior. National Institutes of Health NRSA Postdoctoral Fellowship. P.I., Stephanie M. Rollmann, Sponsors T. F. C. Mackay & R. R. H. Anholt. 2000-2003. $63,900.

19. F31 MH065051. Quantitative trait loci for *Drosophila* mating behavior. National Institutes of Health NRSA Predoctoral Fellowship. P.I., Amanda J, Moehring, Sponsor T. F. C. Mackay. 2001-2003. $40,846.

20. DEB-9976997. Quantitative genetic architecture of inflorescence developmental plasticity. Molecular Evolutionary Ecology of Developmental Plasticity in *Arabidopsis thaliana*. P.I. M. D. Purugganan. National Science Foundation. 1999-2004. $350,329 Mackay component.

21. P01 GM45344. Quantitative trait loci for *Drosophila* lifespan. National Institutes of Health Statistical and Quantitative Genetics Research Program. P.I., B. S. Weir 2000-2005. $955,914 Mackay component.

22. F32 GM66603. QTL for temperature stress resistance in *Drosophila*. National Institutes of Health NRSA Postdoctoral Fellowship. P.I., Theodore J. Morgan, Sponsor T. F. C. Mackay. 2002- 2005. $119,124.

23. R01 GM58260. Genetic basis of species differences in Drosophila. P.I. , J. A. Coyne, sub-contract P. I., T. F. C. Mackay. National Institutes of Health. 2002-2006. $259,816 Mackay sub-contract.

24. R21 AA015348. Genetics of alcohol sensitivity in *Drosophila*. P.I., T. F. C. Mackay. National Institutes of Health. 2004-2006. $273,375.

25. R01 GM59469. Molecular genetics of olfaction in *Drosophila* . P.I., R. R. H. Anholt; co-P. I., T. F. C. Mackay. National Institutes of Health. 2003-2007. $1,125,000.

26. F31 MH74161. Genetic architecture of aggression in *Drosophila*. National Institutes of Health NRSA Predoctoral Fellowship. P.I., Alexis C. Edwards, Sponsor T. F. C. Mackay. 2005-2008. $90,264.

27. R01 GM45146. Quantitative trait loci in *Drosophila.* P.I., T. F. C. Mackay. National Institutes of Health. 2003-2007. $872,000.

28. R01 EY015873. Comparative genomics of glaucoma, P.I., R. R. H. Anholt; co-P.I., T.F. C. Mackay. National Institutes of Health. 2005-2010. $1,237,980.

29. R01 GM058260. Genetics of species differences in *Drosophila*, P.I., J. A. Coyne; sub-contract P. I., T. F. C. Mackay. National Institutes of Health. 2006-2010. $560,678.

30. R01 GM076083. Genetics of aggression in *Drosophila*. P.I., T. F. C. Mackay. National Institutes of Health. 2006-2010. $770,000.

31. 15-ES-101, ARRA Challenge Grant . Oxidative stress and neurogenetic networks in *Drosophila*. Co-P.I., R. R. H. Anholt, T. F. C. Mackay, E. A. Stone. National Institutes of Health. 2009-2011. $483,276.

32. ARRA Administrative Supplement to R01 GM45146. Quantitative trait loci in *Drosophila.* Co-P.I., T. F. C. Mackay, R. R. H. Anholt, E. A. Stone. National Institutes of Health. 2009-2011. $297,270.

33. R01 AA016560. Genetics of alcohol sensitivity in *Drosophila*, P.I., T. F. C. Mackay. National Institutes of Health. 2007-2011. $1,125,000.

34. R01 GM59469. Molecular genetics of olfaction in *Drosophila* . P.I., R. R. H. Anholt; co-P.I., T. F. C. Mackay. National Institutes of Health. 2008-2012. $1,455,547.

35. R01 GM45146. Quantitative trait loci in *Drosophila.* Co-P.I., T. F. C. Mackay, R. R. H. Anholt, E. A. Stone. National Institutes of Health. 2009-2013. $1,400,000 (no-cost extension to 6/30/2014).

36. R21 ES021719. Genetics of lead sensitivity in *Drosophila*. Co-P.I., R. R. H. Anholt (PD), T. F. C. Mackay. National Institutes of Health. 2013-2015. $275,000 (no cost extension to 06/30/2016)

37. R01 GM076083. Genetics of aggression in *Drosophila*. Co-P.I., T. F. C. Mackay (PD), R. R. H. Anholt, E. A. Stone. National Institutes of Health. 2012-2016. $1,264,370 (no cost extension to 04/30/2017).

38. R01 GM59469. Molecular genetics of olfaction in *Drosophila*. Co-P.I., R. R. H. Anholt (PD), T. F. C. Mackay. National Institutes of Health. 2013-2017. $1,174,489.

CURRENT SUPPORT

39. R01 AA016560. Genetics of alcohol sensitivity in *Drosophila*, Co-P.I., T. F. C. Mackay (PD), R. R. H. Anholt. National Institutes of Health. 2012-2017. $1,625,525.

40. R01 AG043490. Systems genetics of *Drosophila* lifespan. Co-P.I., T. F. C. Mackay (PD), R. R. H. Anholt. National Institutes of Health. 2013-2018. $1,250,000.

41. Genomic Selection in Animals and Plants (GenSAP) funded by The Danish Council for Strategic Research. 2013-2018. $300,000.

PENDING

U01 DA041613. Genetics of cocaine and methamphetamine sensitivity in *Drosophila*. Co-P.I., T. F. C. Mackay (PD), R. R. H. Anholt. National Institutes of Health. 2016-2021. $2,826,180.

R35 GM122454. *Drosophila* quantitative genetics. T. F. C. Mackay (P. I.) National Institutes of Health. 2017-2022. $5,034,161.

TRAINING GRANT SUPPORT

42. W. M. Keck Program in Behavioral Biology. R. R. H. Anholt, Program Director; T. F. C. Mackay, participating member. 1999-2004. $800,000.

43. T32 GM 08443. The genetic architecture of quantitative traits. Program Director, T. F. C. Mackay. National Institutes of Health Institutional Training Grant. 1999-2004. $573,914.

44. T32 GM 08443. The genetic architecture of quantitative traits. Program Director, T. F. C. Mackay. National Institutes of Health Institutional Training Grant. 2004-2009. $665,100.

45. R25 GM083242. Initiative for Maximizing Student Diversity. Program directors, T. F. C. Mackay and D. Shafer. National Institutes of Health Institutional Training Grant. 2008-2012. $1,869,824.

46. T32 GM 08443. The genetic architecture of quantitative traits. Program Director, T. F. C. Mackay. National Institutes of Health Institutional Training Grant. 2009-2014. $751,270.

47. R25 GM083242. Initiative for Maximizing Student Diversity. Program directors, T. F. C. Mackay and D. Shafer. National Institutes of Health Institutional Training Grant. 2012-2017. $3,397,645.

PENDING

R25GM083242. Initiative for Maximizing Student Diversity in Biomedical and Behavioral Sciences. Co-P.I., T. F. C. Mackay (P. D.), D. M. Shafer. National Institutes of Health. $5,522,261.

INVITED SYMPOSIA CONTRIBUTIONS

26TH Poultry Breeders Roundtable, 1984. "Jumping genes and quantitative variation"

Hybrid Dysgenesis Workshop, Cambridge, England, 1985. Hybrid dysgenesis-induced response to selection"

Commission of the European Communities Animal Husbandry Research Programme Seminar, Edinburgh, Scotland, 1985. "Transposable elements in genetic selection"

Second International Conference on Quantitative Genetics, Raleigh, North Carolina, 1987. "Transposable element-induced quantitative variation in *Drosophila*"

16TH International Congress of Genetics, Toronto, Canada, 1988. "Transposable elements and fitness in *Drosophila melanogaster*"

4TH International Congress of Systematic and Evolutionary Biology, College Park, Maryland, 1990. "The pleiotropic effects of new polygenic mutations"

4TH World Congress on Genetics Applied to Livestock Production, Edinburgh, Scotland, 1990. "Distribution of effects of new mutations affecting quantitative traits"

Pioneer Hi-Bred Heterosis Conference, Ames, Iowa, 1993. "Quantitative variation and epistasis in *Drosophila*"

17TH International Congress of Genetics, Birmingham, England, 1993. Convener of Symposium entitled "Towards an understanding of the genes controlling quantitative variation", and speaker on "Insertional mutagenesis and quantitative variation"

Gordon Conference on Quantitative Genetics and Biotechnology, Ventura, California, 1995. "Mutations and quantitative traits"

44TH Annual National Breeders Roundtable, St. Louis, Missouri, 1995. "The genetic basis of quantitative variation in *Drosophila melanogaster*"

Society for the Study of Evolution, Montreal, Canada, 1995. "High resolution mapping of QTL affecting bristle number in *Drosophila melanogaster"* and "Mutation and quantitative variation in *Drosophila*"

European Society for Evolutionary Biology, Edinburgh, Scotland, 1995. "The genetic basis of quantitative variation: Candidate genes and *Drosophila* bristle number"

International Plant and Animal Genome V Conference, San Diego, CA, 1997. "The nature of quantitative genetic variation: Lessons from *Drosophila*"

International Conference on Molecular Biology and Evolution, Garmisch-Partenkirchen, Bavaria, Germany, 1997. "Quantitative genetic variation at loci affecting sensory bristle development in *Drosophila melanogaster*"

National Institutes of Health, The Genetic Architecture of Complex Traits, Washington, DC 1997. "QTL and beyond: Lessons from *Drosophila*"

6TH World Congress on Genetics Applied to Livestock Production, Armidale, Australia, January 1998. "The nature of quantitative variation: Lessons from *Drosophila*"

AAAS 1998 Annual Meeting, Philadelphia, PA. Biotechnology and Evolution Symposium. "The nature of quantitative variation: Lessons from *Drosophila*"

National Institutes of Health, International Consortium to Identify Cancer Modifier Genes in Mice, Washington, DC, July 1998

Duke University Genetics Program Mini-Symposium on Quantitative Traits, Durham NC, October 1998. "The nature of quantitative variation: Lessons from *Drosophila*"

28th Annual Meeting of the American Aging Association, 12th Annual Meeting of the American College of Clinical Gerontology. Seattle, WA, June 1999. "QTL mapping of aging genes in *Drosophila melanogaster*"

3rd International symposium on Proteogenomics, Seattle, WA, October 1999. "Complicated genetics of complex traits: Lessons from *Drosophila*"

National Institutes of Health., How Many SNPs are Needed For Disease Gene Mapping Meeting. March 2000, Washington, DC

41st Annual Drosophila Research Conference, Plenary Lecture. Pittsburgh, PA, March 2000."The nature of quantitative genetic variation"

University of California, Davis, Major Issues in Modern Biology, April, 2000."The nature of quantitative genetic variation"

Evolution 2000 Joint Meeting, Symposium on the Genetics of Adaptation, Bloomington, IN, June 2000. Quantitative trait loci for Drosophila lifespan

Genetic Mechanisms of Aging III, Jackson Laboratories, Bar Harbor, ME, August, 2000. "Quantitative trait loci for Drosophila lifespan"

Insect Chemical Ecology in the Molecular Era, Schloss Ringberg, Germany, October, 2000. "Towards an understanding of the molecular genetic basis of adaptation: lessons from *Drosophila*"

National Institute on Alcohol Abuse and Alcoholism, workshop on "QTL Endgame: Strategies for Identifying Genes Influencing Alcohol-Related Behavior", November, 2000, Washington, DC

Gordon Research Conference on Quantitative Genetics and Genomics, February, 2001, Ventura, CA.

Les Treilles Foundation, Workshop on "Quantitative Evolutionary Genetics: Drosophila in the Post-Genome Era", April, 2001, Les Treilles, France

Duke University Genetics Program Mini-Symposium, "My Genes Made Me Do It? Linking Genetics and Behavior"; Durham, NC, October 2001. "The Genetic Architecture of Complex Behaviors"

4th Annual Meeting of the International Behavioural and Neural Genetics Society. San Diego, CA, November 2001. "The Genetic Architecture of Complex Behaviors"

National Human Genome Research Institute, Planning Workshop on Relating Genetic Variation to Health and Disease, August, 2002, Bethesda, MD

Syngenta Torry Mesa Research Institute, Microarray Users Meeting, October 2002, Orlando, FL. "Drosophila Quantitative Genomics"

Gordon Research Conference on Aging, March 2003, Ventura, California. "The Genetic Architecture of Drosophila Lifespan"

BRIDGES to the Future Program Directors meeting, June 2003, Lake Tahoe, CA. "Skills for Scientists in the Post-Genome Era"

XIX International Congress of Genetics, July 2003, Melbourne, Australia. "The Genetic Architecture of Complex Traits: Lessons From Drosophila". (Also co-organizer, Symposium on Genetics of Complex Traits)

Keystone Symposium on Natural Variation and Quantitative Genetics, January, 2004. Breckenridge, Colorado. "Molecular Quantitative Genetics of Drosophila Life Span"

Gordon Research Conference on Behavioral Genetics, February, 2004, Ventura, California. "Genetic Architecture of Drosophila Behavior"

54th Annual Meeting, American Society of Human Genetics, October, 2004, Toronto, Canada. "Genotype-environment interaction: Lessons From a Model Organism"

National Academy of Sciences Colloquium on Systematics and the Origin of Species, on Ernst Mayr's 100th Anniversary, December, 2004, Irvine, California. "Genetics and Genomics of Drosophila Mating Behavior"

UK Genetics Society Meeting on Behavioural Genetics: Has Nature Won?, January, 2005, Edinburgh, Scotland. "Quantitative Genetics and Genomics of *Drosophila* Behaviour"

34th Annual Meeting, American Aging Association, June 2005, San Francisco, California. "Analysis of Gene Expression in *Drosophila*"

International Behaviour and Neural Genetics Society, June, 2005, Sitges, Spain. "Genetics of Locomotor Behavior in *Drosophila*"

Gordon Research Conference on Evolutionary and Functional Genomics, August, 2005, Oxford, England. "The genetic architecture of quantitative traits: Lessons from *Drosophila*"

Evolution and Development: From Molecules to Morphology, Max Planck Institute for Developmental Biology, Tubingen, Germany, September, 2005. "Development and the genetic architecture of quantitative traits: Lessons from *Drosophila*"

Ecological Genomics Symposium, November, 2005, Kansas. "The genetic architecture of quantitative traits: Lessons from *Drosophila*"

GSA Symposium, Genetic Analysis: From Model Organisms to Human Biology, January, 2006, San Diego. "*Drosophila* as a model system for understanding the genetic architecture of complex traits"

Keystone Symposium, Genome Sequence Variation and the Inherited Basis of Common Disease and Complex Traits", January, 2006, Big Sky. "Quantitative trait variation in *Drosophila*"

Genetical Society of Canada Symposium, Genetics and Genomics of Complex Phenotypes, June, 2006, London, Ontario, Canada. "The genetic architecture of quantitative traits: Lessons from *Drosophila*"

The Society for the Study of Evolution Symposium, Evolution of Behavior, June, 2006, Stony Brook, New York. "The genetic architecture of *Drosophila* behavior"

NIGMS Workshop on Systems Genetics and Complex Phenotypes, September 2006, Bethesda, Maryland

Lausanne Genomics Days Symposium, October, 2006, Lausanne, Switzerland. "Quantitative Genomics and the Genetic Architecture of Complex Traits: Lessons from *Drosophila*"

NIH NHLBI Systems Medicine Workshop, January 2007, Bethesda, Maryland. "The genetic architecture of quantitative traits: Lessons from *Drosophila*"

Workshop on "Integrating the Study of Genotype and Phenotype", February, 2007, Florida State University. "The genetic architecture of quantitative traits: Lessons from *Drosophila*"

Gordon Research Conference on Quantitative Genetics and Genomics, February, 2007, Ventura, CA. "The genetic architecture of behavior: Lessons from *Drosophila*"

American Association for Cancer Research, April, 2007, Los Angeles, CA. "The genetic architecture of complex traits: Lessons from *Drosophila*"

NESCent Catalysis meeting, Evolution in Contemporary Human Populations: Medical, Genetic and Behavioral Implications, Durham, NC, May, 2007
NSF Workshop on Motor Pattern Evolution, June 2007, Arlington, VA
Society for Molecular Biology and Evolution, Plenary Speaker, June 2007, Halifax, NS, Canada. "The genetic architecture of complex traits: Lessons from *Drosophila*"
3rd International Conference on Quantitative Genetics, August 2007, Hangzhou, China. "The genetic architecture of complex behaviors: Lessons from *Drosophila*"
GSA Model Organisms Meeting, January 2008, San Diego, CA
Keystone Symposium on Complex Traits: Biologic and Therapeutic Insights (co-organizer and speaker), February 2008, Santa Fe, NM
XX International Congress of Genetics, July 2008, Berlin, Germany (International Organizing Committee)
Duke Systems Biology Institute Annual Symposium, October 2008, Durham, NC
4th Annual Symposium of the University of Florida Genetics Institute, October 2008, Gainesville, FL
Biology of Genomes, May 2009, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
Canadian Genetic Epidemiology and Statistical Genetics Meeting, May, 2009, Harrison Hot Springs, BC Canada
American Genetic Association Annual Symposium, June 2009, Providence, RI
American Society of Naturalists Vice Presidential Symposium, June, 2009, Moscow, ID
Gordon Research Conference on Chronobiology, July 2009, Salve Regina University, Newport, RI
Lecturer on Genetic and Molecular Analysis of Complex Traits, Advanced Course in Drosophila Genetics and Genomics, Wellcome Trust Genome Centre, Hinxton, UK
Keynote speaker, Genomics of Common Diseases, September 2009, Wellcome Trust Genome Centre, Hinxton, UK
Speaker, Entomological Society of America, 2009 meeting, Celebrating the Role of Entomology in the Genomics Revolution Symposium, Indianapolis, IN, December 2009
Gordon Research Conference on Genes and Behavior, Ventura, CA, March 2010
Complex Trait Consortium, Chicago Il, May 2010
Society for the Study of Evolution, 2010 meeting, Towards a Theory of Evolutionary Prediction Symposium, Portland, OR, June 2010
9th World Congress in Genetics Applied to Animal Production, Plenary Speaker, Leipzig, Germany, August 2010
Academia Belgica, Deciphering the Molecular Architecture of Complex Traits, Rome, Italy, September 2010
Centre Intégratif de Génomique, Genetics of Behavior, Lausanne, Switzerland, June 2011
Research Triangle Statistical Genetics Conference, Raleigh, NC, October 2011
Drosophila Research Conference, Plenary Speaker, Chicago, IL, March 2012
NIEHS Symposium, Emerging Issues in Analysis and Design of Large Scale Genetic Studies, invited speaker, Research Triangle Park, NC, May 2012
4th International Conference on Quantitative Genetics, Invited Speaker, Edinburgh, Scotland, June 2012
Workshop on Behavioral Genetics, Guilford, Surrey, December 2012
NSPR-8 Workshop, Plenary Lecturer, Plant and Animal Genome XXI, San Diego, CA, January 2013
Gordon Research Seminar in Quantitative Genetics and Genomics, Plenary Lecturer, Galveston, TX, February 2013
Drosophila Research Conference, Genomic Workshop speaker, Washington, DC, April 2013
European Society for Evolutionary Biology, Plenary Lecturer, Lisbon, Portugal, August 2013
3rd Latin American School of Evolution, Lecturer, Buenos Aires, Argentina, November 2013
Plant and Animal Genome XXII, Plenary Lecturer, San Diego, CA, January 2014

Epistasis Detection in Genetics and Epidemiology, Plenary lecture, Key West, FL, February 2014
Drosophila Research Conference, Plenary Lecturer and workshop speaker, San Diego, CA, March 2014
Systems Genetics of Model (non-Human) Organisms, Invited speaker, Locarno, Switzerland, May 2014
Third Summer Course in Environmental Genomics, Mount Desert Island Biological Lab, Bar Harbor, Maine, August 2014
RTP Illumina User Group Meeting, Research Triangle Park, NC, October 2014
EMBO conference on Experimental Approaches to Evolution and Ecology, Heidelberg, Germany, October 2014
Epistasis Detection in Genetics and Epidemiology, Plenary lecture, Key West, FL, February 2015
Genetics and Environmental Mutagenesis Society Spring Meeting, Plenary Lecturer, Research Triangle Park, NC, April 2015
EMBO Meeting 2015, Invited Speaker, Birmingham, England, September 2015
European Drosophila Research Conference 2015, Plenary Speaker, Heidelberg, Germany, September 2015
Epistasis Detection in Genetics and Epidemiology, Plenary lecture, Key West, FL, February 2016
5th International Conference in Quantitative Genetics, Plenary Speaker, Madison, WI, June 2016
National Symposium on Bridging Genomics and Phenomics, Keynote Speaker, Beijing, China, August 2016
Max Planck Symposium on Complex Trait Genetics, Berlin, Germany, October 2016
Epistasis Detection in Genetics and Epidemiology, Plenary lecture, Key West, FL, February 2017
Alberta Children's Hospital Research institute, Plenary Lecture, Symposium on Precision Medicine and Child Health, Calgary AB, Canada, April 2017

INVITED SEMINARS

Department of Genetics, University of Wisconsin, May 1998
Department of Biology, University of Alabama, November 1998
Department of Embryology, Carnegie Institute, December 1998
Department of Biology, Pennsylvania State University, March 1999
Department of Genetics, University of Georgia, April 1999
Department of Evolution and Ecology, University of California, Irvine, May 1999
Department of Biology, University of Nebraska, September 1999
Department of Biology, University of Toronto at Mississauga, November 1999
Department of Ecology and Evolution, University of California, Davis, April 2000
Department of Biology, The Ohio State University, May 2000
Department of Zoology, University of Florida, Gainesville, September 2000
Department of Molecular and Human Genetics, Baylor College of Medicine, September 2000
Department of Botany, University of Knoxville, November 2000. "Genomics, Present and Future" seminar series
Department of Biology, University of Greensboro, November 2000
Department of Biology, University of Rochester, December 2000
Department of Zoology, North Carolina State University, September 2001
Department of Genetics, Duke University, February 2002
University of North Carolina, Chapel Hill, Carolina Consortium on Human Development, February 2002
Department of Biology, Washington University, St. Louis, March 2002
Department of Biology, Brown University, April 2002
Department of Biology, Michigan State University, April 2002

Department of Biology, Indiana University, September 2002
Department of Biology, Morehouse College, November 2002
Pioneer Hybrid International, January 2003
Department of Human Genetics, University of Chicago, October 2003
Department of Ecology and Evolution, University of Chicago, March 2004
Genomics Training Program Seminar Series, University of Michigan, April 2004
Department of Biology, University of Maryland, May 2004
Samuel Lunenfeld Research Institute, Mt. Sinai Hospital, Toronto, Canada, September 2004
Department of Genetics, Washington University in St. Louis, School of Medicine, November 2004
Department of Biology, University of Maryland Baltimore County, December 2004
Department of Ecology and Evolution, Harvard University, March 2005
Department of Biology, University of North Carolina, Chapel Hill, March 2005
Laboratory of Developmental Genetics, University of Leuven, Belgium, May 2005
Department of Molecular Genetics, University of Antwerp, Belgium, May 2005
Department of Human Genetics, University of Michigan, September 2006
Department of Ecology and Evolution, University of Buenos Aires, November 2006
Department of Biology, Indiana University, January 2007
Center for Quantitative and Computational Biology, Columbus Children's Research Institute, Columbus, Ohio, April 2007
Department of Genetics, University of Wisconsin, October 2007
Institute for Genomic Biology, University of Illinois, November 2007
Cold Spring Harbor Laboratory, Watson Genetics Course, December 2007
Cold Spring Harbor Laboratory, Integrative Statistical Analysis of Genome Scale Data Summer Course, June 2008
Department of Integrative Biology, University of Texas, Austin, TX, September 2008
Baylor College of Medicine Sequencing Center, November 2008, Houston TX
Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill, NC, February 2009
Department of Genome Sciences, University of Washington, Seattle, WA, March 2009
Department of Human Genetics, University of Chicago, Chicago IL, April 2009,
Department of Human Genetics, University of Utah, Salt Lake City, UT, May 2009
Department of Genetics, University of Cambridge, Cambridge, UK, September 2009
Institute of Molecular Biology, University of Zurich, Zurich, Switzerland, September 2009
Huck Distinguished Lecturer, Pennsylvania State University, College Park, PA, November 2009
University of Texas Southwestern Medical School, Dallas, TX, November 2009
Higgins Distinguished Lecture, University of Kentucky, Lexington, KY, Department of Biology, December 2009
University of Arizona Medical School, Tucson, AZ, April 2010
Bauer Center for Systems Biology, Harvard University, Boston, MA, May 2010
Center for Ecology and Evolutionary Biology, University of Oregon, Eugene, OR, October 2010
University of Rochester, Department of Biology, Rochester, NY, March 2011
NIEHS Laboratory of Molecular Genetics, Durham, NC, March 2011
University of Idaho Initiative for Bioinformatics and Evolutionary Studies (IBEST) invited speaker, Moscow, ID, March 2011
Cornell University, Cornell Center for Comparative and Population Genomics (3CPG) invited speaker, Ithaca, NY, April 2011
University of Wisconsin, Department of Animal Science, A. B. Chapman Lectures, Madison, WI, April 2011

Department of Human Genetics, University of California, San Diego, CA, September 2011
Department of Human Genetics, University of Michigan, Ann Arbor, MI, November 2011
Wellcome Trust Center for Human Genetics, Oxford, UK, March, 2012
Center for Systems Genetics, University of North Carolina Chapel Hill, Chapel Hill NC, June 2012
Center for Public Health Genomics, University of Virginia, Charlottesville, VA September, 2012
Department of Genetics, University of Cambridge, Cambridge, UK, October 2012
Department of Genetics, University of Georgia, Athens, GA, March 2013
Center for Integrated Animal Genomics, Iowa State University, March 2013
Duke University Program in Genetics and Genomics, Durham NC, October 2013
Monsanto Biotechnology seminar, March 2014
NIEHS Laboratory of Toxicology and Pharmacology, April 2014
Department of Genetics and Department of Cell and Developmental Biology, University of Pennsylvania, Philadelphia PA, April 2014
Institute of Clinical Research of Montreal (IRCM), Montreal, Canada, June 2014
Jackson Laboratories, Bar Harbor, Maine, August 2014
Department of Ecology and Evolution, University of Lund, Sweden, September, 2014
Department of Biology, University of Birmingham, Alabama, November, 2014
Lieber Institute for Brain Development, Baltimore, Maryland, March, 2015
John A. Lynch Lecture, College of Science, University of Notre Dame, Notre Dame Indiana, October, 2015
Department of Biochemistry and Genetics, Clemson University, Clemson SC, October 2015
Volcani Center, Agricultural Research Organization, Bet Dagan, Israel, May 2016
Robert H. Smith Faculty of Agriculture, Food and Environment, Hebrew University of Jerusalem, Rehovot, Israel, June 2016
Departments of Animal Science, Genetics and Ecology and Evolution, Iowa State University, Ames IA, August 2016
Program in Genetics, Texas A&M University, College Station TX, October 2016
Kjeldgaard Lecture, Department of Molecular Biology and Genetics, University of Aarhus, Aarhus, Denmark, November 2016
Osher Lifelong Learning Institute, NC State University, Raleigh NC, November 2016
Department of Genetics and Biochemistry, Clemson University, Clemson SC, March 2017
Buck Institute for Aging Research, Novato CA, April 2017

PROFESSIONAL SERVICE

NATIONAL / INTERNATIONAL SERVICE

Consulting Editor, *PLoS Genetics* (2005-present)
Editorial Board, *Genome Research* (2010-present)
Editor, *PNAS* (2010-present)
Editorial Board, *Genes, Brain, Behavior* (2012-present)
Editorial Board*, OpenBiology* (2012-present)
Editorial Board, *Axios Reviews* (2013-present)
Executive Editor, American office, *Genetical Research* (1987-2007)
Executive Editor, American office, *Genetics Research* (2008-2009)
Chief Executive Editor, *Genetics Research* (2009-2012)
Associate Editor, *Genetics* (1991-2002)

Associate Editor, *Evolution* (1990-1992)
Committee member, Genetical Society (GB). Biometrical and Statistical Genetics Representative, 1985-1988
ad hoc reviewer, National Institutes of Health Genetics Study Section, February 1990, June 1991, November 1993
National Science Foundation, Population Biology Review Panel, October 1992
Panel member, National Institutes of Health Genetics Study Section, 1995-1999
Participant, National Research Council - National Academy of Sciences Expert Meeting on the Biodemography of Ageing, 1995
Board of Directors, Genetics Society of America, 1999-2001
Council Member, American Genetic Association, 1999-2001
External Review Team, Texas A&M Genetics Program, March, 1999
National Institutes of Health Special Study Section, April 2000
National Institutes of Health, Center for Scientific Review, Genetics IRG Working Group, September-December, 2000
External Advisory Board, "Genetics of Age-Sensitive Traits in Mice" Program Project, The Geriatrics Center, University of Michigan, January 2001
National Institutes of Health, Center for Scientific Review, Genetics Study Sections Boundaries Team, November 2002
National Institutes of Health, Special Study Section, Pre-doctoral fellowships for minority students and students with disabilities, June 2003
Board of Scientific Counselors, National Center for Biotechnology Information, National Library of Medicine, 2003-2008
dbGaP Working Group, NCBI, 2007-2009
Drosophila Board, 2005-2010
President, Drosophila Board, 2006-2007
Treasurer, Genetics Society of America, 2006-2010
Council member, American Genetic Association, 2007-2010
President, American Genetic Association, 2008-2009
National Advisory Council, Stanford University School of Medicine, 2009-2012
Scientific Advisory Board, Max Planck Institute for Developmental Genetics, Tubingen, Germany, 2009-2017 (Chair, 2015-2018)
Scientific Advisory Board, Center for Genome Dynamics, The Jackson Laboratory, Bar Harbor, Maine, 2009-2016
Scientific Advisory Board, FlyBase (2010-present)
Chair-Elect (2009), Chair (2010) and Past-Chair (2011), American Association for the Advancement of Science Section G (Biological Sciences) Steering Committee
Member, Royal Society Sectional Committee 9, 2009-2012
National Institutes of Health Special Study Section, Transdisciplinary Cancer Genomics Research: Post-Genome Wide Association Initiative, October 2009
Board of Regents, National Library of Medicine, 2011-2015 (Chair, 2014-2015)
Rosalind Franklin Award selection committee, 2012, 2015
Board of Electors, Balfour Chair of Genetics, University of Cambridge, Cambridge, UK, 2012
External Review Panel, Genomics, Genetics and Bioinformatics Program, University of California, Riverside CA, 2012
National Academy of Sciences, Class Membership Committee, 2013, 2014
National Academy of Sciences, Council Nominating Committee, 2013, 2014

National Academy of Sciences, John J. Carty Award selection committee, 2013
Member, Duke University Program in Genetics External Review Team, March 2013
Member, Advisory committee to the NIH Director, Working Group on the National Library of Medicine (NLM), 2015
Member, Search committee for Director of the National Library of Medicine (NLM), 2015
Royal Society Newton Advanced Fellowship Committee, 2015-2018
Scientific Advisory Board, Leiber Brain Institute, Baltimore MD, 2016-2018
Scientific Advisory Board, CEXS-UPF, Barcelona, Spain, 2016-2018

UNIVERSITY SERVICE

Member, CALS Structure and Function Subpanel, Strategic Planning Committee, 1993-1994
Member, Search Committee for Department of Statistics Head, 1993-1994
Co-Chair, Department of Genetics Seminar Committee, 1993-1994; 2000-2001
Member, Department of Genetics Admissions Committee, 1988-1993
Department of Genetics Admissions Committee, 1994 to present
Library Representative, Department of Genetics, 1991-1997
Member, Search Committee for Department of Genetics Molecular Evolution Position, 1994-1995
Chair, Search Committee for Department of Genetics Experimental Quantitative Geneticist, 1996-1997
Member, Search Committee for Biomathematics faculty position, 1996-1997
Member, University Research Committee, 1998-2000
Keller Awards Committee, 1998-2002 (Chair, 2001)
William Neal Reynolds Professor Nomination Committee, 2001
Alumni Distinguished Research Award Committee, 2001
Member, Dean's Faculty Advisory Group, 2002-2004
Member, Search Committee for Genetics Department Head, 2008
Member, Genetic Pest Management Search Committee, 2008
Member, Search Committee for Department of Genetics Assistant Professors, 2008-2009
Faculty Committee on Honorary Degrees, 2007-2009
University Promotion and Tenure Committee, 2008-2010
UNC Tomorrow Faculty Team, 2008
Member, NC State University Research Misconduct Investigating Committee, 2008-2009
Member, Provost Search Committee, 2010
Member, Statistics Department Head Search Committee, 2010
Co-Chair (with Daniel Solomon, PAMS Dean), Strategic Planning Task Force on "Faculty Excellence", 2010-2011
Member, NCSU Science Task Force, 2011
Member, Faculty Advisory Committee to the UNC Strategic Directions Initiative, 2012-2013
Chair, Department Head of Biological Sciences Search Committee, 2013-2014
Executive Committee, W. M. Keck Center for Behavioral Biology (2009-present)
Professors of Distinction Review Committee, 2012-present
Director, University-wide Program in Genetics, 2014-present
Director of Graduate Studies, Genetics Graduate Program, 2016-present
Associate Director, Comparative Medicine Institute and Director, Translational Genetics and Genomics Research Group, 2015-present
Member, College of Sciences RPT committee, 2015-present
Outstanding Graduate Faculty Mentor Award Committee, 2015-2016

Member, eRA (electronic research administration) Steering Team, 2016-2017
Member, Research Leadership Academy Task Force, 2016-2019
O. Max Gardner Award Administrative Advisory Committee, 2016-2017

GRADUATE STUDENTS

THESIS SUPERVISOR AND COMMITTEE CHAIR

Pauline D. Ellis, M.Sc., 1985. Department of Genetics, University of Edinburgh
Nicola Wadham, M.Sc., 1986. Department of Genetics, University of Edinburgh
Patricia M. Pignatelli, M.Phil., 1988. Department of Genetics, University of Edinburgh
Chaoqiang Lai, Ph.D., 1990. Department of Genetics, University of Edinburgh. Current position: Scientist, USDA, Tufts University
Robert McMahon, Ph.D., 1992. Department of Genetics, University of Edinburgh. Current position: Senior researcher, Department of Pathology, University of Cambridge, England
Wyatt Mangum, Ph.D. 1995. Department of Genetics, North Carolina State University. Current position: self-employed
Marjorie Gurganus, Ph.D. 1997. Department of Genetics, North Carolina State University. Current position: Patent lawyer
Grażyna Fedorowicz, M.S. 2000. Department of Genetics, North Carolina State University. Current position: Research associate, Genentech
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Indrani Ganguly, Ph.D. 2003. Department of Genetics, North Carolina State University. Current position: Self-employed
Gretchen Geiger-Thornsberry, Ph.D. 2003. Department of Genetics, North Carolina State University. Current position: Assistant Professor, Department of Biological Sciences, Northwest Missouri State University, Maryville, Missouri
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POSTDOCTORAL RESEARCH ASSOCIATES

Anthony E. Shrimpton, Department of Genetics, University of Edinburgh, 1985-1988. (Co-director of research, with A. J. Leigh Brown). Current position: Senior Scientist, Western General Hospital, Edinburgh, UK

Michael S. Jackson, Department of Genetics, North Carolina State University, 1988-1990. Current position: Royal Society Fellow, Department of Genetics, University of Newcastle

Richard F. Lyman, Department of Genetics, North Carolina State University, 1988-1994. Current position: Senior Researcher, Department of Genetics, North Carolina State University

Chaoqiang Lai, Department of Genetics, North Carolina State University, 1990-1991. Current position: Scientist, USDA, Tufts University

James D. Fry, Department of Genetics, North Carolina State University, 1992-1994. Current position: Associate Professor, Department of Biology, University of Rochester

Sergey V. Nuzhdin, Department of Genetics, North Carolina State University, 1993-1997. Current position: Professor, University of Southern California

Elena Pasyukova, Department of Genetics, North Carolina State University and Institute of Molecular Genetics, Moscow, Russia. 1995. Current Position: Head, Laboratory of Genomic Variation, Institute of Molecular Genetics of the Russian Academy of Sciences, Moscow, Russia

Marta L. Wayne, Department of Genetics, North Carolina State University, 1994-1999. Current position: Professor, Department of Zoology, University of Florida, Gainesville

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Maria DeLuca, Department of Genetics, North Carolina State University, 1999-2000; 2002. Current position: Research Assistant Professor, School of Public Health, University of Alabama at Birmingham

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Juan José Fanara, Department of Genetics, North Carolina State University, 1999-2002. Current position: Associate Professor, Department of Ecology, Genetics and Evolution, Ciudad Universitaria Pab II,

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Bryn Gaertner, Department of Genetics, North Carolina State University, 2012-2013. Current position: Postdoctoral fellow, Department of Molecular Biosciences, Northwestern University

Jason Peiffer, Department of Biological Sciences, North Carolina State University, 2012-2014. Current position, Data Analyst, Pioneer Hybrid International

Megan Carnes, Department of Biological Sciences, North Carolina State University, 2014-2015. Current Position: Postdoctoral Fellow, NIEHS

Terry Campbell, Department of Biological Sciences, North Carolina University, 2009-2015. Current Position: unemployed.

Shanshan Zhou, Department of Biological Sciences, North Carolina State University IBC postdoctoral fellow, 2011-present

Wen Huang, Department of Biological Sciences, North Carolina State University IBC postdoctoral fellow, 2011-present

Logan Everett, Department of Biological Sciences, North Carolina State University IBC postdoctoral fellow, 2014-present

Chad Highfill, Department of Biological Sciences, North Carolina State University, 2016-present

TEACHING EXPERIENCE

UNIVERSITY OF EDINBURGH (1980-1987)

Genetics 3A (third year undergraduate general genetics); 8 lectures in population and quantitative genetics; molecular evolution.
Genetics 3B (third year undergraduate). Advanced course in evolutionary genetics; 50 hours of lectures and 40 hours of practicals/tutorials. Lecture topics covered population genetics, quantitative genetics, evolutionary theory (including molecular evolution), and statistics. The practicals were designed to give experience in problem solving and statistical analysis, as well as the execution of a small research project studying evolution in Drosophila populations.
Genetics 4h (genetics honours undergraduates). 12 lectures in population and quantitative genetics.
Diploma/M.Sc in Animal Breeding (postgraduate course). 12 lectures in population and quantitative genetics, plus tutorials.

NORTH CAROLINA STATE UNIVERSITY (1987 - PRESENT)

Genetics 703 Population and Quantitative Genetics; 3 credit hours, 45 lecture hours. 1988-2008.
Genetics 641 Graduate colloquium in genetics; 2 credit hours, 30 lecture hours. Spring 1990. "Mapping Quantitative Trait Loci"; co-taught with C. Stuber and B. S. Weir.
Genetics 810P Graduate colloquium in genetics; 2 credit hours, 30 lecture hours. Fall 1999. “Genetics of Speciation”; co-taught with M. Purugganan.
Summer Institute in Statistical Genetics, Quantitative Genetics Module, 1996-2005; Behavior Genetics Module, 2004-2005.
Genetics 810-001 Evolutionary Genomics Journal Club. Offered yearly Fall semester.
Genetics 820D Professional development course, 2005, 2007, 2010, 2012, 2014, 2016; co-taught with R. R. H. Anholt.
Genetics 810-002 Behavioral Genetics, 2008, 2010; co-taught with R. R. H. Anholt.

PUBLICATION BIBLIOGRAPHY

REFEREED PUBLICATIONS

1. Zouros, E., Golding, B. E. & Mackay, T. F. C. 1977. The effect of combining alleles into electrophoretic classes on detecting linkage disequilibrium. Genetics 85: 543-550. PMCID: PMC1224587

2. Mackay, T. F. C. & Doyle, R. W. 1978. An ecological genetic analysis of the settling behaviour of a marine polychaete. I. Probability of settlement and gregarious behaviour. Heredity 40: 1-12.

3. Mackay, T. F. C. 1980. Genetic variance, fitness, and homeostasis in varying environments: An experimental check of the theory. Evolution 34: 1219-1222.

4. Mackay, T. F. C. 1981. Genetic variation in varying environments. Genet. Res. 37: 79-93.

5. Mackay, T. F. C. 1984. Jumping genes meet abdominal bristles: hybrid dysgenesis-induced quantitative variation in *Drosophila melanogaster.* Genet. Res. 44: 231-237.

6. Mackay, T. F. C. 1985. Transposable element-induced response to artificial selection in

Drosophila melanogaster. Genetics 111: 351-374. PMCID: PMC1202648

7. Mackay, T. F. C. 1985. A quantitative genetic analysis of fitness and its components in *Drosophila melanogaster.* Genet. Res. 47: 59-70.

8. Partridge, L., Mackay, T. F. C. & Aitken, S. 1985. Male mating success and fertility in *Drosophila melanogaster*. Genet. Res. 46: 279-285.

9. Mackay, T. F. C. 1986. Transposable element-induced fitness mutations in *Drosophila melanogaster*. Genet. Res. 48: 77-87.

10. Mackay, T. F. C. 1987. Transposable element-induced polygenic mutations in *Drosophila melanogaster*. Genet. Res. 49: 225-233.

11. Bjorklund, T., Engstrom, G., Mackay, T. F. C. & Liljedahl, L. E. 1988. Search for age-dependent as compared to mutagen-induced mutations on the *X* chromosome affecting viability in *Drosophila melanogaster* males. Gén. Sél. Evol. 20: 409-416.

12. Pignatelli, P. M. & Mackay, T. F. C. 1989. Hybrid dysgenesis-induced response to selection in *Drosophila melanogaster*. Genet. Res. 54: 183-195.

13. Lai, C. & Mackay, T. F. C. 1990. Hybrid dysgenesis-induced quantitative variation on the *X* chromosome of *Drosophila melanogaster.* Genetics 124: 627-636. PMCID: PMC1203956

14. Mackay, T. F. C. & Langley, C. H. 1990. Molecular and phenotypic variation in the *achaete-scute* region of *Drosophila melanogaster*. Nature 348: 64-66.

15. Shrimpton, A. E., Mackay, T. F. C. & Leigh Brown, A. J. 1990. Transposable element-induced response to artificial selection in *Drosophila melanogaster*: Molecular analysis of selection lines. Genetics 125: 803-811. PMCID: PMC1204106

16. Mackay, T. F. C., Lyman, R. F. & Jackson, M. S. 1992. Effects of *P* element insertions on quantitative traits in *Drosophila melanogaster.* Genetics 130: 315-332. PMCID: PMC1204852

17. Mackay, T. F. C., Lyman, R. F., Jackson, M. S., Terzian, C. & Hill, W. G. 1992. Polygenic mutation in *Drosophila melanogaster*: Estimates from divergence among inbred strains. Evolution 46: 300-316.

18. Keightley, P. D., Mackay, T. F. C. & Caballero, A. 1993. Accounting for bias in estimates of the rate of polygenic mutation. Proc. Roy. Soc. Lond. (B) 253: 291-296.

19. Lai, C. & Mackay, T. F. C. 1993. Mapping and characterization of *P*-element-induced mutations at quantitative trait loci in *Drosophila melanogaster.* Genet. Res. 61: 177-193.

20. Lai, C., Lyman, R. F., Long, A. D., Langley, C. H. & Mackay, T. F. C. 1994. Naturally occurring variation in bristle number and DNA polymorphisms at the *scabrous* locus in *Drosophila melanogaster*. Science 266: 1697-1702.

21. Mackay, T. F. C., Fry, J. D., Lyman, R. F. & Nuzhdin, S. V. 1994. Polygenic mutation in *Drosophila melanogaster*: Estimates from response to selection of inbred strains. Genetics 136: 937-951. PMCID: PMC1205898

22. Nuzhdin, S. V. & Mackay, T. F. C. 1994. Direct determination of retrotransposon transposition rates in *Drosophila melanogaster.* Genet. Res. 63: 139-144.

23. Fry, J. D., DeRonde, K. A. & Mackay, T. F. C. 1995. Polygenic mutation in *Drosophila melanogaster*: Genetic analysis of selection lines. Genetics 139: 1293-1307. PMCID: PMC1206457

24. Long, A. D., Mullaney, S. L., Reid, L. A., Fry, J. D., Langley, C. H. & Mackay, T. F. C. 1995. High resolution mapping of genetic factors affecting abdominal bristle number in *Drosophila melanogaster*. Genetics 139: 1273-1291. PMCID: PMC1206456

25. Mackay, T. F. C. 1995. The genetic basis of quantitative variation: numbers of sensory bristles of *Drosophila melanogaster* as a model system. Trends Genet. 11: 464-470.

26. Mackay, T. F. C., Lyman, R. F. & Hill, W. G. 1995. Polygenic mutation in *Drosophila melanogster*: Non-linear divergence among unselected strains. Genetics 139: 849-859. PMCID: PMC1206385

27. Nuzhdin, S. V., Fry, J. D. & Mackay, T. F. C. 1995. Polygenic mutation in *Drosophila melanogaster*: The causal relationship of bristle number to fitness. Genetics 139: 861-872. PMCID: PMC1206386

28. Nuzhdin, S. V. & Mackay, T. F. C. 1995. The genomic rate of transposable element movement in *Drosophila melanogaster*. Mol. Biol. Evol. 12: 180-181.

29. Anholt, R. R. H., Lyman, R. F. & Mackay, T. F. C. 1996. Effects of single *P* element insertions on olfactory behavior in *Drosophila melanogaster*. Genetics 143: 293-301. PMCID: PMC1207262

30. Fry, J. D., Heinsohn, S. L. & Mackay, T. F. C. 1996. The contribution of new mutations to genotype-environment interaction for fitness in *Drosophila melanogaster*. Evolution 50: 2316-2327.

31. Long, A. D., Mullaney, S. L., Mackay, T. F. C. & Langley, C. H. 1996. Genetic interactions between naturally occurring alleles at quantitative trait loci and mutant alleles at candidate loci affecting bristle number in *Drosophila melanogaster*. Genetics 144: 1497-1518. PMCID: PMC1207703

32. Lyman, R. F., Lawrence, F., Nuzhdin, S. V. & Mackay, T. F. C. 1996. Effects of single *P* element insertions on bristle number and viability in *Drosophila melanogaster*. Genetics 143: 277-292. PMCID: PMC1207261

33. Mackay, T. F. C. 1996. The nature of quantitative genetic variation revisited: lessons from *Drosophila* bristles. BioEssays 18: 113-121.

34. Mackay, T. F. C., & Fry, J. D. 1996. Polygenic mutation in *Drosophila melanogaster*: Genetic interactions between selection lines and candidate quantitative trait loci. Genetics 144: 671-688. PMCID: PMC1207559

35. Mackay, T. F. C., Hackett, J. B., Lyman, R. F., Wayne, M. L. & Anholt, R. R. H. 1996. Quantitative genetic variation of odor-guided behavior in a natural population of *Drosophila melanogaster*. Genetics 144: 727-735. PMCID: PMC1207563

36. Nuzhdin, S. V., Pasyukova, E. G. & Mackay, T. F. C. 1996. Positive association between *copia* transposition rate and copy number in *Drosophila melanogaster*. Proc. Roy. Soc. Lond. B 263: 823-831.

37. Nuzhdin, S. V., Pasyukova, E. G., Dilda, C. & Mackay, T. F. C. 1997. Sex-specific quantitative trait loci affecting longevity in *Drosophila melanogaster*. Proc. Natl. Acad. Sci. USA 94: 9734-9739. PMCID: PMC23259

38. Nuzhdin, S. V., Pasyukova, E. G. & Mackay, T. F. C. 1997. Accumulation of transposable elements in laboratory lines of *Drosophila melanogaster*. Genetica 100: 167-175.

39. Schug, M. D., Mackay, T. F. C. & Aquadro, C. F. 1997. Low mutation rates of microsatellite loci in *Drosophila melanogaster*. Nature Genet. 15: 99-102.

40. Wayne, M. L., Hackett, J. B. & Mackay, T. F. C. 1997. Quantitative genetics of ovariole number in *Drosophila melanogaster*. I. Segregating variation. Evolution 51: 1156-1163.

41. zur Lage, P., Shrimpton, A. E., Mackay, T. F. C. & Leigh Brown, A. J. 1997. Genetic and molecular analysis of *smooth*, a quantitative trait locus affecting bristle number in *Drosophila melanogaster*. Genetics 146: 607-618. PMCID: PMC1208001

42. Currie, D. B., Mackay, T. F. C. & Partridge, L. 1998. Pervasive effects of *P* element mutagenesis on body size in *Drosophila melanogaster*. Genet. Res. 72: 19-24.

43. Fedorowicz, G. M., Fry, J. D., Anholt, R. R. H. & Mackay, T. F. C. 1998. Epistatic interactions between *smell-impaired* loci in *Drosophila melanogaster*. Genetics 148: 1885-1891. PMCID: PMC1460070

44. Fry, J. D., Heinsohn, S. L. & Mackay, T. F. C. 1998. Heterosis for viability, fecundity, and male fertility in *Drosophila melanogaster*: Comparison of mutational and standing variation. Genetics 148: 1171-1188. PMCID: PMC1460047

45. Fry, J. D., Nuzhdin, S. V., Pasyukova, E. G. & Mackay, T. F. C. 1998. QTL mapping of genotype-environment interaction for fitness in *Drosophila melanogaster*. Genet. Res. 71: 133-141.

46. Gurganus, M. C., Fry, J. D., Nuzhdin, S. V., Pasyukova, E. G., Lyman, R. F. & Mackay, T. F. C. 1998. Genotype-environment interaction for quantitative trait loci affecting sensory bristle number in *Drosophila melanogaster*. Genetics 149: 1883-1898. PMCID: PMC1460274

47. Lai, C., McMahon, R., Young, C., Mackay, T. F. C. & Langley, C. H. 1998. *que mao*, a *Drosophila* bristle locus, codes for geranylgeranyl pyrophosphate synthase. Genetics 149: 1051-1061. PMCID: PMC1460199

48. Long, A. D., Lyman, R. F., Langley, C. H. & Mackay, T. F. C. 1998. Two sites in the *Delta* gene region contribute to naturally occurring variation in bristle number in *Drosophila melanogaster*. Genetics 149: 999-1017. PMCID: PMC1460197

49. Lyman, R. F. & Mackay, T. F. C. 1998. Candidate quantitative trait loci and naturally occurring variation for bristle number in *Drosophila melanogaster*: The *Delta-Hairless* gene region. Genetics 149: 983-998. PMCID: PMC1460192

50. Mackay, T. F. C. & Lyman, R. F. 1998. Polygenic mutation in *Drosophila melanogaster*: Genotype × environment interaction for spontaneous mutations affecting bristle number. Genetica 102/103: 199-215.

51. Schug, M. D., Hutter, C. M., Wetterstrand, K. A., Gaudette, M. S., Mackay, T. F. C. & Aquadro, C. F. 1998. The mutation rate of di-, tri- and tetranucleotide repeats in *Drosophila melanogaster*. Mol. Biol. Evol.15: 1751-1769.

52. Wayne, M. L. & Mackay, T. F. C. 1998. Quantitative genetics of ovariole number in *Drosophila melanogaster*. II. Mutational variation and genotype-environment interaction. Genetics 148: 201- 210. PMCID: PMC1459805

53. Gurganus, M. C., Nuzhdin, S. V., Leips, J. W. & Mackay, T. F. C. 1999. High resolution mapping of quantitative trait loci affecting sternopleural bristle number in *Drosophila melanogaster*. Genetics 152: 1585-1604. PMCID: PMC1460718

54. Lyman, R. F., Lai, C. & Mackay, T. F. C. 1999. Linkage disequilibrium mapping of molecular polymorphisms at the *scabrous* locus associated with naturally occurring variation in bristle number in *Drosophila melanogaster*. Genet. Res. 74: 303-311.

55. Nuzhdin, S. V., Dilda, C. L & Mackay, T. F. C. 1999. The genetic architecture of selection response: Inferences from fine-scale mapping of bristle number quantitative trait loci in *Drosophila melanogaster*. Genetics 153: 1317-1331. PMCID: PMC1460816

56. Juenger, T. J., Puruggannan, M. D. & Mackay, T. F. C. 2000. Quantitative trait loci for floral morphology in *Arabidopsis thaliana*. Genetics 156: 1379-1392. PMCID: PMC1461322

57. Leips, J. & Mackay, T. F. C. 2000. Quantitative trait loci for lifespan in *Drosophila melanogaster*: Interactions with genetic background and larval density. Genetics 155: 1773-1788. PMCID: PMC1461186

58. Long, A. D., Lyman, R. F., Morgan, A. H., Langley, C. H. & Mackay, T. F.C. 2000. Both naturally occurring insertions of transposable elements and intermediate frequency polymorphisms at the *achaete-scute* Complex are associated with variation in bristle number in *Drosophila melanogaster*. Genetics 154: 1255-1269. PMCID: PMC1460986

59 Pasyukova, E. G., Vieira, C. & Mackay, T. F. C. 2000. Deficiency mapping of quantitative trait loci affecting longevity in *Drosophila melanogaster*. Genetics 156: 1129-1146. PMCID: PMC1461330

60. Vieira, C., Pasyukova, E. G., Zeng, S., Hackett, J. B., Lyman, R. F. & Mackay, T. F. C. 2000. Genotype-environment interaction for quantitative trait loci affecting lifespan in *Drosophila melanogaster*. Genetics 154: 213-227. PMCID: PMC1460900

61. Anholt, R. R. H., Fanara, J. J., Fedorowicz, G. M., Ganguly, I., Kulkarni, N., Mackay, T. F. C. & Rollmann, S. M. 2001. Functional genomics of odor-guided behavior in *Drosophila melanogaster*. Chem. Senses 26: 215-221.

62. Anholt, R. R. H. & Mackay, T. F. C. 2001. The genetic architecture of odor-guided behavior in *Drosophila melanogaster*. Behav. Genet. 31: 17-27.

63. Mackay, T. F. C. 2001. Quantitative trait loci in *Drosophila*. Nature Rev. Genet. 2: 11-20.

64. Mackay, T. F. C. 2001. The genetic architecture of quantitative traits. Annu. Rev. Genet. 35: 303-339.

65. Wayne, M. L., Hackett, J. B., Dilda, C. L., Nuzhdin, S. V., Pasyukova, E. G. & Mackay, T. F. C. 2001. Quantitative trait loci for fitness-related traits in *Drosophila melanogaster*. Genet. Res. 77: 107-116.

66. Dilda, C. L. & Mackay, T. F. C. 2002. The genetic architecture of *Drosophila* sensory bristle number. Genetics 162: 1655-1674. PMCID: PMC1462363

67. Fanara, J. J., Robinson, K. O., Rollmann, S., Anholt, R. R. H. & Mackay, T. F. C. 2002. *Vanaso* is a quantitative trait locus for *Drosophila* olfactory behavior. Genetics 162: 1321-1328. PMCID: PMC1462330

68. Geiger-Thornsberry, G. L. & Mackay, T. F. C. 2002. Association of single nucleotide polymorphisms at the *Delta* locus with genotype-environment interaction for sensory bristle number in *Drosophila melanogaster*. Genet. Res. 79: 211-218.

69. Kulkarni, N. H., Yamamoto, A., Robinson, K. O., Mackay, T. F. C. & Anholt, R. R. H. 2002. The DSC1 channel, encoded by the *smi60E* locus, contributes to odor-guided behavior in *Drosophila melanogaster*. Genetics 161: 1507-1516. PMCID: PMC1462207

70. Leips, J. and Mackay, T. F. C. 2002. The complex genetic architecture of Drosophila life span. Exp. Aging Res. 28: 361-390.

71. Lyman, R. F., Nevo, E. & Mackay, T. F. C. 2002. Variation in *Drosophila* sensory bristle number at "Evolution Canyon". Genet. Res. 80: 215-223.

72. Mackay, T. F. C. 2002. The nature of quantitative genetic variation for *Drosophila* longevity . Mech. Age. Dev. 123(2-3) 95-104.

73. Robin, C., Lyman, R. F., Long, A. D., Langley, C. H. & Mackay, T. F. C. 2002. *hairy*: A quantitative trait locus for Drosophila bristle number. Genetics 162: 155-164. PMCID: PMC1462234

74. Ungerer, M. C., Halldorsdottir, S. S., Modliszewski, J. L., Mackay, T. F. C. & Purugganan, M. D. 2002. Quantitative trait loci for inflorescence development in *Arabidopsis thaliana*. Genetics 160: 1133-1151. PMCID: PMC1462026

75. Weinig, C., Ungerer, M. C., Dorn, L. A., Kane, N. C., Toyonaga, Y., Halldorsdottir, S. S., Mackay, T. F. C., Purugganan, M. D. & Schmitt, J. 2002. Novel loci control variation in reproductive timing in *Arabidopsis thaliana* in natural environments. Genetics 162: 1875-1884. PMCID: PMC1462365

76. Anholt, R. R. H., Dilda, C. L., Chang, S., Fanara, J. J., Kulkarni, N. H., Ganguly, I., Rollmann, S. M., Kamdar, K. P. & Mackay, T. F. C. 2003. The genetic architecture of odor-guided behavior in Drosophila: Epistasis and the transcriptome. Nat. Genet. 35: 180-184.

77. Borrás, T., Morozova, T. V., Heinsohn, S. L., Lyman, R. F., Mackay, T. F. C. & Anholt, R. R. H. 2003. Transcription profiling in Drosophila eyes that overexpress the human glaucoma-associated TIGR/MYOC protein. Genetics 163: 637-645. PMCID: PMC1462450

78. De Luca, M., Roshina, N. V., Geiger-Thornsberry, G. L. Lyman, R. F., Pasyukova, E. G. & Mackay, T. F. C. 2003. *Dopa-decarboxylase* (*Ddc*) affects variation in Drosophila longevity. Nat. Genet. 34: 429-433.

79. Ganguly, I., Mackay, T. F. C. & Anholt, R. R. H. 2003. *Scribble* is essential for olfactory behavior in *Drosophila*. Genetics 164: 1447-1457. PMCID: PMC1462661

80. Norga, K. K., Gurganus, M. C., Dilda, C. L., Yamamoto, A., Lyman, R. F., Patel, P. H., Rubin, G. M., Hoskins, R. A., Mackay, T. F. C. & Bellen, H. J. 2003. Quantitative analysis of bristle number in Drosophila mutants identifies genes involved in neural development. Curr. Biol. 13: 1388-1397.

81. Ungerer, M. C., Halldorsdottir, S. S, Purugganan, M. C. & Mackay, T. F. C. 2003. Genotype-environment interactions at quantitative trait loci affecting inflorescence development in *Arabidopsis thaliana*. Genetics 165: 353-365. PMCID: PMC1462760

82. Weinig, C., Dorn, L. A., Kane, N. C., Ungerer, M. C., Halldorsdottir, S. S., German, Z. M., Toyonaga, Y., Mackay, T. F. C., Purugganan, M. D. & Schmitt, J. 2003. Heterogeneous selection at specific loci in natural environments in *Arabidopsis thaliana*. Genetics 165: 321-329. PMCID: PMC1462755

83. Anholt, R. R. H & Mackay, T. F. C. 2004. Genetic analysis of complex behaviors in *Drosophila*. Nat. Rev. Genet. 5: 838-849.

84. Geiger-Thornsberry, G. L. & Mackay, T. F. C. 2004. Quantitative trait loci affecting natural variation in *Drosophila* longevity. Mech. Ageing Dev. 125: 179-189.

85. Genissel, A., Pastinen, T., Dowell, A., Mackay, T. F. C. & Long, A. D. 2004. No evidence for an

association between common nonsynonymous polymorphisms in *Delta* and bristle number variation in natural and laboratory populations of *Drosophila melanogaster*. Genetics 166: 291-306. PMCID: PMC1470686

86. Harbison, S. T., Yamamoto, A. H., Fanara, J. J., Norga, K. K. & Mackay, T. F. C. 2004. Quantitative trait loci affecting starvation resistance in *Drosophila melanogaster*. Genetics 166: 1807-1823. PMCID: PMC1470806

87. Moehring, A. J. & Mackay, T. F. C. 2004. The quantitative genetic basis of male mating behavior in *Drosophila melanogaster*. Genetics 167: 1249-1263. PMCID: PMC1470936

88. Moehring, A. J., Li, J., Schug, M. D., Smith, S. G., DeAngelis M., Mackay, T. F. C. & Coyne, J. A., 2004. Quantitative trait loci for sexual isolation between *Drosophila simulans* and *D. mauritiana*. Genetics 167: 1265-1274. PMCID: PMC1470931

89. Pasyukova, E. G., Nuzhdin, S. V., Morozova, T. V. & Mackay, T. F. C. 2004. Accumulation of transposable elements in the genome of *Drosophila melanogaster* is associated with a decrease in fitness. J. Heredity 95: 284-290.

90. Pasyukova, E. G., Roshina, N. V. & Mackay, T. F. C. 2004. *shuttle craft*: A candidate quantitative trait gene for *Drosophila* life span. Aging Cell 3: 297-307.

91. Carbone, M. A., Llopart, A., DeAngelis, M., Coyne, J. & Mackay. T. F. C. 2005. Quantitative trait loci affecting the difference in pigmentation between *Drosophila yakuba* and *D. santomea*. Genetics 171: 211-225. PMCID: PMC1456512

92. Harbison, S. T., Chang, S., Kamdar, K. P. & Mackay, T. F. C. 2005. Quantitative genomics of starvation stress resistance in *Drosophila*. Genome Biology 6: R36. PMCID: PMC1088964

93 Lstibùrek, M., Mullin, T. J., Mackay, T. F. C., Huber D. A. & Li, B. 2005. Positive assortative mating with family size as a function of predicted parental breeding values. Genetics 171: 1311-1320. PMCID: PMC1456834

94. Mackay, T. F. C., Heinsohn, S. L., Lyman, R. F., Moehring, A. J., Morgan, T. J. & Rollmann, S. M. 2005. Genetics and genomics of *Drosophila* mating behavior. Proc. Natl. Acad. Sci. USA. 102: 6622-6629. PMCID: PMC1131870

95. Mackay, T. F. C., Lyman, R. F. & Lawrence, F. 2005. Polygenic mutation in *Drosophila melanogaster*: Mapping spontaneous mutations affecting sensory bristle number. Genetics 170: 1723-1735. PMCID: PMC1449762

96. Mackay, T. F. C. & Lyman, R. F. 2005. *Drosophila* bristles and the nature of quantitative genetic variation. Phil. Trans. R. Soc. B 360: 1513-1527. PMCID: PMC1569512

97. Rollmann, S. M., Robinson, K. O., Mackay, T. F. C. & Anholt, R. R. H. 2005. Pinocchio, a novel protein expressed in the antenna, contributes to olfactory behavior in *Drosophila melanogaster*. J. Neurobiol. 63: 146-158.

98. Wayne, M. L., Korol, A. & Mackay, T. F. C. 2005. Microclinal variation for ovariole number and body size in *Drosophila melanogaster*. Genetica 123: 263-270.

99. Carbone, M. A., Jordan, K. W., Lyman, R. F., Harbison, S. T., Leips, J., DeLuca, M., Awadalla, P. & Mackay, T. F. C. 2006. Phenotypic variation and natural selection at *Catsup*, a pleiotropic quantitative trait gene in *Drosophila*. Curr. Biol. 16: 912-919.

100. Edwards, A. C., Rollmann, S. M., Morgan, T. J. & Mackay, T. F. C. 2006. Quantitative genomics of aggressive behavior in *Drosophila melanogaster*. PLoS Genetics 2: e154. PMCID: PMC1564424

101. Jordan, K. W., Morgan, T. J. & Mackay, T. F. C. 2006. Quantitative trait loci for locomotor behavior in *Drosophila melanogaster*. Genetics 174: 271-284. PMCID: PMC1569784

102. Leips, J., Gilligan, P. & Mackay, T. F. C. 2006. Quantitative trait loci with age-specific effects on fecundity in *Drosophila melanogaster*. Genetics 172: 1595-1605. PMCID: PMC1456283

103. Mackay, T. F. C. & Anholt, R. R. H. 2006. Of flies and man: Drosophila as a model for human complex traits. Ann. Rev. Genomics Hum. Genetics 7: 339-367.

104. Moehring, A. J., Llopart, A. Elwyn, S., Coyne, J. A. & Mackay, T. F. C. 2006. The genetic basis of prezygotic reproductive isolation between *Drosophila santomea* and *D. yakuba* due to mating preference. Genetics 173: 215-223. PMCID: PMC1461457

105. Moehring, A. J., Ana Llopart, A., Elwyn, S., Coyne, J. A. & Mackay, T. F. C. 2006. The genetic basis of postzygotic reproductive isolation between *Drosophila santomea* and *D. yakuba* due to hybrid male sterility. Genetics 173: 225-233. PMCID: PMC1461443

106. Morgan, T. J. & Mackay, T. F. C. 2006. Quantitative trait loci for thermotolerance phenotypes in *Drosophila melanogaster*. Heredity 96: 232-242.

107. Morozova, T.V., Anholt, R. R. H & Mackay, T. F. C. 2006. Transcriptional response to alcohol exposure in *Drosophila melanogaster*. Genome Biology 7: R95. PMCID: PMC1794562

108. Rollmann, S. M., Magwire, M. M., Morgan, T. J., Özsoy, E. D., Yamamoto, A., Mackay, T. F. C. & Anholt, R. R. H. 2006. Pleiotropic fitness effects of the *Tre1/Gr5a* region in *Drosophila*. Nat. Genet. 38: 824-829.

109. Sambandan, D., Yamamoto, A., Fanara., J. J., Mackay, T. F. C. & Anholt, R. R. H. 2006. Dynamic genetic interactions determine odor-guided behavior in *Drosophila melanogaster*. Genetics 174: 1349–1363. PMCID: PMC1667092

110. Wilson, R. H., Morgan, T. J. & Mackay, T. F. C. 2006. High resolution mapping of quantitative trait loci affecting increased life span in *Drosophila melanogaster*. Genetics 173: 1455-1463. PMCID: PMC1526659

111. Jordan, K. W., Carbone, M. A., Yamamoto, A., Morgan, T. J. & Mackay, T. F. C. 2007. Quantitative

genomics of locomotor behavior in *Drosophila melanogaster*. Genome Biology 8: R172. PMCID: PMC2375002

112. Lai, C. Q., Parnell, L., Lyman, R. F., Ordovas, J. M. & Mackay, T. F. C. 2007. Candidate genes affecting Drosophila life span identified by integrating microarray gene expression analysis and QTL mapping. Mech. Ageing Dev. 128: 237-249.

113. Lai, C. Q., Leips, J., Zou, W., Roberts, J. F., Wollenberg, K. R., Parnell, L. D., Zeng, Z. B., Ordovas, J. M. & Mackay, T. F. C. 2007. Speed-mapping quantitative trait loci using microarrays. Nat. Methods 10: 839-841.

114. Mackay, T. F. C. & Anholt, R. R. H. 2007. Ain't misbehavin'? Genotype-environment interactions and the genetics of behavior. Trends Genet. 23: 311-314.

115. Morozova, T. V., Anholt, R. R. H. & Mackay, T. F. C. 2007. Phenotypic and transcriptional response to selection for alcohol sensitivity in *Drosophila melanogaster*. Genome Biology 8: R231. PMCID: PMC2246305

116. Riedl, C. A. L., Riedl, M., Mackay, T. F. C. & Sokolowski, M. B. 2007. Genetic and behavioral analysis of natural variation in *Drosophila melanogaster* pupation position. Fly 1: http://www.landesbioscience.com/journals/fly/article/3830

117. Rollmann, S. M., Yamamoto, A., Goossens, T., Zwarts, L., Callaerts, P., Norga, K., Mackay, T. F. C. & Anholt, R. R. H. 2007. The early neurodevelopmental gene *Semaphorin 5c* is essential for olfactory behavior in adult *Drosophila*. Genetics 176: 947-956. PMCID: PMC1894621

118. Wang, P., Lyman, R. F., Shabalina, S. A., Mackay, T. F. C. & Anholt, R. R. H. 2007. Association of polymorphisms in odorant-binding protein genes with variation in olfactory response to benzaldehyde in Drosophila. Genetics 177: 1655-1665. PMCID: PMC2147940

119. Rollmann, S. M., Edwards, A. C., Yamamoto, A., Zwarts, L., Callaerts, P., Norga, K., Mackay, T. F. C. & Anholt, R. R. H. 2008. Pleiotropic effects of *Drosophila neuralized* on complex behaviors and brain structure. Genetics 179: 1327-1336. PMCID: PMC2475736

120. Sambandan, D., Carbone, M. A., Anholt, R. R. H. & Mackay, T. F. C. 2008. Phenotypic plasticity and genotype by environment interaction for olfactory behavior in *Drosophila melanogaster*. Genetics 179: 1079-1088. PMCID: PMC2429861

121. Yamamoto, A., Zwarts, L., Callaerts, P., Norga, K., Mackay, T. F. C. & Anholt, R. R. H. 2008. Neurogenetic networks for startle-induced locomotion in *Drosophila melanogaster*. Proc. Natl. Acad. Sci. USA 105: 12393-12398. PMCID: PMC2527922

122. Ayroles, J. F., Carbone, M. A., Stone, E. A., Jordan, K. W., Lyman, R. F., Magwire, M. M., Rollmann, S. M., Duncan, L. H., Lawrence, F., Anholt, R. R. H. & Mackay, T. F. C. 2009. Systems genetics of complex traits in *Drosophila melanogaster*. Nat. Genet. 41: 299-307. PMCID: PMC2752214

123. Carbone, M. A., Ayroles, J. F., Yamamoto, A., Morozova, T. V., West, S. A., Magwire, M. M., Mackay, T. F. C. & Anholt, R. R. H. 2009. Overexpression of myocilin in the *Drosophila* eye activates the unfolded protein response: Implications for glaucoma. PLoS ONE 4: e4216. PMCID: PMC2615221

124. Edwards, A. C. & Mackay, T. F. C. 2009. Quantitative trait loci for aggressive behavior in *Drosophila melanogaster.* Genetics 182: 889-897. PMCID: PMC2710167

125. Edwards, A. C., Ayroles, J. F., Stone, E. A., Carbone, M. A., Lyman, R. F. & Mackay, T. F. C. 2009. A transcriptional network associated with natural variation in *Drosophila* aggressive behavior. Genome Biology 10: R76. PMCID: PMC2728530

126. Edwards, A. C., Zwarts, L., Yamamoto, A. Callaerts, P. & Mackay, T. F. C. 2009. Mutations in many genes subtly affect aggressive behavior in *Drosophila melanogaster.* BMC Biology 7: 29. PMCID: PMC2707370

127. Flint, J. & Mackay, T. F. C. 2009. Genetic architecture of quantitative traits in mice, flies and humans. Genome Res. 19: 723-733. PMCID: PMC3647534

128. Harbison, S. T., Carbone, M. A., Ayroles, J. F., Stone, E. A., Lyman, R. F. & Mackay, T. F. C. 2009. Co-regulated transcriptional networks contribute to natural genetic variation in *Drosophila sleep.* Nat. Genet. 41: 371-375. PMCID: PMC2683981

129. Harbison, S. T., Mackay, T. F. C. & Anholt, R. R. H. 2009. Understanding the neurogenetics of sleep: Progress from *Drosophila*. Trends Genet. 25: 262-269.

130. Mackay, T. F. C. 2009. The genetic architecture of complex behaviors: Lessons from *Drosophila*. Genetica 136: 295-302.

131. Mackay, T. F. C., Stone, E. A. & Ayroles, J. F. 2009. The genetics of quantitative traits: Challenges and prospects. Nat. Rev. Genet. 10: 565-577.

132. Manolio, T. A., Collins, F. S., Cox, N. J., Goldstein, D. B., Hindorff, L. A., Hunter, D. J., McCarthy, M. I., Ramos, E. M., Cardon, L. R., Chakravarti, A., Cho, J. H., Guttmacher, A. E., Kong, A., Kruglyak, L., Mardis, E., Rotimi, C. N., Slatkin, M., Valle, D., Whittemore, A. S., Boehnke, M., Clark, A., Eichler, E. E., Gibson, G., Haines, J. L., Mackay, T. F. C., McCarroll, S. A. & Visscher, P. M. 2009. Finding the missing heritability of complex diseases. Nature 461: 747-753. PMCID: PMC2831613

133. Morozova, T. V., Ayroles, J. F., Jordan, K. W., Duncan, L. H., Carbone, M. A., Lyman, R. F., Stone, E. A., Govindaraju, D. R., Ellison, C. R., Mackay, T. F. C. and Anholt, R. R. H. 2009. Alcohol sensitivity in Drosophila: Translational potential of systems genetics. Genetics 83: 733-745. PMCID: PMC2766331

134. Yamamoto, A., Anholt, R. R. H. & Mackay, T. F. C. 2009. Epistatic interactions attenuate mutations affecting startle behaviour in *Drosophila melanogaster*. Genet. Res. 91: 373-382.

135. Zhou, S., Stone, E. A., Mackay, T. F. C. & Anholt, R. R. H. 2009. Plasticity of the chemoreceptor repertoire in *Drosophila melanogaster*. PLoS Genetics 5: e1000681. PMCID: PMC2750752

136. Arya, G. H., Weber, A. L., Wang, P., Magwire, M. M., Serrano Negron, Y. L., Mackay, T. F. C. & Anholt, R. R. H. 2010. Natural variation, functional pleiotropy and transcriptional contexts of odorant binding protein genes in *Drosophila melanogaster*. Genetics 186: 1475–1485. PMCID: PMC2998325

137. Clowers, K. J., Lyman. R. F., Mackay, T. F. C. & Morgan, T. J. 2010. Genetic variation in *senescence marker protein-30* is associated with natural variation in cold tolerance in Drosophila. Genet. Res. 92: 103-113.

138. DesRoches, C. E., Busto, M., Riedl, C. A. L., Mackay, T. F. C. & Sokolowski, M. B. 2010. Quantitative trait locus mapping of geotaxis behavior in *Drosophila melanogaster*. Genet. Res. 92: 167-174.

139. Jumbo-Lucioni, P., Ayroles, J. F., Chambers, M. M., Jordan, K. W., Leips, J., Mackay, T. F. C & De Luca, M. 2010. Systems genetics analysis of body weight and energy metabolism traits in *Drosophila melanogaster*. BMC Genomics 11: 297. PMCID: PMC2880307

140. Mackay, T. F. C. 2010. Mutations and quantitative genetic variation: Lessons from *Drosophila*. Phil. Trans. Roy. Soc. B 365: 1229-1239.

141. Magwire, M. M., Yamamoto, A., Carbone, M. A., Roshina, N. V., Pasyukova, E. G., Morozova, T. V. & Mackay, T. F. C. 2010. Quantitative and molecular genetic analyses of mutations increasing *Drosophila* life span. PLoS Genetics 6: e1001037. PMCID: PMC2912381

142. Rollmann, S. M., Wang, P., Date, P., West, S. A., Mackay, T. F. C. & Anholt, R. R. H. 2010. Odorant receptor polymorphisms and natural variation in olfactory behavior in *Drosophila melanogaster*. Genetics 186: 687–697. PMCID: PMC2954467

143. Wang, P., Lyman, R. F., Mackay, T. F. C. & Anholt, R. R. H. 2010. Natural variation in odorant recognition among odorant binding proteins in *Drosophila melanogaster*. Genetics 184: 745-758. PMCID: PMC2845343

144. Zhou, S., Mackay, T. F. C & Anholt, R. R. H. 2010. Tuning the chemosensory window: A fly's perspective. Fly 4: 230-235.

145. Aitman, T. J., Boone, C., Churchill, G. A., Hengartner, M. O., Mackay, T. F. C. & Stemple, D. L. 2011. The future of model organisms in human disease research. Nat. Rev. Genet. 12: 575-582.

146. Ayroles, J. F., Laflamme, B. A., Stone, E. A., Wolfner, M. F. & Mackay, T. F. C. 2011. Functional genome annotation of *Drosophil*a seminal fluid proteins using transcriptional genetic networks. Genet. Res. 93: 387-395.

147. Morozova, T. V., Mackay, T. F. C. & Anholt, R. R. H. 2011. Transcriptional networks for alcohol sensitivity in *Drosophila melanogaster*. Genetics 187: 1193–1205. PMCID: PMC3070527

148. Zwarts, L., Magwire, M. M., Carbone, M. A., Yamamoto, A., Versteven, M., Anholt, R. R. H., Callaerts, P. & Mackay, T. F. C. 2011. Complex genetic architecture of *Drosophila* aggressive behavior. PNAS 108: 17070-17075. PMCID: PMC3193212

149. Anholt, R. R. H. & Mackay, T. F. C. 2012. Genetics of aggression. Annu. Rev. Genet. 46: 145-164.

150. Huang, W., Richards, S., Carbone, M. A., Zhu, D., Anholt, R. R. H., Ayroles, J. F., Duncan, L., Jordan, K. W., Lawrence, F., Magwire, M. M., Warner, C. B., Blankenburg, K., Han, Y., Javaid, M., Jayaseelan, J., Jhangiani, S. N., Muzny, D., Ongeri, F., Perales, L., Wu, Y.-Q., Zhang, Y., Zou, X., Stone, E. A., Gibbs, R. A. & Mackay, T. F. C. 2012. Epistasis dominates the genetic architecture of *Drosophila* quantitative traits. PNAS 109: 15553-15559. PMCID: PMC3465439

151. Jordan, K.W., Craver, K. L., Magwire, M. M., Cubilla, C. E., Mackay, T. F. C. & Anholt, R. R. H. 2012. Genome wide association for sensitivity to chronic oxidative stress in *Drosophila melanogaster*. PLoS ONE 7: e38722. PMCID: PMC3371005

152. Jumbo-Lucioni, P., Bu, S., Harbison, S. T., Slaughter, J. C., Mackay, T. F. C., Moellering, D. R. & De Luca. M. 2012. Nuclear genomic control of naturally occurring variation in mitochondrial function in *Drosophila melanogaster*. BMC Genomics 13: 659. PMCID: PMC3526424

153. Mackay, T. F. C., Richards, S., Stone, E. A., Barbadilla, A., Ayroles, J. F., Zhu, D., Casillas, S., Han, Y., Magwire, M. M., Cridland, J. M., Richardson, M. F., Anholt, R. R. H., Barrón, M., Bess, C., Blankenburg, K. P., Carbone, M. A., Castellano, D., Chaboub, L., Duncan, L., Harris, Z., Javaid, M., Jayaseelan, J. C., Jhangiani, S. N., Jordan, K. W., Lara-Garduno, F., Lawrence, F., Lee, S. L., Librado, P., Linheiro, R. S., Lyman, R. F., Mackey, A. J., Munidasa, M., Muzny, D. M., Nazareth, L., Newsham, I., Perales, L., Pu, L.-L., Qu, J., Ràmia, M., Reid, J. G., Rollmann, S. M., Rozas, J., Saada, N., Turlapati, L., Worley, K. C., Wu, Y.-Q., Yamamoto, A., Zhu, Y., Bergman, C. M., Thornton, K. R., Mittelman, D. & Gibbs, R. A. 2012. The *Drosophila melanogaster* Genetic Reference Panel. Nature 482: 173-178. PMCID: PMC3683990

154. Massouras, A., Waszak, S. M., Albarca, M., Hens, K., Ayroles, J. F., Dermitzakis, E. T., Stone, E. A., Mackay, T. F. C. & Deplancke, B. 2012. The *cis*-regulatory architecture of gene expression variation in *Drosophila*. PLoS Genetics 8: e1003055. PMCID: PMC3499359

155. Morozova, T. V., Goldman, D. Mackay, T. F. C. & Anholt, R. R. H. 2012. The genetic basis of alcohol consumption: Multiple phenotypes, many genes, complex networks. Genome Biology 13: 239. PMCID: PMC3334563

156. Ober, U., Ayroles, J. F., Stone, E. A., Richards, S., Gibbs, R. A., Stricker, C., Gianola, D., Schlather, M., Mackay, T. F. C. & Simianer, H. 2012. Using whole genome sequence data to predict phenotypic traits in *Drosophila melanogaster*. PLoS Genetics 8: e1002685. PMCID: PMC3342952

157. Swarup, S. Harbison, S. T., Hahn, L. E., Morozova, T. V., Yamamoto, A., Mackay, T. F. C. & Anholt, R. R. H. 2012. Extensive epistasis for olfactory behavior, sleep and waking activity in *Drosophila melanogaster*. Genet. Res. 94: 9-20. PMCID: PMC3283907

158. Weber, A. L., Khan, G. F., Magwire, M. M., Tabor, C. L., Mackay, T. F. C. & Anholt, R. R. H. 2012. Genome-wide association for oxidative stress resistance in *Drosophila melanogaster*. PLoS ONE 7: e34745. PMCID: PMC3319608

159. Zhou, S., Campbell, T. G., Mackay, T. F. C. & Anholt, R. R. H. 2012. Phenotypic plasticity of the *Drosophila* transcriptome. PLoS Genetics 3: e11002593. PMCID: PMC33154

160. Harbison, S. T., McCoy, L. J. & Mackay, T. F. C. 2013. Genome-wide association study of sleep in *Drosophila melanogaster*. BMC Genomics 14: 281. PMCID: PMC3644253

161. Swarup, S., Huang, W., Mackay, T. F. C & Anholt, R. R. H. 2013. Analysis of natural variation reveals neurogenetic networks for *Drosophila* olfactory behavior. Proc. Natl. Acad. Sci. USA. 110:1017-1022. PMCID: PMC3549129

162. Wilson, R. H., Lai, C. Q., Lyman, R. F. & Mackay, T. F. C. 2013. Quantitative genetics and genomics of postponed senescence in *Drosophila*. Mech. Ageing Dev. 134: 79-88. PMCID: PMC3918434

163. Anholt, R. R. H. & Mackay, T. F. C. 2014. Dissecting the genetic architecture of behavior in *Drosophila melanogaster*. Curr. Opinion Behav. Sci., in press.

164. Ellis, L. L., Huang, W., Quinn, A. M., Ahuja, A., Alfrejd, B., Gomez, F. E., Hjelmen, C. E., Moore, K. L., Mackay, T. F. C., Johnston, J. S. & Tarone, A. M. 2014. Intrapopulation genome size variation in *D. melanogaster* reflects life history variation and plasticity. PLoS Genetics 10: e1004522. PMCID: PMC4109859.

165. Huang, W., Massouras, A., Inoue, Y., Peiffer, J., Ràmia, M., Tarone, A. M., Turlapati, L., Zichner, T., Zhu, D., Lyman, R. F., Magwire, M. M., Blankenburg, K., Carbone, M. A., Chang, K., Ellis, L. L., Fernandez, S., Han, Y., Highnam, G., Hjelmen, C. E., Jack, J. R., Javaid, M., Jayaseelan, J., Kalra, D., Lee, S., Lewis, L., Munidasa, M., Ongeri, F., Patel, S., Perales, L., Perez, A., Pu, L., Rollmann, S. M., Ruth, R., Saada, N., Warner, C., Williams, A., Wu, Y.-Q., Yamamoto, A., Zhang, Y., Zhu, Y., Anholt, R. R. H., Korbel, J. O., Mittelman, D., Muzny, D. M., Gibbs, R. A., Barbadilla, A., Johnston, J. S., Stone, E. A., Richards, S., Deplancke, B. & Mackay, T. F. C. 2014. Natural variation in genome architecture among 205 *Drosophila melanogaster* Genetic Reference Panel lines. Genome Res. 24: 1193-1208. PMCID: PMC4079974.

166. Mackay, T. F. C. 2014. Epistasis and quantitative traits: Using model organisms to study gene-gene interactions. Nat. Rev. Genetics 15: 22-33. PMCID: PMC3918431

167. Montgomery, S. L., Huang, W., Anholt, R. R. H., Mackay, T. F. C & Rand, M. D. 2014. Genome-wide association analysis of tolerance to methylmercury toxicity in Drosophila implicates myogenic and neuromuscular developmental pathways. PLoS ONE 9: e110375. PMCID: PMC4215868

168. Morozova, T. V., Mackay, T. F. C. & Anholt, R. R. H. 2014. Genetics and genomics of alcohol sensitivity. Mol. Genet. Genomics 289: 253-269. PMCID: PMC4037586

169. Zhou, S., Mackay, T. F. C. & Anholt, R. R. H. 2014. Transcriptional and epigenetic responses to

mating and aging in *Drosophila melanogaster*. BMC Genomics 15: 927.

170. Anholt, R. R. H & Mackay, T. F. C. 2015. Dissecting the genetic architecture of behavior in *Drosophila melanogaster*. Curr. Opin. Behav. Sci. 2: 1-7. PMCID: PMC4507818

171. Arya, G. H., Magwire, M. M., Huang, W., Serrano-Negron, Y. L., Mackay, T. F. C. & Anholt, R. R. H. 2015. The genetic basis for variation in olfactory behavior in *Drosophila melanogaster*. Chem. Senses 40: 233-243. PMCID: PMC4398050

172. Carnes, M. U., Campbell, T. Huang, W. , Butler, D. G., Carbone, M. A., Duncan, L. H., Harbajan, S. V., King, E. M., Peterson, K. R., Weitzel, A., Zhou, S., & Mackay, T. F. C. 2015. The genomic basis of postponed senescence in *Drosophila melanogaster*. PLoS ONE 10: e0138569. PMCID: PMC4574564

173. Gaertner, B. E., Ruedi, E. A., McCoy, L. J., Moore, J. M., Wolfner, M. F. & Mackay, T. F. C. 2015. Heritable variation in courtship patterns in *Drosophila melanogaster*. G3 5: 531-539. PMCID: PMC4390569

174. Dembeck, L. M., Böröczky, K., Huang, W., Schal, C., Anholt, R. R. H. & Mackay, T. F. C. 2015. Genetic architecture of natural variation in cuticular hydrocarbon composition in *Drosophila melanogaster*. eLife 4: e09861. PMCID: PMC4749392

175. Dembeck, L. M., Huang, W., Carbone, M. A. & Mackay, T. F. C. 2015. Genetic basis of natural variation in body pigmentation in *Drosophila melanogaster*. Fly 9: 75-81.

176. Dembeck, L. M., Huang, W., Magwire, M. M., Lawrence, F., Lyman, R. F. & Mackay, T. F. C. 2015. Genetic architecture of abdominal pigmentation in *Drosophila melanogaster*. PLoS Genetics PLoS Genet 11: e1005163. PMCID: PMC4416719

177. Garlapow, M. E., Huang, W., Yarboro, M. T., Peterson, K. R. & Mackay, T. F. C. 2015. Quantitative genetics of food intake in *Drosophila melanogaster*. PLoS ONE 10: e0138129. PMCID: PMC4574202

178. Huang, W. Carbone, M. A., Magwire, M. M., Peiffer, J. A., Lyman, R. F., Stone, E. A., Anholt, R. R. H. & Mackay, T. F. C. 2015. Genetic basis of transcriptome diversity in *Drosophila melanogaster*. PNAS 112: E6010-E6019. PMCID: PMC4640795

179. Ivanov, D. K., Escott-Price, V., Ziehm, M., Magwire, M. M., Mackay, T. F. C., Partridge, L. & Thornton, J. M. 2015. Longevity GWAS using the *Drosophil*a Genetic Reference Panel. J. Gerontol. A Biol. Sci. Med. Sci. 70: 1470-1478. PMCID: PMC4631106

180. Morozova, T. V., Huang, W., Pray, V. A., Whitham, T., Anholt, R. R. H. & Mackay, T. F. C. 2015. Polymorphisms in early neurodevelopmental genes affect natural variation in alcohol sensitivity in adult Drosophila. BMC Genomics 16: 865. PMCID: PMC4624176

181. Morgante, F., Sørensen, P., Sorensen, D. A., Maltecca, C. & Mackay, T. F. C., 2015. Genetic architecture of micro-environmental plasticity in *Drosophila melanogaster*. Scientific Reports 5: 9785. PMCID: PMC4421828

182. Ober, U., Magwire, M. M., Huang, W., Schlather, M., Simianer, H. & Mackay, 2015. Accounting for genetic architecture improves sequence based genomic prediction for a *Drosophila* fitness trait. PLoS One 10: e0132980. PMCID: PMC4500411

183. Ramaswami, G., Deng, P., Zhang, R., Carbone, M. A., Mackay, T. F. C. & Li, J. B. 2015. Genetic mapping uncovers *cis*-regulatory landscape of RNA editing. Nat. Comm. 6: 8194. PMCID: PMC4573499

184. Shorter, J. R., Couch, C. R., Huang, W., Carbone, M. A., Peiffer, J., Anholt, R. R. H. & Mackay, T. F. C. 2015. Epistasis and the genetic architecture of *Drosophila* aggressive behavior. PNAS 112: E3555-E3563. PMCID: PMC4500262

185. Shorter, J. R., Geisz, M., Özsoy, E., Magwire, M. M., Carbone, M. A. & Mackay, T. F. C. 2015. The effects of royal jelly on fitness traits and gene expression in *Drosophila melanogaster*. PLoS ONE 10: e0134612. PMCID: PMC4520568

186. Sorensen, P. S., de los Campos, G., Morgante, F., Mackay, T. F. C. & Sorensen, D. 2015. Genetic control of environmental variation of two quantitative traits of *Drosophila melanogaster* revealed by whole-genome sequencing. Genetics 201: 487-497. PMCID: PMC4596664

187. Zwarts, L., Vanden Broeck, L., Cappuyns, E., Ayroles, J. F., Magwire, M. M., Vulsteke, V., Clements, J., Mackay, T. F. C & Callaerts, P. 2015. The genetic basis of natural variation in mushroom body size in *Drosophila melanogaster*. Nat. Comm. 6: 10115. PMCID: PMC4682101

188. Carbone, M. A., Yamamoto, A., Huang, W., Lyman, R. A., Meadors, T. B., Yamamoto, R., Anholt, R. R. & Mackay, T. F. C. 2016. Genetic architecture of natural variation in visual senescence in *Drosophila*. PNAS 113: E6620-E6629. PMCID: PMC5087026

189. Edwards, S. M., Sørensen, I. F., Sarup, P., Mackay, T. F. C. and Sørensen, P. 2016. Genomic prediction for quantitative traits is improved by mapping variants to Gene Ontology categories in *Drosophila melanogaster*. Genetics 203: 1871-1883. PMCID: PMC4981283

190. Friedenberg, S. G., Meurs, K. M. & Mackay, T. F. C. 2016. Evaluation of artificial selection in Standard Poodles using whole genome sequencing. Mamm. Genome, in press.

191. Garlapow, M. E., Everett, L. J., Zhou, S., Gearhart, A. W., Fay, K. A., Huang, W., Morozova, T. V., Arya, G. H., Turlapati, L., St. Armour, G., Hussain, Y. N., McAdams, S. E., Fochler, S., & Mackay, T. F. C., 2016. Genetic and genomic response to selection for food consumption in *Drosophila melanogaster*. Behav. Genet., in press.

192. Gerken, A. R., Mackay, T. F. C. & Morgan, T. J. 2016. Artificial selection on chill-coma recovery time in *Drosophila melanogaster*: Direct and correlated responses to selection. J. Thermal Biol. 59: 77-85.

193. He, X., Zhou, S., St. Armour, G. E., Mackay, T. F. C. & Anholt, R. R. H. 2016. Epistatic partners of neurogenic genes modulate Drosophila olfactory behavior. Genes, Brain, Behav. 15: 280-290. PMCID: PMC4841442

194. Huang, W., Lyman, R. F., Lyman, R., Carbone, M. A., Harbison, S. T., Magwire, M. M and Mackay, T. F. C. 2016. Spontaneous mutation and the origin and maintenance of quantitative genetic variation. eLife 5: e14625

195. Huang, W. & Mackay, T. F. C. 2016. The genetic architecture of quantitative traits cannot be inferred from variance component analysis. PLoS Genetics 12): e1006421. PMCID: in progress.

196. Hunter, C. M., Huang, W., Mackay, T. F. C. & Singh, N. D., 2016. The genetic architecture of natural variation in recombination rate in *Drosophila melanogaster*. PLoS Genetics 12: e1005951. PMCID: PMC4817973

197. Reidl, C., Oster S., Busto, M., Mackay, T. F. C. & Sokolowski, M. 2016. Natural variability in Drosophila larval and pupal NaCl tolerance. J. Insect. Physiol. 88: 15-23. PMCID: PMC4811728

198. Shorter, J. R., Dembeck, L. M., Everett, L. J., Morozova, T. V., Arya, G. H., Turlapati, L., St. Amour, G. E., Schal, C., Mackay, T. F. C. & Anholt, R. R. H. 2016. *Obp56h* modulates mating behavior in *Drosophila melanogaster*. G3: Genes, Genomes, Genetics, 6: 3335-3342. PMCID: PMC5068952

199. Vonesch, S. C., Lamparter, D., Mackay, T. F. C., Bergmann, S. & Hafen, E. 2016. Genome-wide analysis reveals novel regulators of growth in *Drosophila melanogaster*. PLoS Genetics 12: e1005616. PMCID: PMC4709145

200. Zhou, S., Morozova, T. V., Hussain, Y. N., Luoma, S. E., McCoy, L., Yamamoto, A., Mackay, T. F. C. & Anholt, R. R. H. 2016. The genetic basis for variation in sensitivity to lead toxicity in *Drosophila melanogaster*. Environ. Health Perspect. 124: 1062-1070. PMCID: PMC4937873

INVITED PAPERS (CONFERENCE PROCEEDINGS, REVIEWS, COMMENTARIES)

1. Mackay, T. F. C. 1984. Jumping genes and quantitative variation. In *Proceedings of the 26th British Poultry Breeders Roundtable.*

2. Mackay, T. F. C. 1986. Transposable elements in genetic selection. pp. 113-121 in *Exploiting New Technologies in Animal Breeding: Genetic Developments*. Edited by C. Smith, J. W. B. King and J. C. McKay. Clarendon Press, Oxford.

3. Mackay, T. F. C. 1987. Speciation: Finding pieces of the puzzle. Nature 327: 279-280.

4. Mackay, T. F. C. 1988. Transposable element-induced quantitative genetic variation in *Drosophila.* pp. 219-235 in *Proceedings of the 2nd International Conference on Quantitative Genetics*. Edited by B. S. Weir, E. J. Eisen, M. M. Goodman and G. Namkoong. Sinauer, Sunderland, Mass.

5. Mackay, T. F. C. 1989. Transposable elements and fitness in *Drosophila melanogaster*. In *Proceedings of the XVI th International Congress of Genetics.* Genome 31: 284-295.

6. Mackay, T. F. C. 1989. Mutation and the origin of quantitative variation. pp. 113-119 in *Evolution and Animal Breeding: Reviews on Molecular and Quantitative Approaches in Honour of Alan Robertson.* Edited by W. G. Hill and T. F. C. Mackay. C. A. B. International, Wallingford.

7. Mackay, T. F. C. 1990. Alan Robertson (1920-1989). Genetics 125: 1-7.

8. Mackay, T. F. C. 1990. Distribution of effects of new mutations affecting quantitative traits. pp. 219-227 in *Proceedings of the 4th World Congress on Genetics Applied to Livestock Production.* Edited by W. G. Hill, R. Thompson and J. A. Woolliams. Organizing Committee, 4th World Congress on Genetics Applied to Livestock Production, Edinburgh.

9. Lai, C. & Mackay, T. F. C. 1990. Mapping and characterization of *P* element-induced polygenic mutations in *Drosophila melanogaster*. pp. 349-352 in *Proceedings of the 4th World Congress on Genetics Applied to Livestock Production*. Edited by W. G. Hill, R. Thompson and J. A. Woolliams. Organizing Committee, 4th World Congress on Genetics Applied to Livestock Production, Edinburgh.

10. Mackay, T. F. C. 1998. The nature of quantitative variation: Lessons from Drosophila. *Proceedings of the 6th World Congress on Genetics Applied to Livestock Production*.

11. Mackay, T. F. C. 1998. Quantitative genetics and phenotypic evolution. Evolution 52: 635-640

12. Mackay, T. F. C. 2000. Aging in the post-genomic era: simple or complex? Genome Biology 1(4): reports4018.1-4018.6. http://genomebiology.com/2000/1/4/reports/4018

13. Gibson, G. & Mackay, T. F. C. 2002. Enabling population and quantitative genomics. Genet. Res. 80: 1-6.

14. Hill, W. G. & Mackay, T. F. C. 2004. Douglas Falconer. Genetics 167: 1529-1536.

15. Mackay, T. F. C. 2004. The genetic architecture of quantitative traits: lessons from Drosophila. Curr. Opin. Genet. Dev. 14: 253-257.

16. Mackay, T. F. C. 2004. Douglas Scott Falconer (1913-2004). Heredity 93: 119-121.

17. Mackay, T. F. C. 2004. Methods for genetic dissection of complex traits. Sci. Aging Knowl. Environ. 2004 (17), pe17. [DOI: 10.1126/sageke.2004.17.pe17]

18. Mackay, T. F. C. 2004. Complementing complexity. Nat. Genet. 36: 1145-1147.

19. Mackay, T. F. C. 2007. Wild populations are smaller than we think: a commentary on 'Effective population size/adult population size ratios in wildlife: a review' by Richard Frankham. Genet Res. 89: 489.

20. Mackay, T. F. C. 2007. What prevents transposable elements from taking over the genome? A commentary on 'A test for the role of natural selection in the stabilization of transposable element copy number in a population of *Drosophila melanogaster*' by Elizabeth Montgomery, Brian Charlesworth and Charles H. Langley. Genet Res. 89: 433-434.

21. Mackay, T. F. C. 2009. Q&A: Genetic analysis of quantitative traits. J. Biol. 8: 23.

22. Mackay, T. F. C. 2009. A-maize-ing diversity. Science 325: 688-689.

23. Mackay, T. F. C. & Moore, J. H. 2014. Why epistasis is important for tackling complex human disease genetics. Genome Med. 6: 42. PMCID: PMC4062066.

24. Laland, K., Uller, T., Feldman, M., Sterelny, K., Müller, G. B., Moczek, A., Jablonka, E., Odling-Smee, J., Wray, G. A., Hoekstra, H. E., Futuyma, D. J., Lenski, R. E., Mackay, T. F. C., Schluter, D. & Strassmann, J. E. 2014. Does evolutionary theory need a rethink? Nature 514: 161-164.

BOOKS AND BOOK CHAPTERS

1. Hill, W. G. & Mackay, T. F. C. 1989. *Evolution and Animal Breeding: Reviews on Molecular and Quantitative Approaches in Honour of Alan Robertson*. 313 pp. C. A. B. International, Wallingford.

2. Falconer, D. S. & Mackay, T. F. C. 1996. *Introduction to Quantitative Genetics*, 4/e. Addison Wesley Longman.

3. *Encyclopedia of Ecology and Environmental Management.* 1996. Contributor, quantitative genetics and transposable element entries. Blackwell Science, Oxford.

4. Mackay, T. F. C. 2001. The genetic architecture of quantitative traits: Inferences from *Drosophila* sensory bristle number. Pp. 389-409 in *The Character Concept in Evolutionary Biology*, edited by G. P. Wagner. Academic Press, San Diego, CA.

5. Mackay, T. F. C. 2004. Genetic dissection of quantitative traits. Pp. 51-73 in *The Evolution of Population Biology: Modern Synthesis*, edited by. R. Singh and M. Uyenoyama. Cambridge University Press.

6. Mackay, T. F. C., Roshina, N. V., Leips, J. W. & Pasyukova, E. G. 2006. Complex genetic architecture of Drosophila longevity. Pp. 181-216 in *Handbook of the Biology of Aging, Sixth Edition*, edited by E. J. Masaro and S. N. Austad.

7. Anholt, R. R. H. & Mackay, T. F. C. 2010. *Principles of Behavioral Genetics*. Elsevier, Inc.

8. Anholt, R. R. H., Mackay, T. F. C. & Stone, E. A. 2014. Systems genetics of behavior in *Drosophila*. In *Handbook of Behavioral Genetics of* Drosophila melanogaster, edited by J. Dubnau.

9. Mackay, T. F. C. 2015. Epistasis for quantitative traits in *Drosophila*. Methods Mol. Biol. 1253: 47-70.

10. Mackay, T. F. C. 2015. The nature of quantitative genetic variation. Encyclopedia of Evolutionary Biology.

Dr. Trudy Mackay Campus Visit

Monday, May 29, 2017

7:00am depart from RDU	9:11am arrive at DFW (AA Flight 1349)
1:10pm depart from DFW	2:04pm arrive at CLL (AA Flight 2804)
Lodging	Guest Suites – University Center Reservation Number: 101856 Arrival Date: 5/29/17 Departure Date: 5/31/17 Suite: 1504 POC: Joni Groce 845-8901
2:30pm – 3:00pm	Tour of Texas A&M University
3:00pm – 3:45pm	Meet with Jerome Menet, BSBW 354 (Biological Sciences Bldg. West)
4:00pm – 4:30pm	Tour of lab with Drew Hillhouse and David Threadgill
4:30pm – 5:00pm	Meet with James Cai
5:30pm	Dinner at Madden's Casual Gourmet - 202 S Bryan Ave, Bryan, TX 979-779-2558 David Threadgill, Evelyn Castiglioni, Loren Skow

Tuesday, May 30, 2017

7:45am – 8:45am	Breakfast – The Hilton Breakfast Buffet – Penny Riggs, Fuller Bazer, Robert Burghardt, Terje Raudsepp
9:00am – 10:00am	Tour of the Equine Complex
10:00am – 10:30am	Break
10:30am – 11:30am	Drs. Mackay and Womack meeting with Dr. Junkins Jack K Williams Administration Building, Suite 305 *Park in Lot 54 in reserved space labeled "Hagler Institute for Advanced Study"
11:45am – 1:15pm	Lunch – Spencer Johnston, Vaishali Katju, Ulfar Bergthorsson
1:30pm – 2:00pm	Meet with Juliana Rangel Posada, HPCT 315
2:00pm – 2:30pm	Meet with Aaron Tarone, HPCT 420
2:30pm – 3:00pm	Meet with Zach Adelman, HPCT
3:00pm – 3:30pm	Meet with Spence Johnston, HPCT
3:45pm – 4:15pm	Meet with Jason Karpa (HSC Molecular & Cellular Med) 440 Reynolds Medical Building, room 238 – phone# 979-436-0767
4:30pm – 5:00pm	Meet with Dean Green
5:00pm	Escort Dr. Mackay back to MSC Suites
6:30pm	Dinner at Cenare - 404 University Dr E, College Station, TX 696-7311 Jane Welsh, David Threadgill, Ramesh Vemulapalli, Larry Suva
	Escort Dr. Mackay back to MSC Suites

Wednesday, May 31, 2017

7:45am – 9:00am	Breakfast – First Watch – Evelyn Castiglioni, Loren Skow, David Threadgill
10:32am depart from CLL	11:31am arrive at DFW (AA Flight 2819)
1:45pm depart from DFW	5:22pm arrive at RDU (AA Flight 2601)

5/25/2017 3:16 PM REVISED