

**2014 LARGE-SCALE APPLIED RESEARCH PROJECT COMPETITION:
GENOMICS AND FEEDING THE FUTURE
PRE-APPLICATION FORM**

Project Title: Genomics of Abiotic Stress Resistance in Wild and Cultivated Sunflowers

Estimated Total Budget: \$6,770,000

Amount Requested from Genome Canada (maximum 40% of Total Budget): \$2,708,000

Project Duration (up to a maximum of 4 years): 4 years

Project Leader

Name ¹	Loren H. Rieseberg
Affiliation	University of British Columbia
Address	Botany Department 3529-6270 University Blvd Vancouver, BC V6T 1Z4
Telephone	604-827-4540
E-mail	lriesebe@mail.ubc.ca
Date	
Signature ²	

Co-Project Leader

Name	John M. Burke
Affiliation	University of Georgia
Address	Department of Plant Biology Miller Plant Sciences Athens, GA 30602 USA
Telephone	706-583-5511
E-mail	jmburke@uga.edu
Date	
Signature ²	

Lead Organization (CEO, President or authorized representative)

Name of organization	University of British Columbia
Name of representative	Martin Kirk
Title	Director of Research Services
Date	
Signature ²	

Genome Centre CEO(s) or authorized representative(s)

Lead Centre ³	Genome BC	Co-lead Centre (if applicable)	
Name	Alan E. Winter	Name	
Date		Date	
Signature ²		Signature ²	
Additional Centre (if applicable)			
Name			
Date			
Signature ²			

¹ Project Leader is responsible for administrative and financial responsibilities of the project

² Signatures confirm acceptance of terms as outlined in the Meaning of Signatures

³ Administrative Centre for projects which have been identified as being co-led by two or more Genome Centres

RESEARCH AREAS AND KEYWORDS

Select the area(s) that relate(s) to the research proposed. If relevant to more than one area, use numbers to indicate the relative weighting (i.e., 1 = primary focus; 2 = secondary focus, etc.)

<input type="text" value="1"/>	Agriculture	<input type="text"/>	Energy	<input type="text"/>	Environment
<input type="text"/>	Fisheries	<input type="text"/>	Forestry	<input type="text" value="2"/>	GE ³ LS
<input type="text"/>	Human Health	<input type="text"/>	Mining	<input type="text"/>	Technology Development

Provide a **maximum** of five (5) words or phrases for each category (i.e., Research, and Methods and Technologies) that describes the proposed investigation.

CATEGORY	KEYWORDS
Research	Abiotic stress resistance, agricultural genomics, ecophysiology, evolutionary genomics, wild and cultivated sunflowers
Methods & Technologies	Association mapping, high-throughput genotyping and phenotyping, gene regulatory analyses, physiology of abiotic stress resistance, population genomic analyses

Provide a **maximum** of five (5) words or phrases for each category (i.e., Research questions, and Methods) that describes the proposed integrated GE³LS investigation.

CATEGORY	KEYWORDS
Research questions	Access and benefit sharing, international treaty framework, genetic resources, genomic data sharing, proprietary interests
Methods	Literature review, legal framework analysis, policy analysis, IP landscape review, interviews

Sharing of application and reviews

Where applicable, Genome Canada seeks your consent to share the information included in your pre-application and pre-application reviews, on a confidential basis, with the funding partners referenced in the RFA as well as co-funding partners arranged for by you and your Genome Centre(s).

I, the Project Leader **consent** to the sharing of the application and reviews with the organizations indicated above.

I, the Project Leader **do not consent** to the sharing of the application and reviews with the organizations indicated above.

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I. SUMMARY OF THE PROJECT

Food production must increase by 70 to 100% by 2050 to keep pace with predicted population growth and changes in diet. This task is exacerbated by ongoing changes in climate, heightened competition for land and water, and continued deceleration of yield increases from conventional breeding. To meet this challenge, crops must be developed that combine high yield with resistance to biotic and abiotic stress, and require lower inputs. Here we propose to identify traits and alleles that will allow such cultivars to be developed and to deliver these alleles to public and private breeding programs. Our focus is on sunflower, a globally important oilseed with production valued at \$20B/year, but we will apply new genome editing methods to determine the extent to which our discoveries can be applied to the improvement of other oilseeds.

Sunflower is ideal for the proposed research because of its diverse extremophile and cross-compatible wild relatives, which can be exploited for research and breeding. Because oilseed sunflower is grown widely in developing countries for food, it is the only oilseed in the Global Crop Diversity Trust's list of 25 priority food security crops. Canada is the world's 13th largest exporter of sunflower, but there is a supply deficit in North America of this healthy vegetable oil. Canadian production is now limited by salt and flooding, while low nutrients and drought limit sunflower production in Sub-Saharan Africa (and worldwide) and will become increasingly important in the southern prairies of Canada due to climate change. Wild plants have mechanisms to mitigate these challenges, but crops are far less resilient. System-level understanding of abiotic stress resistance can facilitate the development of improved varieties that can be grown on marginal farmlands currently unsuitable for crops.

The specific goals of this project are to: (1) assess resistance to drought, flooding, salt, and low nutrient stress in cultivated sunflower and its wild relatives using traditional and high-throughput phenotyping approaches; (2) associate variation in abiotic stress resistance with specific genes, regulatory networks, and/or causal variants; (3) determine the mechanistic basis of stress resistance via physiological and transcriptomic characterization of genotypes with divergent stress responses; (4) address major biological questions concerning the types of genes, their network positions, and the nature of physiological trade-offs involved in the evolution of abiotic stress resistance; (5) identify suitable stress resistance alleles (i.e., those exhibiting resistance in multiple genetic backgrounds, ideally with minimal tradeoffs) for use in sunflower breeding programs and potentially for improvement of other oilseeds; and (6) explore strategies for addressing significant negative impacts of international treaties on the use of plant genetic resources by private and public sector breeding programs in Canada and worldwide as part of our GE³LS research.

Deliverables are: (1) "next generation" germplasm resources (resistance alleles with minimal trade-offs in relevant genetic backgrounds), enabling sunflower breeders to put resistant, high-yielding cultivars in the field within three years of project end; and (2) strategies for mitigating barriers to R&D (e.g., uncertainties in IP and profit sharing) caused by international treaties.

The PIs are world leaders in plant genomics and are responsible for most of the genomic tools and resources available for sunflower. Many end-users are involved, including sunflower breeders from Canada, the USA, EU, S. America, and Sub-Saharan Africa, and are able to translate the findings to market. The GE³LS team has high expertise developed during, e.g., the Genome Canada-funded Genomics of Sunflower project, and has relationships with the Treaty Secretariat, industry leaders, legal and policy scholars, and non-governmental organizations.

Ten years out, if just 5% of Canadian lands affected by related soil problems became suitable for sunflowers, this would add 0.7 million hectares to production, with a gross production value ~\$1 billion annually, accompanied by reduced greenhouse gases through sunflower's nitrate mining. Stress-resistant cultivars will stabilize production in the face of abiotic stress in Sub-Saharan Africa, reducing the potential for famine. Worldwide impacts will be massive, as no other oilseed can maintain stable yields across as wide a range of environmental conditions as can improved sunflower cultivars.

II. RESEARCH PROPOSAL

A. INTRODUCTION

Over human history, the domestication and improvement of crop plants has achieved spectacular increases in yield over wild plants, enough to support a population explosion and the rise of modern civilization^{1,2}. However, in striving for maximal yield, the genetic changes caused by domestication were not entirely beneficial. Crop plants often exhibit reduced stress resistance compared to their wild relatives^{3,4}, perhaps due to selection for performance in optimal environments and to loss of resistance via trade-offs with productivity under ideal conditions⁵. This loss of resistance is especially troubling in the 21st century, as we struggle to increase crop productivity in the face of climate change, rapid population growth, and heightened competition for land and water⁶.

To reduce stress-induced yield loss and improve food security, efforts have increasingly focused on the development of stress-resistant crops. However, such improvement efforts require knowledge. What is the genetic basis of stress resistance? Can alleles be found within crop or wild gene pools that confer resistance across broad genetic backgrounds, but with minimal yield trade-offs? What is the influence of factors such as the position of a gene within a regulatory network on the occurrence and severity of possible trade-offs? How often are the same mutations, genes, and gene networks exploited by natural selection in the evolution of stress resistance across different species? We propose to address these basic biological questions through an investigation of the genomic and physiological basis of resistance to drought, flooding, salt, and low nutrient stress in wild and cultivated sunflowers. Cultivated sunflower, *Helianthus annuus*, is an ideal study system for this work because the productivity of this globally important oilseed and food security crop is limited by such stresses⁷, while it retains reproductive compatibility with wild relatives that are adapted to a variety of extreme environments, including desert, swamp, saline, and sand dune habitats.

The availability of cost-effective and efficient genomic technologies sets the stage for linking genomic information to agriculturally relevant phenotypes. However, it remains challenging to phenotype traits that are important for stress resistance on sufficiently large numbers of plants to permit genetic dissection^{8,9}. Multiple approaches are needed to meet this challenge, such as leaf carbon isotope ratio ($\delta^{13}\text{C}$), which can be used to efficiently estimate water-use efficiency integrated over the lifetime of the leaf^{10, 11} and sensor-based high-throughput phenotyping (HTP) systems, which have emerged as promising non-destructive approaches¹². Expected trade-offs between plant productivity and stress resistance represent another concern¹³. However, some stress resistance traits can evolve independently of growth potential or yield^{14,15} making it feasible to develop genotypes with both high yield potential and stress resistance.

A complementary approach to determining the genetic basis of abiotic stress resistance is the use of comparative population genomic data to identify adaptively important genes¹⁶. Such approaches, which associate allelic variation with relevant environmental variables, do not require the up-front collection of phenotypic data. As such, they serve as a useful complement to more intensive, trait-based approaches and provide an avenue for the efficient discovery of putatively adaptive alleles from materials that might otherwise not be evaluated.

The overarching goals of this project (Figure 1) are to:

- 1) Assess abiotic stress resistance (drought, flooding, salt, and low nutrients) in sunflower and its wild relatives using traditional phenotyping and sensor-based HTP approaches;
- 2) Associate variation in abiotic stress resistance and related traits in cultivated and wild sunflower with specific genes, regulatory networks, and/or causal genetic variants using genetic map-based and population genomics approaches;
- 3) Determine the mechanistic basis of stress resistance via in-depth physiological and transcriptional characterization of lines identified as being divergent in stress resistance in our large-scale, population-level phenotypic screens;

- 4) Identify suitable abiotic stress resistance alleles (i.e., those exhibiting resistance in a variety of genetic backgrounds, ideally with minimal trade-offs) for improvement of sunflower cultivars for Canadian and international markets and subsistence farming – and potentially for improvement of other oilseeds, especially soybean and canola;
- 5) Develop, characterize, and distribute “next generation” germplasm resources in the form of a multi-species, advanced generation intercross (MAGIC) population that will facilitate the efficient genetic analysis of complex trait variation in *Helianthus* and enable the rapid deployment of exotic alleles in breeding programs; and
- 6) Explore strategies for addressing significant negative impacts of international treaties on the use of plant genetic resources by private and public sector breeding programs in Canada and worldwide as part of our GE³LS research.

Our efforts align well with the RFA. Our project addresses:

“challenges that are relevant both in the Canadian context and also to Canada's international development priorities by providing sustainable, genomic-based solutions to problems of agriculture ... in developing countries. For example, research on how plants can better respond to abiotic and biotic stresses has the potential for considerable impact on global food security with applications in Canada and the developing world.” (RFA, p. 4).

In addition, the genomic information and resistance alleles provided by our project are expected to contribute the following focal topics of the RFA (p. 5): meeting the caloric demands of population growth, improving crop health, adapting crops to climate change, and lessening their footprint on the environment (by reducing need for external inputs such as fertilizers or water).

Our project was designed in collaboration with end-users (sunflower breeders) representing four government agencies (Ag Canada, INRA, the National Semi-Arid Resources Research Institute in Uganda, and the USDA) and five companies (Advanta Seeds, Biogemma, Dow AgroSciences, KWS Seeds, and NuSeed Americas), who are also contributing to the project by providing some of their most promising cultivars for inclusion in multi-parent advanced generation intercross (MAGIC) mapping population (see below), assistance with the crosses needed to develop this population, field-based evaluation of both association populations, and co-funding. The extensive involvement of sunflower breeders, combined with the financial backing of the Global Crop Diversity Trust for the developing country component of the project, will ensure that the genomic and physiological information generated by the project, as well the stress resistance alleles we identify, are rapidly deployed in breeding programs.

B. STUDY SYSTEM

Sunflower is one of the world's most important oilseed crops, with production valued at ca. \$20B/year (<http://faostat.fao.org>). Because sunflower is grown widely in developing countries and used primarily for food, it is the only oilseed included in the Global Crop Diversity Trust's list of 25 priority food security crops. Sunflower is also an important ornamental crop and source of confectionery seeds – the current focus of Canadian production. Canadian production is now limited by salt and flooding (yield loss is 100% when flooding or extreme salt stress occurs), while low nutrients and drought limit sunflower production in Sub-Saharan Africa (and worldwide) and will become increasingly important in the southern prairies of Canada due to climate change. Sunflower belongs to the genus *Helianthus*, which includes 49 wild species¹⁷, many of which are cross-compatible with the cultivated sunflower and occur in extreme environments, and therefore represent important reservoirs of valuable resistance alleles.

Sunflower has excellent genomic resources (<http://www.sunflowergenome.org>), which will be utilized in the current project for genomic-based agricultural applications. These resources, developed mainly by the PIs as part of a previously funded Genome Canada project, include numerous genetic mapping populations, SNP and expression arrays, a sequence-based physical map, ultra-dense genetic maps, an extensive transcriptome collection, a high quality reference sequence, and whole genome shotgun (WGS) re-sequencing data for 550 cultivated

and wild sunflower genotypes, including our full association mapping population (see below).

Sunflower germplasm collections comprise ~40,000 cultivated and wild accessions globally and have served as the basis for our development of a cultivated sunflower association mapping (SAM) population. This population is composed of 288 inbred lines that capture ca. 90% of the allelic diversity in the cultivated sunflower gene pool¹⁸. Genotypic characterization of this population using a 10,000 SNP array revealed that linkage disequilibrium (LD) decays rapidly across much of the genome¹⁹, thereby enabling high-resolution genetic studies of abiotic tolerance traits in a highly diverse population.

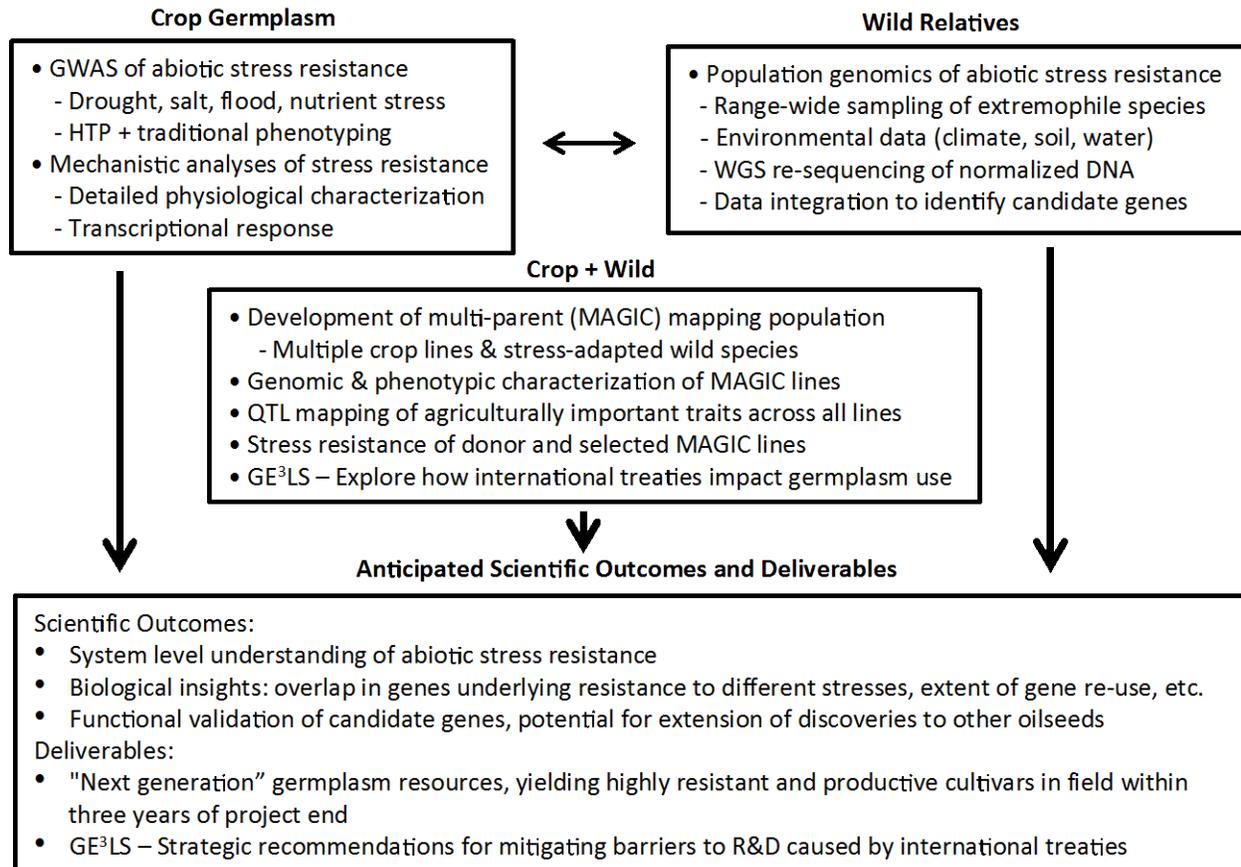


Figure 1. Overview of proposed activities, anticipated scientific outcomes, and deliverables

C. EXPERIMENTAL APPROACHES

Activity 1: Investigating abiotic stress resistance in cultivated sunflower

To assess the genetic and physiological basis of abiotic stress resistance in cultivated sunflower, we will phenotype stress resistance and related traits in separate, large-scale screens for drought, flooding, salt, and low nutrient stress, followed by GWAS to determine the genetic basis of variation in those traits. We will then select lines that exhibit notable differences in resistance to each stress for further characterization to better understand the mechanistic basis of the stress resistance under multiple stress levels relevant to field conditions.

Activity 1.1 - Phenotyping in large-scale screens

We will perform large-scale screens of cultivated sunflower (SAM population, 288 lines) for stress resistance and associated traits in separate experiments for drought, flooding, salt, and low nutrients. Depending on the stress, the screens will be conducted in the field, greenhouse, and/or growth room (Table 1). For each screen, we will implement two treatments (control and stressed) and three replicates. Where possible, the intensity and timing of the stress will be

chosen based on the results of preliminary studies that identify a level of stress that will reduce growth and/or yield by an average of ~30%.

Table 1. Large-scale phenotyping of SAM population.

Screen(s)	Location	Phenotypes
Drought stress	Field – Uganda and DREC ^a	Leaf and canopy traits (DREC only), phenological traits, leaf N and $\delta^{13}\text{C}$, yield traits, seed oil traits, and root architecture
Seedling drought stress	Growth rooms ^b	Biomass allocation (roots, stems, and leaves), root architecture, stem height and diameter, number of true leaves, and leaf N and $\delta^{13}\text{C}$
Flood stress ^b	Greenhouse	Relative height growth, biomass allocation, adventitious rooting, constitutive and induced lenticels, and constitutive and induced aerenchyma (stem and roots).
Flood stress	Field - Saskatchewan	Survivorship, relative height growth, phenological traits, yield traits, seed oil traits
Salt stress ^b	Greenhouse	Relative height growth, leaf characteristics, N, biomass allocation at harvest, and leaf ion concentrations (Na, K, Mg, Ca)
Salt Stress	Field- Saskatchewan	Relative height growth, leaf ion concentrations (Na, K, Mg, Ca), phenological traits, yield traits, seed oil traits
Low nutrient stress ^b	Greenhouse	Relative height growth, leaf characteristics, N, biomass allocation, N resorption proficiency and efficiency
Low nutrient stress	Field – Uganda	Phenological traits, leaf N and $\delta^{13}\text{C}$, yield traits, seed oil traits

^a Sensor-based HTP approaches for leaf and canopy traits will using tractor-mounted sensors will take place at the University of California's Desert Research & Extension Center (DREC)²⁰.

^bTwo screens will be performed, one at the seedling stage and one at the late vegetative stage.

Activity 1.2 - Genome-wide association studies of abiotic stress resistance and related traits

Following phenotypic characterization of the SAM population, we will use GWAS to identify alleles associated with variation in abiotic stress resistance and related traits, and to determine their potential suitability for use in marker-assisted breeding. This phase of our research will make use of the phenotypic data described above, as well as genotypic information (SNPs, structural variants and multi-locus haplotypes) extracted from WGS re-sequencing data previously obtained for the SAM population. These analyses are fairly straightforward, though care will be taken to minimize false positives due to population structure and relatedness^{21,22}. We also will test for genetic correlations between traits to identify alleles that lack severe antagonistic correlations that could result in unacceptable trade-offs with performance.

Activity 1.3 - Detailed ecophysiological characterization

For ecophysiological characterization, we will carry out a series of greenhouse, growth chamber, and field studies using multiple phenological stages and multiple levels of stress. For each stress, the most and least resistant lines (15 of each) will be replicated within treatments using experimental designs appropriate for the stress applications and characterized for a core set of traits including gas exchange (photosynthesis, stomatal conductance, instantaneous water-use efficiency), leaf lifetime, and specific root length^{23,24}.

Activity 1.4 - Transcriptomic analyses

In addition to the extensive ecophysiological characterization described above, we will compare the transcriptional responses of the lines that are most and least resistant to each stress. The evaluation of transcriptional responses will be conducted in growth rooms using four lines from the SAM population (2 resistant and 2 susceptible), 3 biological replicates, 4 stresses, 2 treatments (control and stressed), 5 time points, and 2 tissues (960 samples total). Stress

treatments will be applied at the 4-leaf stage and will continue for 10 days. Leaf and root tissue from seedlings will be harvested 24 hours after stress application to monitor expression changes due to acute stress, after 5 and 10 days to identify chronically expressed transcripts, and at 2 time points after initiation of recovery to determine the extent to which expression changes persist after a plant has recovered from a stress. RNAseq libraries from leaf and root tissue will be sequenced on an Illumina HiSeq, and gene co-expression network analysis will be employed to identify co-expression modules associated with specific stress responses, as well as modules that respond to multiple stresses^{25,26}. These co-expression networks will also provide insights into the putative functional modules within which our candidate stress resistance genes reside and their network positions and degree of connectedness to other members of a module²⁷.

Activity 2: Population genomic analyses of stress adaptation in the wild

To further dissect genomic regions underlying abiotic stress resistance, we will search for associations between SNPs and important ecological variables (climate, water, and soil characteristics) in natural populations of the wild species contributing to our multi-species mapping population (see below). We will obtain soil samples and seeds from 50 populations across the full range of each 4 extremophile species: *H. annuus* (tolerance to drought, flooding, and salt stress), *H. argophyllus* (drought, flooding, and low-nutrient stress), *H. debilis* (drought, salt, and low nutrient stress), and *H. petiolaris* (drought and low-nutrient stress). As far as possible, we will sample from geographically proximate, but ecologically divergent populations to reduce neutral correlations caused by population structure populations¹⁶. For genotypic characterization, we will conduct WGS re-sequencing of normalized libraries from 2,000 genotypes (50 populations x 10 individuals per population x 4 species). Sequencing from normalized libraries represents a cost-effective strategy for comprehensively sampling the gene space in sunflower, as well as providing sufficient SNPs for haplotype reconstruction.

To identify locally adapted alleles, we will search for correlations between SNP genotypes and spatially explicit environmental variables, including soil fertility data from each site and climatic variables from the WorldClim database²⁸. Analyses will be performed for each species independently using a Bayesian statistical method that controls for the neutral correlations due to population structure¹⁶. The results from these analyses will allow us to address major biological questions, including the extent of overlap in genes under selection for various stresses, the extent of gene re-use during adaptation in the different species, the types of genes under selection, and the positions of these genes within regulatory networks.

Activity 3: Development and characterization of a multi-species mapping populations

To facilitate the efficient genetic analysis of complex trait variation and to produce materials containing exotic alleles that can be readily deployed in breeding programs, we will develop a modified multi-parent advanced generation intercross (MAGIC) mapping population²⁹ that includes both cultivated and wild sunflower donors. Such populations combine the high power to detect quantitative trait loci (QTL) offered by biparental populations with the ability to assay a broader spectrum of diversity and improved resolution afforded by association mapping. Because sunflower is a hybrid crop, we will develop separate male and female populations. For each population, our crossing design will involve four elite breeding lines and four wild donors. Each wild donor will be successively combined with three elite lines to produce four different intermated populations that will ultimately be intercrossed in all pairwise combinations. We will then develop 600 recombinant inbred lines (RILs) for each population with equal representation from each of the six intercross pairs via multiple rounds of self-pollination.

The elite and wild donors have been chosen in consultation with our public and private partners to represent a broad cross-section of cultivated and wild sunflower diversity, including the four wild species chosen for population genomic analyses. The initial crosses are underway at UBC, with subsequent generations to be produced by our partners. The use of winter nurseries will speed population development, and we anticipate RIL availability by year 3 of the project. The populations will be genotyped using a 50k SNP array developed from our population genomic

analyses (above). We will evaluate these populations using the same general design and phenotyping methods outlined above for the SAM population. In addition, our public and private partners will evaluate one or both of these populations at multiple locations worldwide (e.g., Argentina, California, France, Saskatchewan, and Uganda). Map construction and QTL detection will follow established procedures³⁰. This work will thus result in the production and baseline characterization (including the mapping of QTLs underlying a variety of agriculturally important traits) of a highly valuable germplasm resource for the sunflower research and breeding community. This next generation germplasm resource and the accompanying genotypic information can be directly employed by our end users to rapidly move desired traits and alleles into their breeding programs through marker-assisted and/or genomic selection. In addition, for each stress, the 25 most and least resistant MAGIC lines from each population will be subjected to in-depth phenotypic characterization under control and stressed conditions to validate the results of our population genomic analyses.

Activity 4: Functional validation of candidate stress resistance genes

A subset of genes that are thought to have large impacts on drought, flooding, salt, or low nutrient resistance will be targeted for functional validation. We will prioritize genes that: (1) exhibit strong associations with resistance to one or more abiotic stresses; (2) show unusually strong correlations with the relevant environmental parameter(s) in natural populations; (3) display notable differences in sequence or gene expression; and/or (4) exhibit the signature of divergent natural selection. Several approaches will be employed for functional analyses, including transformation and RNAi in sunflower, complementation of homozygous knock-out lines in *Arabidopsis*, and the use of genome editing approaches to locate causal mutations³¹. For mutations displaying expected effects in *Arabidopsis*, we will introduce them into other crops as time and technology permits, starting with soybean and canola. Rieseberg's lab has had success with such approaches in sunflower and *Arabidopsis*³² and collaborator Parrott's group brings experience with the CRISPR/Cas system in soybean.

Activity 5: international treaties and use of plant genetic resources (GE3LS)

The goal of the GE3LS research is to ensure that the social and economic benefits of this project can be realized. At present, the Convention on Biological Diversity (CBD) and related International Treaty for Plant Genetic Resources in Food and Agriculture (Treaty) present hurdles to uptake of innovations in agricultural genomics.

The CBD, developed to address access and benefit-sharing of indigenous biological resources in developing nations, allows national regimes to restrict access to these resources, resulting in barriers to research and development. The Treaty was intended to alleviate these barriers by facilitating access to plant genetic resources under uniform benefit sharing terms. Signatories to the Treaty, which include Canada, Europe, and most developed and developing countries commit *inter alia* to share plant genetic resources for 64 key crops (including sunflower) according to a Standard Material Transfer Agreement (SMTA), which includes benefit sharing "from the use, including commercial, of plant genetic resources for food and agriculture [covered under the Treaty]." While not a signatory of the Treaty, the U.S. has made clear that it will honor SMTA obligations for materials in its National Plant Germplasm System (NPGS).

The Treaty has opened access to many resources. However, the impacts of SMTA obligations remain unclear: there is no guidance in the Treaty or SMTA, for example, on what use of Treaty resources triggers benefit sharing obligations, or how such obligations are modified by combination of Treaty resources with other non-Treaty germplasm. Further, it remains unclear whether the SMTA obligations apply to derivative or improved germplasm or to germplasm modified via new genome editing technologies. Even more, there is ambiguity as to whether data generated from Treaty resources (i.e. plant genomes) are also subject to the SMTA.

The net result of these uncertainties is that some companies avoid use of any genetic resources subject to the SMTA (H. Dempewolf, Global Crop Diversity Trust, pers. comm.), and may not

access innovative germplasm such as that proposed by this project. The Rieseberg lab recently witnessed this when a multinational corporation expressed interest but ultimately declined to use pre-bred germplasm generated by the Rieseberg lab because of the germplasm was subject to the Treaty SMTA.

To address such potential issues, the GE3LS team will communicate with scientific researchers throughout the process of identifying, accessing, and developing sunflower germplasm to track incorporation of Treaty and non-Treaty resources, as well as modifications to the material. In addition, the GE3LS team will interface with, among others, the Treaty Secretariat (including via participation in ongoing Working Groups), industry stakeholders, and legal and policy experts to develop strategies for navigating and resolving the ambiguities in interpretation of the CBD and Treaty. In addition to benefiting this project, the GE3LS work will also be of considerable interest in the legal/policy community as these are issues that face stakeholders for other crops.

Ultimately, the GE3LS team will generate (1) ongoing feedback to the project team on how to track use of SMTA and non-SMTA covered materials; (2) a publishable set of strategic recommendations for the project team and for other crop research teams about development in the context of these treaties; and (3) an analysis of potential pathways forward under the CBD and Treaty regimes, including recommended modifications in the SMTA language, to maximize innovation in agricultural genomics.

The GE3LS team has a high level of expertise on issues related to the CBD, Treaty and sharing of agricultural genomics data³³, developed in part during the Genome Canada-funded Genomics of Sunflower project. Emily Marden is involved in ongoing consultations with the Treaty Secretariat, and the governance working group of DivSeek, an emerging effort to share data related to crop diversity. She is thus well positioned to interface with entities in developing a strategic position for the project and conveying recommendations for change.

(D) SCIENTIFIC OUTCOMES AND DELIVERABLES

Our project will identify strategies, mechanisms, traits, and alleles that can be used to produce sunflower lines that are more resistant to drought, flooding, salt, and low nutrient stress, but with little or no impact on productivity under ideal conditions. We will also determine the types of genes (and their network positions) that are most likely to confer resistance across broad genetic backgrounds and with minimal yield trade-offs. This knowledge will move us closer to a systems-level understanding of the interactions between plants and their environment and will enable the development of smarter and more efficient strategies for breeding environmentally resilient cultivars in sunflower and has the potential to positively impact other crops.

Knowledge of the mechanisms and genetic architecture of abiotic stress resistance, coupled with identification and functional validation of key resistance alleles (and associated genotypic information), will lead to our main deliverables:

(1) “Next Generation” germplasm resources in the form of multi-species, advanced generation intercross populations (i.e., resistance alleles with minimal trade-offs in relevant genetic backgrounds) that will allow end-users to rapidly deploy exotic alleles in breeding programs using marker-assisted and/or genomic selection, yielding new highly resistant and productive cultivars; and

(2) Strategic recommendations for mitigating barriers to public and private breeding programs (e.g., uncertain IP and profit sharing obligations) resulting from international treaties; and our GE³LS team will suggest refinements to Working Groups of the Treaty Secretariat and other stakeholders to reduce the barriers found in the CBD and the Treaty.

We expect the new sunflower cultivars to be in the field within three years of project end, with significant economic benefits through expansion of sunflower production onto marginal lands and important social benefits through increased food security in Uganda and other developing countries.

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GANTT CHART

Genomics of Abiotic Stress in Cultivated and Wild Sunflowers Loren H. Rieseberg & John M. Burke

ACTIVITY	PLANNED START (01/10/15)	PLANNED DURATION (#Quarters)	ACTUAL START (dd/mm/yy)	ACTUAL DURATION (#Quarters)	% COMPLETE	QUARTER - 3 months Start Date 10/15															
						1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Activity 1: Abiotic stress resistance in cult. sunflower																					
Activity 1.1 - Phenotyping in large-scale screens	01/10/15	8																			
Activity 1.2 - GWAS of abiotic stress resistance	01/10/16	8																			
Activity 1.3 - Detailed ecophysiological characterization	01/10/16	8																			
Activity 1.4 - Transcriptomic analyses	01/10/16	8																			
Activity 2: Population genomics -stress adaptation in wild																					
Activity 2.1 - Collections	01/04/16	2																			
Activity 2.2 - Genotyping	01/10/16	4																			
Activity 2.3 - Analyses & publication	01/10/17	4																			
Activity 3: Development & characterization of MAGIC populations																					
Activity 3.1 - Population development	01/10/15	10																			
Activity 3.2 - Phenotyping in large-scale screens	01/04/17	6																			
Activity 3.3 - QTL analyses	01/04/17	6																			

Activity 3.4 - Detailed ecophysiological characterization	01/04/17	6																		
Activity 4: Functional validation of stress resistance genes	01/10/16	12																		
Activity 5: GE³LS																				
Activity 5.1 Tracking germplasm used and output	01/10/16	16																		
Activity 5.2 – Literature and policy review	01/10/16	8																		
Activity 5.3 – Develop strategies and interface with Treaty et al.	01/01/17	12																		
Activity 5.4 – Recommendation s for changes in policy & SMTA	01/01/18	8																		

planned

III. PROJECT TEAM

Last Name	First Name	Affiliation	Role ⁴	Time Commitment (hrs/week)	Description of Contribution & Reasons for Inclusion in Proposal
Rieseberg	Loren	University of British Columbia	Project co-leader	15	Will lead overall project. Past experience in managing large genomics projects. Pioneer in plant ecological genomics.
Burke	John	University of Georgia	Project co-leader	15	Will provide leadership on association mapping. Expert on sunflower genetics & genomics.
Donovan	Lisa	University of Georgia	Co-investigator	10	Will provide leadership on ecophysiological analyses. Expert on plant ecophysiology.
Langlade	Nicolas	INRA Toulouse	Co-investigator	10	Will lead transcriptomics component. Expert on sunflower molecular physiology.
Marden	Emily	University of British Columbia	Co-investigator	10	Will lead GE3LS component. Expert in CBD, Treaty & sharing of genomics data.
Hulke	Brent	USDA Fargo, ND	Co-investigator / End User	10	Will lead MAGIC pop. development & deploy resistance alleles in breeding program. Strong track record in molecular breeding.
Yeaman	Sam	University of Calgary	Co-investigator	10	Will lead population genomics component of project. Expert in population genomics & bioinformatics.
Stewart	Megan	University of British Columbia	Project Manager	40	Will provide project management & coordination.
Xiao	Jinhua	Dow Agrosiences	Collaborator / End User	5	Will contribute to MAGIC population development & evaluation & will deploy resistance alleles in breeding program. Strong track record in

⁴ Role includes: Project Leader, Co-Project Leader, Co-Applicant, End-User, Collaborator etc. Definitions of participant categories are provided in the [Guidelines for Funding Research Projects](#).

					molecular breeding.
Coque	Marie	Biogemma	Collaborator / End User	5	Will contribute to MAGIC population development & evaluation & will deploy resistance alleles in breeding program. Strong track record in molecular breeding.
Wieckhorst	Silke	KWS Seeds	Collaborator / End User	5	Will contribute to MAGIC population development & evaluation & will deploy resistance alleles in breeding program. Strong track record in molecular breeding.
Zambelli	Andrés	Advanta Seeds	Collaborator / End User	5	Will contribute to MAGIC population development & evaluation & will deploy resistance alleles in breeding program. Strong track record in molecular breeding.
May	Bill	Ag Canada	Collaborator / End User	5	Will lead field- based salt tolerance experiments & will deploy resistance alleles in breeding program. Strong track record in sunflower breeding.
Anyanga	Walter	National Semi-arid Resources Research Institute, Uganda	Collaborator / End User	10	Will contribute to MAGIC population evaluation & deploy resistance alleles in breeding program. Strong track record in sunflower breeding.
Gerdes	Jim	NuSeed Americas	Collaborator / End User	5	Will contribute to MAGIC population development & evaluation & will deploy resistance alleles in breeding program. Strong track record in molecular breeding.
Dechaine	Jennifer	Central Washington University	Collaborator	5	Will contribute to ecophysiological analyses. Expert in sunflower ecophysiology
Andrade-Sanchez	Pedro	University of Arizona	Collaborator	5	Will lead HTP at DREC. Expert in agricultural engineering.
Parrott	Wayne	University of Georgia	Collaborator	5	Will lead genome editing component. Expert in crop biotechnology.

IV. SOCIAL AND/OR ECONOMIC BENEFITS

A. BACKGROUND

Food production must double by 2050 to address population growth, but climate change will reduce yield gains of conventional crops. Crops are needed that combine high yield with resistance to biotic and abiotic stress, require lower inputs, and produce less environmental harm. Sunflower can partly fulfill this need because of its diverse extremophile and cross-compatible wild relatives, whose alleles can be exploited for breeding. It also is a major crop in its own right, ranking 12th in terms of area harvested (<http://faostat3.fao.org/home/E>), with a gross value of \$20 billion per year. Worldwide, it is an important food security crop in developing countries, with global use increasing rapidly (Khoury et al. 2014; *PNAS* 111:4001-4006). But barriers arise because of international treaties such as the Convention on Biological Diversity (CBD) and the International Treaty for Plant Genetic Resources in Food and Agriculture (Treaty), to the extent that some end users avoid use of genetic resources subject to the Treaty, and will not access innovative germplasm if Treaty resources are employed.

B. PROJECT DELIVERABLES AND SOCIAL AND ECONOMIC BENEFITS

The project will deliver new sunflower cultivars incorporating alleles from wild sunflower relatives, conferring resistance to drought, salt, flooding, and low nutrients. Knowledge of the genetic basis of stress resistance, plus identification and validation of resistance alleles (and associated genotypic information), will lead to our key deliverables: (1) “Next Generation” germplasm resources in the form of multi-species, advanced generation intercross populations (i.e., resistance alleles with minimal trade-offs in relevant genetic backgrounds) that will allow end-users to rapidly deploy exotic alleles in breeding programs using marker-assisted and/or genomic selection, yielding new highly resistant and productive cultivars; and (2) Strategies for mitigating barriers to public and private breeding programs (e.g., uncertain IP and profit sharing obligations) resulting from international treaties; and our GE³LS team will suggest refinements to the Treaty Secretariat to reduce the barriers found in the CBD and the Treaty.

Because of extensive participation of end-users in our project, strategies by our GE³LS team to minimize barriers to uptake, and the commercialization experience of the project lead, these new cultivars are expected in the field within three years of project end. Longer-term, other important oilseeds can be improved with similar techniques or more directly through the use of genome editing approaches, which may allow mutations that confer resistance in sunflower to be introduced into other oilseeds.

Canada has ~38 million ha of marginal farmlands (<http://www.nrel.gov/docs/fy10osti/46209.pdf>; Fig. 1). These lands are currently unsuitable for crops for a variety of reasons, including low nutrient soils (25% of land), salty soils (6%), and poor drainage (5%). Such marginal lands are, however, potentially suitable for improved sunflower cultivars. Within five years of the project’s end, we expect 1% of such marginal lands to be planted with improved cultivars, with a gross production value of ~\$200 million annually. After ten years, we expect 5% of these lands will be planted, adding 0.7 million ha to Canadian production (and ~\$1 billion annually). A market for this increase exists: North America can now absorb an additional 350,000 metric tons of oilseed sunflower per year, which would require 0.2 million ha. (J. Sandbakken, Natl. Sunflower Assoc., pers. comm.). The public is also demanding higher oleic content in vegetable oil (lower saturated fat), which sunflower can provide, and the FDA is moving close to a ban on partial hydrogenated oils in the US, opening even more opportunities

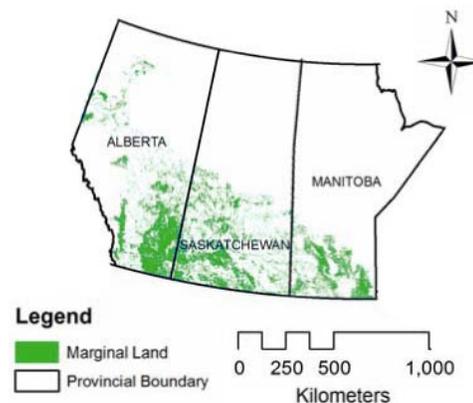


Fig.1. Marginal lands in the Canadian Prairies (from Liu et al. Proc. 2012 Intl. Conf. Agro-Geoinformatics, pp. 1-6)

for sunflower oil (which does not need hydrogenation). Best US industry projections are that, by 2016, an additional 0.7-0.8 million ha need to be seeded in oil-type sunflowers to meet demand – and 90-95% of US imports come from Canada (J. Sandbakken, Natl. Sunflower Assoc., pers. comm.). The new cultivars will be non-GMO, easing grower and market acceptance.

Internationally, the impact of the proposed research on food security in developing countries is potentially massive. If the information and germplasm from this project were to increase sunflower yields in Uganda to levels currently enjoyed by Canadian farmers, this would add ~214 calories per day to the diets of each Ugandan (current caloric intake is 1,970 calories, which is below minimum requirement of 2,200 calories). Similar gains are estimated for other sunflower growing regions in sub-Saharan Africa. Most importantly, stress-resistant cultivars will stabilize production in the face of abiotic stress, thereby reducing the potential for famine.

Finally, there will also be reduced greenhouse gas production because of sunflowers' soil nitrate mining ability (the only major herbaceous crop able to do so), especially following grain crop rotation (Hulke, B.S., & L.W. Kleingartner (2014) Sunflower. p. 433-57. In: CSSA Pub. 33).

C. PLAN FOR DISSEMINATION AND USE OF DELIVERABLES

This proposal includes many end users (plant breeders) who have contributed advice and valuable germplasm and are committed to population development and phenotyping. Thus they have 'skin in the game' and are highly likely to incorporate valuable germplasm and alleles into their breeding programs. Second, germplasm will be made publicly available by Genebanks in Canada and the USA, and project data will be deposited into public databases such as GenBank. Further, following functional validation, we will patent a handful of the most valuable genes/mutations in all major sunflower markets in the developed world. This will likely involve a collaboration with one or more industry partners who would (1) file the patents, (2) provide trait introgression into multiple genetic backgrounds, and (3) provide the trait to licensees who would pay to utilize the technology. For mutations with similar effects in other crops, IP would be extended accordingly. This is working well for a crop protection trait the Rieseberg lab is currently commercializing with a large multinational AgroBiotech firm. We are aware that IP issues for this project are potentially complex and IP policy will be developed to align with Genome Canada's policy (guidance will be provided by co-investigator Marden, who has published extensively on this topic).

Dissemination of GE³LS results will include a White Paper directed at the project team and other crop research teams for managing CBD and Treaty obligations to maximize uptake, and publications and presentations to stakeholders, scholars and policymakers about these recommendations. Co-investigator Marden will engage relevant bodies, including the Treaty Secretariat, the Global Crop Diversity Trust, the Canadian Senate Standing Committee on Agriculture and Forestry, and Plant Gene Resources of Canada to move forward refinements to reduce barriers and facilitate innovation. Genomics, physiological, and evolutionary knowledge will occur through the Sunflower Genome Database (<http://www.sunflowergenome.org>) and Heliagene (<https://www.heliagene.org>); publication in high-profile journals; presentations at conferences, universities, and companies; and hands-on training at our sunflower genomics workshop following the PAG Conference in San Diego.

D. ENGAGEMENT OF END-USERS

Our project was designed in collaboration with sunflower breeders from four government agencies (Ag Canada, INRA, the National Semi-Arid Resources Research Institute in Uganda, and the USDA) and 5 companies (Advanta Seeds, Biogemma, Dow AgroSciences, KWS Seeds, and NuSeed Americas), who provide germplasm, population development, phenotyping and evaluation, and co-funding. This will ensure that the genomic and physiological findings, as well as stress resistance alleles, are rapidly deployed in breeding programs. We also obtained advice from major sunflower markets in Europe, Argentina, and the USA. Many of these end-users are formally involved in the project as co-investigators or collaborators.

APPENDIX I. BUDGET AND CO-FUNDING SUMMARY

APPENDIX II. SHORT CVs

Last Name	First Name	Affiliation	Role⁵
Rieseberg	Loren	UBC	Project Leader
Burke	John	UGA	Co-Project Leader
Donovan	Lisa	UGA	Co-Applicant
Hulke	Brent	USDA	Co-Applicant
Langlade	Nicolas	INRA	Co-Applicant

⁵ Role includes: Project Leader, Co-Project Leader, Co-Applicant, End-User, Collaborator, etc. Definitions of participant categories are provided in the [Guidelines for Funding Research Projects](#).

Curriculum Vita
LOREN H. RIESEBERG

Address:

Mail: Botany Department
University of British Columbia
3529-6270 University Blvd.
Vancouver, B.C. V6T 1Z4
Phone: (604) 827-4540
Fax: (604) 822-6089
E-mail: lriesebe@interchange.ubc.ca

Work Experience

2006- Professor, Department of Botany, University of British Columbia
2004- Distinguished Professor, Department of Biology, Indiana University
2000-04 Associate Chair for Research and Facilities, Department of Biology, Indiana U.
1997-04 Professor, Department of Biology, Indiana University
1996-00 Director, Plant Sciences Program, Indiana University
1993-97 Associate Professor, Department of Biology, Indiana University
1987-93 Assistant Professor of Botany, Claremont Graduate School, CA

Academic and Training Background

1987 Ph.D., Botany, Washington State University, Pullman
1984 M.S., Botany, University of Tennessee, Knoxville
1981 B.A., Biology, Southern College, Chattanooga

Selected Accomplishments and Honours

1. Darwin–Wallace Medal (medal awarded by the Linnean Society of London for "major advances in evolutionary biology")
2. Fellow, Royal Society of Canada, 2010-
3. Fellow, Society of Biology, 2010-
4. Fellow, Royal Society (UK Academy of Science), 2010-
5. Canada Research Chair (Tier 1) in Plant Evolutionary Genomics, 2006-
6. President, American Genetics Association, 2006
7. Fellow, American Academy of Arts and Sciences, 2004-
8. Stebbins Medal (medal given for the best book, monograph, or article published on plant systematics and plant evolution the previous year), 2004
9. Guggenheim Fellowship, 2004
10. MacArthur Fellowship (Unrestricted \$500,000 fellowship awarded to "individuals who have shown extraordinary originality and dedication in their creative pursuits"), 2003-08
11. Fellow, American Association for the Advancement of Science, 2003-
12. A.R. Wallace – R.E. Franklin Medal for significant contributions to the life sciences, 2003
13. David Starr Jordan Prize (International prize given once every three years to a scientist under 40 years of age for "innovative contributions to the study of evolution, ecology, population, or organismal biology"), 1998

Selected Peer-Reviewed Publications (from > 300 publications total; Web of Science: >15,500 citations, h-index = 68; Google Scholar: >22,000 citations, h-index = 82)

- Khoury, C.K. et al. 2014. The crops that feed the world: increasing homogeneity in global food supplies. *Proceedings of the National Academy of Sciences USA* 111:4001-4006. (ranked #42 in media interest out 21,392 articles published in *PNAS*; Faculty of 1000, new finding).
- Renaut, S. et al. 2013. Genomic islands of divergence are not affected by geography of speciation in sunflowers. *Nature Communications* 4, 1827.
- Mandel, J.R. et al. 2013. Association mapping and the genomic consequences of selection in sunflower. *PLoS Genetics* 9, e1003378.
- Blackman, B.K. et al. 2011. Sunflower domestication alleles support single domestication center in eastern North America. *Proceedings of the National Academy of Sciences USA* 108:14360–14365.
- Mayrose, I. et al. 2011. Recently-formed polyploids diversify more slowly than their diploid relatives. *Science* 333:1257.
- Blackman, B.K., J.L. Strasburg, S.D. Michaels, and L.H. Rieseberg. 2010. The role of recently derived FT paralogs in sunflower domestication. *Current Biology* 20:629–635.
- Wood, T.E. et al. 2009. The frequency of polyploid speciation in vascular plants. *Proceedings of the National Academy of Sciences USA* 106:13875-13879. (Faculty of 1000, exceptional)
- Rieseberg, L.H., and J.H. Willis. 2007. Plant speciation. *Science* 317:910-914.
- Rieseberg, L.H., T.E. Wood, and E. Baack. 2006. The nature of plant species. *Nature* 440:524-527. (Faculty of 1000, exceptional)
- Harter, A.V. et al. 2004. Origin of extant domesticated sunflowers in eastern North America. *Nature* 430:201-205.
- Rieseberg, L.H. et al. 2003. Major ecological transitions in annual sunflowers facilitated by hybridization. *Science* 301:1211-1216. (Faculty of 1000, recommended)
- Burke, J.M., and L.H. Rieseberg. 2003. The fitness effects of transgenic disease resistance in wild sunflowers. *Science* 300:1250.

Selected Grant and Fellowship Support

1. CFI / BCDKF, Construction of Envirotron, 2,120,060 CAD, 2013-18
2. NSF, Repeatability of Adaptive Introgression, 690,000 USD, 2013-19 (PI: K. Whitney)
3. Canada Research Chair in Plant Evolution Genomics, 1,200,000 CAD, 2013-20
4. Six Seed Companies, Sunflower Genomics Resources Consortium, 840,000 CAD, 2012-16
5. Global Crop Diversity Trust, Sunflower Genetic Diversity, Pre-breeding and Evaluation, 273,000 USD, 2011-14
6. Genome Canada/Genome BC, AdapTree, 4,700,000 CAD, 2011-14 (S. Aitken, PI)
7. NSERC, Evolutionary Genomics of Plant Adaptation and Speciation, 600,000 CAD, 2011-16
8. NSERC, Biodiversity Research: Integrative Training & Education, 1,650,000 CAD, 2009-15 (PI: S. Otto)
9. Genome Canada/Genome BC, Genomics of Sunflower, 10,491,589 CAD, 2009-13
10. NSF, Compositae Genome Project, 8,091,000 USD, 2009-13
11. ARC, Natural Selection and Speciation, 210,000 AUC, 2009-11 (PI: D. Ortiz-Barrientos)
12. NSERC, Canadian Pollination Initiative, 5,000,000 CAD, 2009-14 (PI: P. Kevan)
13. NSERC SRO, Genetics of Invasiveness, 991,000 CAD, 2008-10
14. NSF, Colonization of Texas by weedy sunflowers, 578,000 USD, 2007-12 (PI: K. Whitney)
15. CIDA, Genetic diversity of noug, 225,000 CAD, 2007-10
16. NSERC Discovery, Plant adaptation and speciation, 379,000 CAD, 2006-11
17. Canada Research Chair in Plant Evolution Genomics, \$1,200,000 CAD, 2006-13

NAME AND AFFILIATION

John M. Burke
Department of Plant Biology
University of Georgia
Athens, GA 30602

WORK EXPERIENCE

2011- Professor, Univ of Georgia, Department of Plant Biology
2011-2014 Director, The Plant Center at UGA
2006-2011 Associate Professor, Univ of Georgia, Department of Plant Biology
2002-2006 Assistant Professor, Vanderbilt Univ, Department of Biological Sciences
1999-2002 Postdoctoral Fellow, Indiana Univ, Department of Biology
1996 Teaching Assistant, Univ of Georgia, Genetics
1994-1999 Graduate Research Assistant, Univ of Georgia, Department of Genetics
1994 Teaching Assistant, Univ of Minnesota, Laboratory in Genetics
1993-1994 Junior Scientist, Dept of Genetics and Cell Biology, Univ of Minnesota

ACADEMIC AND TRAINING BACKGROUND

Univ of Minnesota. Major: Genetics and Cell Biology, Minor: Statistics. B.S. 1993.
Univ of Georgia. Major: Genetics. Ph.D. 1999.
Indiana Univ Dept of Biology. Postdoctoral Fellow, 1999-2002.

SELECTED ACCOMPLISHMENTS AND HONOURS

National Academies Education Fellow in the Life Sciences – 2013
University of Georgia Creative Research Medal – 2013
NSF Young Investigator Award in Plant Genome Research – 2003-2008
Univ of Georgia Franklin College Distinguished Doctoral Assistantship – 1998-1999
Univ of Georgia University-Wide Graduate Fellowship – 1995-96, 1996-97, 1997-98
NSF/USDA/DOE Training Grant Fellowship in Plant Evolution – 1994-1999

SELECTED PEER-REVIEWED PUBLICATIONS, PATENT APPLICATIONS AND PATENTS

Barb, J.G., J.E. Bowers, S. Renaut, J.I. Rey, S.J. Knapp, L.H. Rieseberg, and J.M. Burke. 2014. Chromosomal evolution and patterns of introgression in *Helianthus*. **Genetics** 197: 969-979.
Pearl, S.A., J.E. Bowers, S. Reyes Chin-Wo, R.W. Michelmore, and J.M. Burke. 2014. Genetic analysis of safflower domestication. **BMC Plant Biol.** 14: 43.
Mandel, J.R., E.V. McAssey, S. Nambeesan, E. Garcia-Navarro, and J.M. Burke. 2014. Molecular evolution of candidate genes for crop-related traits in sunflower (*Helianthus annuus* L.). **PLoS ONE** 9: e99620.
Renaut, S., C.J. Grassa, S. Yeaman, B.T. Moyers, Z. Lai, N.C. Kane, J.E. Bowers, J.M. Burke, and L.H. Rieseberg. 2013. Genomic islands of divergence are not affected by geography of speciation in sunflowers. **Nat. Commun.** 4: 1827.
Ziebell, A.L., J.G. Barb, S. Sandhu, B. Moyers, R.W. Sykes, C. Doeppke, K.L. Gracom, M. Carlile, L.F. Marek, M.F. Davis, S.J. Knapp, and J.M. Burke. 2013. Sunflower as a biofuels crop: an analysis of lignocellulosic chemical properties. **Biomass Bioenergy** 59: 208-217.

- Mandel, J.R., R.B. Dikow, V.A. Funk, R.R. Masalia, S.E. Staton, A. Kozik, R.W. Michelmore, L.H. Rieseberg, and J.M. Burke. A target enrichment method for gathering phylogenetic information from hundreds of loci: an example from the Compositae. **Appl. Plant Sci.** 2: 1300085.
- Mandel, J.R., S. Nambeesan, J.E. Bowers, L.F. Marek, D. Ebert, L.H. Rieseberg, S.J. Knapp, and J.M. Burke. 2013. Association mapping and the genomic consequences of selection in sunflower. **PLoS Genetics** 9: e1003378.
- Chapman, M.A., S. Tang, D. Draeger, J.G. Barb, S.J. Knapp, and J.M. Burke. 2012. The genetics of floral symmetry in van Gogh's sunflowers reveals independent recruitment of *CYCLOIDEA* genes in the Asteraceae. **PLoS Genetics** 8: e1002628.
- Bowers, J.E., E. Bachlava, R.L. Brunick, L.H. Rieseberg, S.J. Knapp, and J.M. Burke. 2012. Development of a 10,000 locus genetic map of the sunflower genome based on multiple crosses. **G3: Genes, Genomes, Genetics** 2: 721-729.
- Bowers, J.E., S. Nambeesan, J. Corbi, M.S. Barker, L.H. Rieseberg, S.J. Knapp, and J.M. Burke. 2012. Development of an ultra-dense genetic map of the sunflower genome based on single-feature polymorphisms. **PLoS ONE** 7: e51360.
- Staton, S.E., B. Hartman Bakken, B.K. Blackman, M.A. Chapman, N.C. Kane, S. Tang, M.C. Ungerer, S.J. Knapp, L.H. Rieseberg, and J.M. Burke. 2012. The sunflower (*Helianthus annuus* L.) genome reflects a recent history of biased accumulation of transposable elements. **Plant J.** 72: 142-153.
- Kane, N.C., N. Gill, M.G. King, J.E. Bowers, H. Berges, J. Gouzy, E. Bachlava, N.B. Langlade, Z. Lai, M. Stewart, J.M. Burke, P. Vincourt, S.J. Knapp, and L.H. Rieseberg. 2011. Progress towards a reference genome for sunflower. **Botany**, 89: 429-437.
- Blackman, B.K., D.A. Rasmussen, J.L. Strasburg, A.R. Raduski, J.M. Burke, S.J. Knapp, S.D. Michaels, and L.H. Rieseberg. 2011. Contributions of flowering time genes to sunflower domestication and improvement. **Genetics**, 187: 271-287.
- Chapman, M.A., J.H. Leebens-Mack, and J.M. Burke. 2008. Positive selection and expression divergence following gene duplication in the sunflower *CYCLOIDEA* gene family. **Mol. Biol. Evol.**, 25: 1260-1273.
- Chapman, M.A., C.H. Pashley, J. Wenzler, J. Hvala, S. Tang, S.J. Knapp, and J.M. Burke. 2008. A genomic scan for selection reveals candidates for genes involved in the evolution of cultivated sunflower (*Helianthus annuus* L.). **Plant Cell** 20: 2931-2945.

SELECTED RESEARCH FUNDING

- NSF Plant Genome Research Program** (Award #DBI-0820451). 03/15/09-02/28/13 (no-cost extension through 02/28/15). Comparative genomics of phenotypic variation in the Compositae. **\$8,000,000** (one of 7 co-PIs; \$1,986,382 + \$345,003 supplement to UGA).
- Industry Consortium**. 01/15/12-01/14/16. Sunflower genomic resources. **\$840,000** (one of 3 co-PIs; \$280,000 to UGA).
- NSF Plant Genome Research Program** (pending). Evolutionary genomics of abiotic stress resistance in wild and cultivated sunflowers. **\$3,995,017** (one of 8 co-PIs).
- NSF Integrative Organismal Systems** (pending). Investigating a hypothesized spectrum of adaptive drought resistance traits in *Helianthus*. **\$792,206** (one of 2 co-PIs).

NAME AND AFFILIATION

Lisa A. Donovan
Department of Plant Biology
University of Georgia
Athens, GA 30602

WORK EXPERIENCE

2014- Distinguished Research Professor & Department Head, Univ of Georgia,
Department of Plant Biology
2005-2014 Professor, Univ of Georgia, Department of Plant Biology
2001-2005 Associate Professor, Univ of Georgia, Department of Plant Biology
1995-2001 Assistant Professor, Univ of Georgia, Department of Plant Biology
1992-1995 Postdoctoral Fellow, Univ of California, Davis
1986-1992 Graduate Research/Teaching Assistant, Univ of Utah, Department of Biology
1982-1986 Research Technician, Savannah River Ecology Laboratory, Aiken SC
1980-1982 Research Assistant, Univ of Delaware, College of Marine Studies

ACADEMIC AND TRAINING BACKGROUND

Salisbury State University. Major: Biology. B.S. 1980.
University of Delaware. Major: Marine Biology. M.S. 1982.
University of Utah. Major: Biology. Ph.D. 1992.

SELECTED ACCOMPLISHMENTS AND HONOURS

American Association for the Advancement of Science Fellow, 2012
University of Georgia Creative Research Medal, 2006
Fulbright Visiting Professor: Radboud University, Nijmegen Netherlands, 2009
Stebbins Medal award for collaboration (Rieseberg et al. 2003 Science paper) 2004
University of Georgia Lilly Teaching Fellow, 1996-1998
Graduate Research Fellow, University of Utah 1989-1991
American Fellow, American Association University Women 1990-1991

SELECTED PEER-REVIEWED PUBLICATIONS, PATENT APPLICATIONS AND PATENTS

Brouillette, L.C., C.M. Mason, R.Y. Shirk, L.A. **Donovan**. 2014. Adaptive differentiation of traits related to resource use in a desert annual along a resource gradient. New Phytologist 183: 868-879.
Donovan, L.A., C.M. Mason, A.W. Bowsher, E.W. Goolsby, C.D.A. Ishibashi. 2014. Ecological and evolutionary lability of plant traits affecting carbon and nutrient cycling. Journal of Ecology 102: 302-314.
Auchincloss, L., H.M. Easlon, D. Levine, L.A. **Donovan**, J.H. Richards. 2014. Predawn stomatal opening does not substantially enhance early morning photosynthesis in *Helianthus annuus*. Plant Cell and Environment 37: 1364-1370.
Sack, L., C. Scoffoni, G. John, H. Poorter, C. Mason, R. Mendez-Alonzo, L.A. **Donovan**. 2013. How do leaf veins influence the worldwide leaf economic spectrum? A critical review and synthesis. Journal of Experimental Botany 64: 4053-4080.

- Mason, C.M., S.E. McGaughey, L.A. **Donovan**. 2013. Ontogeny strongly and differentially alters leaf economic and other key traits in three diverse *Helianthus* species. Journal of Experimental Botany 64: 4053–4808.
- Milton, E.F., E.W. Goolsby, L.A. **Donovan**. 2013. Cultivated *Helianthus annuus* differs from two wild relatives in germination response to simulated drought stress. Helia 36: 35-46.
- Gevaert, S.D., J.R. Mandel, J.M. Burke, L.A. **Donovan**. 2013. High genetic diversity and low population structure in Porter's sunflower (*Helianthus porteri*). Journal of Heredity 104: 407-415.
- Mandel, J.R., E.F. Milton, L.A. **Donovan**, S.J. Knapp, J.M. Burke. 2013. Genetic diversity and population structure in the rare Algodones sunflower (*Helianthus niveus* ssp. *tephrodes*). Conservation Genetics 14: 31-40.
- Donovan**, L.A., H. Maherali, C.M. Caruso, H. Huber, H. de Kroon. 2011. The evolution of the worldwide leaf economics spectrum. Trends in Ecology and Evolution 26: 88–95.
- Brouillette, L.C., L.A. **Donovan**. 2011. Relative growth rate and functional traits of a hybrid species reflect adaptation to a low fertility habitat. International Journal of Plant Sciences 172:509-520.
- Brouillette, L.C., L.A. **Donovan**. 2011. Nitrogen stress response of a hybrid species: A gene expression study. Annals of Botany 107:101-108.
- Rosenthal, D.M., V. Stiller, J.S. Sperry, L.A. **Donovan**. 2010. Contrasting drought tolerance strategies in two desert annuals of hybrid origin. Journal of Experimental Botany 61: 2769–2778.
- Donovan**, L.A., F. Ludwig, D.M. Rosenthal, L.H. Rieseberg, S. Dudley. 2009. Phenotypic selection on leaf ecophysiological traits in *Helianthus*. New Phytologist 183: 868–879.
- Howard A.R., M.W. van Iersel, J.H. Richards, L.A. **Donovan**. 2009. Nighttime transpiration can decrease hydraulic redistribution. Plant Cell Environment 32:1060-1070.
- Sapir, Y, M.L. Moody, L.C. Brouillette, L.A. **Donovan**, L.H. Rieseberg. 2007. Patterns of genetic diversity and candidate genes for ecological divergence in homoploid hybrid sunflower *Helianthus anomalus*. Molecular Ecology 16:5017-5029
- Brouillette, L.C, D.M. Rosenthal, L.H. Rieseberg, C. Lexer, R.L. Malmberg, L.A **Donovan**. 2007. Genetic architecture of leaf ecophysiological traits in *Helianthus*. Journal of Heredity 98:142-146.
- Brouillette, L.C., M. Gebremedhin, D.M. Rosenthal, L.A. **Donovan**. 2006. Testing hypothesized evolutionary shifts toward stress tolerance in hybrid *Helianthus* species. Western North American Naturalist 66:409-419.
- Donovan**, L.A., J.H. Richards, M.J. Linton. 2003. Magnitude and mechanisms of disequilibrium between predawn plant and soil water potentials. Ecology 84: 463–470.
- Rieseberg, L.H., O. Raymond, D.M. Rosenthal, Z. Lai, K. Livingston, T. Nakazato, J.L. Durphy, A.E. Schwarzbach, L.A. **Donovan**, C. Lexer. 2003. Major ecological transitions in wild sunflower facilitated by hybridization. Science 301: 1211–1216

SELECTED RESEARCH FUNDING

- NSF Integrative Organismal Systems** (2011-2015). The evolution of the worldwide leaf economic spectrum in *Helianthus* **\$638,003** (one of 2 co-PIs).
- NSF Plant Genome Research Program** (pending). Evolutionary genomics of abiotic stress resistance in wild and cultivated sunflowers. **\$3,995,017** (one of 8 co-PIs).
- NSF Integrative Organismal Systems** (pending). Investigating a hypothesized spectrum of adaptive drought resistance traits in *Helianthus*. **\$792,206** (one of 2 co-PIs).

CURRICULUM VITAE

Brent S. Hulke

Sunflower and Plant Biology Research Unit
Red River Valley Agricultural Research Center
USDA-ARS
1307 18th St. N.,
Fargo, ND 58102-2765
Ph. 701-239-1321, FAX: 701-239-1346
Email: brent.hulke@ars.usda.gov

Work Experience

2010-present Research Geneticist GS-13, Sunflower and Plant Biology Research Unit, USDA-ARS, Fargo, ND
2008-present Adjunct Professor, Plant Sciences Dept., North Dakota State University, Fargo, ND
2007-2010 Research Geneticist GS-12, Sunflower Research Unit, USDA-ARS, Fargo, ND
2005-2007 Research Assistant, University of Minnesota, St. Paul, MN
2004-2005 Graduate School Fellow, University of Minnesota, St. Paul, MN
2002-2004 Research Assistant and Plant Sciences Institute Fellow, Iowa State University, Ames, IA

Academic and Training Background

Ph.D. *Applied Plant Sciences* University of Minnesota, St. Paul, MN
August 2007
Dissertation: "Using wild and landrace germplasm and current breeding methods to improve winterhardiness in perennial ryegrass (*Lolium perenne* L.)."

M.S. *Plant Breeding* Iowa State University, Ames, IA
May 2004
Thesis: "Influence of reduced phytate on the agronomic and seed characteristics of soybean lines with reduced palmitate."

B.S. *Agronomy, With Highest Honor* South Dakota State University, Brookings, SD
May 2002

Selected Professional Membership and Service

2012 – present Editor, Theoretical and Applied Genetics
2012 – present Mentor, New Scientist Mentorship Program, USDA-ARS-Northern Plains
2012 – present Research Position Evaluation System (RPES) panelist, USDA-ARS
2008 – present International Sunflower Association member
2003 – present Crop Science Society of America member

Selected Honours

2013 USDA-ARS Northern Plains Area – No Revision Award (joint award with other unit scientists – based on quality and merit of our new 5-year CRIS plan).

2011	USDA-ARS-Northern Plains Area – Leadership Training award
2006	Western Seed Association – President’s Award
2006	National Council of Commercial Plant Breeders – Graduate Student Award

Peer-Reviewed Publications this year (*graduate students/postdocs in italics*)

1. *Chirumamilla, A., J.J. Knodel, L.D. Charlet, B.S. Hulke, S.P. Foster, and P.J. Ode.* 2014. Ovipositional preference and larval performance of the banded sunflower moth and its larval parasitoids on resistant and susceptible lines of sunflower, *Helianthus annuus*. *Environ. Ent.* 43:58-68.
2. **Hulke, B.S.**, and L.W. Kleingartner. 2014. Sunflower. p. 433-457. In: *Yield Gains in Major US Field Crops: CSSA Special Publication 33.* S. Smith, B. Diers, J. Specht, and B. Carver (Eds.) ASA-CSSA-SSSA, Madison, WI.
3. *Kantar, M.B., K. Betts, J.-M. Michno, J.J. Luby, P.L. Morrell, B.S. Hulke, R.M. Stupar, and D.L. Wyse.* 2014. Evaluating an interspecific *Helianthus annuus* × *Helianthus tuberosus* population for use in a perennial sunflower breeding program. *Field Crops Res.* 155:254-264.
4. Pearson, T.C., J.R. Prasifka, D.L. Brabec, R.P. Haff, and **B.S. Hulke.** 2014. Automated detection of insect-damaged sunflower seeds by X-ray imaging. *Applied Engineering in Agriculture* 30:125-131.
5. Prasifka, J.R., **B.S. Hulke,** and G.J. Seiler. 2014. Pericarp strength of sunflower and its value for plant defense against the sunflower moth, *Homoeosoma electellum*. *Arthropod-Plant Interactions* 8:101-107.
6. Qi, L.L., L. Gong, S.G. Markell, G.J. Seiler, T.J. Gulya, and B.S. Hulke. 2014. Registration of two confection sunflower germplasm lines HA-R10 and HA-R11, resistant to sunflower rust. *J. Plant Registrations* doi: 10.3198/jpr2014.02.0010crg
7. *Talukder, Z.I., L. Gong, B.S. Hulke, V. Pegadaraju, Q. Song, Q. Schultz, and L. Qi.* 2014. A high-density SNP map of sunflower derived from RAD-sequencing facilitating fine-mapping of the rust resistance gene *R₁₂*. *PLoS One* doi: 10.1371/journal.pone.0098628
8. *Talukder, Z.I., B.S. Hulke, L. Marek, and T.J. Gulya.* 2014. Sources of resistance to sunflower diseases in a global collection of domesticated USDA plant introductions. *Crop Sci.* 54:694-705.
9. *Talukder, Z.I., B.S. Hulke, L.L. Qi, B.E. Scheffler, V. Pegadaraju, K. McPhee, and T.J. Gulya.* 2014. Candidate gene association mapping of Sclerotinia stalk rot resistance in sunflower (*Helianthus annuus* L.) uncovers the importance of *COII* homologs. *Theor Appl Genet* 127:193-209.

Selected Grants Awarded (in USD)

1. May, W., **B. Hulke,** and D. Petty. 2013-2016. Developing sunflower hybrids for Saskatchewan with improved oil profiles. Saskatchewan Agricultural Development Fund, awarded \$36,500 in 2013, \$36,500 in 2014, \$36,500 in 2015, and \$1,500 in 2016.
2. **Hulke, B.S.** 2013-2014. Revising the fatty acid profile of sunflower to meet new industry and consumer demands (postdoc salary award). USDA-ARS, awarded \$70,000 in 2013 and \$70,000 in 2014.
3. **Hulke, B.** 2013. Identifying and mapping modifiers of high oleic and high oleic, low sat fatty acid composition. National Sunflower Association, awarded \$38,700.
4. **Hulke, B.** 2014. Using genomic selection to optimize prediction of Sclerotinia and agronomic phenotypes for more efficient breeding. USDA-ARS-NSI, awarded \$89,049.

NICOLAS B. LANGLADE

AFFILIATION

INRA (French National Institute for Agricultural Research)

Laboratory of Plant-Microbe Interactions (UMR CNRS/INRA 2594/441)

24 chemin de Borde Rouge - Auzeville

CS 52627

31326 CASTANET TOLOSAN CEDEX

FRANCE

WORK EXPERIENCE

2007- Senior Researcher, INRA (French National Institute for Agricultural Research),
Department of Plant Breeding

2006-2007 Postdoctoral Fellow, ENS Lyon, (France)

2002-2006 Postdoctoral Fellow, John Innes Centre, (United-Kingdom)

1998-2002 Teaching Assistant, Univ. of Neuchatel (Switzerland)

ACADEMIC AND TRAINING BACKGROUND

Univ. of Poitiers (France). Major: Biochemistry, Minor: Plant Physiology. B.S., 1998.

Univ. of Neuchatel (Switzerland). Major: Plant Physiology. PhD., 2002.

John Innes Centre, Cell & Development Biology Dept. (United-Kingdom) Postdoctoral Fellow,
2002-2006.

ENS Lyon, Laboratory of Plant Development and Reproduction (France) Postdoctoral Fellow,
2006-2007.

SELECTED ACCOMPLISHMENTS AND HONOURS

Conception and creation of the High-Throughput Phenotyping platform Heliaphen

Conception and creation of the Sunflower Genomics Webportal Heliagene

SELECTED PEER-REVIEWED PUBLICATIONS, PATENT APPLICATIONS AND PATENTS

Langlade N.B., Messerli G., Weisskopf L., Plaza S., Tomasi N., Smutny J., Neumann G.,
Martinoia E., Massonneau A. (2002) ATP citrate lyase: cloning, heterologous expression
and possible implication in root organic acid metabolism and excretion
Plant, Cell & Environment

Langlade N.B., Feng X., Dransfield T., Copsey L., Hanna A.I., Thébaud C., Bangham A., Hudson A., Coen E. (2005) Evolution through genetically controlled allometry space. **Proceedings of the National Academy of Sciences of the United States of America**

Whibley, A.C.*, Langlade, N.B.*, Andalo, C., Hanna, A.I., Bangham, A., Thebaud, C., Coen, E. S. (2006) Evolutionary paths underlying flower color variation in *Antirrhinum* **Science**

** These authors contributed equally to this work.*

Marchand, G., Huynh-Thu, V. A., Kane, N., Arribat, S., Varès, D., Rengel, D., Balzergue, S., Rieseberg, L., Vincourt, P., Geurts, P., Vignes, M. and Langlade, N. B. (2014) Bridging physiological and evolutionary time scales in a gene regulatory network. **New Phytologist**

Marchand, G., Mayjonade, B., Varès, D., Blanchet, N., Boniface, M.C., Maury, P., Andrianasolo Nambinina F., Burger, P., Debaeke, P., Casadebaig, P., Vincourt, P., Langlade N.B. (2013) A biomarker based on gene expression indicates plant water status in controlled and natural environments. **Plant, Cell & Environment**

Rengel, D., Arribat, S., Pierre Maury, P., Martin-Magniette, M.L., Hourlier, T., Laporte, M., Varès, D., Carrère, C., Grieu, P., Balzergue, S., Gouzy, J., Vincourt, P., Langlade, N.B. (2012) A Gene-Phenotype Network Based on Genetic Variability for Drought Responses Reveals Key Physiological Processes in Controlled and Natural Environments. **PLoS ONE**

Bellec A., Bergès H., Gouzy J., Langlade N.B., Marande W., Mayjonade B., Muñoz S., Vincourt P. Protocole for high-throughput BAC-end sequencing **Patent Application**

SELECTED RESEARCH FUNDING

(External funding for the lab in brackets)

2012-2019 ANR project SUNRISE, Sunflower resources to improve yield stability in a changing environment, (2683K€)

Coordination from July 1, 2014

2010-2015 INRA BAP projects and consortium: French participation to the Sunflower Genome sequencing project and consortium, (total 300 k€).

Coordination of the French side (including transcriptomics, genetic map production, BAC-end production and annotation)

2010 Genoscope project SYSTEMSUN, Systems biology: analysis of sunflower hormonal regulatory networks and identification of evolutionary adaptations of these networks to contrasted abiotic environments (47 k€)

Coordinator

2009-2013 OLEOSOL project, Sunflower Geneics and Genomics Resources (3 378 k€)

Coordinator of phenotyping, physiological and molecular analysis

2008-2011 ANR project SUNYFUEL, Improving sunflower yield and quality for biofuel production by genomics and genetics (472 k€)

Coordinator of phenotyping, physiological and molecular analysis,