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Subject:	09-105 Revise Manuscript
Date:	Tuesday, September 01, 2009 2:08:00 PM
Attachments:	Genome 09-105 Revision.doc

Alistair:

Yesterday, we submitted the revisions to the manuscript 09-105. Unfortunately we resubmitted with a earlier title. If possible, can you please change the title to the correct title? The information is as follows.

CORRECT TITLE: Early-generation Germplasm Introgression from *Sorghum macrospermum* into Sorghum (*S. bicolor)*

SUBMITTED TITLE: Introgression Breeding using *S. macrospermum* and Analysis of Recovered Germplasm

I logged on today in an attempt to change it, but since it had been submitted I was unable to make any changes.

I've also attached the document in case you can change it.

Thanks,

bill

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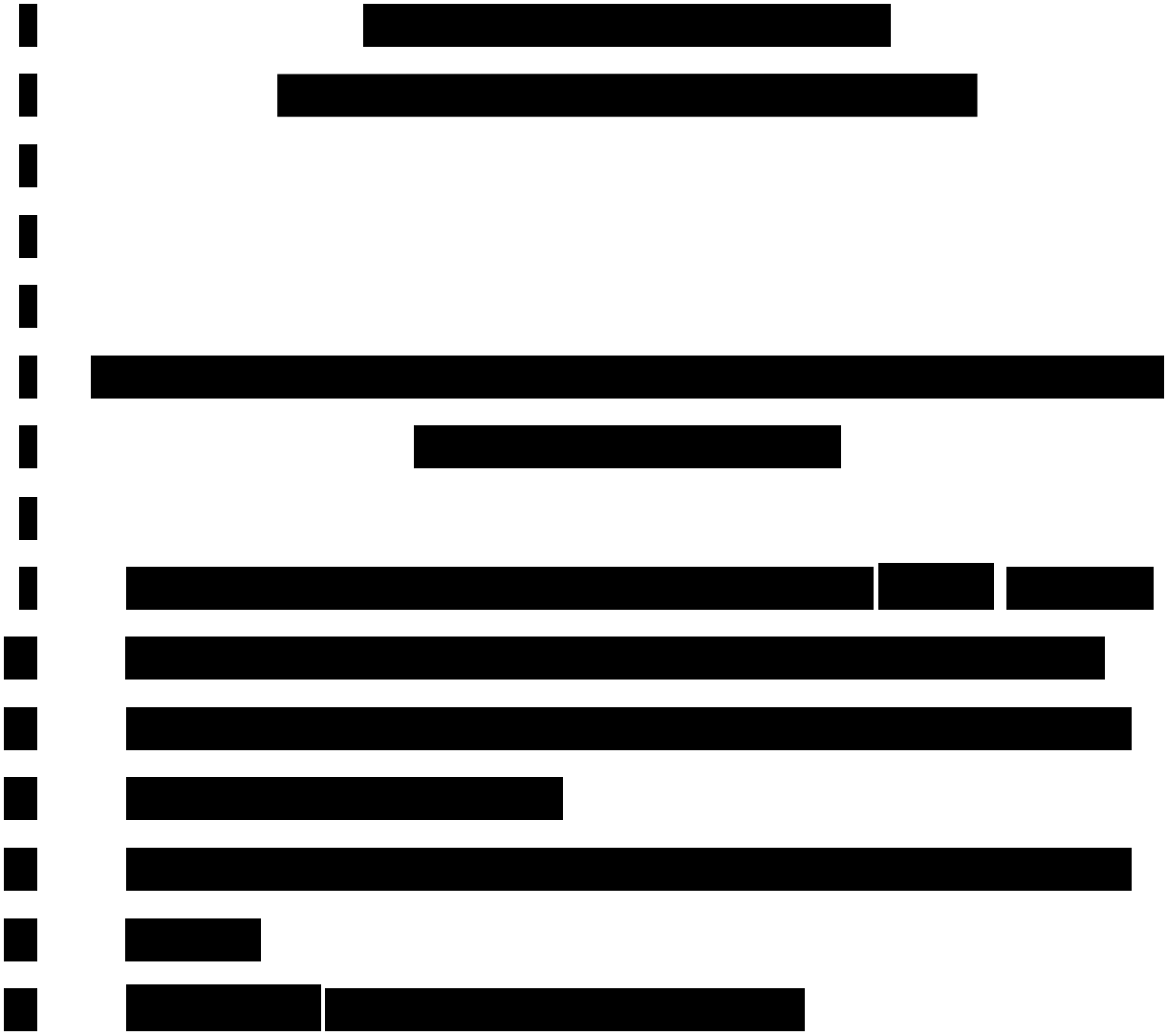

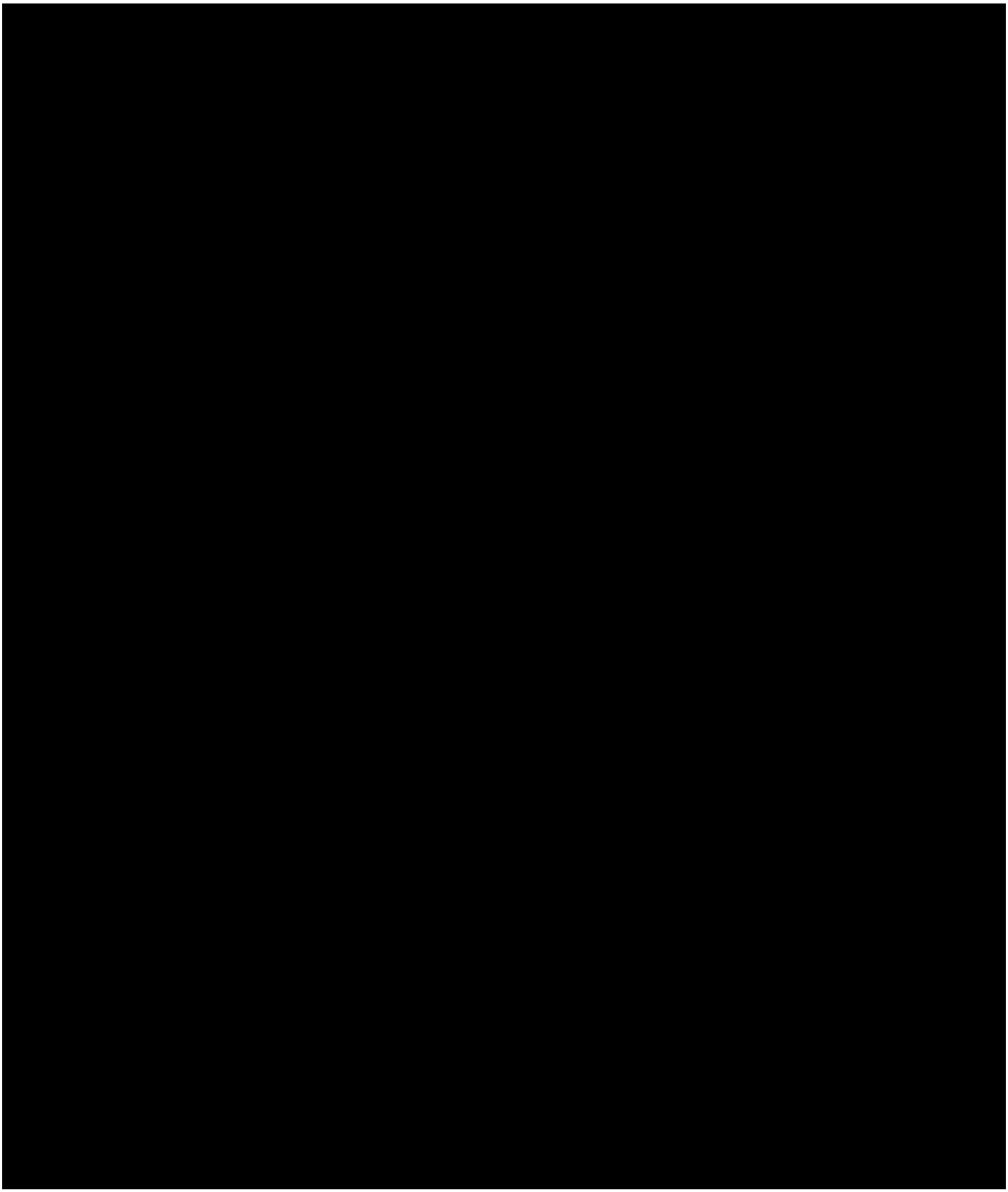

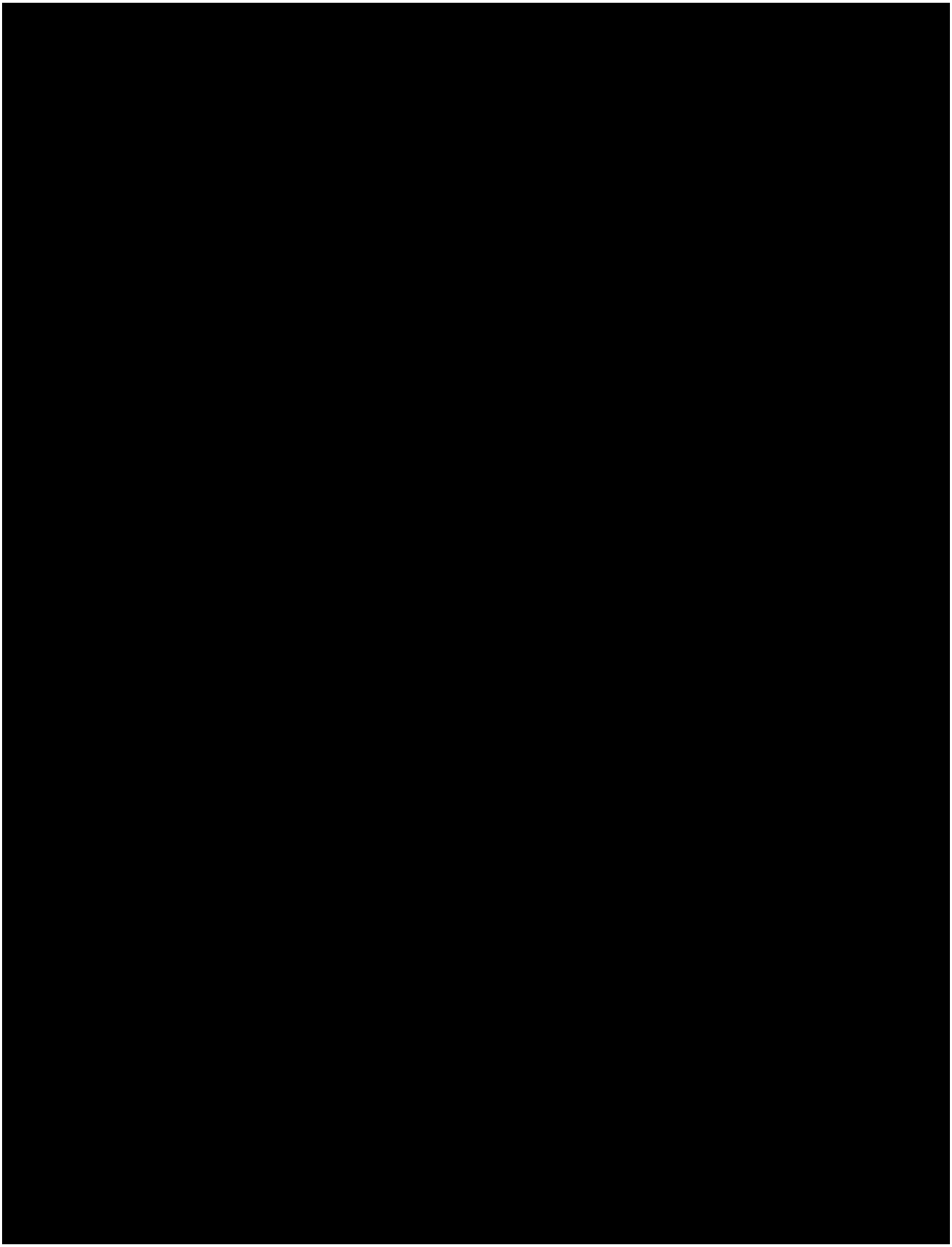

recently, this gene pool was completely inaccessible as no hybrids had ever been recovered despite numerous efforts (Karper and Chisholm, 1936; Ayyanger and Ponnaiya, 1941; Garber, 1950; Endrizzi, 1957; Tang and Liang, 1988; Wu, 1990; Sun et al., 1991; Huelgas et al., 1996).

The cause of reproductive isolation between sorghum and the tertiary gene pool was unknown until Hodnett et al., (2005) determined that it was due to pollen-pistil incompatibilities. Pollen tube growth of wild species was inhibited in the stigma and style which prevented successful fertilization. The reproductive barriers proved to be strong but not complete as Price et al., (2005) finally recovered one interspecific hybrid between cytoplasmic male-sterile (CMS) sorghum and *S. macrospermum*. The efficiency of producing this hybrid improved dramatically by using a *S. bicolor* genotype homozygous for the *iap* allele. The *Iap* locus (*I*nhibition of *A*lien *P*ollen) controls a pistil barrier that prevents foreign species pollen tube growth; whereas, the recessive genotype (*iap iap*) allows pollen tube growth of maize as well as wild sorghum species (Laurie and Bennett, 1989; Price et al., 2006). Price et al., (2006) recovered hybrids between sorghum and *S. macrospermum*, *S. nitidum*, and *S. angustum* but only hybrids with *S. macrospermum* survived to maturity.

S. macrospermum (2*n* = 40) is the only member of the *Chaetosorghum* section and it is native to the Katherine area in the Northern Territory of Australia (Lazarides et al., 1991). While this species does not possess any obvious agronomically desirable traits, it does have significant pest resistance. It is either a non-host or has ovipositional non-preference to sorghum midge (*Stenodiplosis sorghicola* Coquillett) (Franzmann and

Hardy, 1996; Sharma and Franzmann, 2001). It is not susceptible to sorghum downy mildew (*Peronosclerospora sorghi* Weston and Uppal (Shaw)) (Kamala et al., 2002) and has high tolerance to shoot fly (*Atherigona soccata* Rond.) (Sharma et al., 2005). These beneficial traits, as well as the possibility that it holds other valuable unique genetic variation, make it attractive to use in an introgression breeding program.

Until recently, the genomic relationship between *S. macrospermum* and *S. bicolor* was not known. Several authors have described *S. bicolor* ($2n = 4x = 20$; AAB_1B_1) has an ancient tetraploid; its genomic formula was derived by analyzing meiosis in hybrids with *S. halepense* ($2n = 8x = 40$; $AAAAB_1B_1B_2B_2$) (Hadley, 1953; Celerier, 1958; Tang and Liang, 1988). Meiotic chromosome pairing behavior in interspecific hybrids between *S. bicolor* and *S. macrospermum* revealed that moderate levels of allosyndetic recombination occurred and the genomic formula AAB_1B_1YYZZ was proposed for *S. macrospermum* ($2n = 8x = 40$) (Kuhlman et al., 2008). Allosyndetic recombination was observed in subgenomes A and B_1, but the frequency was 2.5 times higher in subgenome A. The authors attempted to produce backcrosses using the interspecific hybrid as a male, but were not successful.

The tertiary gene pool species *S. macrospermum* is now available to plant breeders because hybrids can now be recovered by using specific *S. bicolor* germplasm (*iap iap*). The sorghum and wild species genomes undergo moderate levels of allosyndetic recombination; therefore, recovering introgression in backcross progeny is likely (Kuhlman et al. 2008). The remaining obstacle to using this species in an introgression program is determining how to recover backcrosses. The objectives of this