

ditions, the interaction between the nucleus and different cytoplasm can be evaluated at the morphological and molecular level. Cytoplasmic organelles (mitochondria and chloroplast) have been implicated in multiple plant-pathogen interaction pathways.

Our project is to measure differential responses of various alien cytoplasm in a specific nuclear background to various pathogens to provide a better understanding on the effect of nuclear-cytoplasmic interactions on biotic stress tolerance. In this study, we analyzed the nuclear donors of 56-1 (tetraploid), and Chris and Selkirk (both hexaploid), alloplasmic lines. Fifty selected alloplasmic lines were tested for their diseases response to *Pyrenophora tritici-repentis* (Ptr) isolates BR15 (produces ToxA, B, and C) and Pti2 (produces ToxA and C), one of the more virulent isolates in our collection. Results indicated that *Aegilops bicornis* cytoplasm provided reduced sensitivity to isolate BR15 as identified in alloplasmic lines of Selkirk and Chris, whereas *Ae. variabilis* cytoplasm provided reduced sensitivity to isolate BR15 as identified in alloplasmic lines 56-1 and Chris. Selkirk alloplasmic lines showed a similar reaction to the euplasmic parent to isolate Pti2. These alloplasmic lines, and others that showed significant increases in resistance or susceptibility, are being screened with additional Ptr isolates. Further investigations determining the mechanism of increased resistance or sensitivity by measuring the changes in the production of reactive oxygen species in those selected alloplasmic lines are underway. In conclusion, cytoplasm variability can improve resistance to plant diseases.

Poster 70. The function of *scs*, *Rf*, and *vi* for proper compatibility of durum wheat nucleus in alien cytoplasm.

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Interactions between alien cytoplasm and particular species cytoplasm specific, *scs*, genes from *Triticum timopheevii* or common wheat (*T. aestivum*) transferred to the nuclear genome of durum wheat (*T. turgidum*) produce male-sterile, A lines that are maintained by crossing to normal counterparts (B lines). Our objective was to study the function of fertility restorer (*Rf*), *scsti*, and *vitality* (*vi*) genes in alloplasmic lines of durum wheat to provide partial (sterile) and full compatibility (fertile) between alien cytoplasm and nucleus. We crossed A lines of durum wheat with cytoplasm from different related species, including *T. timopheevii* (Tt), *T. araraticum* (Ta), and *Aegilops speltoides* (Spt) to the (*Ae. longissima*) double-ditelosomic 1B ((lo) dDt 1B) having *scsti scsti* and *vi vi* and the durum lines having *scsti scsti* or *vi vi*. The crosses of (lo) dDt 1B with the *scsti scsti* and *vi vi* gene pairs produced fertile F₁s, showing that *scsti* and *vi* produce fertile F₁s, whereas crosses to durum lines having a *scsti scsti* or *vi vi* produced male sterile F₁s, showing that *scsti* or *vi* alone do not produce fertility in A lines with alien cytoplasm. Also, crosses of (lo) *scsti*-durum to the R lines having *Rf* genes and cytoplasm of Tt, Ta, spt, or other related species produced plump and viable seeds having *scsti* and *Rf* and fertile F₁s, but seeds having *Rf* genes alone were shriveled and inviable, like those from a cross to control durum. In summary, the (lo) *scsti vi* or (lo) *scsti Rf* produced plump seeds and fertile F₁, whereas (lo) *vi* produced plump seeds with greatly reduced fertility and plant vigor, and *Rf* produced shriveled and inviable seeds.

Poster 71. Homoeoallelic relationship of two speciation genes involved in the evolution of allopolyploid wheat.

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The evolution of wheat is a very complex process involving both nuclear and extranuclear genomes. Here we present work on homoeologous relationship between two speciation genes affecting nuclear-cytoplasmic (NC) interactions, critical in the development of allopolyploid wheat. Disruption of such NC interactions leads to multiple incompatibilities, such as lack of seed viability or low vigor. These incompatibilities create genetic barriers, playing an important role in the speciation process, and preclude the commercial production of hybrid wheat and the full exploitation of the secondary and tertiary gene pools in breeding of *Triticum* ssp. The species-cytoplasm specific (*scs*) genes restore adequate compatibility between durum wheat nucleus and *Aegilops longissima* (S¹S¹; 2n=2x=14) cytoplasm. Classical mapping using

5,932 F₂s and radiation hybrid (RH) mapping using 237 RH1 semi-durum lines, treated with 150 Gy gamma rays, were employed to position the *scsti* and *scsae* loci, respectively. The two compatibility genes were mapped, with ten common markers (out of 49 EST-based markers used), onto homoeologous chromosomes 1D (introduced to durum from *T. aestivum* (AABBDD; 2n=6x=42) and 1A (with the *scsti* locus introduced from *T. timopheevii* (A'A'GG; 2n=4x=28)). The *scsti* locus was mapped within 0.3-cM region of chromosome 1A, whereas the region of *scsae* was narrowed to ~6.9 centiRads (cR; units of RH maps). Wheat Zapper, an online application developed to localize orthologous relationships with model species, was used to compare wheat and rice sequence in the *scs* region. A conserved colinearity between wheat and chromosomes 10 and 5 of rice (*Oryza sativa*) was observed. The syntenic relationship between two *scs* genes and the fact that both loci restore identical phenotypes in the same alloplasmic line provide firm evidence for their homoeoallelic identity. Our observations also support the 'Maan hypothesis', which states that each species had pre-established unique compatible NC interactions before undergoing evolutionary polyploidization and cytoplasm exchange with other species. The map-based cloning of the *scs* genes will allow the employment of multiple NC genes into wheat cultivars to produce interspecific hybrids and to provide breeders with a novel set of tools to adapt wheat to the fast changing environment.

Poster 72. Re-evolution of wheat mitochondria.

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Mitochondria are centers of energy metabolism in the cell. The cross talk between the genomes present in the mitochondria and nucleus in a cell are critical to all eukaryotes. Thousands of phenotypic variations in plants and other organisms are known to be the result of changes in nuclear-mitochondrial (NM) communication. Recent data indicates that a mixture of more than one type of the mitochondrial genome exists within a cell (namely heteroplasmy), which adds a level of complexity to NM communication. Because plants cannot escape from adverse environmental conditions, a high level of heteroplasmy and changes in frequencies of different mitotypes could play an important role in stress tolerance. Analyzing the NM interaction in an alloplasmic line of wheat (line with alien cytoplasm), having *Aegilops longissima* cytoplasm but a *Triticum durum* nucleus, revealed the presence of a particular nuclear encoded species cytoplasm specific (*scs*) gene is critical for proper NM communication required for several developmental processes. High-resolution mapping of *scsti* (from *T. timopheevii*) and *scsae* (from *T. aestivum*) by a combination of radiation-hybrid and genetic mapping, located these genes on the same region of chromosome 1A and 1D of wheat, respectively. Because both loci restore identical phenotypes in the same alloplasmic line, the two genes seems to be homoeologous genes playing an important role in Triticeae speciation. Detailed analysis of the mitochondrial genome composition of the same alloplasmic line revealed alteration of the mitochondrial genome and gene expression patterns relative to parental lines. These changes are dramatic considering the timeframe. We also identified a high level of heteroplasmy in addition to the new mitotypes in this alloplasmic line leading to increased variation of this organelle, possibly because of an alien nuclear genome. Our analysis also indicates differential response of various alloplasmic wheat lines with the same nucleus to the fungal pathogen *Pyrenophora tritici-repentis* (tan spot) providing additional evidence on the importance of cytoplasm in response to biotic stresses. Re-evolution of wheat by introducing a new cytoplasm and a compatible *scs* gene in the nucleus may provide a further mechanism for tolerating biotic and abiotic stresses.