5,932 F_2s 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^tA^tGG; 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 centi Rads (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.