

Poster 73. Accelerated, mitochondrial genome evolution of a *Triticum alloplasmic* line.A.K. Noyszewski¹, L. Al-Nimer², F. Ghavami¹, Y. Q. Gu³, N. Huo³, A. Soltani¹, S. Meinhardt⁴, and S.F. Kianian¹.¹ Department of Plant Science, North Dakota State University, Fargo, ND 58108, USA; ² Department of Computer Science, North Dakota State University, Fargo, ND 58108, USA; ³ Genomics and Gene Discovery, USDA, Albany, CA, USA; and ⁴ Department of Plant Pathology, North Dakota State University, Fargo, ND 58108, USA.

Making an alloplasmic line (a line with alien cytoplasm) of durum wheat (*Triticum turgidum*) with *Aegilops longissima* cytoplasm is impossible, resulting in nonviable seeds unless the species cytoplasm specific, *scs*, gene regulating the nuclear–cytoplasmic compatibility is introduced to the nucleus of alloplasmic line. To find out the possible changes in the mitochondrial genome of *Ae. longissima* in the alloplasmic conditions, the mitochondrial genomes of the alloplasmic wheat and its parents were sequenced and described. All mitochondrial genes characterized previously in the *T. aestivum* genome were present in the sequenced mitochondria. The genome comparison showed major differences in the *atp6*, *nad9*, *nad6*, and *rps19-p* genes. We were able to identify species specific ORFs, e.g., orf113, as one of chimeric ORFs found only in alloplasmic line. We recognized that the orf359 in alloplasmic line is the most polymorphic region when compared to *T. turgidum* and that it is entirely missing in *Ae. longissima*. Nucleotide polymorphism across the genomes indicated possible mitochondrial heteroplasmy. Structural differences between three *Triticum* mitochondrial genomes were observed where conserved gene blocks and gene pairs remained together among species but were rearranged within the genome. Three possible recombination events in gene blocks, I, V, and VI, were found. Significant differences in the alloplasmic line mitochondrial genome were observed when compared to its donor based on gene sequence, ORFs, single nucleotide polymorphism, and overall synteny. These results indicate accelerated evolution of the mitochondrial genome as a result of nuclear genome substitution and may have significant evolutionary and genetic implications in terms of adaptation and stress tolerance.

Poster 74. Changes in gene expression of mitochondrial genes in alloplasmic wheat lines carrying restorer genes.Ali Soltani¹, Farhad Ghavami¹, Andrzej Noyszewski¹, Filippo M. Bassi¹, Anantharama Rishi¹, Steven Meinhardt², and Shahryar F. Kianian¹. ¹ Department of Plant Sciences and ² Department of Plant Pathology, North Dakota State University, Fargo, ND 58108-6050, USA.

The replacement of a particular nucleus with the nucleus of another species in alloplasmic lines of wheat is an unique approach to analyze nuclear–cytoplasmic (NC) communication events. Usually these replacements produce non-viable, sterile, or weak progenies due to the incompatibility in NC interaction. The incompatibility in (lo) durum wheat, where the nucleus of *Aegilops longissima* has been replaced with that of *Triticum turgidum*, can be improved by the addition of the *scs* (species cytoplasm specific) and *Vi* (vitality) gene pairs. These two genes can recover plant vigor and male fertility in (lo) durum lines, respectively. In many cases, cytoplasmic male sterility is associated with the expression of particular mitochondrial orfs. Therefore, the relative expression level of several ORFs and mitochondrial genes were analyzed in (lo) durum lines having different combinations of *scs* and *Vi* genes as well as normal lines using 2^{-ΔΔC_t} method with SYBR green real-time PCR. Our preliminary analysis revealed higher expression of several orfs in (lo) durum lines compared with the cytoplasm donor (*Ae. longissima*) and nuclear donor (*T. turgidum*). These data support the hypothesis that the expression of mitochondrial orfs is suppressed by gene(s) in the nucleus of the normal plants. It appears the normal suppression mechanism are affected in alloplasmic conditions increasing the expression of certain orfs and eventually leads to decrease in male fertility and/or plant vigor. Based on our data, the nuclear *scst1* (*T. timopheevi*-derived *scs*) gene product can down regulate the expression of orf48–orf25 in (lo) durum line. The mechanism of this down regulation is still unclear and needs more investigation.