

**Oat evolution revealed in the maternal lineages of 25 *Avena* species.**

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**Summary:**

Over the last several years, I have conducted a phylogenetic analysis of 25 oat species by searching for maternal evolutionary signals. The hope was to provide a supplementary view of oat evolution. This was done using a multiplexed shotgun procedure to acquire sequence data from the chloroplast and mitochondrial genomes of 25 *Avena* species. Phylogenetic analyses of the organellar SNP data revealed a new maternal pathway of oat genome evolution leading to the formation of the hexaploids. This new pathway involves three diploid species (*A. ventricosa*, *A. canariensis*, and *A. longiglumis*) and two tetraploid species (*A. insularis* and *A. agadiriana*). The cultivated hexaploid *A. sativa* acquired its maternal genome from an AC genome tetraploid closely related to *A. insularis*. In turn, both *A. insularis* (AC genome) and *A. agadiriana* (AB genome) derived their maternal genomes from an ancient A genome diploid closely related to *A. longiglumis*. The data show that the C genome species diverged 19.9-21.2 million years ago (Mya), that the oldest A genome *A. canariensis* diverged 13-15 Mya, and that species of the clade including the hexaploids diverged 8.5-9.5 Mya. Comments are welcome and further exploration of this topic towards a better understanding of oat evolution and utilization is encouraged.