



Comparative linkage mapping of diploid, tetraploid, and hexaploid *Avena* species suggests extensive chromosome rearrangement in ancestral diploids

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Summary:

Oat (*Avena*) species can be diploid, tetraploid, or hexaploid, and four genome types (named A through D) are generally recognized. We used Genotyping-by-Sequencing (GBS) markers to construct linkage maps of an A genome diploid oat cross (*Avena strigosa* x *A. wiestii* (SW), $2n = 14$), and an AB genome tetraploid oat cross (*A. barbata*, $2n = 28$).

The *A. barbata* cross had been mapped previously using AFLP markers (Gardner and Latta, 2006), and the SW cross had been mapped previously using mostly RFLP markers (Portyanko, *et al.* 2001). With the addition of the GBS markers, both new maps have greatly improved coverage, which allowed for the identification of seven complete linkage groups (chromosomes) in SW and 14 in *A. barbata*. The seven SW linkage groups showed very strong homology and synteny to seven of the linkage groups in the *A. barbata* cross. The other seven *A. barbata* linkage groups showed much less conservation with the SW linkage groups, implying that *A. barbata* is an allopolyploid formed from the crossing of distinct A and B genome diploid ancestors. Several translocations were found between chromosomes within each subgenome (A or B) of *A. barbata*. However, no translocations were observed between A and B genome chromosomes.

The SW and *A. barbata* maps were compared to a consensus map of the cultivated ACD hexaploid oat *A. sativa* ($2n = 42$) (Bekele, *et al.* 2018). The A and D genomes of *A. sativa* showed parallel rearrangements when compared to the A genome diploid and the A genome of the tetraploid. While translocations between chromosomes from different genomes are well known in polyploid *Avena* species, our results are best explained if translocations also occurred in the A, B, and D genome diploid ancestors of polyploid *Avena* species.

References:

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