Analysis of TE population in polyploid oat reveals subgenome specific activity patterns

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Abstract

Oat (*Avena sativa*) is an allohexaploid cereal comprising three large and highly repetitive subgenomes (A, C and D). The C subgenome separated _˜8 million years ago (MYA) while A and D separated _˜3.5 MYA. We analyzed over 22.000 full length retrotransposons belonging to four high-copy and two centromere-specific families. Out of these, we found four families to be subgenome specific. The analyzed TE families were active during different times in *A. sativa* evolution, allowing to study how they evolved in different species lineages. For example, we found two *Gypsy* families with a distinct activity pattern differing between the C subgenome and the A and D subgenomes. Additionally, detailed characterization of subgenome-specific TEs showed them to be excellent markers for chromosomal translocations that occurred after polyploidization events.

The *Copia* family *RLC_Angelina* is highly abundant in all three subgenomes. Interestingly, we identified two *RLC_Angelina* sub-populations one comprising autonomous and one non-autonomous elements. This demonstrates that pairs of autonomous and non-autonomous TEs can persist over millions of years. In the A and D genome the *RLC_Angelina* family went mostly silent before their separation and in the C genome before the tetraploidisation that brought together the C and D genomes _˜1.5. MYA. (CCDD).

In addition, we identified the *Gypsy* family *RLG_Cereba* in the centromeres of the A and D subgenomes while we found a different family, *RLG_Ava*, to dominate the C subgenome centromeres. Interestingly, the *RLG_Cereba* family was absent in the C subgenome and *vice versa* for the *RLG_Ava* family. This suggests a competition between centromere specific retrotransposon families.

Surprisingly, we found no evidence of TEs specifically activated after polyploidisation events. On the contrary, we identified TE families that were highly active before the polyploidisation events, but went silent after. This challenges the notion that polyploidization is followed by a ”genomic shock”.

Keywords: Avena sativa, Retrotransposons, Genome Evolution

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