

The most widely cultivated allohexaploid common wheat (*Triticum aestivum*) originates from two natural polyploidizations. The first hybridization occurred between two diploid ancestors carrying the A (*Triticum urartu*) and B genome, producing a tetraploid wheat (*Triticum turgidum*, AABB). The second one was between the cultivated tetraploid wheat and the diploid goat grass (*Aegilops tauschii*, DD). Recently, a near-completed high-quality genome sequences of common wheat and its wild tetraploid and diploid ancestors were published, providing a precious opportunity to explore how common wheat overcomes the intergenomic incompatibilities, the so-called evolutionary ‘dead end’, and successfully establishes nascent polyploids. Here we systematically compared three wheat A (sub) genomes with different ploidy levels to present changes in gene and transposon during the evolution of *T. urartu*, emmer and Chinese Spring from their common ancestor. The diploid progenitor of the A subgenome has experienced extraordinarily frequent gene loss and duplication, resulting in greatly improve adaptability to large-scale genetic changes that occur in a short period of time. Further studies on the chromosomal distribution and functional preferences of the lost and duplicated genes demonstrate how the diploid ancestor keeps its stability under the highly dynamic genetic background. As for transposable elements, the tetraploidization dominantly activated four Gypsy families and accelerated TE eliminations in two Copia families. However, the hexaploidization did not induce any change in TE families. Our comparative analysis of the wheat A (sub-) genome at three ploidy levels reveal critical genomic features that determine the successful polyploidization and genomic remodeling through wide hybridizations.