Sequence composition, organization, and evolution of the core Triticeae genome

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evaluated using the ratio of EST number in a TE family to the copy number of the TE family in the D-genome. Transcription levels were the highest for Ty3-gypsy elements (1.7%), lowest for Ty1-copia elements (0.6%), and moderate for non-LTR (1.4%) and CACTA elements (1.2%). The highly transcribed were the Ty3-gypsy element Latidu and the CACTA

Defective TE elements can arise during transposition or retrotransposition by internal deletion (see reviews by Bennetzen, 2000; Feschotte et al.

The genome appears to control the retroelement invasion at the level of transcription and/or integration. A high correlation between the level of transcription and amplification was observed in Tos17 (Hirochika et al., 1996). However, Bare-1 was highly transcribed in barley, but its retrotransposition was rarely detected (Suoniemi et al., 1997). In our results, Latidu was highly expressed but only accounted <1% of the D-genome. Therefore, integration, rather than transcription, is likely the major restriction factor for retrotransposition in the large genomes of wheat and barley. We can further infer that the insertion spectrum of a retroelement is a determinant of its copy number in a large genome. The narrower the spectrum, the lower the copy number, and vice versa. Studies in yeast showed that insertion specificity was determined by an interaction between the integration complexthe

implying that this family has a broad insertion spectrum and

and the number of active (hypomethylated) elements. Inspection of the CG and CNG frequencies in the tmf library showed that variation in frequencies was approximately fourfold higher for Ty3-gypsy and CACTA than for Ty1-copia

Ty3-gypsy and CACTA elements. Therefore, Ty1-copia

sequenced a small-insert genomic library of bread wheat generated from the slow-association fraction collected at C_0t >1600. The preliminary result indicated that the repeat

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