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Detection of *Ty1-copia* like Retrotransposons from Common Buckwheat (*Fagopyrum esculentum*)

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Objectives

RT domains of *Ty1-copia* retrotransposons were isolated from common buckwheat (*Fagopyrum esculentum*) genome through PCR using degenerate primers and characterized with respect to their sequence heterogeneity and phylogenetic relationships among themselves as well as with the plants from different taxonomic groups.

Materials and Methods

1. Plant materials: Buckwheat (*Fagopyrum esculentum*)
2. Methods: Genomic PCR, Sequencing analysis, Similarity analysis, Phylogenetic analysis

Results and Discussion

The *copia* primers amplified a single product of about 280bp, which was cloned and one hundred randomly isolated clones were sequenced. Among these, 72 clones showed sequence homologies with the *copia-RT* sequences of other plants. Translation of nucleotide sequences of these clones to their amino acids and alignment of putative amino acid sequences showed presence of properly translated primer sequences at their both ends (5'-QMDVK and 3'-YVDDM). About 24% clones revealed presence of stop codons or frame shift or both within their translational frames. Analysis with multiple sequence alignments and construction of N-J tree (based on pair wise distance method) showed great sequence heterogeneity with an overall average distance of 32% among *copia-RT* domains, which is quite high for the elements of the same class. These results indicate the presence of a large population of *Ty1-copia* like retrotransposons with a rich diversity of sequences in buckwheat genome.

All the *copia-RT* sequences were assigned to seven distinct groups. Each group was defined as a set of related sequences having more than 90% identity in their amino acids. Phylogenetic analysis of buckwheat *copia-RT* sequences with that of other unrelated plants showed that some buckwheat clones are more closely related with *Ipomoea*, *Orobancha* and *Silene* (dicots) or with some monocots like wheat, rice and barley rather than to other buckwheat clones. These results indicate that majority of buckwheat *copia-like* retrotransposons are of very ancient origin and support the hypothesis of both vertical as well as horizontal modes of their transmissions. Moreover, significantly low level of translational mutations in their RT sequences indicates the possibility of presence of some active retroelements in buckwheat genome.

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