



The Subtelomeric khipu Satellite Repeat from *Phaseolus vulgaris*: Lessons Learned from the Genome Analysis of the Andean Genotype G19833

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Subtelomeric regions in eukaryotic organisms are known for harboring species-specific tandemly repeated satellite sequences. However, studies on the molecular organization and evolution of subtelomeric repeats are scarce, especially in plants. Khipu is a satellite DNA of 528-bp repeat unit, specific of the *Phaseolus* genus, with a subtelomeric distribution in common bean, *P. vulgaris*. To investigate the genomic organization and the evolution of khipu, we performed genome-wide analysis on the complete genome sequence of the common bean genotype G19833. We identified 2,460 khipu units located at most distal ends of the sequenced regions. Khipu units are arranged in discrete blocks of 2-55 copies and are heterogeneously distributed among the different chromosome ends of G19833 (from 0 to 555 khipus per chromosome arm). Phylogenetically related khipu units are spread between numerous chromosome ends, suggesting frequent exchanges between non-homologous subtelomeres. However, most subclades contain numerous khipu units from only one or few chromosome ends indicating that local duplication is also driving khipu expansion. Unexpectedly, we also identified 81 khipu units located at centromeres. All the centromeric khipu units belong to a single divergent clade also comprised of a few units from several subtelomeres, suggesting that a few sequence exchanges between centromeres and subtelomeres took place in the common bean genome. The divergence and low copy number of these centromeric units from the subtelomeric units could explain why they were not detected by FISH (Fluorescence in situ Hybridization) although it can not be excluded that these centromeric units may have resulted from errors in the pseudomolecule assembly. Altogether our data highlight extensive sequence exchanges in subtelomeres between non-homologous chromosomes in common bean and confirm that subtelomeres represent one of the most dynamic and rapidly evolving regions in eukaryotic genomes.

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