

Comparative cytogenetic analysis in *Vigna* sp. revealed by BAC-FISH

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Abstract/Resumo

Vigna Savi species constitute a group of worldwide legumes of great socioeconomic importance. Progress in its genomic resources allowed the development of a consensus genetic map with a high-density of SNP markers and construction of Bacterial Artificial Chromosome (BAC) libraries. Fluorescent in situ hybridization (FISH) using BAC clones as probes (BAC-FISH) became a powerful tool for synteny and collinearity analyses among closely related species in several groups of plants. Previous work using BAC-FISH with probes of the *P. vulgaris* 'BAT93' library of *V. unguiculata* (Vu) and *V. aconitifolia* (Vac) chromosomes showed partial conservation of macrosynteny with chromosomal rearrangements. For a better understanding of the genomic organization and karyotype evolution in *Vigna*, we performed a comparative cytogenetic study with three *Vigna* species ($2n = 22$), using BAC-FISH. Four single-copy BACs of chromosome 3 and chromosome 11 of *V. unguiculata* (Vu3 and Vu11, respectively) were hybridized in situ on mitotic metaphase chromosomes of *V. angularis* (Van) and *V. radiata* (Vr). For chromosome 3, two Vu3 BACs (H31G07 and H50P11) were located in the same orientation at Vu, Van and Vr chromosomes, in interstitial regions in the short and long arms, respectively. These results suggest a conservation of synteny for both markers. On the other hand, H49E24 and H85I15 BACs were located respectively in terminal region in the short arm and subterminal region in the long arm of Vu11, while a distinct pattern was observed in Van, which showed both BACs at adjacent positions in the short arm. This suggests that a pericentric inversion involving BAC H85I15 occurred in one of these species. Based on the present results, associated with our previous works, the inversion observed on Vu11 seems to have occurred in *V. unguiculata* after *Vigna* and *Phaseolus* separation, since position of other BAC clones were different in Vu when compared to Vac, Van and Pv. These data demonstrate the feasibility of the BAC-FISH technique in comparative chromosome mapping, showing a break of macrosynteny among species of Phaseoloid clade. This is an initial step of an extensive macrosynteny study with BAC-FISH in *Vigna*.

Keyword/Palavras-chave: Bacterial Artificial Chromosome (BAC); Chromosome-specific markers; Comparative Analysis; *Vigna*

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