

Deciphering the repetitive DNA landscape in *Phaseolus* beans and allied genera (*Cajanus* and *Vigna*) by a comparative cytogenomic approach

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Abstract/Resumo

Several bean species (Fabaceae) have been undergoing intensive genomic research, which includes the generation of massive amount of DNA sequence data. We performed a comparative investigation of the repetitive DNA composition in some bean species (*Phaseolus vulgaris* - *Pvu*, *P. acutifolius* - *Pac*, *P. coccineus* - *Pco*, *Cajanus cajan* - *Cca*, *Vigna angularis* - *Van* and *V. nakashimae* - *Vna*). Genomic sequences were obtained from the NCBI public database (*Cca*/SRX031567, *Pac*/SRX1182015), *Pco*/SRX1182014, *Pvu*-andean accession/SRX1182008 and mesoamerican accession/SRX1182013, *Vna*/SRX758247 and *Van*/SRX7575509) and run in the Repeat Explorer pipeline using an all-to-all comparison analysis. Physical mapping of the most abundant repetitive elements was performed by FISH using mitotic chromosomes. Overall, the repetitive DNA fraction makes up around 30% of the genomes, except for both *Vigna* species (9.7% and 14.6%, for *Van* and *Vna*, respectively). LTR-retrotransposons represented the major class, with Ogre-Tat elements showing a large variation, followed by LTR-Chromovirus, satellite DNA repeats, LINEs and DNA transposons. The composition of satellite repeats was variable and four new families were identified, together with five previously described. All satellites were genus- or species-specific. Chromosomal mapping of LTR sequences (Chromovirus and Ogre) showed a differential accumulation on the pericentromeres of most chromosomes, particularly on *Phaseolus*. Among the satellite repeats, five were used for FISH (four newly identified). The three satellite families from *Phaseolus* showed different species-specific distribution. *PacSAT363* was detected in 12 pericentromeres. *PcoSAT36* and *PcoSAT336* were accumulated at pericentromeres, but *PcoSAT336* were also located in some chromosome termini co-localized with 45 rDNA, suggesting that this satellite have probably originated from ribosomal sequences. *Cajanus cajan* and *Vigna* showed only one satellite repeat each. *CcaSAT100* was located in 18 centromeres, while *VanSAT174* corresponded to the 45 rDNA in *Vna*, but appeared also as an independent centromeric satellite repeat in *Van*. Our analysis indicates a very dynamic landscape on the evolution of repetitive DNA among beans. Retrotransposons appeared as the main component of genomes and showed higher accumulation in the pericentromeric heterochromatin of *Phaseolus* species. Satellite repeats were mostly centromeric or pericentromeric and frequently species-specific, suggesting a fast evolution of this type of sequence in the bean genomes.

Keyword/Palavras-chave: Next generation sequencing (NGS); satellite DNA; Transposable elements; PCR; Fluorescent in situ Hybridization (FISH)

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