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Transposable elements and microsatellites in the *Passiflora edulis* genome: A first view

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The passion fruit (*Passiflora edulis*) is a tropical crop of economic importance for industrialized juice production and consumption as fresh fruit. However, very little is known about the genome of the species. Therefore, we have constructed a large-insert BAC library of *P. edulis*, consisted of 82,944 clones that are deposited at CNRGV/INRA, Toulouse. Then, we have entirely sequenced 109 BAC inserts, obtaining about 10 Mb of data. Identification and characterization of repeat sequences is an important part of the description of a genome, since a large portion of plant genomes is composed of repeated elements, and some of them play important roles in the cell. The aim of the present study was to search for repeat sequences in the 10 Mb of *P. edulis* data. We used REPET/PASTEC pipeline for identifying transposable elements (TEs) and MISA tool for microsatellite identification. The totality of all TE sequences correspond to ~20% of data, and 437 TEs were found, of which 250 belong to class I (194 LTRs, 36 LARDs, 11 DIRSs, 7 LINEs, 2 SINEs), eight to Class II (6 TIRs, 2 HELITRONs), four to TRIM order and one to MITE order; the remaining 174 TEs were not yet classified to class or order level (Figure 1). In addition, 10,918 microsatellites were found, of which 1,979 were mono-, 1,458 di-, 6,086 tri-, 947 tetra-, 296 penta- and 152 hexa-nucleotides, corresponding to ~122 Kb of sequence data. The percentages of each microsatellite class found herein are different from those previously reported in P. edulis BAC-end sequences analyzing ~6 Mb. This is the first analysis on the structure and content of the repeat portion of P. edulis genome, particularly TEs and microsatellites.

Biography

Zirlane Portugal da Costa has done her degree in Agronomic Engineering (Federal University of Ceará, Brazil). She has worked on *Cucumi melo* breeding in order to develop hybrid varieties for the Brazilian market. During her Master's degree (University of São Paulo, College of Agriculture, Brazil), she has worked with two cultivated Passiflora species, *P. edulis* and *P. alata* with the objective of developing putative functional markers (SSRs and SNPs) by prospecting of *P. edulis* transcripts expressed in response to *Xanthomonas axonopodis* infection. During her PhD studies (University of São Paulo, College of Agriculture, Brazil), she has investigated a large-insert BAC library of *P. edulis*. She is particularly working on transposable elements for their identification and classification into class, order, superfamily and family levels, using appropriate bioinformatics tools.

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