Development of retrotransposon-based markers IRAP and REMAP for cassava (*Manihot esculenta*)

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ABSTRACT. Retrotransposons are abundant in the genomes of plants. In the present study, inter-retrotransposon amplified polymorphism (IRAP) and retrotransposon-microsatellite amplified polymorphism (REMAP) markers were developed for the cassava genome (*Manihot esculenta* Crantz). Four cassava cultivars (Fécula Branca, IPR-União, Olho Junto, and Tamboara, two samples per cultivar) were used to obtain IRAP and REMAP fingerprints. Twelve designed primers were amplified alone and in combinations. The 42 IRAP/REMAP primer combinations amplified 431 DNA segments (bands; markers) of which 36 (8.36%) were polymorphic. The largest number of informative markers (16) was detected using the
primers AYF2 and AYF2xAYF4. The number of bands for each primer varied from 3 to 16, with an average of 10.26 amplified segments per primer. The size of the amplified products ranged between 100 and 7000 bp. The AYF2 primer generated the highest number of amplified segments and showed the highest number of polymorphic bands (68.75%). Two samples of each cassava cultivar were used to illustrate the usefulness and the polymorphism of IRAP/REMAP markers. IRAP and REMAP markers produced a high number of reproducible bands, and might be informative and reliable for investigation of genetic diversity and relationships among cassava cultivars.

**Key words:** Retrotransposons; Cassava; Diversity; Primer design