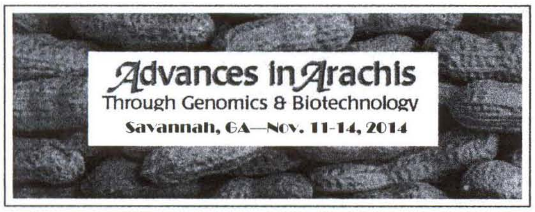

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Genetic variability and marker detection for rust resistance in recombinant inbred lines and backcross inbred lines of groundnut (*Arachis hypogaea* L.)

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A F_6 mapping population and backcross populations (BC_1F_4 and BC_2F_3 BC_3F_2) were developed from the cross between the susceptible parent GPBD-5 and resistant parents ICGV 86699 and ICGV 99005 to dissect the genetic variation and SSR markers linked to the rust resistance in groundnut. Genetic variability revealed that there were highly significant differences among recombinants for rust reaction. Less differences were observed between PCV and GCV for rust reaction in both crosses, which indicated a greater role of genetic components. High values of heritability (>80%) genetic advance and genetic advance as percent mean was observed for rust reaction in F_6 and backcross populations. Bulk segregant analysis in the segregating populations of both crosses (GPBD-5 × ICGV 86699 and GPBD-5 × ICGV 99005) indicated Tc4g10 marker was putatively linked to the rust resistant gene. The association of the putative marker identified based on DNA pooling from the selected segregants was established by single marker analysis (SMA). In the F_6 population of both crosses GPBD-5 × ICGV 86699 and GPBD-5 × ICGV 99005, the Tc4g10 marker accounted for 72.40% and 50.60% total variation, respectively. Tc4g10 marker accounted for 67.10%, 38.40% and 61.30% total variation in the cross GPBD-5 × ICGV 86699, and the same marker accounted for 73.8%, 54.7% and 84.4% total variation in the cross GPBD-5 × ICGV 99005 in BC_1F_4, BC_2F_3 and BC_3F_2, respectively. This marker can be used in marker assisted selection for rust resistance in groundnut improvement programs.

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