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Preliminary Analysis of the Genetic Determinism of the Resistance to Rotylenculus Reniformis in the Backcross Progeny of [(G.hirsutum x G. thurberi)2 x G. longicalyx] Hybrid

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The purpose of the investigation was to verify if the resistance to the reniform nematode observed in the backcross progeny of [(*G.hirsutum* x *G. thurberi*)^2 x *G. longicalyx*] (HTL) hybrid was controlled by a sole DNA fragment coming from *G. longicalyx* chromosome homeologous to chromosome-11 of *G. hirsutum* as observed in the backcross progeny of other trispecific hybrids involving *G. longicalyx*. In order to reach this objective, 13 BC1, 28 BC2 and 24 BC3 plants issued from the backcrossing to two *G. hirsutum* cultivars of HTL hybrid and highly resistant HTL backcross derivatives were screened in growth chambers for their resistance to the reniform nematode. The host status of the tested plants was assessed according to a scale where relative plant resistance is based on egg production per gram of root expressed as a percentage of egg production per gram on *G. hirsutum* control plants within the test. The limits of the five classes of the scale were: 0% = immune (I), 1-10% = highly resistant (HR), 11-25% = resistant (R), 26-40% = moderately resistant (MR), 41-100% = susceptible as check (S) and above 100% = very susceptible (VS). Among the 65 BC plants tested, we counted 20 (31%) HR, 25 (38%) R, and 20 (31%) S. None of them were I or MR. According to the BC generation, the percentage of sensitive plants varied from 20 % (BC2) to 40% (BC3). The phenotypic segregation was compared with the segregation of SSR markers BNL 3279_114 and BNL 836_215 specific to *G. longicalyx* mapped respectively at 1.4 and 4.4 cM of the *G. reniformis* resistance locus in the LONREN lines developed by USDA. Globally, only about 50% of the tested HR and R plants carried the SSR markers specific to *G. longicalyx* while 75 % of the S plants presented only *G. hirsutum* specific SSR alleles. No significant distortion was observed regarding the transfer through the ovule of both SSR markers specific to *G. longicalyx* in the different backcross generations. A recombination between the two marker loci was observed for 6% of the 65 analysed BC plants. These results indicate that the resistance to *R. reniformis* might be controlled by more than one gene. A screening of larger populations issued from highly resistant plants using molecular markers distributed all over the genome of *G. hirsutum* is necessary to check this hypothesis and map the other DNA fragment(s) of *G. longicalyx* and *G. thurberi* that could be involved in the control of the resistance to the reniform nematode.