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Resistance gene analogs colocalized with white spot disease resistance QTLs in maize

Lana, UGP[1,2]; Souza, IRP[1]; Noda, RW[1]; Magalhães, JV[1]; Guimarães, CT[1].

[1]Embrapa Milho e Sorgo, Sete Lagoas, MG; [2]Centro Universitário de Sete Lagoas, UNIFEMM, Sete Lagoas, MG

ubiraci.lana@embrapa.br

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Maize white spot (MWS) is considered one of the most important foliar maize diseases prevalent in tropical and subtropical areas that can cause significant yield losses. In spite of its economic importance, QTLs and resistance gene analogs (RGAs) associated with MWS are scarce. The aim of this study was to map QTLs associated with MWS resistance in a tropical maize population and to identify functional RGAs underlying these QTLs. A population composed by 148 F_2 individuals derived from a cross between L31.2.1.2, resistant, and L726, susceptible maize inbred lines was genotyped with 200 microsatellite markers and their $F_{2:3}$ progenies were evaluated for the response to MWS disease in two locations. Heritability estimate based on progeny mean was high (81.89%) and eight QTLs were mapped on chromosomes 1, 2, 3, 4, and 8, explaining approximately 92% of the genetic variance of MWS resistance. Data mining using 93 full-length plant R-genes revealed 939 RGAs distributed in clusters along the maize genome that were classified according to predicted functional domains. Out of them, 123 RGAs were colocalized in silico with MWS resistance QTLs, accounting for 0.4% of all maize genes. Candidate genes *Pto20, Pto99* and *Xa26.151.4* were genetically mapped and colocalized with MWS resistance QTLs on chromosomes 4 and 8. Furthermore, these candidate genes were up-regulated in the resistant line infected by MWS under field conditions. Interestingly, these RGAs share a serine/threonine protein kinase domain, which could be used to infer about resistance mechanisms and as putative targets for MWS resistance. Financial Support: Embrapa, Fapemig, and CNPq