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Identification of molecular markers associated with sudden death syndrome resistance in soybean

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Sudden Death Syndrome (SDS) is a disease that affects soybean production and is caused by four different species of the soil fungus *Fusarium*, all of them observed in Argentina, being *F. tucumaniae* the most frequent. SDS infections can result in severe yield losses, and the severity depends on different factors, including the susceptibility of the cultivar and the stage of growing period when the infection occurs. The most effective strategy of management is host plant resistance, which is determined by several genes. 14 QTLs located in the C2, G, I, D2, N, F and H linkage groups are known. The objective of this study was to identify molecular markers (MM) associated with the resistance to SDS in a RILs population coming from a cross between the Argentine cultivars NA4613RG and ADM4800. To characterize 149 RILs F2: F9 during four agricultural seasons, the incidence and severity of the disease was evaluated in each plot and the disease index (IE) was calculated. In addition, 200 MM were analyzed in 20 linkage groups, finding 25 polymorphic. The association between MM and IE was determined by ANOVA. Finally, two MM associated with IE were found in regions previously described ($p < 0.05$), proving there are resistance regions associated with SDS in the mentioned linkage groups in Argentine germplasm.