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'MN1606SP' by 'Spencer' filial soybean population reveals novel quantitative trait loci and interactions among loci conditioning SDS resistance

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Soybean sudden death syndrome (SDS) reduces soybean yield in most of the growing areas of the world. The causal agent of SDS, soil borne fungus *Fusarium virguliforme* (Fv), releases phytotoxins taken up by the plant to produce chlorosis and necrosis symptoms in the leaves. Planting resistant cultivars is the most successful management practice to control the disease. The objective of this study was to identify quantitative trait loci (QTL) associated with the resistance response of MN1606SP to SDS. A mapping population of F2:3 lines created by crossing the highly resistant cultivar 'MN1606SP' and the susceptible cultivar 'Spencer' was phenotyped in the greenhouse at three different planting times, each with three replications. Plants were artificially inoculated using SDS infested sorghum homogeneously mixed with the soil. Data were collected on three disease criteria, foliar disease incidence (DI), foliar leaf scorch disease severity (DS), and root rot severity. Disease index (DX) was calculated as $DI \times DS$. Ten QTL were identified for the different disease assessment criteria, three for DI, four for DX, and three for root rot severity. Three QTL identified for root rot severity and one QTL for disease incidence are considered novel, since no previous reports related to these QTL are available. Among the QTL, two interactions were detected between four different QTL. The interactions suggest that resistance to SDS is not only dependent on additive gene effects. The novel QTL and the interactions observed in this study will be useful to soybean breeders for improvement of SDS resistance in soybean germplasm.