عنوان مقاله:

Unraveling genotype-isolate interaction in sunflower (Helianthus annuus L.)- Sclerotinia pathosystem using GGE biplot method

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خلاصه مقاله:

Sunflower (Helianthus annuus L.) is one of the most important oilseed crops in the world. Basal stem rot, caused by Sclerotinia spp., is an important disease of sunflower causing considerable yield losses worldwide. Effective improvement for disease resistance relies on the understanding of the interaction between pathogen and host. A total of ۱۰۰ sunflower genotypes from different worldwide agricultural research institutions were evaluated for their responses to three isolates of each of the S. sclerotiorum and S. minor at the seedling stage in the controlled conditions. Remarkable significant host-pathogen isolate interaction indicates the existence of vertical or isolate-specific resistance in the studied sunflower germplasm against Sclerotinia spp. Genotype-by-pathogen biplot analysis was performed to observe the pathogenicity of the two fungi on host genotypes and facilitate the simultaneous visualization of the relationship among the pathogens and genotypes. The first two principal components accounted for ۹۵.۸۶% and ۷۹.۷۷% of the total variation of the genotype-isolate interaction of S. sclerotrium and S. minor, respectively. The GGE biplot related to S. Sclerotiorum isolates depicted that out of the studied genotypes, "H۱۰۰A/LC۱۰۶۴" was resistant against the A۳۷ isolate of S. Sclerotiorum. Among the examined germplasm, the genotype "۱۰۵۹" was identified as the resistant genotype against the J۲ isolate of S. Sclerotiorum. None of the genotypes were resistant to the J۱ isolate of S. Sclerotiorum. Regarding the generated biplot for S. minor, "۸A*/LC۱۰۶۴C" was the most resistant sunflower genotype against the M۱ isolate of S. minor. The genotype "H۲۰۵A/۸۳HR۴" was located in vertex near to A۱ and G۲ isolates and, therefore, was resistant to these isolates of S. minor. The genetic variation detected within the sunflower collections can be utilized for the selection of diverse parents in the resistant breeding programs as well as the development of mapping populations for the QTL analysis of resistance to .S. sclerotiorum and S. minor

کلمات کلیدی:

Biplot analysis, Disease resistance, Genotype-by-pathogen interaction, Isolate specific resistance, Sclerotinia basal stem rot, Sunflower