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Whole genome sequencing reveals population structure of *Cercospora beticola* to resistant sugar beet cultivars in Germany.

Cercospora leaf spot (CLS), caused by the fungal pathogen *Cercospora beticola*, is the most destructive sugar beet foliar disease. Management of CLS relies heavily on fungicide applications, however the emergence of fungicide-resistant populations emphasizes the importance of developing resistant cultivars. Understanding the interactions between cultivar resistance and *C. beticola* is essential for sustainable CLS management. To gain better insight into the structure of *C. beticola* populations collected from cultivars bearing distinct resistance properties, field trials were conducted with four sugar beet cultivars with different resistance properties in four geographical locations in Germany in 2022 and 2023. Experimental plots were inoculated with CLS-infested leaf material in 2022. Leaf material from each variety was harvested separately at the end of the season as inoculum for 2023. A population of 25 *C. beticola* isolates was obtained from each cultivar at each location, resulting in a total number of 800 isolates in both years. Isolates were subjected to whole genome sequencing and variant discovery to perform population genomic analysis. Principal component analysis showed little variation among populations obtained from different locations or cultivars, although location-specific lineages were identified in both years from one of the trial locations. Population genomic scans revealed eight genomic regions associated with certain host genotypes. Further experiments will focus on validating the functions of genes underlying these associated regions.