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**Extreme-phenotype GWAS identified genomic variation associated with resistance to *Aphanomyces* root rot in sugar beet.**

*Aphanomyces* root rot (ARR) can result in significant damage to newly emerged sugar beet seedlings. ARR is primarily managed by incorporation of factory waste-lime, use of fungicide seed treatments and use of moderately resistant varieties. Limited breeding efforts have focused on improving adult plant resistance although the mechanisms of resistance are unclear. Ninety-six USDA-ARS pre-breeding lines were screened for ARR resistance using a zoospore inoculation method and scored using a standardized 0-3 ARR rating scale. Individual plants within an accession were selected and pooled into equally sized (n=106) highly resistant or highly susceptible pools. Genomic sequencing was conducted on the pools for an extreme phenotype genome-wide association study (XP-GWAS) to identify genomic variants associated with ARR resistance. A total of 5,286,985 biallelic SNPs were identified and 29 of those were found to be statistically significant. These highly significant variants between pools were used to identify novel regions of the genome associated with ARR resistance.