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Abstract

Titanium dioxide nanoparticle (nTiO₂) is one of the most produced nanoparticles worldwide. Its mechanism on crop development and performance is unclear as it is hard to predict their toxicity or benefit. Therefore, understanding the genetics of crop development under nTiO2 is a prerequisite for their applications in agriculture and crop improvement. Here, we aimed to examine the influence of 300 ppm nTiO₂ on seed germination, seedling morphology, root-related traits in 121 worldwide spring barley (Hordeum vulgare L.) accessions. Results show that nTiO2 significantly affected all traits scored in this study. Response to nTiO₂ treatment, clear wide natural variation among accessions was detected. Remarkably, 10 genotypes showed increased root length under nTiO₂ at the seedling stage indicating that nTiO₂ enhanced the root elongation. Genome-wide association scan (GWAS) was applied using 9K single nucleotide polymorphism (SNPs) in a mixed-linear model that revealed 86 significant marker-trait associations with all traits scored in this study. Many significant SNPs were physically located near candidate genes, of which 191





genes were detected within the linkage disequilibrium and distributed over all barley chromosomes. Mostly, the genes harboured by chromosome 2H, specially calcium-binding genes family, regulate the variation of seedling length-related traits. Candidate genes on 7H encode zinc finger protein that controls the rate of germination. Therefore, these genomic regions at 2H and 7H can be targeted to select for improved seedling development and seed germination under nTiO₂ stress in soils. These results improve understanding the genetic control of seed germination and seedling development under high levels of nTiO₂ that can support plant breeding and crop improvement programmes.

Keywords: abiotic stress, barley, candidate genes, crop improvement, germination, GWAS, nanoparticles, nTiO₂, root length, seedling.