

Association mapping for common bunt resistance in wheat

Philipp Matthias Steffan | Anders Borgen | Anna Maria Torp | Søren K. Rasmussen | Gunter Backes

UCPH, current KWS | Agrologica | UCPH | University of Copenhagen | University of Kassel

Philipp.Steffan@kws.com | borgen@agrologica.dk | a.torp01@gmail.com | skr@plen.ku.dk | gunter.backes@uni-kassel.de

Presented by: Søren K. Rasmussen

Common bunt is a seed borne disease of wheat whose importance is anticipated to increase with a growing organic seed market which, in addition to seed phytosanitary measures, relies on genetic resistances towards common bunt. Genome wide association studies have been proven a useful tool in the detection of genetic polymorphisms underlying phenotypic trait variation in wheat. We screened 248 wheat accessions for two years for their resistance reactions towards common bunt. The majority of lines exhibited high levels of susceptibility towards common bunt, but 25 accessions had less than 10 % infection. Using Diversity Array Technology (DArT) markers for genotyping and correcting for population stratification by using a compressed mixed linear model, we identified two significant marker trait associations for common bunt resistance, designated Q Cbt-cph-2 B and Q Cbt-cph-7 A, located on wheat chromosomes 2 B and 7 A, respectively. We show that genome wide association studies are applicable in the search for genetic polymorphisms for resistance towards rare plant diseases in the context of an under-representation of resistant lines.