



Finding new sources of rust resistance from Watkins wheat landraces and wild relatives in Egypt through resistance gene enrichment breeding  
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The use of genetic diversity from wheat wild progenitor species and landraces has made a significant contribution to improving wheat productivity and provide new sources of resistance to different wheat diseases. In the present study, we have applied enabling technology resistance gene enrichment sequencing (RenSeq) to define the functional resistance gene repertoire against rusts and mildew in a diverse panel of 300 wheat lines. A diverse set of 300 Watkins bread wheat landraces were evaluated in Egypt in four different locations including Sids, Sakha, Nubaria and Gemmeiza Agricultural research stations, Agricultural Research Center during three consecutive seasons 2018-2019, 2019-2020 and 2020-2021 for disease resistance under natural field conditions. The obtained phenotypes were analysed by coupling association genetics to resistance gene enrichment sequencing (AgRenSeq) to define functional resistance genes in wheat. Candidate genes were identified for resistance to stripe rust on chromosomes 7A, 7D and 3B, leaf rust on chromosomes 1A and 6B and stem rust chromosomes 2B and 6B. In addition, one powdery mildew candidate resistance gene was identified on chromosome 5D which confers resistance at seedling and adult plant stages. Future work will focus on genetic confirmation of the identified genes and their incorporation into Egyptian wheat breeding programmes.