RESISTANCE GENE

A new mapping strategy

Nat. Biotechnol. **37**, 139–143 (2019).

Wild germplasm of crops contains abundant, yet underexplored, disease resistance (R) gene resources. The application of existing methods for cloning R genes from wild crops is hindered by the requirement for segregating or mutant progenies. Sanu Arora, from the John Innes Centre, and colleagues now report a strategy for rapid R gene cloning by coupling association genetics with R gene enrichment sequencing (AgRenSeq).

To test the AgRenSeq method, the researchers obtained a panel of *Aegilops tauschii* (diploid wheat) lines that were phenotyped using six races of the wheat stem rust pathogen. A sequence capture bait library was designed and optimized for capturing nucleotide-binding/leucine-rich (NLR) sequences encoded by the R genes in this population. The enriched R gene sequences were then assembled into NLR contigs and NLR *k*-mers were extracted for each accession. After a pre-filtering step, *k*-mer-based association mapping was conducted to identify *k*-mers associated with the resistance trait.

Four stem rust resistance genes, *Sr33*, *Sr45*, *Sr46* and *SrTA1662*, against three races of the stem rust pathogen were identified using this approach. The function of these genes in conferring resistance was underpinned by previous map-based or mutagenesis cloning and transgenic data, indicating the power of AgRenSeq. Rapid R gene cloning by AgRenSeq will facilitate marker-assisted breeding and broad-spectrum resistance engineering in genetically modified crops without a need for a reference genome.

However, AgRenSeq will likely miss atypical R genes because it relies on the capture of NLR sequences. Additionally, its performance is affected by sample size and population structure.

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Published online: 8 March 2019
https://doi.org/10.1038/s41477-019-0391-2