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Study Identifies Genetic Markers for Scald Resistance in Winter Malting Barley

Researchers analyzed 14,789 SNPs across 374 barley lines to help breeders screen resistant plants earlier.

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JoVE Visualize highlighted a genome-wide association study on Sept. 29 that identified genetic markers linked to resistance to scald in winter malting barley, offering breeders a clearer map for selecting plants that can better withstand one of the crop’s persistent

diseases.

The study focused on an adapted multiparent winter malting barley population and used 14,789 single nucleotide polymorphisms, or SNPs, across 374 barley lines. Those numbers matter because genome-wide association analysis depends on comparing many genetic differences across a broad set of plants to detect which parts of the genome are consistently tied to a trait. In this case, the trait was resistance to scald.

Scald is a plant disease that can damage barley growth and grain quality. In malting barley, disease pressure can affect both farm yields and the consistency of raw material moving into malt houses. That makes disease resistance an agricultural issue and, potentially, a supply issue for brewers that rely on stable barley quality for beer production.

The work described by JoVE Visualize is aimed at helping breeding programs move from observing resistance in the field to identifying genetic signals that can be tracked in the lab. Instead of waiting for several growing seasons to see which lines hold up best under disease pressure, breeders can use DNA markers to screen plants earlier and more efficiently. That does not replace field testing, but it can narrow the number of lines that need to be advanced and reduce time in the selection process.

Genome-wide association studies are widely used in crop science because they can connect natural genetic variation to useful traits without requiring a single simple inheritance pattern. In barley, as in other crops, disease resistance is often influenced by multiple genomic regions rather than one gene alone. A multiparent population can be especially useful in that setting because it captures more genetic diversity than a population derived from just two parents. More diversity can improve the chances of finding markers that remain useful across breeding material.

The study’s scale also suggests an effort to balance depth and practical breeding relevance. A panel of 374 lines is large enough to provide a broad comparison across related material, while nearly 15,000 SNP markers give researchers dense coverage of the genome. Together, those data can help identify chromosome regions associated with resistance and distinguish stronger signals from background noise.

For breeders, the value of this kind of result depends on whether the markers can be validated and used in routine selection. A marker is most useful when it reliably predicts resistance across different environments and breeding populations. The findings highlighted by JoVE Visualize therefore point to a step in the breeding pipeline rather than a finished commercial product. Further testing is usually needed before a marker becomes part of standard selection protocols.

Even so, the direction is important for the barley sector. Winter malting barley must meet agronomic demands in the field and quality demands from the malt and brewing industries. A line that performs well against disease but fails on malting quality will have limited value. The same is true in reverse. Research that looks at disease resistance within winter malting germplasm is notable because it is working directly in plant material that is closer to industry use, rather than in a broad collection with little commercial relevance.

That could have practical consequences beyond the breeding station. If barley breeders are able to use validated markers to improve scald resistance more efficiently, growers may face fewer losses from disease in affected environments. Over time, that could support more stable malt barley supplies for maltsters and brewers, with potential benefits for cost control and planning. Those effects would depend on adoption, field performance, and local disease conditions, but the breeding objective is closely tied to the supply chain for beer.

The study also reflects a broader shift in crop improvement toward combining classical plant breeding with genomic tools. Traditional selection remains central because yield, disease response, winter hardiness, and malting quality all need to be measured under real conditions. But marker-assisted approaches can make those programs more targeted. When researchers can identify genomic regions associated with resistance, they can select promising offspring earlier, stack useful traits more deliberately, and reduce the number of weaker lines carried forward.

For barley, that matters because breeding cycles are long and disease pressure can change from year to year. A genomic tool that improves the odds of selecting resistant material can make programs more efficient even if it does not eliminate uncertainty. It

can also help breeders preserve other important traits while improving resistance, since they can track several markers at the same time instead of selecting on visible disease response alone.

The JoVE Visualize material does not present the work as a final answer to scald in barley. Rather, it points to a set of genetic associations that can support breeding decisions and future validation work. In applied crop research, that is often how progress happens: first by locating useful genomic signals, then by testing them across more material and environments, and finally by converting them into routine tools for breeding programs working to deliver more resilient malting barley.