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## Genome of Barley Disease Reveals Surprises

**Scientists have sequenced the genome of a major fungal disease that affects barley and other cereal crops, a breakthrough that could lead to significant advances in our understanding of how plant diseases evolve. The research, published in the journal *Science*, suggests that parasites within the genome of the fungus help the disease to adapt and overcome the plant's defences.**

The study could help with the development of new agricultural techniques for protecting cereal crops from infection. Barley grains are the basis of many staple foods, and also central to the brewing and malting industries, so keeping the plants disease-free is becoming increasingly important for food security. This latest research, led by Dr Pietro Spanu from the Department of Life Sciences at Imperial College London, decodes the genome of *Blumeria*, which causes powdery mildew on barley.

Powdery mildew affects a wide range of fruit, vegetable and cereal crops in northern Europe. Infected plants become covered in powdery white spots that spread all over the leaves and stems, preventing them from producing crops, and having a devastating impact on the overall agricultural yield. Farmers use fungicides, genetically resistant varieties and crop rotation to prevent mildew epidemics, but the fungi often evolve too rapidly for the techniques to be effective. The mildew is able to evolve so quickly because multiple parasites within the genome, known as 'transposons', help it to disguise itself and go unrecognised by the plant's defences. It is as if the transposons confuse the host plant by changing the target molecules that the plant uses to detect the onset of disease.

The researchers discovered that *Blumeria* had unusually large numbers of transposons within it. "It was a big surprise," said Dr Spanu, "as a genome normally tries to keep its transposons under control. But in these genomes, one of the controls has been lifted. We think it might be an adaptive advantage for them to have these genomic parasites, as it allows the pathogens to respond more rapidly to the plant's evolution and defeat the immune system."

The authors believe that their research will contribute significantly to the design of new fungicides and resistance in food crops, as they now understand how the mildew can adapt so quickly. "With this knowledge of the genome we can now rapidly identify which genes have mutated, and then can select plant varieties that are more resistant," said Dr Spanu. The genetic codes will also help scientists monitor the spread and evolution of fungicide resistance in an emerging epidemic. "We'll be able to develop more efficient ways to monitor and understand the emergence of

resistance, and ultimately to design more effective and durable control measures."

Mildew pathogens are a type of 'obligate' parasite, which means they are completely dependent on their plant hosts to survive, and cannot live freely in the soil. Because they are so dependent, the pathogens have devised a way to disguise themselves in order to avoid the immune response of the host plant and overcome its defences.

"We've now found this happening in lots of fungi and fungal-like organisms that are obligate pathogens," said Dr Spanu, adding that the costly genome inflation could therefore be a trade-off that makes these pathogens successful. "Non-obligate pathogens are not so dependent on their hosts, as they can live elsewhere," said Dr Spanu, "so they are less dependent on rapid evolution."

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**Journal Reference:** Pietro D. Spanu, James C. Abbott, Joelle Amselem, Timothy A. Burgis, Darren M. Soanes, Kurt Stüber, Emiel Ver Loren Van Themaat, James K. M. Brown, Sarah A. Butcher, Sarah J. Gurr, Marc-Henri Lebrun, Christopher J. Ridout, Paul Schulze-Lefert, Nicholas J. Talbot, Nahal Ahmadinejad, Christian Ametz, Geraint R. Barton, Mariam Benjdia, Przemyslaw Bidzinski, Laurence V. Bindschedler, Maïke Both, Marin T. Brewer, Lance Cadle-Davidson, Molly M. Cadle-Davidson, Jerome Collemare, Rainer Cramer, Omer Frenkel, Dale Godfrey, James Harriman, Claire Hoede, Brian C. King, Sven Klages, Jochen Kleemann, Daniela Knoll, Prasanna S. Koti, Jonathan Kreplak, Francisco J. López-Ruiz, Xunli Lu, Takaki Maekawa, Siraprapa Mahanil, Cristina Micali, Michael G. Milgroom, Giovanni Montana, Sandra Noir, Richard J. O'Connell, Simone Oberhaensli, Francis Parlange, Carsten Pedersen, Hadi Quesneville, Richard Reinhardt, Matthias Rott, Soledad Sacristán, Sarah M. Schmidt, Moritz Schön, Pari Skamnioti, Hans Sommer, Amber Stephens, Hiroyuki Takahara, Hans Thordal-Christensen, Marielle Vigouroux, Ralf Weßling, Thomas Wicker, and Ralph Panstruga. Genome expansion and gene loss in powdery mildew fungi reveal functional tradeoffs in extreme parasitism. *Science*, 2010; 330 (6010): 1543-1546 DOI: 10.1126/science.1194573