**RRES Press Release 7th January 2025 Pathogen-host database refocuses on genes**

***PHI-base provides a comprehensive resource for deeper insights into pathogens and their hosts***

A new version of the influential [Pathogen–Host Interactions Database (PHI-base)](https://phi5.phi-base.org/#/home) has been developed and aims to provide more depth on how genes affect the outcome of interactions between pathogens and their hosts. PHI-base 5 increases the amount of information that can be pulled from peer-reviewed publications about pathogen–host interactions, say researchers, and with information now recorded in standardised way, should make it easier for both humans and machine learning systems to use the data.

PHI-base has been freely available for use by the scientific community for almost 20 years and will surpass 10,000 genes curated in total by mid-2025.

Kim Hammond-Kosack, lead scientist and PHI-base co-founder, says ‘This latest advancement of the precision of the information we are capturing will make PHI-base even more useful for discovery research, disease control, and monitoring for changes in pathogens that are of the most concern’.

The redesigned PHI-base 5 website displays all information about a given pathogen or host gene on a single page (one page per gene), which is intended to make it easier for researchers to explore genes of interest, and to identify findings in the literature that either confirm, or conflict with, existing knowledge. This change also makes it easier for information from PHI-base to be integrated with other biological databases, such as [UniProtKB](https://www.uniprot.org/) and [KnetMiner](https://knetminer.com/).

PHI-base 5 allows the curation of information that is either entirely new to the system or delivered in more detail than before. This includes:

* changes to pathogen genes that cause resistance to antibiotics or antifungals;
* changes to host genes that improve the host’s ability to resist infection;
* phenotypes for interactions that are common in plants, such as gene-for-gene interactions; and
* comparisons between the normal phenotype causally linked to a gene to what happens when the gene is mutated or deleted.

‘Within the [One Health](https://www.fao.org/one-health/en) concept, there is growing recognition of the multiple interconnectedness between crop health, animal health, human health and ecosystem health’ says Professor Martin Broadley, a science director at Rothamsted Research. ‘PHI-base allows researchers to rapidly explore the rules of life underpinning multiple pathogen types. Having this species breadth readily accessible allows exploitable common and species-specific mechanisms to stand out from the crowd.’

Nearly a fifth of the database (17%) focuses on pathogens of rice and wheat – the two most eaten cereal grains – and almost half (45%) focuses on crop species. In the UK and Europe, the overall production stability and economic success of the wheat crop is now under threat from climate change and an increasing diversity of pathogens and pests. PHI-base provides up to date new knowledge on pathogens and interaction phenotypes at various experimental scales. This is being used by researchers to deliver novel types of genetic and other improvements to advance the resilience of the wheat crop.

Full summary of improved features can be found [here](https://www.rothamsted.ac.uk/sites/default/files/Documents/PHI-base%205%20improvement%20summary.pdf).

Publication

Martin Urban, Alayne Cuzick, James Seager, Nagashree Nonavinakere, Jahobanta Sahoo, Pallavi Sahu, Vijay Laksmi Iyer, Lokanath Khamari, Manuel Carbajo Martinez, Kim E Hammond-Kosack, PHI-base – the multi-species pathogen–host interaction database in 2025, *Nucleic Acids Research*, Volume 53, Issue D1, 6 January 2025, Pages D826–D838, <https://doi.org/10.1093/nar/gkae1084>