

# New database for vital model organism launched

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A new database promises to be an invaluable resource to scientists who use a unique single-celled fungus to study human diseases.

The new database for the fission yeast *Schizosaccharomyces pombe*, called PomBase, was launched today by a consortium of researchers at the University of Cambridge, the European Bioinformatics Institute (EBI), and University College London (UCL).

Fission yeast is a single-celled fungus (yeast). Because their cells function much like our own, and it is an important model for studying [cellular processes](#) frequently associated with heritable diseases and cancers.

Scientists have already discovered that fission yeast has equivalents of many [human genes](#) which are known causes of rare genetic diseases and syndromes (including Batten', Bloom's, Birt-Hogg-Dube, Liddle, Lowe, Niemann-Pick). Additionally, fission yeast have counterparts of human genes implicated in diseases with multiple causes, to include many cancers, deafness, [neurological diseases](#), heart disease, Parkinson's, and anaemia.

Biologists today are very dependent on computer databases that catalogue the functions of the genes of the organisms they study and give access to other supporting information. The PomBase website will therefore prove to be an important tool for researchers studying fission yeast.

Its [launch](#) is the first stage of a 5-year project funded by the Wellcome Trust to provide a [model organism](#) database that allows researchers around the world to participate directly in the curation process in addition to using automated procedures based on the [genetic blueprint](#) of the fission yeast. The project uses Ensembl software for genome browsing, which is already used to present data for many other important experimental species. Novel tools and resources generated by this project will also be available to researchers working on other species, including [human pathogens](#), to create similar databases.

Steve Oliver, Professor of [Systems Biology](#) & Biochemistry, who is spearheading the initiative, commented: "Organism specific database projects frequently have limited resources, and large backlogs of uncurated literature. An important novel component of this project is the construction of intuitive tools to allow the research community to involve itself in database curation, and ensure that the scientific information published in their papers is visible to the entire biological research community. These tools can also be shared with other groups and implemented for their organism of interest."

Valerie Wood, PomBase Manager and co-investigator, said: "PomBase is not only establishing a [database](#) for this important model, it is also adapting the EBI's Ensembl Genomes platform and constructing tools to allow the research community to curate their own publications. The PomBase protocols will enable other research communities to establish and sustain similar databases for other experimental organisms. We have already identified counterparts for over 300 human disease genes in PomBase and many of these are being studied to elucidate the cellular basis of a diverse range of diseases."

Jurg Bahler, fission yeast researcher and PomBase co-investigator from UCL, added: "Many basic cellular processes are conserved between yeast and humans, and PomBase will be used extensively by biological and

biomedical researchers world-wide to study mechanisms involved in cell growth and division."

Paul Kersey, PomBase co-investigator from EBI, said: "PomBase has adapted the EBI's Ensembl platform to provide a multi-faceted resource dedicated to the needs of [fission yeast](#) researchers. These developments will enable other research communities to establish and sustain similar databases for their favourite experimental organisms."

The community curation initiative for PomBase will be launched in Spring 2012.

Provided by University of Cambridge

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