



FunPath: Genomewide search for disease-relevant mechanisms of the yeast *Candida glabrata*

Project Coordinator



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Project Description

In healthy individuals, yeasts of the *Candida* genus are nothing more than normal inhabitants of the body. They are generally to be found on the skin, in the mouth as well as in the intestines or mucous membranes. However, when the immune system is weakened, for example after a transplantation, long-term therapy in hospital, in cancer patients or babies, *Candida* species are able to transform into aggressive disease-provoking agents that are often responsible for systemic infections. Alongside *Candida albicans* the species *Candida glabrata* is becoming increasingly well known for causing illnesses, but treatment is difficult, as the yeasts have developed a resistance to the most common drugs used in fungal therapies.

Seven researcher teams from four different countries have now founded the FunPath Initiative under the umbrella of the *ERA-NET Pathogenomics*, with the specific aim of uncovering the disease relevant characteristics of the yeasts on a genetic level. Previous studies have shown that *Candida glabrata* is not greatly similar to other *Candida* species, but shares many characteristics with the genome of the non-pathogenic *Saccharomyces cerevisiae*, commonly used in baking and brewing. Today, this yeast is a vital ingredient in the economy, serving in a number of industrial processes as a genetically engineered organism. As part of the ERA-NET initiative, the researchers will be taking a close look at the genes that help to shield *Candida glabrata* from the immune system during infections. To shed some light on this ability, the scientists hope to analyse all relevant signalling pathways discovered in previous studies whilst using the existing knowledge about the close relative *Saccharomyces cerevisiae*. Ultimately, the researchers want to gain an insight into around 1000 genes, whose role will be made clear with the help of genetic engineering methods and large-scale screening systems. The most relevant factors to emerge following this scrutiny will then be analysed in animal models, mice or insects for example, to provide further information on possible therapeutic approaches.

