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For human beings, microorganisms play a crucial part in a number of respects: they can be both useful inhabitants of the body and dangerous pathogens. This dual role has long made them a fascinating branch of scientific research. Particularly on a genetic level, disease-causing microorganisms are increasingly being analysed in the hope of identifying critical factors that might be therapeutically applicable. This will also be the aim of twelve European research consortia within the ERA-NET PathoGenoMics network, which have recently started their work.

The ERA-NET PathoGenoMics network was initiated in 2004 and is one of around 80 ERA-NET networks aimed at counteracting the fragmentation of the European Research Area. The ERA-NET scheme is a funding instrument of the European Commission, first introduced in the Sixth Framework Programme. The underlying intention is to step up the cooperation associated with research activities carried out at a national or regional level in the member states. The ERA-NET PathoGenoMics was initiated by a group of research ministries and funding agencies from ten different countries to promote genomic research on pathogenic microorganisms (pathogenomics) in Europe. In the meantime, 15 partners from Austria, Finland, France, Germany, Hungary, Israel, Latvia, Portugal, Slovenia and Spain are cooperating under this single umbrella. As Julio Barbas from the Spanish Ministry of Research says, "In view of the multitude of data in the field of pathogenomics, we need the closest possible cooperation in Europe to bring together the best heads and to avoid the needless repetition of research in different countries."

The first transnational call for projects, issued last year, was well received: a total of 44 project applications were submitted, including 216 participating scientists. A jury has finally chosen twelve consortia for funding and these are now beginning their work. "By the year 2010, we will be allocating a total sum of around 14 million Euro, which will be provided by the respective national funding agencies of the research groups participating", said Prof. Frank Laplace from the German Federal Ministry of Education and Research.

Many of the research teams are focusing on specific groups of microorganisms, including the bacterial genera *Helicobacter*, *Escherichia*, *Listeria*, *Streptococcus* and *Chlamydia* and the fungal genera *Candida* and *Pneumocystis*. The diseases caused by these microorganisms are as varied as the microorganisms themselves but the key question is often the same: why do largely harmless bacteria or fungi mutate into dangerous, disease-causing agents? To get to the bottom of this and other mysteries, the researcher groups are using the latest genomics tools and a variety of different approaches. One aim is to shed some light on the microorganisms themselves. Thanks to the huge quantity of genome sequences that have previously been decoded, scientists will concentrate in particular on the complex network of protein interactions, screening them for signalling pathways relevant to disease. In addition, the researchers are looking at the respective host cells, again with the hope of identifying the factors that play an essential part in the development of disease. Based on their results, the scientists' long-term aim is to find new approaches for diagnostic, preventive and therapeutic strategies.

More information: <http://www.pathogenomics-era.net>

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