

Who are we?

"ERA-NET" is a Coordination Action (CA) scheme supported by the European Commission, aiming to strengthen the scientific basis in Europe and to support the structure of the European Research Area (ERA).

Within this framework, ERA-Net PathoGenoMics has created an internal market for pathogenomics research, fostering trans-national exchange of information, mobility of human resources, trans-national support of innovation and technology transfer and proposes a European Research and Training agenda on pathogenomic research as part of a European Research policy.

Twelve European research consortia were selected for funding by the review board of the ERA-NET PathoGenoMics network. In the next three years these research teams will work on identifying critical factors in the biological processes and life cycles of pathogenic bacteria and fungi.

ERA-Net PathogenoMics: Shedding light on microorganisms that cause disease

For humans, microorganisms can be useful inhabitants of the body or dangerous pathogens, creating a fascinating branch of scientific research, particularly on a genetic level.

The ERA-NET PathoGenoMics network initiated in 2004 is one of around 80 ERA-NET networks. The scheme, funded by the European Commission, was first introduced in the Sixth Framework Programme to increase cooperation in research activities carried out in member states. The ERA-NET PathoGenoMics was initiated by a group of research ministries and funding agencies from ten countries to promote genomic research on pathogenic microorganisms (pathogenomics) in Europe. Fifteen partners from Austria, Finland, France, Germany, Hungary, Israel, Latvia, Portugal, Slovenia and Spain are cooperating under this single umbrella.

The first trans-national call for projects was issued last year resulting in 44 project applications, including 216 participating scientists. Twelve consortia were chosen for funding and these are now beginning their work.

Many research teams are focusing on specific groups of microorganisms, and fungal genera, using the latest genomics tools and a variety of different approaches. Thanks to the huge quantity of genome sequences previously decoded, scientists will concentrate in particular on the complex network of protein interactions, screening them for signalling pathways relevant to disease, with the long-term aim of finding new approaches for diagnostic, preventive and therapeutic strategies.

More information: www.pathogenomics-era.net

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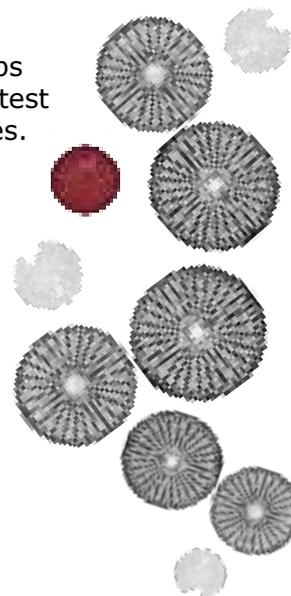
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SPATELIS Initiative: Exploring Listeria's sophisticated Infection strategies

Listeria bacteria, usually acquired through consuming contaminated food, will be investigated by the SPATELIS network, consisting of ten research teams representing five countries. The group's aim is to analyze the disease-causing factors in Listeria monocytogenes infections. Their study will fully exploit genomic and post genomic data and technologies to identify proteins, host ligands and cellular processes in an attempt to interrupt and limit bacterial growth.

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RNAi-Net: Functional analysis of the human genome during bacterial infections

A network of 16 research groups from seven countries will jointly analyze in detail the mechanisms of the host aspects of human diseases. Identification of host functions acting in disease as positive defense or negative elements of the host-pathogen cross talk is the major aim of the project. The recently established RNAi platform will be used by these key European key laboratories.

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Focusing on Escherichia coli: What causes a useful intestinal bacterium to become a health risk?

E.coli, the intestinal bacterium, is essential to body function although some variants are dangerous. Dealing with these species (ExPEC) is an ever increasing challenge. Fourteen research groups from seven countries will work together to develop therapeutic and preventive approaches in the fight against diseases caused by ExPEC strains. The molecular basis of infection will be integrated with genomics and functional studies. Uncovering the mechanisms responsible for the widespread resistance to antibiotics is also one of the group's goals.

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Shedding light on Streptococcus pathogenesis by comparative molecular analysis

The Streptococcus genus is responsible for approximately one third of all human bacterial infections. Six research teams from three countries have joined forces and are focusing on the bacterial surface molecules to uncover their role in infection processes. GAS and GBS gene expression in cellular and animal models will be studied, as well as bacterial-host interactions. The findings are expected to lead to the discovery of new basic disease-causing mechanisms and the development of new drugs.

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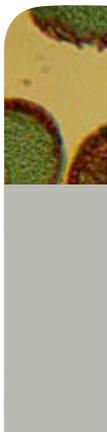


Glycoshield initiative: Exploring the role of fungal cell surfaces in infective processes

The Glycoshield initiative group comprises seven research teams from three countries. Its aim is to determine the role of selected surface components in the host response to the fungal pathogen. The scientists hope to shed light on the complex interactions between molecules present on the fungal cell surface during the infective processes and the different stages of pathogenicity. These will serve as a basis for developing innovative therapeutic approaches.

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Genome-wide analysis of the mechanisms of Enterococcus faecalis infections

Five research groups from four countries have joined forces to identify potential key mechanisms in the development of Enterococcus infections, determine virulence and fitness factors and define the fine line between the bacterial status as a gut commensal and opportunistic pathogen. Based on the results, key disease-relevant mechanisms of infective processes will be studied in an animal model to facilitate the identification of immunotherapeutic targets.

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

The FunPath Initiative founded by seven research groups from four countries aims to pursue a pathogenomics approach to identify the virulence genes at the genome scale of the opportunistic yeast *Candida glabrata*. Basic as well as applicable knowledge of the disease-relevant characteristics at a genetic level, analysis of immune and cellular factors and information applicable to therapeutic approaches are the group's objectives.

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ECIBUG: Tackling malicious Chlamydia infections using genomic analysis

To understand the pathobiology of *Chlamydia* on the basis of pathogen and host genomics, the ECIBUG consortium of nine research groups from four countries will explore the pathogenic *Chlamydia* species on a molecular level. In an attempt to tackle the organism's resistance to therapeutics.

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EPS-Matrix Initiative: Exploring the bacterial biofilm matrix at the protein level

This project aims to use an in vitro mature biofilm model combined with proteomic analysis to identify proteins playing nonstructural roles within the biofilm matrix. The investigation will be carried out by five research groups with complementary expertise from two countries. The work will involve four model organisms together with in-silico analyses of the biofilm to investigate protein secretion pathways and the potential biofilm-related role of the identified proteins.

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Pneumocystis: Revealing the shift from fungal colonization to lung disease

The Pneumocystis group, composed of three research teams from three countries, is aiming to determine the biological changes undergone by the organisms, that allows extensive proliferation of the fungus in the lungs of susceptible hosts. This culminates in severe pneumonitis and, ultimately, in respiratory failure. By targeting *Pneumocystis jirovecii*, which is often detected in human pulmonary disease, the scientists hope to generate efficient models for continuous monitoring of infection mechanisms.

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HELDIVNET: Analysing the genetic variability of the Helicobacter pylori bacterium

Helicobacter is a genus often responsible for gastrointestinal ulcerations, infections and infection-associated tumors, especially gastric cancers.

Seven research teams from four countries are working to broaden our understanding of *Helicobacter pylori*'s genetic diversity. The role of human genetic variation in determining susceptibility to infections is also being investigated by using comparative genomics and post genomic functional analysis.

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Unravelling the role of a key enzyme family in the pathogenicity of Candida albicans

Genome wide analysis of the function of the enzymes kinase and phosphatase in the human pathogen *Candida albicans* will be carried out by three research groups from three countries. They will investigate the role of these important enzyme families and how they affect the pathogenicity of *Candida albicans* in order to identify novel anti-fungal targets.

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