Worldwide Grid helps in the fight against heart disease

Catania, Tuesday, 3 March 2009

The latest work on the genetic causes of one of the world's biggest killers, coronary artery disease, will be published in the March 2009 issue of *Nature Genetics*. The research done by teams from the Cardiogenics consortium used the Enabling Grids for E-sciencE (EGEE) infrastructure. EGEE manages the world's largest multi-disciplinary computing grid and enabled the researchers to do two years' work in fewer than 45 days. This allowed them to identify possible genetic candidates for the causes of a disease which kills over two million people a year in Europe alone.

Coronary artery disease (CAD) is the most common form of heart disease and is a leading cause of death worldwide. It is one of the root causes of angina, heart failure and arrhythmias. This work could allow researchers to better understand why the disease develops and may offer new approaches for pharmacological prevention and treatment.

"Until recently, we looked at one variation at a time when trying to find new genes associated with disease", said David Tregouet, Pierre & Marie Curie University (UPMC), France.

"In this work we are using an original approach which lets us look at several variations at once. So, instead of investigating the effect on CAD risk of the 378,000 individual genetic markers available in this project, more than 8.1 million combinations were tested. We could do this large number of calculations thanks to EGEE".

The work was done in three stages to successfully narrow down the genetic sequences within a person's chromosomes that could make them susceptible to CAD. In the first stage, almost 8.1 million configurations of genetic markers were examined and 29 specific combinations were identified as possibly associated with susceptibility to CAD. Focussing on these 29 combinations, the second stage was able to bring this number down to just one combination of four genetic markers confirmed to be strongly associated with the risk of CAD. When these four genetic markers were investigated in additional studies, covering a total of almost 12,000 individuals, there was a strong correlation between their presence and the risk of having CAD.

One of the possible explanations behind why these four genetic markers seem to indicate that a person may be at an increased risk of CAD, is that they overlap with genes that regulate an enzyme called lipoprotein (a). A raised level of lipoprotein (a) is used by doctors around the world to diagnose CAD. When the Cardiogenics consortium compared the levels of the enzyme in one of the studies, they found that there was a strong correlation between high lipoprotein levels and the presence of the identified gene sequences.

Notes for Editors

Follow the EGEE User Forum live via GridCast at **http://gridtalk-project.blogspot.com/** and Twitter at **http://twitter.com/EnablingGrids**. Photos from the conference will be tagged on Flickr with "egeeuf09."

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Cardiogenics, an EU-project coordinated in Lübeck, Germany, aims to discover genetic variations leading to coronary artery disease, to uncover the underlying disease mechanisms and help to develop new treatments. For more information see www.cardiogenics.eu.

The Enabling Grids for E-sciencE (EGEE) project is co-funded by the European Commission. The project aims to provide researchers, in both academia and industry, with access to major computing resources, independent of their geographic locations.

EGEE's main aims are:

1. To build a secure, reliable and robust grid infrastructure
2. To supply a computing service for many scientific disciplines
3. To attract, engage and support a wide range of users from science and industry, and provide them with extensive technical and training support.

For more information see **http://www.eu-egee.org** or contact Catherine Gater, EGEE Dissemination, Outreach and Communications Manager, on + 41 (0)22 767 41 76 or email Catherine.Gater@cern.ch.