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HapMap Revolutionizing Genetic Research

The HapMap is revolutionizing the way scientists conduct genetic research. It has already been used to find genes related to several diseases, and many other promising studies are in progress. Around the world, the samples collected for the Project are being used by hundreds of investigators in many other studies. These studies are enhancing our understanding of both the disease process and of many basic aspects of biology.

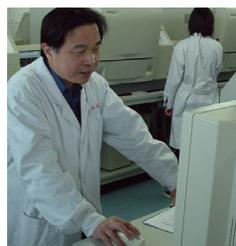
Across the globe, researchers are using the HapMap in exciting new ways to speed up the process of finding genes that contribute to health and disease. Several biotechnology companies have developed new technologies – called “platforms” – based on the analysis of HapMap data. These platforms are leading to exciting new methods for screening DNA samples. The HapMap has created a shortcut that now makes it possible for scientists to screen blood samples from hundreds or even thousands of people with and without certain diseases. This allows them to

detect associations between certain genetic variations and diseases.

Since the discovery of two major genes associated with macular degeneration (reported in the last issue of HapMap News) researchers – using the HapMap data – have found genes related to other important diseases, including:

- ◆ autism
- ◆ celiac disease
- ◆ childhood obesity
- ◆ diabetes
- ◆ multiple sclerosis

continued



“Having the HapMap freely and publicly available on the Internet to researchers around the world is greatly accelerating the pace of biomedical research internationally.”

- Dr. Huanming Yang, Director of the Beijing Genomics Institute

About the Coriell Institute

The Coriell Institute for Medical Research in Camden, New Jersey is a not-for-profit basic research institute with an international reputation based on its accomplishments in genetics research and cell banking. Its cell repositories contain one of the world's largest cell culture collections for use in research, forming a central and irreplaceable resource for the worldwide scientific community.



How to Contact Us

We encourage your community, through your Community Advisory Group, to let us know what other types of information you wish to receive. At the Coriell Institute, Dr. Donald Coppock oversees the Institute's involvement in the HapMap Project. Dr. Coppock also coordinates outreach to participating communities and researchers. He can be reached at:

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Major Autism Gene Found with Help of HapMap

Using data from the HapMap, along with DNA samples collected from many families who have affected children, researchers have discovered a genetic variation linked to autism. Autism – a condition usually diagnosed in childhood – causes severe problems in thinking, feeling, language, and the ability to relate to other people. It affects more than 3 of every 1,000 children ages 3-10.

Autism is one of the most heritable mental health conditions. If one identical twin has autism, so will the other in nearly 9 out of 10 cases. If one sibling has the disorder, the other siblings run a 35-fold greater-than-average risk of having it. Until recently, however, researchers have had little success in

identifying the genes involved.

Now, with the help of the HapMap (and samples from many families with affected children), researchers have achieved an important breakthrough. They found a variation in the sequence of a gene – called the “MET receptor tyrosine kinase gene” – that is associated with autism. This gene is involved in brain development, immune function, and digestive system repair. The genetic variation causes less of the gene to be expressed. People who have the variation are more than twice as likely as others to have “autism spectrum disorders,” ranging from the most severe form (autism) through intermediate and much milder developmental disorders.



Dr. Antonio Persico in his office.

According to study researcher Dr. Antonio Persico of the Department of Experimental Neurosciences at IRCCS

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Santa Lucia (Rome, Italy), “Autism probably involves complicated interactions between many different genetic and environmental factors. But this is a very important gene related to autism, from the largest family genetics study that has been done so far. This research, which builds on the HapMap, brings us one step closer to unlocking the mysteries of this disorder.”

HapMap Revolutionizing Genetic Research

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Without the HapMap, these groundbreaking discoveries would have taken years longer to achieve. While it will probably be some time before the identification of these genes translates into treatments or cures for these diseases, finding the genes is a crucial first step.

As Dr. Huanming Yang, Director of the Beijing Genomics Institute, states, “having the HapMap freely and publicly available on the Internet to researchers around the world is greatly accelerating the pace of biomedical research internationally.” For example, building on the HapMap, researchers in Japan, the U.K., Estonia, and several other countries are now launching large national biobanks to learn more about both the

genetic and the non-genetic factors that influence a wide range of diseases. In the U.S., a major public-private partnership was recently formed – called the Genetic Association Information Network (GAIN) – which is aimed at identifying the major genetic components of certain common diseases, including diabetes, schizophrenia, bipolar disorder, depression, psoriasis, and attention deficit/hyperactivity disorder (ADHD). In the UK, a similar project is looking at coronary heart disease, type 1 diabetes, type 2 diabetes, rheumatoid arthritis, Crohn disease and ulcerative colitis, bipolar disorder, and hypertension, as well as at tuberculosis and malaria in Ghana. In China, the U.S., and several other coun-

tries, researchers are discussing large projects to find the genes associated with several types of cancer.

In addition to using the data in the HapMap resource, many investigators around the world are studying the samples themselves, to help find the answers to a variety of other basic biological questions. So far, HapMap samples have been distributed to 138 investigators in 16 countries, ranging from China and Singapore to Iceland, Poland, South Africa and Spain. These investigators’ studies, like the HapMap itself, will expand our knowledge about human health and human relatedness.

Special Feature

This issue highlights four communities participating in the HapMap Project.

Japanese in Tokyo, Japan

The Japanese samples studied in the first two phases of the Project were collected in Tokyo, which has a population of over 12 million people, and is the largest city in Japan. Many of the sample donors were people who had already participated in other biomedical research projects. However, discussions about the Project were held with many people in addition to those who decided to donate samples, mostly in the Kanto area surrounding Tokyo.

In these discussions, some people expressed concerns about how the samples collected in Japan would be labeled; they did not want future research based on the HapMap to be used to discriminate

against Japanese people who are members of a minority population in countries outside of Japan. Some people also raised concerns about privacy and confidentiality, but these worries were lessened when people understood that no names or identifying information would be collected with the samples. Some wondered about potential commercial uses of the stored samples by biotechnology companies in

the West, and about how adequate oversight over the samples would be ensured once the samples had been sent to the Coriell Institute. In response to some of these concerns, the Coriell Institute modified some of its policies, to obtain more detailed information from researchers who order the samples that can be communicated back to the Japanese Community Advisory Group (CAG).



Many donors in Japan have previously participated in other biomedical research projects.



The Meenakshi Temple in Pearland, Texas is an important meeting place for members of the Houston Gujarati Indian community.

Gujarati Indians in Houston, Texas

These samples, which will be studied in the next phase of the HapMap Project, were collected from people living in Houston, Texas, whose ancestors came

from the Gujarat region in India. Gujarat is located in the northwestern part of the Indian subcontinent, and is one of the most industrialized states in India. “Gujarati” is a general term used to describe people who trace their ancestry to

this general geographic area, where people speak the Gujarati language.

Most people in the Houston Gujarati community with whom the Project was discussed expressed few concerns about genetic variation research and had high

hopes for the ability of this research to shed light on the causes of disease and contribute to the general good of humanity. They were especially interested in participating because people with ancestry from India often are not as well represented in biomedical research studies as people from other parts of the world. South Asian Indians living in the U.S. are especially underrepresented in research studies, because they are often “lumped together” with people from other Asian groups. People in the Houston Gujarati community hoped that the HapMap findings would spark greater interest in studying the special health problems of Indians — both those living in India and those living in other parts of the world.

Yoruba in Ibadan, Nigeria

The Yoruba samples studied in the first two phases of the Project were collected in Ibadan, which has a population of almost 2 million and is the second largest city in Nigeria. The Yoruba are mostly urban dwellers who have a complicated population history and a complex political and social organization. About 40 million people throughout West Africa, about 30% of the people in Nigeria, and the majority of people in Ibadan, are Yoruba.

Most people in the Yoruba community that discussed the Project were very enthusiastic about being approached to take part in this research. They were especially interested in the “Out of Africa” theory of human population history, under which all of the world’s population originated in Africa. Some people



Members of the Yoruba CAG hope that genetic variation research will help bring the world’s people closer together.

expressed the opinion that genetic variation research, by helping to show how people are biologically related to each other, might in some way help bring the world’s people together – especially Yoruba people or others with African ancestry who had been separated from their roots through slavery. People in the Yoruba community understand that the health benefits from the Project would

take some time to reach Nigeria, but were still interested in taking part so that future generations could benefit. Some have children and relatives in the recent Nigerian diaspora in the United States, Britain, and other countries, and thought these people might benefit even during their lifetimes if the Project yields short term health benefits in those countries.

Toscani in Italia

These samples, which will be studied in the next phase of the Project, were collected from people of Tuscan descent in Tuscany, a large region in central Italy. The samples were collected from residents of a flourishing industrial town near the city of Florence that has long and active history dating back to the Etruscans and a strong sense of local identity.

The people who were approached for the Project were generally quite open to participation if not highly engaged in or informed about the topic. The ethical and social implications of the Project generated much discussion among some, including debate about what it means to be a town resident, what it means to be “Tuscan” and the importance of social, in contrast to

biological, definitions of individual and group identities. The participants in a working group set up for the Project, in collaboration with the investigators who collected the samples, drafted a written statement that expresses their position regarding the potential risks and benefits of the Project and their aspirations “. . . that the research that will be carried out with and on our blood not be utilized for social or political discrimination against which we have fought so hard – nor for military purposes, nor

for reproductive cloning.” The Coriell Institute will include this statement in every box of samples from this community it sends out to investigators. For a link to the full text of the statement, see <http://ccr.coriell.org/nhgri/tuscan.html>.



Members of the Toscani CAG debated the implications of the HapMap Project for their community.

Enhanced Oversight Established for HapMap Samples

Management of the repository at the Coriell Institute where the HapMap samples are stored has been reorganized to provide stronger oversight over how the samples are used by future investigators and to accommodate greater input from the donor communities (through the Community Advisory Groups). The repository, which is now managed by the National Human Genome Research Institute (NHGRI), will continue to be operated by the same staff at the Coriell Institute, under the direction of Dr. Donald Coppock, who has worked at the Coriell Institute with the Hap Map Project for more than 4 years. The location of the samples will remain



Donald Coppock, Ph.D., Principal Investigator (left) and Christine Beiswanger, Ph.D., Co-Principal Investigator, (right) with the staff of the Coriell Cell Culture Laboratories who worked with the HapMap samples.

unchanged. However, the reorganization will make it possible for staff of the Coriell institute to be more proactive in

monitoring future uses of the samples and reporting back to the donor communities.

The next issue of HapMap News will highlight other participating communities and continue to provide general information about the HapMap Project and its important discoveries.

Electronic versions of this issue of HapMap News are available at: <http://www.coriell.org/index.php/content/view/65/120/> in each of the following languages: Chinese, English French, Italian, Japanese Spanish, Swahili, and Yoruba. Additional information of interest can also be found on the website of the International HapMap Project, <http://www.hapmap.org>.



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