vectors or mediators of disease. RNAi occurs in the protozoan parasite *Trypanosoma brucei* where it is being actively used as a reverse genetics tool [23] but there is also the potential that the same strategy could be adapted to down-regulate genes involved in the replication and/or maturation of this organism so blocking its natural life cycle. In mammalian cells we have used small dsRNA to rescue the cellular toxicity induced by plasmids expressing transcripts encoding an expanded polyglutamine tract, a defect associated with several dominant genetic disorders [24].

These studies only hint at the ways that dsRNA-triggered gene silencing could be used to block gene expression, but as our understanding of PTGS and RNAi improves it is probable that methods that use these pathways will prove to be versatile reverse genetics tools in a wide range of species and potentially a novel means of treating disease.

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Meeting Report

Genes, technology and public dialogue in Tartu, Estonia

Andres Metspalu

The Gene Technology Forum 2001 was held in Tartu, Estonia, 13–15 September 2001.

The success of the implementation of gene technologies in improving everyday life, including healthcare and food production, depends on one single and major issue – whether the general public will love (or hate) it. The key to this issue is to continue the dialog between the scientific community and the general public. Advances in human genetics and pharmacogenetics, directed either to gene discovery or drug trials, straightforwardly depend on large-scale population-based studies. Estonia has launched the Estonian Genome Project (see http://www.genomics.ee) with the major goal of creating the largest health database, and including genetic data of the participating individuals. As a part of public dialog and education devoted to human genetics and the development of gene technologies, Tartu has been hosting international meetings since 1999.

This year, about 400 medical doctors, scientists, students and specialists with diverse backgrounds gathered and the meeting started with a minute of silence to remember those who perished in the World Trade Center and the Pentagon.

The keynote speaker of the conference, Klaus Lindpaintner (Roche Genetics, the genetics division of F. Hoffmann-La Roche AG, Basel, Switzerland) offered his interpretation of genomics- and genetics-based healthcare. Elaborating on the increasing importance of genetics in healthcare, he explained how individualized, more efficient medicines developed on the basis of gene technology will help to reduce healthcare costs and how genome research will permit the prevention of diseases earlier and on a larger scale than at present. He emphasized that we should handle genetics as any other big advance in medicine and not mystify it – genomic approaches are not going to change the paradigm of how medicine is or will be practiced, they will just provide new tools

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to understand and treat disease and promote health.

Human genetics

This topic was represented by leaders of the field and covered genetic aspects of vision, hearing, cardiovascular disease and cancer. Thomas Meitinger (GSF, Neuherberg, Germany) focused on genes and mutations involved in degenerative eye disorders, including multifactorial diseases such as glaucoma and age-related macular dystrophy. François Cambien (INSERM, Paris, France) gave an excellent lecture on genetics of multifactorial diseases including cardiovascular disease. He reminded the audience and 'newcomers' to the field to carefully study the achievements of past 15 years and take a lesson from them. Much of what we are discussing today has been around for some time and quite often the 'new' is just the forgotten 'old'. He stressed the importance of explaining the biological basis behind disease and made it clear that to understand complex diseases we need to develop a catalog of all common polymorphisms and determine their roles. Finally, he stated that new tools need to be developed in the field of population genetics and although epidemiology and classical Mendelian genetics are helpful, they might also obscure the 'big' picture. Nicholas Short (UVS Iceland Genomics Corporation, Reykjavik, Iceland) presented the corporate vision of cancer studies using Icelandic cancer patients, Icelandic Cancer Registry and National Hospital System. They are using a clinical genomics approach to find the correlations between molecular biology of the patient's tumor and the mutations that give rise to it.

The most surprising presentation for many members of the audience was the one by Ralf Baumeister (Genome Center, Munich, Germany). He demonstrated very elegantly how the model organisms (*Caenorhabditis elegans* in his case) could be and have to be used in human genome research. His talk, full of animations and superb slides, offered unexpected insights, for example showing that even Duchenne muscular dystrophy has a *C. elegans* model or that simple organisms can have a temperature control using only a small number of neurons. According to the after-meeting feedback from the participants, his talk was one of the best.

Technology

A haplogroup map of the human genome will be the 'next big thing' in human genomics and the National Institutes of Health have proposed a new program similar to that of the SNP (single nucleotide polymorphism) consortium. The key question is which technology to choose? Therefore, and because of the Estonian Genome Project and the massive genotyping effort, several lectures were devoted to technology. Andreas Braun (Sequenom Inc., San Diego, CA, USA) gave an extensive review of SNP genotyping based on DNA MassArray™.

'The key ... is to continue the dialog between the scientific community and the general public.'

The validation process for the most comprehensive set of working SNP assays all over the human genome is close to completion and is intended to be used for elucidating the major genetic factors involved in human diseases. Roger Derbyshire (Orchid BioSciences, Abingdon, UK) presented his company's platform for genotyping based on primer extension on microarrays on the bottom of each well of a special 384-well plate. However, the winning solution, as many in the field said afterwards, was suggested by Mark Chee (Illumina Inc., San Diego, CA, USA). Illumina Inc. has combined the 192-plex oligonucleotide ligation-based assay with read-out on miniaturized arrays of universal capture probes attached to microbeads. The latter are assembled into arrays at the ends of optical fiber bundles and color-coding is used for the identification of SNPs. To be even more competitive, they have developed their in-house oligonucleotide production facility. In a few years time the technology will be mature enough to offer genotyping of one SNP for less than 1 US cent. Olli-Pekka Kallioniemi (NHGRI, NIH, Bethesda, MD, USA) described a tissue array technique (the pathologists' dream) in which tissue samples can be analyzed in a massive parallel format (e.g. 1000 samples) enabling the researcher to ask biological questions never asked before.

Genomics

Ian Dunham (The Sanger Centre, Hinxton, UK) offered an up-to-date view of the human genome sequencing and analysis of the data. In more detail, he presented the preliminary data on linkage disequilibrium structure and extent in chromosome 22. Wojciech Makalowski (NIH, Bethesda, MD, USA) gave a dynamic presentation on computational genomics. Gene prediction in eucaryotes is still a big problem and it is naïve to think that it can be solved using computational methods alone. Comparative genomics and synteny were suggested as the first handles we should reach for. The current status of the Estonian Genome Project was presented by the author and Kalev Kask (University of Stanford, CA, USA). A pilot phase (database of 10 000 individuals) is in preparation and we should be ready for sampling from Spring 2002.

Two lectures were devoted to equally important issues in present-day science. Ford N. Goldman (Minz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., Boston, MA, USA) gave a classroom-clear picture of how to raise capital in biotech from start-up to initial public offering (IPO). It was very useful for scientists hoping to start their own business and brought common sense to those in academic research who tend to overestimate science in the long process of introducing a product to the market.

Finally, everyone enjoyed the perfect lecture delivered by Gísli Pálsson (University of Iceland, Reykjavik, Iceland), 'For whom the cells toll: debates about biomedicine'. Ethical problems are of utmost importance in any population-based genetic study. He has the Icelandic health database experience at hand and gave an in-depth view of the matter from inside.

Conclusion

This meeting is not one of the 'world championship conferences' where labs and companies present fireworks of their results and data, but rather a performance where world class scientists communicate science to people – science to society on a large scale. At present, I believe that this is what we need more than ever. We can come up with a treatment or diagnostic procedure, but however sophisticated or modern it is, if people do not like or understand it, they will not accept it.

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