Ben Lehner wins Eppendorf Young Investigator Award 2013

presented in partnership with *Nature*

The Eppendorf Award for Young European Investigators was established in 1995 to recognize outstanding work in biomedical science. It also provides the opportunity for young European researchers to showcase their work and communicate their research to a scientific audience. *Nature* is pleased to partner with Eppendorf to promote the award and celebrate the winner's work in print and online. Thea Cunningham talks to the 2013 winner Ben Lehner about his work, and how it felt to win the award. To listen to the full interview, visit: **nature.com/nature/awards/eppendorf**.

Eppendorf and *Nature*

Ben Lehner is the eighteenth recipient of the Eppendorf Award for Young European Investigators, which recognizes talented young individuals working in the field of biomedical research in Europe. The Eppendorf Award is presented in partnership with *Nature*. The winner is selected by an independent jury of scientists under the chairmanship of Reinhard Jahn, Director of the Max Planck Institute for Biophysical Chemistry, Göttingen, Germany. *Nature* and Eppendorf do not influence the selection. For more information see: **eppendorf.com/award.**

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Thea Cunningham: **What research are you working on?**

Ben Lehner: Our main interest is in why individuals are phenotypically different. We are particularly interested in why a genome sequence is not enough information to predict an individual's character.

TC: **What is meant by phenotype?**

BL: The phenotype is all the characteristics and properties of an individual. We are looking at severe phenotypes like life and death. We know from studying model organisms like mice and the nematode *Caenorhabditis elegans* that when you have organisms with identical genomes carrying the same harmful mutation, sometimes only some of the individuals are affected. This variation is not down to their environment, because they are in the same environment. It is not due to their genome sequence either, because they have the same genome. It is not nature and it is not nurture, it is something else.

TC: **If genes or environment are not determining this variation in phenotype, what is?**

BL: We think some variation happens in early development. We all start as one cell with half of our genome inherited from our mother, and half from our father. Whether a genetic mutation you inherit has an effect can depend on the extent to which other genes are switched on or off at particular stages of development.

TC: **So this interplay between genes can have a dramatic effect?**

BL: We know that this is true in single celled organisms like bacteria and yeast, and in simple multicellular animals like nematodes. Nearly everything we know about human diseases comes from work on bacteria, yeast, viruses and other simpler systems. These phenotypes are

(Left to right) Maria Leptin, Axel Jahns, Ben Lehner, Francisco Chavarri and Reinhard Jahn. Image couresty of EMBL PhotoLab 2013.

obviously different but the general principles of genetics still apply.

TC: **What type of change in gene expression can result in a different phenotype?**

BL: One example we study in *C. elegans* is a mutation in a transcription factor that controls the expression of other genes. Half of the nematodes inheriting this mutation die after embryogenesis. The remainder are absolutely fine. The effect of this mutation depends on the activity of two other genes during development. One is another transcription factor, and the other is part of the core cell machinery, proteins that help the folding of other proteins. If we measure the levels of these two other genes, how much they're being switched on or off, then we can better predict whether this mutation will have an effect.

TC: **Are we able to predict whether a person will be born with a certain trait or risk of disease?**

BL: This would be very difficult in humans. The reason we can do it in model organisms is because we can measure how much genes are being switched on and off during development. For adult phenotypes, it might work if you find a phenotypic trait to measure that reflects this variation, such as a protein in the blood or a metabolite, and you knew how to connect that with genetics. For predictive or personalised medicine, it will have to be a combination of understanding the genetics and measuring something about each person, and then combining those data together to make predictions. I don't think you will be able to do it with the genome sequence alone. We know of thousands of genes associated with particular diseases. This is very different, however, to being able to sequence a person's genome and predict what is going to happen to them. That is still a long way off for most common diseases.

TC: **Is this something you are working towards?**

BL: A patient going into hospital does not want to know the typical outcome for a patient with the same mutation: they want to know what will actually happen to them. We are using these simple organisms to figure out how to do that. How can you measure something about an individual after they develop, and use that information in combination with genetics to make accurate predictions? This is what we really want to understand.

APPLICATION DEADLINE — 15 JANUARY 2014

We invite biological and biomedical researchers not older than 35 years, working in Europe, to apply for the 2014 Eppendorf Award. The deadline for entries is 15th January 2014. The prize ceremony will take place at the EMBL Advanced Training Centre (ATC) in Heidelberg, Germany. To find out more visit **eppendorf.com/award**.