



Professor Dr Nils Stein

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Q&A >



Nils, can you tell us where you are based and how your career has taken you there?



I am based at the IPK Leibniz Institute of Plant Genetics and Crop Plant Research in Gatersleben in Germany. I've been working here for over 20 years now. I started out studying biology at the University of Kaiserslautern and after finishing my studies I moved on to do my PhD at the University of Hohenheim. This prepared me for taking a post-doctorate position at the University of Zurich where we worked on map-based cloning of wheat. I stayed there for three to four years and it was at a time when there were no genomic resources for

wheat and barley in place yet, but this period of genetics and map-based cloning prepared me to take the next step. I moved to IPK and first became a lab manager of Andreas Graners' team to organise his research projects in barley genetics. Soon after that I became a joint group leader and in 2015 I became an independent group leader. Since 2018 I have been dual affiliated with the University of Goettingen and IPK.

Professor Dr Nils Stein



You work with a range of crop species, what is it about barley that makes it a unique and useful crop for your type of research?



We work on all the small grain cereals but barley is the second most important crop in Europe and in Germany it is very important for different purposes. At IPK, Barley was chosen as an important lead crop species for research in the early 2000s because the German Ministry of Education began a programme for plant genome research and there was a greater emphasis on looking at these crops. Wheat is economically more important than barley globally, but it has a more

complicated genome so there has been more genetic work undertaken on barley.

Since the early 20th Century barley has been used as a genetic model in research and that has generated a lot of genetic material available here in Germany and through international collaboration over the past two decades, which has provided a lot of opportunities for research.

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QUESTION 3



In this era of greater capacity to generate genomic information and greater capability to deal with the data, what do you think are the main bottlenecks in dealing with global issues through breeding?



Being able to access the genome sequence of one genotype of wheat and barley has already facilitated a lot of research to allow us to understand the genetic control of a number of traits and reduce bottlenecks. This is not only interesting for geneticists, but also can have an immediate applied value. The fact that we can generate genome sequences much more easily today also allows us to unlock the entire genetic diversity of the species and allows application and research at a broad scale.

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How are you and colleagues working to identify and characterize novel barley genes and gene networks? What benefits will this bring?



In order to improve certain traits in breeding, it is important to understand the biology behind it. Considering certain things like: what is the genetic control? Which gene networks are involved? When we study genetics, we take advantage Mendel's laws and typically use a genetic mapping approach. We cross parents that differ in character and follow the segregation for parental characteristics in the mapping population. We then use the molecular tools to identify the genomic location and you can do that with the information available today. You can then narrow down at very high resolution to the gene which controls the trait. If it is possible for one gene you can do this for many genes.

This is important in combination with other tools in genomics for instance, in the systematic profiling of gene expression. It allows you to discover what additional regulatory networks are involved in the control of a trait of interest. If you relate this to breeding characters that are of interest and usually controlled by many genes. We are, however, far away from really understanding the complexity of gene regulatory networks on many quantitative traits that are important for crop improvement.

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We face a number of serious global challenges around crop production and food security. How does your research work to address these?



There are a number of challenges, no one will deny that. Food security is a really important part of that, but I do think that we need to be careful in thinking that genetics or breeding has the answer to all of those challenges. There are a number of areas that can make a big impact. Genetic control to climatic adaptation is an area where we can contribute knowledge to changing the direction of or improving breeding. I think there our research is really key because without the genomic information it would not be very straightforward to improve complicated complex traits.

More importantly, we also need to discover novel genes that we may have not yet used in breeding before and which we now have to unlock from the existing genetic resources globally and make them available for breeding. The genomics research and genome sequencing we do here really goes beyond the sequence of a single genotype. Our intention is to use these modern methods to unlock the global entire diversity of a species and really catalogue the available variation that can then be exploited in breeding.

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QUESTION 6



How important is collaboration across the wider crop industries in driving forward solutions to many of these challenges?



International collaboration was always key in the barley community, and we are a much smaller cohort compared to wheat, rice and maize and we have to take advantage of those people in that area and work efficiently together. All the work in genome sequencing in barley was part of an international effort from the very beginning. Early on it was impossible to think of genome sequencing in wheat and barley without an international consortium, not only because of the labour, but also because of the funding. Most of the work was funded jointly through national initiatives and this has changed.

Today the technologies are so far advanced that individual teams can sequence the genome of one barley genotype or wheat genotype in an individual PhD project. But, if we think now about unlocking global genome diversity, we talk here about cataloguing the genetic diversity of gene bank collections that may comprise many, many thousands of different genotypes. This is definitely where we need an international collaborative effort, and in fact we have already started with such a collaboration at the EU level.

I'm the coordinator of the Horizon 2020 project called AGENT, where we have brought together a network of gene banks at the EU level to systematically genotype germplasm collections of genetic resources. We are looking for the overlap or the uniqueness and try to establish an actively collaborating scientific network that generates phenotypic data, activates historical phenotypic data for these collections and starts enabling predictions over the collections in international collaboration.

There is also a lot of biology we don't understand in barley and often it is just the amount of work, and the amount of analysis just goes beyond the capacity of an individual group. Research is really interdisciplinary and you have to work with different people of different perspectives and expertise to understand more. All the research that goes into functional understanding of barley biology underpins also the breeding effort. It will be most efficient if it is done in national and international collaboration.

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QUESTION 7



How can we encourage greater numbers and more diverse groups to study plant science given the need to enhance the vitally important research that underpins the future of our planet?



Yeah, well there are different aspects to that problem and one aspect is really the community. That's the responsibility of the more experienced scientists in the community to try to mentor early career scientists and explain to them or give them examples of why it is so rewarding to go into this area of research and why it is so important for young people specifically.

But I think the economic circumstances for individuals are also key. If there are no job opportunities in barley research we will not find the people to go into this area. A lot of the work that is related to big data, for example, which has a real impact in genomics and breeding.

We need more and more people that have a bioinformatics training. If we cannot provide a competitive funding then we will have a hard time to secure younger generations to become interested in our area.

We also find talent through individual interaction. But to really make barley pangenomics efficient information for breeding, we have to also have a long breath in funding to understand the biology of the crops because the challenges we are facing in adaptation to climate change are going to be really fundamental in the mechanisms of plant biology. It's not simple, and to really make a difference in breeding, we have a lot more to do.

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