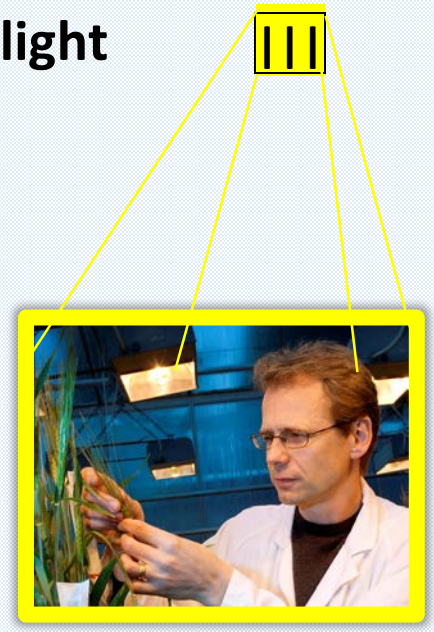
PlantLink Researcher in the spotlight

Mats Hansson



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This month we turn the spotlight to Prof Mats Hansson, head of the Molecular Cell Biology unit at Lund University. Mats studies molecular processes in plants related to design of plant architecture, time to flowering, chlorophyll biosynthesis and wax biosynthesis. In his research he often uses barley (Hordeum vulgare L.) mutants which were isolated more than 50 years ago!

-What is currently on top of your research agenda?

I am currently involved in four projects where the common nominator is barley. The last days have mostly been focused on 50 years old mutants with an altered plant architecture. We are doing crosses in the greenhouse to eventually obtain double mutants, which we hope will give us a solid material for studying the interaction of the involved genes. The genes are mostly involved in brassinosteroid signalling and metabolism.

-Tell us about your latest publication?

It was my PhD student Lizette Schneider who published her identification of three genes, *Cer-c*, *Cer-q* and *Cer-u*, involved in wax biosynthesis in barley. She did a lot of SNP marker analyses and then she found the genes in the end of chromosome 2. Champagne!

-What led you into your particular field of research?

As a PhD student, I studied heme biosynthesis in *Bacillus subtilis*. Heme is a tetrapyrrole and I went on to study another tetrapyrrole derivative, chlorophyll, as a postdoc using barley as a model organism. Since then, I have worked more with barley and less with *B. subtilis*. However, I miss all elegant genetic tricks I can do in *B. subtilis* and not in barley.

-What are the implications of your research for the society?

We are sorting out the function of various genes, which will make it possible to know how to combine them to create advantageous crop plants. I am collaborating with bright plant breeders at Nordic Seed outside Aarhus in Denmark and I hope I can help them more in the close future when the barley genome sequence has been published.

-Finally, let´s say you got unlimited research funds; where would your research be five years from now?

Then I would be able to establish a bioinformatic node as well as a node working with protein structures in my group. This would help me to follow the barley mutants we are studying from the DNA level to protein level, in order to obtain full understanding of the mutants and the effect of the mutations at the molecular level.