

Einladung

zum

Botanischen Kolloquium

Freitag, den 18. Mai 2018, 12 c.t.

Nussallee 4, Hörsaal Botanik

Referent: Prof. Dr. Nils Stein

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Gatersleben*

Thema: „*From one to 20,000 genomes - the barley pan-genome is shaping up*”

A first reference sequence of barley comprising chromosome –like assemblies was recently made available by the International Barley Sequencing Consortium (IBSC). Since then this resource is a game changer for gene cloning and capturing global barley diversity. One genome is very useful; however, it is telling only part of the story of genome diversity of a given species. In barley we know that up to 10% of the coding sequence may be affected by any kind of structural variation. This problem is currently being addressed in frame of a barley pan-genome project including the development of at least three additional reference quality genome assemblies of diverse haplotypes. Full sequencing of thousands of 5 Gbp genomes to reference quality is not exactly needed and would still be prohibitively expensive, however, if looking at this problem from a breeders or seed bank manager`s perspective it most likely exists the future vision and desire to fully understand the species genome complexity and re-sequence genomes as a routine at real-time in the field. To get a first step into this direction we characterized the genomic complexity of all 20,000 barley seed accessions at IPK Gatersleben, Germany, hosting the largest international ex situ seed bank of crop plants in the EU27. This unprecedented level of resolution about barley genome diversity is facilitating diversity studies, allele mining and GWAS but also potentially changing ex situ seed banks in the future from storage facilities into general information hubs for research and breeding.

Diskussionsleitung: Prof. Dr. F. Hochholdinger, INRES, Crop Functional Genomics

Die Dozenten der Botanischen Institute

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