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Special Seminar 2013

Estimating heritability and predictive accuracy of genomic prediction in plant breeding programs

Prof. Hans-Peter Piepho

Bioinformatics Unit, University of Hohenheim, Stuttgart, Germany

Date: Wednesday, 27 November 2013

Time: 5.00 - 6.00 pm

Place: Agriculture Lecture Theatre (G.013, Agriculture North Wing)

Parking: Hackett Drive, Entrance No. 2, 3 and 4 (paid visitor parking; alternatively: free parking in yellow car bays)



Heritability is often used by plant breeders and geneticists as a measure of a trial's precision, or the precision of a series of trials. For computing its main use is the response to selection.

Most formulas proposed for calculating heritability implicitly assume balanced data and independent genotypic effects. While both of these assumptions are often violated in plant breeding trials, equations assuming balanced data are still in common usage.

This talk reviews various approaches to assessing heritability and derived quantities for unbalanced plant breeding trial data.

Furthermore, the seminar will also discuss the related problem of assessing predictive accuracy in genomic selection.

Professor Hans-Peter Piepho was appointed Professor of Bioinformatics at the University of Hohenheim, Stuttgart, Germany in 2001. He has been working as an applied statistician in agricultural research for almost 20 years.

His main interests are related to statistical procedures as needed in plant genetics, plant breeding and cultivar testing. He has worked for many years on modelling of genotype-environment interaction in series of experiments using mixed model procedures.

Recent interests include marker-assisted breeding (genomic selection), spatial methods for field trials and experimental design for various applications including cDNA microarrays and series of experiments.

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