Dr. AARON J. LORENZ

Department of Agronomy and Plant Genetics University of Minnesota 1991 Upper Buford Circle, St. Paul, MN 55108 Email: lore0149@umn.edu

Education

PhD, University of Wisconsin, 2008, Plant Breeding and Plant GeneticsM.S., Iowa State University, 2005, Plant BreedingB.S., University of Minnesota, 2002, Science in Agriculture-Plant Science Employment

Employment

- Assistant Professor (75/25 Research/Teaching), University of Minnesota, Department of Agronomy and Plant Genetics, April 2015 Present.
- Assistant Professor (80/20 Research/Teaching), University of Nebraska, Department of Agronomy and Horticulture, July 2010 March 2015.
- Postdoctoral Research Associate, USDA-ARS/Cornell University, Jan 2009 June 2010. Graduate Research Assistant, Maize silage breeding program, University of Wisconsin, Aug 2005 – Dec 2008.
- Graduate Research Assistant, Maize breeding and genetics, Iowa State University, May 2003 Aug 2005.

The 5 most cited papers

- 1. Jannink, J. L., Lorenz, A. J., & Iwata, H. (2010). Genomic selection in plant breeding: from theory to practice. *Briefings in Functional Genomics*, 9(2), 166-177.
- Heffner, E. L., Lorenz, A. J., Jannink, J. L., & Sorrells, M. E. (2010). Plant breeding with genomic selection: gain per unit time and cost. *Crop Science*, 50(5), 1681-1690.
- 3. Lorenz, A. J., Chao, S., Asoro, F. G., Heffner, E. L., Hayashi, T., Iwata, H., ... & Jannink, J. L. (2011). Genomic selection in plant breeding: knowledge and prospects. In *Advances in Agronomy* (Vol. 110, pp. 77-123). Academic Press.
- Yu, L. X., Lorenz, A., Rutkoski, J., Singh, R. P., Bhavani, S., Huerta-Espino, J., & Sorrells, M. E. (2011). Association mapping and gene–gene interaction for stem rust resistance in CIMMYT spring wheat germplasm. *Theoretical and Applied Genetics*, 123(8), 1257-1268.
- Lorenz, A. J., Hamblin, M. T., & Jannink, J. L. (2010). Performance of single nucleotide polymorphisms versus haplotypes for genome-wide association analysis in barley. *PLoS One*, 5(11), e14079







ZNANSTVENI CENTAR IZVRSNOSTI ZA BIORAZNOLIKOST IMOLEKULARNO OPLEMENJIVANJE BILJA

CENTRE OF EXCELLENCE FOR BIODIVERSITY AND MOLECULAR PLANT BREEDING

Genomska selekcija u oplemenjivanju bilja radionica

Poljoprivredni fakultet Sveučilišta J.J. Strossmayera u Osijeku, Vladimira Preloga 1, Aula magna, Osijek

25. 5. 2018. (petak) u 9:30 sati

Predavač: Dr. Aaron J. Lorenz, University of Minnesota, SAD

PROGRAM

- 9:30 Uvod molekularni markeri, povezanost između markera i svojstva
- 10:30 Genomska selekcija što, zašto i kako
- 12:30 Ručak
- 13:15 Uporaba genomskih predviđanja u oplemenjivačkom procesu
- 14:15 Optimizacija točnosti predviđanja
- 16:15 Kava
- 16:30 Primjeri uporabe genomske selekcije

Prijevod na hrvatski nije osiguran



WORKSHOP ON GENOMIC SELECTION FOR PLANT BREEDING

Faculty of Agriculture, J.J. Strossmayer University in Osijek, Croatia; May 25, 2018

Lecturer: **Dr. Aaron J. Lorenz**, University of Minnesota, Twin Cities, MN, USA

- I. Introduction (1 hr)
 - a. Application of molecular markers to breeding programs
 - b. Description of marker technologies
 - i. Choices of marker platforms
 - 1. Pros/cons of various platforms
 - ii. Quality control of marker data for breeding applications
 - c. Marker-trait associations
 - i. Methods
 - ii. Applications

II. <u>Genomic selection (2 hrs)</u>

- a. What is genomic selection?
 - i. Terminology/definitions
- b. Why use genomic selection?
- c. How to do genomic selection?
 - i. Description of models
 - ii. Calculating predictions
 - iii. The G-BLUP approach
 - Calculation of various realized relationship matrices and how they relate to one another
 - 2. Use of realized relationships to make predictions
 - iv. How to evaluate success and accuracy
 - 1. Cross-validation
 - 2. Deterministic formula to predict prediction accuracy

12:30-13:15 Lunch (provided)

- III. Application of genomic prediction to a breeding pipeline (1 hr)
 - a. Framework for determining value of predictions in terms of genetic gain
 - b. Strategies for using genomic selection to enhance genetic gain
 - c. Review of examples of genomic selection being performed from literature

IV. Optimization of prediction accuracy (2 hrs)

- a. Model choice (including prediction of non-additive effects)
- b. Training population size
- c. Marker number/type
- d. Training population composition
 - i. Strategies for updating training population
- e. Importance of relationship between training population and target population
- f. Genotype-by-environment interactions
- g. Multi-trait genomic prediction
- 16:15 Coffee Break (provided)
 - V. Special applications (1 hr)
 - a. Hybrid prediction
 - b. Prediction of germplasm collections
 - c. Predicting potential (mean and variance) of breeding crosses
 - d. Crop modeling/GxE predictions

The workshop is organized as part of the HRZZ project "Genetics and physiology of multiple-stress tolerance in maize"

