

a. **Course Code: PBT-810**

b. **Title: Plants; Genotypes to Phenotypes**

c. **Credit Hours: 3(3-0)**

d. **Learning Objectives**

- (i) To help students understand the fundamental genetic and evolutionary processes that shape levels and patterns of genetic variation in populations
- (ii) To enable them to apply population genetic concepts to interpret genetic data from populations
- (iii) To make them familiar with a number of approaches to analyzing and inferring biological function from data
- (iv) To enable them to write and discuss knowledgeably about the methods, analyses and interpretation of recent literature.

e. **Outcomes**

Students will be able to interpret quantitative genetics research

Effectively present research findings from landmark papers in quantitative genetics theory

Describe the impacts of quantitative genetics theory in shaping modern plant improvement and genetics research

Demonstrate critical thinking of how to apply quantitative genetics theory to solving novel or emerging breeding problems

f. **Content**

QTL mapping

History of quantitative trait locus (QTL) analysis

Review the principles of QTL mapping

Establish the main advantages and disadvantages of QTL mapping

Review QTL analysis methods

Linkage disequilibrium (LD) and coalescent theory

Major considerations of experimental design prior to undertaking a QTL

analysis Challenges of having too few or too many markers when

doing

QTL analysis and their solutions

Factors affecting the detection of small effect QTLs

Dominance/additivity (d/a) statistic; use of the -1, 0 and 1 values

Method for analyzing GXG (two-locus interactions among QTL) and the main difficulties of this method

Transgressive variation and the underlying genetic architecture to explain it

Distributional analysis or selective mapping and its importance at the time of its proposal

Genetic Architecture

Structure and Mixed Models

Genomic Selection

Genomic BLUP decoded

Genomic heritability

Multivariate approaches

Genotype x Environment interaction

Factors affecting Genomic selection accuracy and long-term genetic gain

Genomic selection using low vs. high marker density

g. **Details of lab work (if applicable)**

Not applicable

h. **Recommended Reading**

- S. Tanksley (1993). *Mapping polygenes*. Annual Review Genetics 27:205-233. Doi: 10.1146/annurev.ge.27.120193.001225
- Lander & Botstein (1989). *Mapping Mendelian factors underlying quantitative traits using RFLP linkage maps*. Genetics 121:185-199.
- Rosenberg, N. a., and M. Nordborg. 2002. Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. Nat. Rev. Genet. 3(5): 380–390.
- Slatkin, M. 2008. Linkage disequilibrium – understanding the evolutionary past and mapping the medical future. Nat. Rev. Genet. 9(6): 477–485
- Gibson, G. (2012) *Rare and Common Variants: twenty arguments*. Nature Reviews Genetics 13: 135-145. doi:10.1038/nrg3118

- Brown et al. (2011) *Distinct genetic architectures for Male and Female inflorescence traits in maize*. PLOS Genetics 7(11):e1002383. doi:10.1371/journal.pgen.1002383
- Yu, J. et al (2006) *A unified mixed- model method for association mapping that accounts for multiple methods of relatedness*. Nature Genetics 38(2): 203-208. doi:10.1038/ng1702
- Piepho et al. (2003) *A hitchhiker's guide to mixed models for randomized experiments*. J. Agronomy and Crop Science 189:310-322. DOI: 10.1046/j.1439-037X.2003.00049.x
- G. K. Robison (1991) *That BLUP is a Good Thing: The Estimation of Random Effects*. Stat. Sci. 6: 15-32.
- Gianola, D. and R. Fernando (1986) *Bayesian Methods in Animal Breeding Theory*. J. Anim. Sci. 63:217-244.
- Meuwissen, et al. (2001) *Prediction of total genetic value using genome-wide dense marker maps*. Genetics 157: 1819-1829.
- Lorenz et al. (2011) *Genomic selection in Plant Breeding: Knowledge and Prospects*. Advances in Agronomy 110:77- 123. DOI: 10.1016/B978-0-12-385531-2.00002-5.
- Habier, D., R.L. Fernando, and D.J. Garrick. 2013. *Genomic BLUP Decoded: A Look into the Black Box of Genomic Prediction*. Genetics 194(3): 597–607.
- Habier, D., R.L. Fernando, and J.C.M. Dekkers. 2007. *The Impact of Genetic Relationship Information on Genome-Assisted Breeding Values*. Genetics 177(4): 2389–2397
- de Los Campos, G., A.I. Vazquez, R. Fernando, Y.C. Klimentidis, and D. Sorensen. 2013. *Prediction of complex human traits using the genomic best linear unbiased predictor (ME Goddard, Ed.)*. PLoS Genet. 9(7): e1003608–e1003608.
- de los Campos, G., D. Sorensen, and D. Gianola. 2015. *Genomic Heritability: What Is It?* PLoS Genet. 11(5): e1005048.

- Krishna Kumar, S., M.W. Feldman, D.H. Rehkopf, and S. Tuljapurkar. 2016. Limitations of GCTA as a solution to the missing heritability problem. *Proc. Natl. Acad. Sci. U. S. A.* 113(1): E61–70.
- Gianola et al. (2008) *Reproducing Kernel Hilbert Spaces Regression Methods for Genomic Assisted Prediction of Quantitative Traits*. *Genetics* 178:2289-2303.
- Legarra et al. (2009) *A Relationship Matrix Including Full Pedigree and Genomic Information*. *J. Dairy Sci.* 92:4656-4663.
- Jia, Y., and J.-L. Jannink. 2012. Multiple Trait Genomic Selection Methods Increase Genetic Value Prediction Accuracy. *Genetics* 192(4): 1513–1522.
- Stephens, M. 2013. A unified framework for association analysis with multiple related phenotypes. *PLoS One* 8(7): e65245.
- Burgueño, J., G. de los Campos, K. Weigel, and J. Crossa. 2012. Genomic Prediction of Breeding Values when Modeling Genotype × Environment Interaction using Pedigree and Dense Molecular Markers. *Crop Sci.* 52(2): 707–707.
- Jarquín, D., J. Crossa, X. Lacaze, P. Du Cheyron, J. Daucourt, J. Lorgeou, F. Piraux, L. Guerreiro, P. Pérez, M. Calus, and Others. 2014. A reaction norm model for genomic selection using high-dimensional genomic and environmental data. *Theor. Appl. Genet.* 127(3): 595–607.
- Heslot, N., D. Akdemir, M.E. Sorrells, and J.-L. Jannink. 2013. Integrating environmental covariates and crop modeling into the genomic selection framework to predict genotype by environment interactions. *Theor. Appl. Genet.* 127(2): 463–480.
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- Meuwissen and Goddard (2010) *Accurate prediction of genetic values for complex traits by whole-genome resequencing*. *Genetics* 185: 623–631. DOI: 10.1534/genetics.110.116590
- Habier et al (2009) *Genomic selection using low-density marker panels*. *Genetics* 182: 343–353. DOI: 10.1534/genetics.108.100289
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