

W554**Genomic Selection for Heterosis without Dominance in Multiplicative Traits: Case Study of Bunch****Production in Oil Palm**

Date: Sunday, January 11, 2015

Time: 2:10 PM

Room: Towne - Meeting House

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To study the potential of genomic selection for heterosis resulting from multiplicative interactions between additive and antagonistic components, we focused on oil palm, where bunch production is the product of bunch weight and bunch number. We simulated two realistic breeding populations and compared over four generations the current reciprocal recurrent selection (RRS) with reciprocal recurrent genomic selection (RRGS). All breeding strategies aimed at selecting the best individuals in parental populations to increase bunch production in hybrids. For RRGS, we obtained the parental genomic estimated breeding values using GBLUP with hybrid phenotypes as data records and population specific allele models. We studied the effects of four RRGS parameters on selection response and genetic parameters: (1) the molecular data used to calibrate the GS model: in RRGS_PAR, we used parental genotypes and in RRGS_HYB we also used hybrid genotypes; (2) frequency of progeny-tests (model calibration); (3) number of candidates and (4) number of genotyped hybrids in RRGS_HYB. We concluded that RRGS could increase the annual response to selection compared to RRS by decreasing the generation interval and by increasing the selection intensity. With 1,700 genotyped hybrids, calibration every four generations and 300 candidates per generation and population, response to selection of RRGS_HYB was 71.8% higher than RRS. RRGS_PAR with calibration every two generations and 300 candidates was a relevant alternative, as a good compromise between annual response, risk around expected response, increase in inbreeding and cost. Finally, RRGS required inbreeding management because of higher annual increase in inbreeding than RRS.

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Meeting Information**When:**

January 10 - 14, 2015

Where:

San Diego, CA

