Life Sciences Seminar

A model experiment of parallel selection for elucidating the architecture of complex traits

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Attempts to replicate genetic studies of highly complex traits are often misguided, compromised due to the almost inevitable differences in the sampling of alleles and their frequencies between studies. The inferential consequences of this frequently unavoidable biological and analytical reality can be frustrating for some researchers. This can also have the effect of obscuring the relative strengths and weaknesses of the range of experimental and analytical approaches applied in studies aimed at identifying QTLs or elucidating the genetic architecture of highly complex traits. In an effort to explore multiple approaches within the same biological experiment we established a 15 generation pedigree incorporating > 1700 single pair crosses and >90,000 phenotyped individuals. This was done using Drosophila melanogaster for the phenotypic trait: length of the pupal case (h2= 0.44 ?0.04 SE & H2= 0.58). The use of an automated phenotyping and data recording system made it possible to record the complete ancestry of every individual within the pedigree. The pedigree was initiated using 8 autosomes, 2 Y-chromosomes and 2 mito-types. Within part of the pedigree a select and re-sequence approach with x28 independent replicates was performed.Within, this common biological framework we can conduct the following analytical approaches to assess their relative strengths and weaknesses in minimising the degree of missing heritability: association, random-forest, reproduced allele-frequency changes in response to selection, extended family-analysis and tests of epistasis. This analysis was based on >300 complete sequenced genomes. It is anticipated that this study and phenotype could represent a rich resource with which to examine analytical approaches when it is placed on-line.

Monday, July 16, 2018 10:00am - 11:00am
Meeting room 1st floor / Central Bldg. (I01.1OG - Zentralgebäude)

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