BiRC talk– open to all

Speaker: Frédéric Hospital,

INRA UMR Génétique Animale et Biologie Intégrative (GABI)

Jouy-en-Josas, France

Title: Detection of traces of selection with numerous SNP in small experimental populations undergoing directional selection.
Time: Tuesday, 3 December 2013 at 14.15 – 15.00
Place: Bioinformatics Research Centre, Build.1110, Aud. 223, C.F. Møllers Allé 8, 8000 Aarhus C

Abstract:

Three lines of chickens (L1, L2, L3) have been selected for 12 generations for three different immune response traits. A fourth line (L4) was a contemporary random bred Control (Minozzi et al. 2008). Each generation, 200 chicks per line were hatched in a single batch. Selection for each trait was done by mass selection based on individual phenotype. Individuals from the three selected lines and the control line at generation G9, as well as individuals from the founding population (G0) were sampled (20 individuals/line) and genotyped with a 60K SNP chip. We present the use of this dataset to detect traces of selection in the three selected Chicken lines.

An original method was designed to detect traces of selection by comparing the SNP allele frequencies between generations G0 and G9 for each line. The method was able to pinpoint a dwarfing gene known to have undergone strong selection hence, serving as a validation. In addition it highlights numerous SNPs that seem to behave non-neutrally, providing candidate regions for future search for selected genes.

While classical approaches generally focus on traces of 'historical' (long term) selection, this work demonstrates that it is possible to detect short-term selection in experimental population using SNPs.

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