



Plant & Animal Genomes XI Conference

January 11-15, 2003
Town & Country Convention Center
San Diego, CA

Poster: Equine

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PEDIGREE ANALYSIS FOR RACING PERFORMANCE IN HORSES

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The aim of this work was to determine the hereditary background of horse-phenotypes using statistical pedigree-analysis. Segregation analysis models were used, and genotypes of the major gene(s) for animals were estimated.

A large 6-generation pedigree of 9183 French Trotters horses was designed according to an apparent non-normal distribution of performance. Trait 1 was a performance index published by French Haras Nationaux (population-adjusted log of earnings per start, 3295 records). Trait 2 was record time (best racing time par km, with fixed effect, 3249 records). Models were fitted with a variable number of major genes and standard continuous genetic variation (polygenes), and using Bayesian inference the most probable model (number and sizes of major genes and amount of polygenic variation) was assessed.

Model solutions indicated one clear major gene for each trait; there was some, but not very strong evidence, for presence of more than one major gene, especially for the trait-1. In a bivariate model, presence of pleiotropic genes was tested, yielding very similar results, indicating that the major gene found for the trait-1 and trait-2 was actually one pleiotropic gene controlling both traits. Examining the fitted genotypes in the pedigree showed that two elite sires were both homozygous.

Based on the results from the analysis, families with largest genetic variances can be

indicated and could be used to find DNA markers.

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