BAYESIAN EPISTATIC QUANTITATIVE TRAIT LOCI ANALYSIS FOR BODY WEIGHT AND ADIPOSITY.

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Abstract

Though highly heritable, the genetic architecture of obesity-related traits is quite complex and may not be successfully uncovered by considering single genetic effects in isolation. Hence, we investigate the effects of quantitative trait loci (QTL) on three obesity traits (body weight at 12 weeks, sum of subcutaneous and epididymal fat pads, and gonadal fat) and an organ character trait (liver weight) in mice. The mapping sample was produced from a cross of the F1 between CAST/Ei (wild strain) and M16i (selected for rapid growth rate) back to M16i. To identify genes that influence obesity in an interactive fashion, we performed a Bayesian mapping method using both non-epistatic and epistatic models to infer genetic effects and map positions of putative QTL for the four phenotypic traits. Also maximum likelihood (ML) interval mapping methods were performed. For all analyses, QTL effects were detected on many of the 19 chromosomes with several chromosomes carrying more than one QTL. Furthermore, additional putative QTL reflecting small effects were discovered for all traits only when assessing main effects and epistatic effects simultaneously. Moreover, Bayesian analyses within an epistatic framework suggested possible pleiotropic QTL, which could not be detected if only main effects were included in the model. Results indicate that complex interactions among multiple genes played an important role in controlling obesity traits and organ character traits and may pave the way toward detection of specific genes.