

Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice.

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**Abstract:** Although mice are the most widely used mammalian model organism, genetic studies aimed at drug abuse relevant traits have suffered from limited mapping resolution due to extensive linkage disequilibrium (LD) that is characteristic of crosses among inbred strains. Carworth Farms White (CFW) mice are a commercially available outbred mouse population that harbor enormous genetic diversity and exhibit rapid LD decay in comparison to other available mouse populations. We performed a genome-wide association study (GWAS) of behavioral, physiological and gene expression phenotypes using 1,200 male CFW mice. We used genotyping by sequencing (GBS) to obtain genotypes at 92,734 SNPs. We also measured gene expression using RNA sequencing in three brain regions. We identified numerous behavioral, physiological and expression quantitative trait loci (QTLs). We integrated the behavioral QTL and eQTL results to implicate specific genes, including *Azi2* in sensitivity to methamphetamine. The integration of CFW mice, GBS and RNA sequencing constitutes a powerful approach to GWAS in mice.