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## A Tail of Two Cohorts: Genetic Investigation of a Novel Complex Behavioral Trait

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Exploratory activity in the novel open field remains a standard means of assessing simple forms of hippocampal-dependent learning and memory in rodent models. Our initial research demonstrated that interleukin-7 receptor knockout/congenic (Il7r<sup>-/-</sup>) mice acquired in 2001 (IL7R-V cohort) exhibit significantly decreased habituation in the open field relative to C57BL/6J (B6/J) controls. Using a series of complementation tests designed to discern between target gene and 129-derived flanking region effects, our data suggested that the Il7r locus is responsible for this recessive phenotype. Surprisingly, the habituation phenotype could not be replicated using Il7r<sup>-/-</sup> mice acquired in 2004 from the same supplier (IL7R-A cohort). Analysis of these data indicates that the difference between the two Il7r<sup>-/-</sup> cohorts is likely genetic and is not attributable to environmental variables. Whole genome genotyping has confirmed the genetic background of both cohorts to be primarily homozygous B6/J. However, we identified genetic regions that are homozygous (B6/N or 129S6) in the IL7R-V cohort but display variability in the IL7R-A cohort. In an effort to narrow the list of putative candidate gene regions, we are correlating genotypic data at these regions of interest with habituation performance for both Il7r<sup>-/-</sup> cohorts. To further elucidate the genetic mechanism(s) underlying the phenotypic difference between cohorts, we have performed microarray analyses to determine whether they differ in hippocampal gene expression. Furthermore, we are assessing mossy fiber morphometry for both Il7r<sup>-/-</sup> cohorts, as previous studies have indicated that hippocampal mossy fiber length correlates with some learning and memory phenotypes.