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## Presentation Abstract

Program#/Poster#: 186.09/SS8

Presentation Title: Cis-regulatory evolution of the *avpr1a* locus and its pseudogene among New World voles

Location: Hall A-C

Presentation time: Sunday, Nov 13, 2011, 8:00 AM - 9:00 AM

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Abstract: Gene duplication is a common process with profound consequences for the function and evolution of a locus. Once a gene has been duplicated, either copy can be lost or can assume a new function, and it is necessary to examine both copies across related species to make correct inferences about the evolution of the locus. Voles are increasingly important models for the molecular mechanisms of social behavior. The evolution of *avpr1a* locus, which codes for the vasopressin 1a receptor, has been a major focus of this work. The *avpr1a* locus has undergone a duplication thought to be unique to the socially monogamous prairie voles, *Microtus ochrogaster*. However, the locus and its duplicate have not been systematically investigated across *Microtus* species. To do so, we PCR-amplified the 1100 bp of cis-regulatory sequence of the *avpr1a* locus and its putative pseudogene, as well sequence from two neutral loci (LCAT introns 2-4 and exons 3-5, ~700bp; b-fibrinogen intron 7, ~700bp) from 7 species of New World *Microtus* with well-characterized mating systems: *M. ochrogaster*, *M. pinetorum*, *M. agrestis*, *M. arvalis*, *M. californicus*, *M. pennsylvanicus* and *M. richardsonii*. The first 2 species are socially monogamous, and the remaining 5 are all promiscuous. We first used Bayesian methods to

reconstruct a phylogeny for these species based on neutral markers, using *Myodes glareolus* as an outgroup. The phylogenetic analysis gave substantially higher resolution than has been previously reported. Remarkably, this included a strongly supported pairing of the two monogamous species, *M. ochrogaster* and *M. pinetorum* (posterior probability = 0.99), which suggests that monogamy may have evolved a single time within this clade. This is a novel pairing, but accords with historic groupings based on tooth structure. Preliminary analysis suggests the *avpr1a* amplicons were more closely related to one another than to the pseudogene amplicons, which would indicate that the duplication of the locus predated diversification of the clade. Together, our data highlight how phylogenetic analyses can inform our understanding of the evolution of genes regulating social behavior and other complex phenotypes.

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Posterior cingulate cortex

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