40TH ANNUAL MEETING

NEUROSCIENCE 2010

SOCIETY FOR NEUROSCIENCE

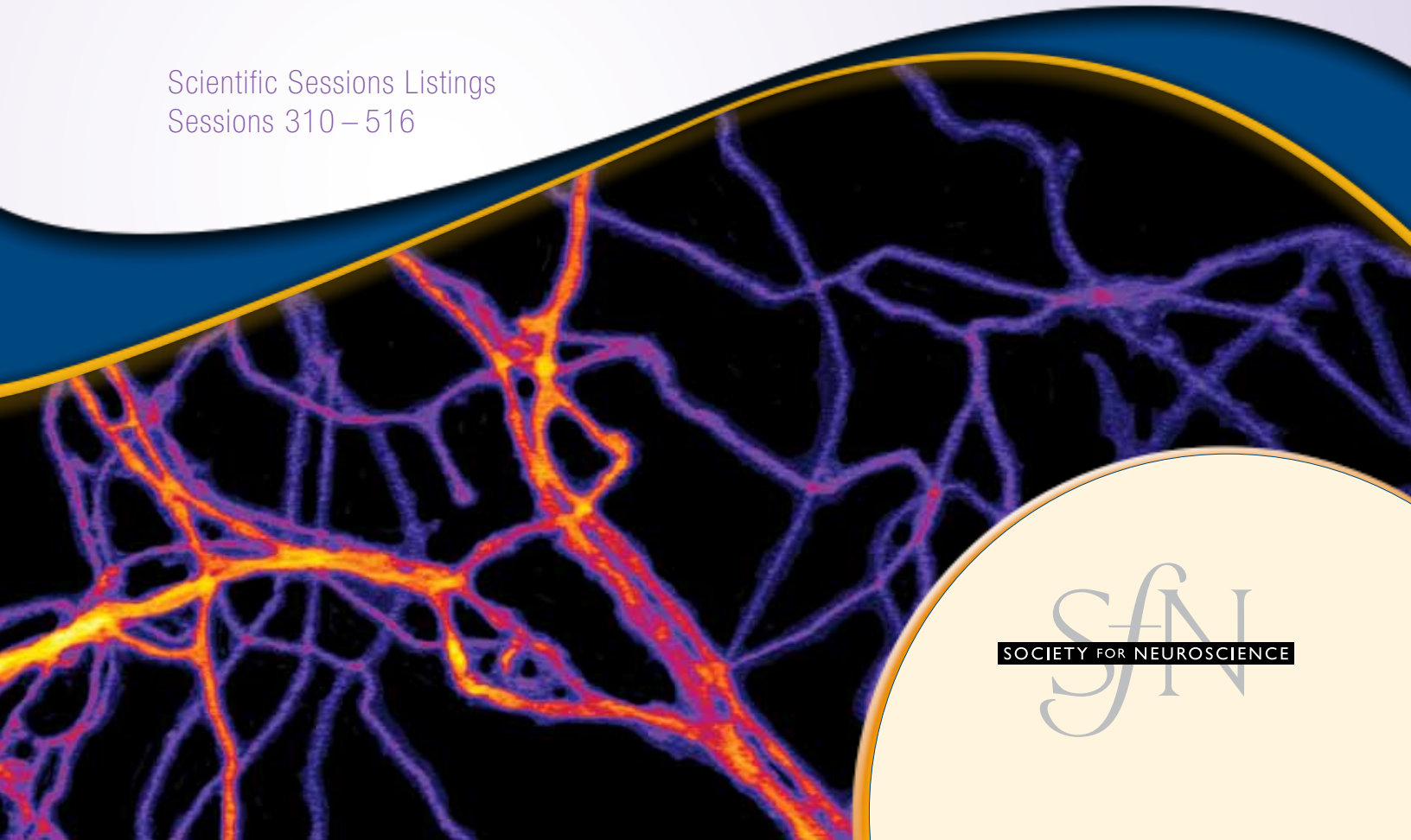
FINAL PROGRAM

Monday

NOVEMBER 15, 2010

SAN DIEGO CALIFORNIA

Scientific Sessions Listings
Sessions 310 – 516



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Presentation Abstract

Program :	387.12/EEE4
Title:	Evolution of cis-regulatory variation at the avpr1a locus and its pseudogene
Location:	Halls B-H
Presentation Time:	Monday, Nov 15, 2010, 11:00 AM -12:00 PM
Authors:	***A. BERRIO**, N. S. LYSAK, D. V. BLONDEL, J. L. PINO, S. M. PHELPS; Biol., Dept. of Biology/University of Florida, Gainesville, FL
Abstract:	Individual and species differences in gene expression underlie a tremendous diversity of behavior. Expression of the vasopressin 1a receptor (V1aR), for example, governs behavioral differences between the monogamous prairie vole (Microtus ochrogaster) and the promiscuous montane vole (M. montanus). Field data demonstrate that natural selection favors pair-bonding by male prairie voles; such selection may promote uniformly high levels of V1aR in the ventral pallidum (VPal), a region central to male pairing. In contrast, field data suggest selection actively maintains variation in the retrosplenial cortex (RSctx), a region implicated in spatial memory, territorial intrusions and sexual infidelity. Differences in gene expression are often due to variation in cis-regulatory sequences; alternatively, duplicated loci can also function as regulators of the original locus. We examined the evolution of cis-regulatory sequences of the prairie and montane vole avpr1a loci, as well as an avpr1a-pseudogene thought to be unique to prairie voles. We first tested for evidence of selection acting on the prairie vole avpr1a. To do so, we sequenced 20 avpr1a alleles from wild-caught prairie voles for ~2.5kb upstream of the translation start site, and homologous sequence from the montane vole. We compared the ratio

of between- and within-species nucleotide polymorphisms at the avpr1a locus (36:18) with that at neutral loci (21:20). We found a trend toward reduced polymorphism at the prairie vole avpr1a ($p<0.10$), suggesting overall purifying selection at the locus. A single 50bp region seems to have been under stronger purifying selection than the locus as a whole ($p<0.05$), and much stronger selection than is evident for neutral loci ($p<0.01$). This is consistent with the fitness value of V1aR-mediated pair-bonding, and suggests a novel enhancer for high pallidal V1aR. A 300bp segment exhibited a trend toward higher levels of standing variation ($p=0.11$), a signature of balancing selection. Remarkably, this same segment contained SNPs associated with individual differences in RSctx V1aR. Lastly, we sequenced 20 alleles of the pseudogene to determine whether its cis-regulatory sequences have been under selection since divergence from the avpr1a locus. We found much lower standing variation (between:within, 19:1) than predicted based on neutral loci (21:20), indicating strong purifying selection on the pseudogene cis-regulatory region ($p<0.001$). Together, our data suggest novel regulators of avpr1a expression, including the possible involvement of a pseudogene previously assumed to be non-functional.

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Keyword(s): Microtus

Social Behavior

Posterior Cingulate

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