Sexual dimorphism is found in many organisms, so it is not surprising that sexually biased gene expression is also common. Many of these genes with sexually biased expression are involved in reproductive success, and would be important for conservation. Experiments using microarrays have shown that a significant number of genes in many organisms have a sexual bias in expression. Sexually antagonistic mutations or mutations beneficial to one sex but harmful to the other account for some of these differences in gene expression. If a particular gene product is very deleterious to one sex, the expression of it may be reduced or eliminated in the other sex, thus reducing the "sexual conflict". Sex chromosome theory predicts that sexually antagonistic mutations should accumulate in tight linkage with a new sex-determining gene, even when the harm to benefit ratio is high. Salmonid fishes have the XX/XY mode of sex determination, but the male-determining region is located on a different linkage group in almost every species, so most of the species have "new" sex chromosomes containing genes that are autosomal in the other species. Sockeye salmon (*Oncorhynchus nerka*) is especially interesting because the Y chromosome is a fusion between the coho salmon (*O. kisutch*) Y and a chromosome arm that is autosomal in coho salmon. Theoretically, divergent selection between the sexes on sex-linked genes can be identified by analysis of population data. Results of an analysis of signatures of selection on sex-linked genetic markers in natural populations of both species will be presented along with suggestions on how future genomic data may be used to address these questions.

115-6 Conservation Implications of Widespread Misclassification and Hybridization of the Endangered *Aplochiton zebra* and *A. taeniatus* in South America

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Aplochiton zebra and *Aplochiton taeniatus* are two galaxiid fishes endemic to Patagonia and, in the case of *Aplochiton zebra,* also present in the Falklands Islands where they are threatened by salmonid invasions. Identification of *Aplochiton* is complicated because the two species are ecologically and morphologically very similar and include resident as well as migratory ecotypes that may confound classification. We used DNA barcoding (COI, cytochrome b) and a new developed set of microsatellite markers to identify *Aplochiton zebra* from *Aplochiton taeniatus* and to assess the validity of *in-situ* field identification in Chilean Patagonia. We also assessed the extent of cross-species amplification of recently developed microsatellite DNA primers for *A. zebra*. Cross-species amplification was demonstrated in 11 of 13 loci tested. On a sample of 456 *Aplochiton,* phenotypic misclassification ranged from 0 % for *A. zebra* and 70 % for *A. taeniatus,* the latter species being more widespread than previously thought. We also report on the potential of hybridization between both species with findings of first generation hybrids in rivers where both species co-exist. *Aplochiton* zebra populations showed strong population structuring in relation to both life-history differences (anadromous bversus landlocked populations) and post-galcial origin. We will discuss the implications of our results for the conservation and management of *Aplochiton* populations.

115-7 Early Life History Transcriptome Differences and Temperature Adaptation in Brown Trout