**Title:**

Salmon River steelhead population genetics with evidence of gene flow between headwaters.

**Presenter:**

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Poster

Salmon River steelhead population genetics with evidence of gene flow between headwaters

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As one part of our Snake River genetic monitoring program, we sampled wild *Oncorhynchus mykiss* from 23 locations in each of the major Salmon River sub basins. More than 2500 fish were genotyped using the 15 standardized SPAN microsatellite loci. Results showed genetic isolation by distance and a high degree of genetic structure differentiating populations both within and among drainages. Sample locations from different drainages in this study showed an unexpected genetic affinity between their respective headwaters, suggesting a possible gene flow corridor between headwaters of two very geographically distinct river drainages—the Middle Fork Salmon River and upper main stem of the Salmon River. We explore various scenarios to explain this unexpected genetic similarity between locations separated by hundreds kilometers of river distance. We conclude that episodic events such as flooding or some form of human intervention may have permitted limited gene flow between otherwise highly differentiated genetic lineages.