

### Introduction



**Figure I:** Life cycle of resident and migrant *O*. mykiss, diverging following the juvenile stage.

## Results

Migrant x Migrant Family Chromosome Resident x Resident Family Chromosome Figure 6: Manhattan plots for the migrant family (top) and the resident family (bottom). Each point represents one marker and its association with life history determination, shown in its respective chromosomal position. The red line represents the 0.01 level of significance; every point above the red line is a marker that is significantly associated with smoltification.

**Figure 2:** Adult resident (top)

and migrant (bottom) O. mykiss.





# Should I Stay or Should I Go? Analyzing the Genetic Basis of Migration-Related Traits in Rainbow Trout (Oncorhynchus mykiss).

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Figure 3: Study area of Sashin Creek and Lake, Baranof Island, Alaska. Migrants are native to the lower creek. Juvenile individuals were transported above two barrier waterfalls into the lake in 1926; the lake has since developed a largely resident population.



Figure 4: One of the two barrier waterfalls that blocks upstream fish passage into the lake. Migrants produced in the lake can move downstream but are unable to return to the lake to spawn; that genetic material is consequently lost to the lake population.



	Chromosome	Start Position	End Pos
	omy06	82137635	8213802
Apoptosis	omy07	78259944	7826327
	omy09	54514509	5451773
Phototransduction _	omy04	679023	1282575
	omy16	1946000	1980894
	omy27	1547273	1576062
	omy02	53713259	5373009
Lipid/Fatty Acid	omy08	9245714	9294768
Metabolism	omy09	51478701	5148957
	omy16	52253283	5226452
	omy01	14034893	1407572
	omy01	61470543	6157964
	omy02	74185429	7418999
	omy04	679023	1282575
	omy07	11474375	1147682
Growth and -	omy08	76874702	7688280
Development	omy14	59706925	5971574
_	omy21	44434836	4443580
_	omy22	28173844	2855079
_	omy22	32457242	3246618
	omy28	11228455	1126869
	omy01	52900204	5298171
_	omy01	55613945	5561931
_	omy07	72345554	7286422
Ion Homoostasis -	omy09	44791396	4482443
	omy22	2791347	3084253
	omy22	47354055	4737820
	omy23	9020635	9022818
	omy28	5952093	6379074

Table 3: Genes identified through BLAT analysis as spanning the same portions of the genome as significant markers in both the Resident x Resident and Migrant x Migrant families.

Chromosome	Start Position	<b>End Position</b>	Annotation
omy02	65249829	65709098	si:dkey-153m14.1
omy02	66720536	67198313	basic helix-loop-helix family, member e41
omy16	55765846	55782186	interleukin 17 receptor E-like
omy16	55805949	55837272	intraflagellar transport 122 homolog
omy29	7014767	7044810	NSA2 ribosome biogenesis homolog

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myosin, light chain 1, alkali; skeletal, fast epidermal growth factor receptor SPARC related modular calcium binding 2 transmembrane protein 72 solute carrier family 39, member 8 catenin, beta interacting protein 1 sodium leak channel, non-selective transmembrane protein 237 calcium homeostasis modulator 3 solute carrier family 26, member 5

Continued work includes developing a model based on a number of the significant markers to predict an individual's life history trajectory prior to the individual undergoing smoltification or reaching sexual maturity. This has use to fisheries managers in restoring and maintaining populations of migratory O. mykiss.

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We took fin clips from age-2 individuals that had either undergone smoltification or reached sexual maturity. In the lab, DNA was extracted and the individuals were sexed [9].

We genotyped 192 individuals (Table 1) on an Affymetrix SNP chip at 57,501 known polymorphic locations across the genome.

We used TASSEL to identify SNPs associated with phenotype, using an FDR corrected p-value at alpha = 0.01.

Using the updated O. mykiss genome [10], we mapped markers using the R package 'qqman'.

We performed a BLAT analysis to identify genes linked with significant markers.

**Table I:** Breakdown of the genotyped individuals by family, sex, and phenotype.

	Migrant x Migrant	Resident x Resident
nolts	38	16
molts	37	18
tures	38	24
sidents	11	10
notyped	124	68

\* Within the migrant and resident families, respectively, 5002 and 429 markers were significant at an FDR-corrected p-value of 0.01 and could be mapped to

The resident population of O. mykiss in Sashin Lake is genetically isolated from the population in Sashin Creek, so we expect to find fewer significant markers within the resident family due to overall decreased genetic diversity.

Previous research identified markers on nearly every chromosome associated with successful migration in adult O. mykiss, suggesting that migration is controlled via a complex, polygenic pattern of inheritance [11]. In this study, in both familial crosses, markers significantly associated with life history were found on nearly every chromosome (Fig. 6), providing further support for this

Through the BLAT analysis we identified, in the Migrant x Migrant family, significant markers associated with 28 genes whose functions are connected to pathways previously hypothesized to be important in smoltification (Table 2).

Five genes on three chromosomes (**Table 3**) were associated with smoltification in both families, suggesting that these regions of the genome are important in life history determination regardless of familial origin.



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