Introduction

Rainbow trout (Oncorhynchus mykiss) exhibit partial migration (Fig. 1), in which populations consist of both resident and migrant individuals [1-2]. Which life history path an individual will take is highly heritable [2-4], but is also influenced by the environment [5-7].

Scotmid, smoltifying, or remaining resident can be influenced by a variety of factors. Scotmid individuals are less likely to migrate and are selected for the presence of a genetic component that results in the expression of a reduced gene expression of candidate genes for the migration response. In the case of smoltifying individuals, genetic components associated with reduced gene expression may also be expressed. This may result in the genetic makeup of the individual becoming a genetic marker for smoltification or remaining resident. This is a complex process, and it is important to find candidate genes that confer a reduced genetic component for the expression of smoltification or remaining resident.

Discussion

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 O. mykiss genome.

The resident population of O. mykiss in Sassin Lake is genetically isolated from the population in Sassin 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 in the migration of each chromosome (Fig. 6), providing further support for this idea.

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 migration in both families, suggesting that these regions of the genome are important in life history determination regardless of familial origin.

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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References