Nuclear and mitochondrial SNPs provide high-throughput resolution for migratory studies of Chinook salmon

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Abstract

Much is known of the freshwater life history and ecology of Chinook salmon; far less is known of the oceanic migration patterns and relative marine survival of individual stocks. Migration following stock-specific corridors may lead to differing marine survival and varying rates of return among stocks during periods of fluctuating marine conditions. We are developing markers based on single nucleotide polymorphisms (SNPs) to rapidly genotype large number of individual from high sample volumes. Nuclear and mitochondrial SNPs provide useful and complementary information. We compare SNPs from representative populations originating from throughout the range of Chinook salmon to equivalent data from allosyhm and microsatellite markers. Results to date show that SNP markers have the potential of becoming a rapid and cost-effective approach to the analysis of large numbers of samples from complex mixtures.

Introduction

Studies of the ecological genetics of fish may require the analysis of thousands of individuals at many loci to characterize populations and estimate the composition of complex fisheries. Often results of fish may require the analysis of electrophoresis. Often results of fish may require the analysis of electrophoretic or management, because of great use to management. Provide information potentially described in the literature.

Methods

Ten 5'-nuclease reaction SNP genotyping assays (Fig 2) were developed in order to facilitate large-scale examination of several loci known a priori to be informative in Chinook salmon on smaller scales (Table 1). These 10 assays were tested on 1473 individuals from 16 sites around the Pacific basin (Fig 1). Data from the SNP loci were compared to data from other genetic markers commonly used for high-throughput fishery applications: allozymes and microsatellites. Microsatellite loci examined in this study were: Omsl, Oms2, Oms3, Oms4, Oms5, Oms6, Oms7, Oms8, Oms9, and Oms10. A total of 29 allozyme loci were also analyzed in all samples. Genetic distances based on the three different marker types were compared graphically with multidimensional scaling plots and statistically by examining correlations between pairwise-genetic distances between all populations. Statistical significance of each correlation was tested using a permutation procedure.

Results and Conclusions

Conversion of genetic markers from PCR-RFLP, DNA sequencing and DGGIE (high-throughput SNP genotyping assays was successful. These SNP assays are cheaper and faster to run than genetic markers presently being used for stock structure analyses (Fig 7). Further, since the required number of individuals in baseline samples increases with increasing numbers of alleles per locus, SNP baselines should be relatively smaller and thus cheaper to produce.

A second advantage of SNP markers over microsatellites and allozyme is that SNP data are discrete (nucleotide bases) rather than continuous (relative mobilities). This is because the SNP assays require electrophoresis samples, and much less time to generate new data (Fig 3) than the genotyping of microsatellites or allozymes.

Fig 1. Allozyme and microsatellite alleles both distinguished known lineages of Chinook salmon

Table 1. Locus for which SNPs assays were developed

<table>
<thead>
<tr>
<th>Locus</th>
<th>Description</th>
<th>Published assay type</th>
<th>Genotyping assay</th>
</tr>
</thead>
<tbody>
<tr>
<td>APGRO_poly</td>
<td>Polymorphic Oms locus (10)</td>
<td>DNA sequencing</td>
<td>DNA sequencing</td>
</tr>
</tbody>
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Fig 4. SNPs revealed geographic groupings similar to the ones indicated by the other marker types

Results to date show that SNP markers have the potential of becoming a rapid and cost-effective approach to the analysis of large numbers of samples from complex mixtures.