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Supplement D: Variation in Progeny Admixture

Background

We sought to identify the amount of variation present among progeny within hybrid classes. If the variation is low, using familial admixture (the average admixture of the two parents) would be an appropriate technique for estimating the admixture in progeny. However, if the variation in admixture among progeny is large, each offspring would need to be genotyped independently to determine its admixture.

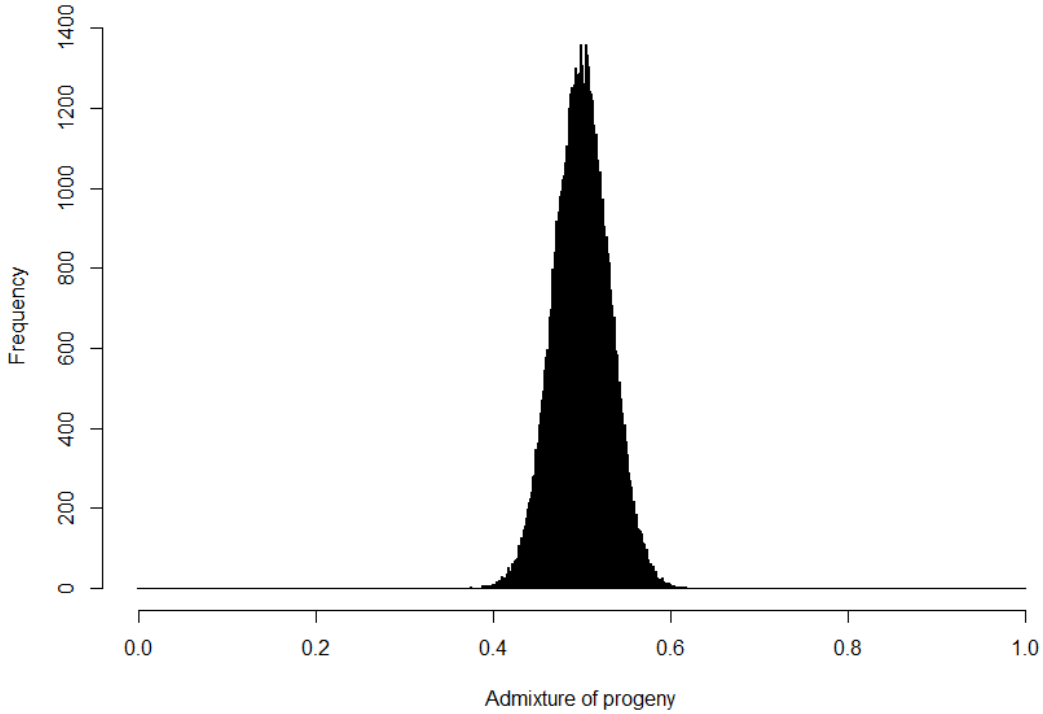
Methods

We simulated 100,000 progeny from an $F_1 \times F_1$ cross. $F_1 \times F_1$ crosses are the only hybrid cross with the ability to produce offspring across the range of admixture levels, depending on the recombination patterns. Therefore, an $F_1 \times F_1$ cross is expected to have the highest variance in progeny admixture.

Salmonids have approximately 50 pairs of chromosome arms (Allendorf and Thorgaard 1983). Salmonids have almost complete interference, where only one recombination occurs per chromosome arm (Thorgaard et al. 1983; Guyomard et al. 2006; Brieuc et al. 2014). We used published estimates of single (90%), double (2.6%), and zero (7.4%) recombinations (Brieuc et al. 2014) to simulate recombination in our F_1 parents. Recombination was allowed to occur randomly across the chromosome arm and arms were assumed to be the same size. Simulations were performed using R (R Core Team 2012).

Results

The variation of admixture within progeny was low. The mean admixture was 0.50, with a 95% confidence interval of 0.44 to 0.56 (see the figure below).



Supplemental References

Brieuc, M. S. O., C. D. Waters, J. E. Seeb, and K. A. Naish. 2014. A dense linkage map for Chinook Salmon (*Oncorhynchus tshawytscha*) reveals variable chromosomal divergence after an ancestral whole-genome duplication event. G3: Genes, Genomes, Genetics 4:447–460.

Guyomard, R., S. Mauger, K. Tabet-Canale, S. Martineau, C. Genet, F. Krieg, and E. Quillet. 2006. A type I and type II microsatellite linkage map of Rainbow Trout (*Oncorhynchus mykiss*) with presumptive coverage of all chromosome arms. BMC Genomics [online serial] 7:302.

R Core Team 2012. R: a language and environment for statistical computing. R Foundation for Statistical Computing, Vienna.

Thorgaard, G. H., F. W. Allendorf, and K. L. Knudsen. 1983. Gene-centromere mapping in Rainbow Trout: high interference over long map distances. Genetics 103:771–783.

R Code

```
# F1 x F1
# recombination occurs randomly
progeny <- c()

# produce 100,000 progeny
for(i in seq(1:100000)){
  female <- c(); male <- c()

  for(j in seq(1:50)){
    recomb <- runif(1) # draw a rand. Num. from a uniform dist.
to see if recombination occurs

    if (recomb > 0.974){ # double recombination
      position1 <- runif(1);
      position2 <- runif(2);
      admixture <- abs(position1-position2); # determine region
of genome that recombined
      female[j] <- sample(c(admixture, (1-admixture)), 1)
    }
    else if (recomb > 0.90){ # zero recombination
      female[j] <- sample(c(0,1), 1)
    }
    else { # single recombination
      admixture <- runif(1)
      female[j] <- sample(c(admixture, (1-admixture)), 1)
    }

    recomb <- runif(1)

    if (recomb > 0.974){ # double recombination
      position1 <- runif(1);
```

```
      position2 <- runif(2);
      admixture <- abs(position1-position2);
      male[j] <- sample(c(admixture, (1-admixture)), 1)
    }
    else if (recomb > 0.90){ # zero recombination
      male[j] <- sample(c(0,1), 1)
    }
    else { # single recombination
      admixture <- runif(1)
      male[j] <- sample(c(admixture, (1-admixture)), 1)
    }

  }
  progeny[i] <- mean(c(male, female))

}

hist(progeny, xlim=c(0,1), breaks=seq(0,1, by=0.001),
xlab="Admixture of progeny", main="")
round(quantile(progeny, c(0.0275, 0.975)), digits=2)
```