

## Can we identify wild-born salmon from parentage assignment data? A case study in the Garonne-Dordogne rivers salmon restoration programme in France



Parentage assignment with genomic markers provides an opportunity to monitor salmon restocking programs. Most of the time, it is used to study the fate of hatchery-born fish in those programs, as well as the genetic impacts of restocking. In such analyses, only fish that are assigned to their parents are considered. In the Garonne-Dordogne river basin in France, native salmon have disappeared, and supportive breeding is being used to try to reinstate a self-sustained population. It is therefore of primary importance to assess the numbers of wild-born returning salmon, which could appear as wrongly assigned or not assigned, depending on the power of the marker set and on the size of the mating plan. We used the genotypes at nine microsatellites of the 5800 hatchery broodstock which were used from 2008 to 2014, and of 884 upstream migrating fish collected from 2008 to 2016, to assess our ability to identify wild-born salmon. We simulated genotypes of hatchery fish and wild-born fish and assessed how they were identified by the parentage assignment software Accurassign. We showed that 98.7% of the fish assigned within the recorded mating

plan could be considered hatchery fish, while 93.3% of the fish in other assignment categories (assigned out of the mating plan, assigned to several parent pairs, not assigned) could be considered wild-born. Using a Bayesian approach, we showed that 31.3% of the 457 upstream migrating fish sampled from 2014 to 2016 were wild-born. This approach is thus efficient to identify wild-born fish in a restoration program. It remains dependent on the quality of the recording of the mating plan, which we showed was rather good (<5% mistakes) in this program. To limit this potential dependence, an increase in the number of markers genotyped (17 instead of 9) is now being implemented.

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