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COMBINING VITASSIGN AND COLONY: AN EFFICIENT PRACTICAL PROCEDURE FOR PARENTAL ASSIGNMENT WITH MISSING PARENTS

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The contribution of parentage assignment in selective breeding of aquaculture species is undeniable. However, breeding programs often face practical management problems and it is not uncommon that some broodstock genotypes miss because of premature death, traceability problems or sample quality problems. This may lead to unexpectedly low parentage assignment and decrease markedly the potential of genetic improvement. In this study, we explored the potential of combining two softwares, VITASSIGN and COLONY, for obtaining parentage assignment in the case of a few missing parental genotypes in a full factorial mating design. Nine dams were crossed to 60 sires in a full factorial mating scheme and 2000 offspring were reared in a single batch. Biological samples of offspring and parents (caudal fin or sperm) were genotyped for 12 microsatellite markers at Labogena (Jouy-en-Josas, France). Due to low sample quality, 2 dams, 2 sires and 9 offspring could not be genotyped. First pedigree assignment trials were run with this partial dataset (1991 offspring, 7 dams and 58 sires). Using VITASSIGN, an exclusion-based parentage assignment software, 40.8% of offspring were assigned to single parent pair (55.8% allowing up to 2 mismatches). Using Colony, a maximum likelihood parentage software, highly probable pedigree was obtained for 52.6% of the offspring. The average posterior probabilities of 259 additional potential dams genotypes generated by Colony were collected over 7 plausible configurations, and 2 dams showing posterior probabilities higher than 0.95 were identified. The next pedigree assignment included those two inferred dam genotypes, and resulted in 78.0% perfect match in VITASSIGN (92.4% allowing up to 2 mismatches) and in 77.1% assignment in Colony. Finally, candidate sires and dams with missing loci or genotyping errors were corrected based on the genotypes inferred by Colony (12 more parent genotypes were corrected or completed, for a total of 29 corrected alleles). In the end, using VITASSIGN, 96.4% of the offspring were uniquely assigned (86.1% with perfect match and 96.4% with up to 2 mismatches allowed), and only 3.4% of the offspring could not be assigned.

Keywords: pedigree assignment, VITASSIGN, Colony, missing genotypes

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