Accuracy of genomic predictions using different imputation error rates in aquaculture breeding programs: A simulation study

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In breeding programs, genetic evaluations can be performed using phenotypic information from the selection candidates per se or from relatives to obtain breeding values (EBV) by the traditional method known as the Best Linear Unbiased Predictor (BLUP). Using phenotypic information from relatives (e.g. sib-testing) is a common practice particularly in aquaculture, because some economically important traits, including disease resistance and carcass quality, would require the slaughtering of animals before they could become breeders. The ability to better predict genetic merit has made the incorporation of genomic information into genetic evaluation a common practice in livestock and aquaculture species. Genomic selection uses genotypic information from single nucleotide polymorphism (SNP) arrays or genotyping-by-sequencing assays to increase the accuracy of selection by means of exploiting realized within and between family trait information. The cost of genotyping dense SNP panels in the training population and selection candidates limits the practical implementation of genomic selection. Imputation from low- to high-density genotypes represents an alternative which decreases the cost of genotyping while maintaining prediction accuracies. The present study compared EBV accuracies obtained with BLUP and genomic selection (GBLUP) methods using simulation. We simulated five generations of a rainbow trout (Oncorhynchus mykiss) breeding program, using 1662 individuals with real genotypic data from 42,822 SNP as a founder population. The scenarios varied using three heritability levels ($h^2 = 0.1$; 0.2 and 0.4) and four imputation error rates (10%, 5%, 1% and 0%), mimicking different densities of low-density SNP panels (0.5 K, 3 K, 7 K and 42 K, respectively). The simulations showed: (1) an increase in accuracy ranging from 3% to 25% when comparing GBLUP against BLUP across all

scenarios, (2) a non-linear increase in accuracy for both BLUP and GBLUP across generations and heritability levels, and (3) comparable performance between GBLUP0.5 K, GBLUP3K and GBLUP7K models in terms of accuracy. We conclude that low cost genomic selection can be applied in aquaculture breeding programs using a combined approach of low-density SNP panels (e.g. 500 SNPs) and genotype imputation.