OPTIMISING GENOTYPE IMPUTATION TO IMPROVE GENOMIC SELECTION FOR DISEASE RESISTANCE IN ATLANTIC SALMON

Smaragda Tsairidou[1], Alastair Hamilton[2], Diego Robledo[1], James E. Bron[3], Ross D. Houston[1]

[1] The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, EH25 9RG, United Kingdom
[2] Hendrix Genetics Aquaculture BV// Netherlands Villa 'de Körver', Spoorstraat 695831 CK Boxmeer, The Netherlands
[3] Institute of Aquaculture, University of Stirling, FK9 4LA, United Kingdom

INTRODUCTION

- Seafood (including fish, shellfish and crustaceans) is a major source of high quality animal protein, healthy fats (e.g. omega-3 fatty acids), and essential nutrients
- Controlling disease is a key challenge for ensuring sustainable aquaculture production
 - **Sea lice: the most costly disease-related problem in salmon farming industry**

- Genomic selection using genotype data can help reduce disease and accelerate response to selection for economically important traits such as disease resistance
- Genome-wide genetic marker data on large populations can be obtained in a cost-effective manner via genotype imputation

Aim of Study:
Optimise the use of low-density genotypes and evaluate genotype imputation strategies for cost-effective genomic selection in Atlantic salmon breeding programmes

MATERIALS & METHODS

a) Identification of optimal SNP panel density and SNP composition
  - Using a custom software pipeline integrating R, Shell, and ASReml, the genomic prediction accuracy was estimated using multiple replicates of five-fold cross-validation, through a GBLUP approach

b) Systematic assessment of the imputation accuracy when:
  - Parents were genotyped for the optimal SNP panel
  - Offspring were genotyped for a range of lower density imputation panels and imputed to the optimal SNP panel using FImpute

c) Comparison of genomic prediction accuracies of genomic selection for each of the datasets, with and without imputation
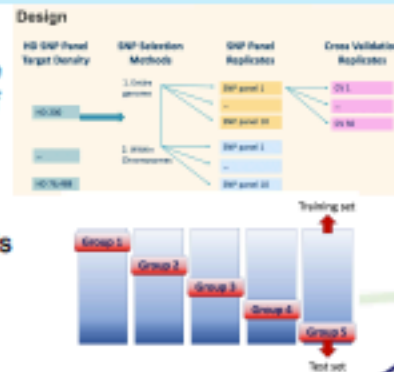
RESULTS

- Genomic heritability:
  0.19 (0.07) for sea lice resistance
  0.57 (0.07) for body weight
- Reducing SNP density from HD to 200 SNPs resulted in a 14.5% decrease in prediction accuracy for sea lice resistance, and a 27.9% decrease for weight

Average prediction accuracy over 10 SNP panel replicates
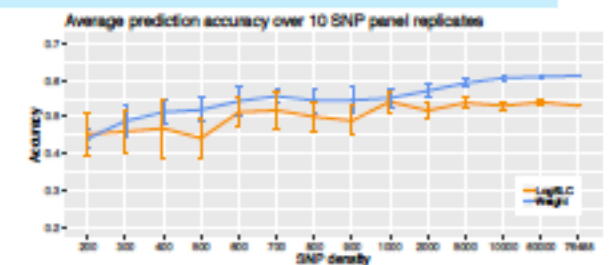
❖ The asymptote was between 2,000 and 5,000 SNPs, and therefore 5000 SNPs was chosen as the optimal SNP panel

Accuracy of imputation to 5000 SNPs
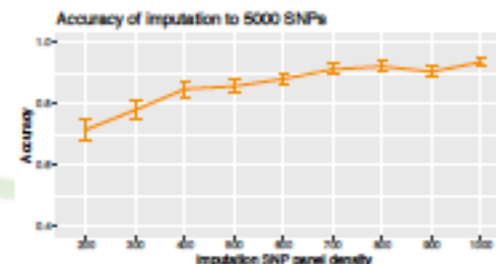
- Imputation accuracy increased with increasing imputation panel density
- Less variability across individuals when imputing from higher densities

❖ Genomic prediction accuracy when offspring were genotyped for 200 SNPs and imputed, and parents were genotyped for 5,000 SNPs, was 0.53
❖ This accuracy was similar to the full high density and optimal density dataset, and markedly higher than using 200 SNPs without imputation

Sea lice resistance prediction accuracy for imputed SNP panels
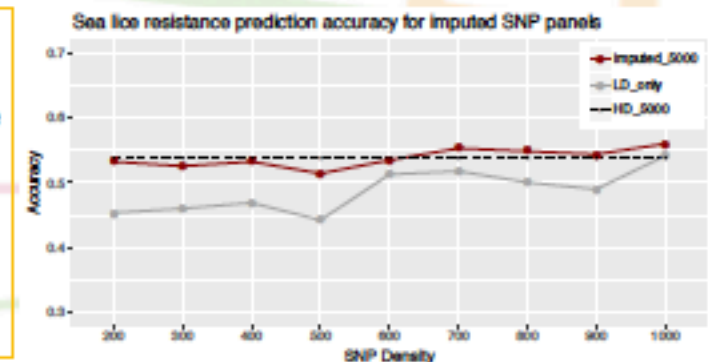
CONCLUSIONS

- Genomic selection using very low density genotypes imputed to medium density (e.g. 5000 SNPs) can provide prediction accuracies similar to those obtained from full high density genotype data
- Using low density SNP panels with imputation can be a cost effective tool for genomic prediction in Atlantic salmon breeding programmes