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Fatty acid composition prediction and phenomic selection in rainbow trout by Raman spectroscopy

In this study, Raman scattering spectroscopy was used to predict fatty acid (FA) composition in rainbow trout (Oncorhynchus mykiss), providing a cost-effective alternative to gas chromatography (GC). Fatty acid composition was analysed in visceral adipose tissue from 268 individuals fed three different diets. Ridge regression was used to calibrate a model against GC results. The FA profile of 1,382 trout from 831 families of the "Les Sources de l'Avance" selection programme was then predicted from Raman spectra obtained from visceral fat sample, and phenotypic data for growth, processing and quality traits, including a cross-sectional steak image using magnetic resonance imaging, were also collected. A 57k Axiom™ single nucleotide polymorphism genotyping array was also used to provide heritability (h2) estimates along wavenumbers. Heritability is the proportion of observed variation in a trait among individuals in a population that can be attributed to genetic factors, indicating how much a trait is likely to be passed from parents to offspring.
The results yielded cross-validated R² values of 0.79 for total PUFAs, 0.83 for omega-6 PUFAs and 0.66 for omega-3 PUFAs. Individual omega-3 fatty acids such as alpha-linolenic acid (ALA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) also showed strong predictive performance with R² values of 0.82, 0.76 and 0.81 respectively. The heritability results show that the Raman spectra are significantly heritable with three interesting wavenumbers (h2 from 0.15 to 0.28). Phenomic selection showed higher correlations with corrected phenotypes for traits such as body weight and fatty acid composition, outperforming genomic selection in these cases. Further validation in future generations will be required to confirm these findings.
Taken together, these results demonstrate the potential of the Raman spectroscopy and multivariate statistics principle to improve aquaculture breeding programmes by integrating high-throughput FA composition prediction by Raman spectroscopy and phenomic selection to support more efficient large-scale phenotyping [1,2].

References

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