Pixels to feed: Digital phenotyping potential for genetic analysis of feed intake and efficiency in *Atlantic salmon*

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Acknowledgements

Precision Vision

Valid Win

Background

- Feed efficiency (FE) is a high-value trait
- *Atlantic salmon* exhibit significant genetic variation and the potential to improve FE
- However, aquaculture systems are complex, making it challenging to phenotype individual feed intake (IFI)
- Digital technologies are offering accurate and high-throughput phenotyping strategies

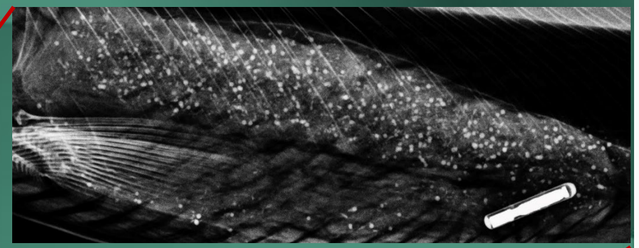
Study objective

The current study aims to uncover the genetic basis of FE

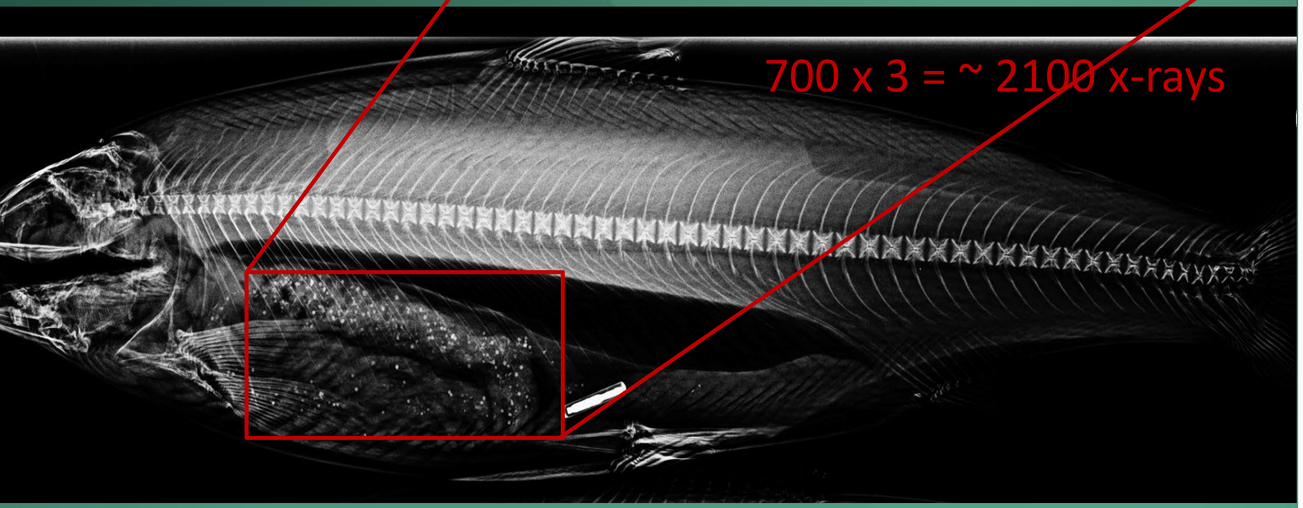
- Develop a reliable method to phenotype IFI under a commercial setting
- Train and evaluate deep learning model (BeadDetect) for object detection
- Study the genetic parameters of FE and related traits
- GWAS and Gene Mapping to identify key genomic regions linked with FE

Study Design

!!! Challenge



Hundreds of beads in fish



- 35 full sibs Atlantic salmon families
- 2021-year class of MOWI Genetics
- **Traits recorded**

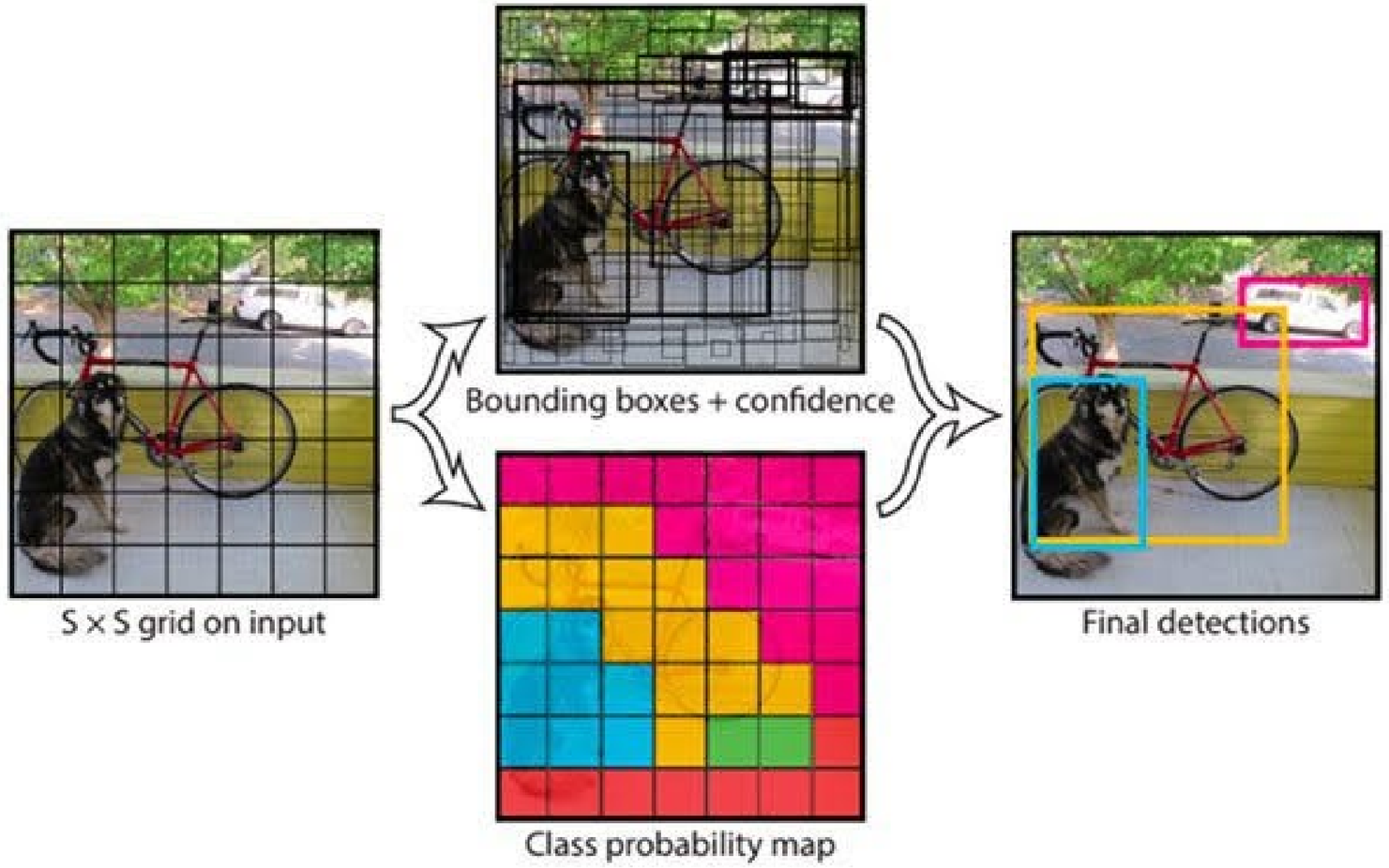
  3 measurement time points **(80, 194 and 297 g)**

  - ✓ Individual feed intake
    - X-ray imaging
  - ✓ Whole-body fat (WBF)
    - Near-infrared spectroscopy
  - ✓ Feed conversion ratio (FCR)
  - ✓ Residual feed intake (RFI)

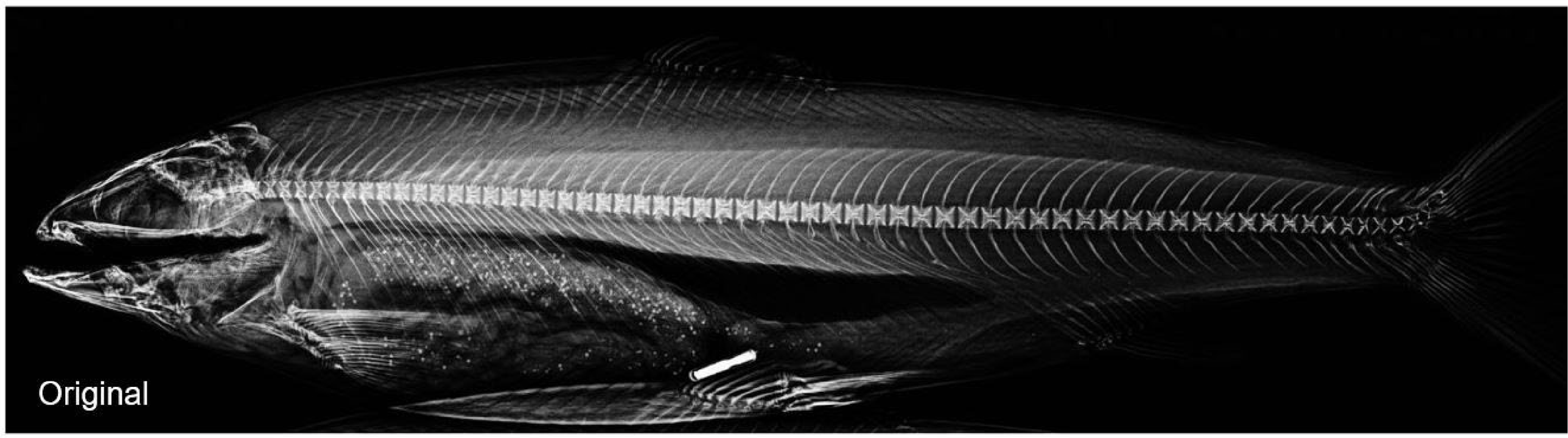
Deep learning for bead detection

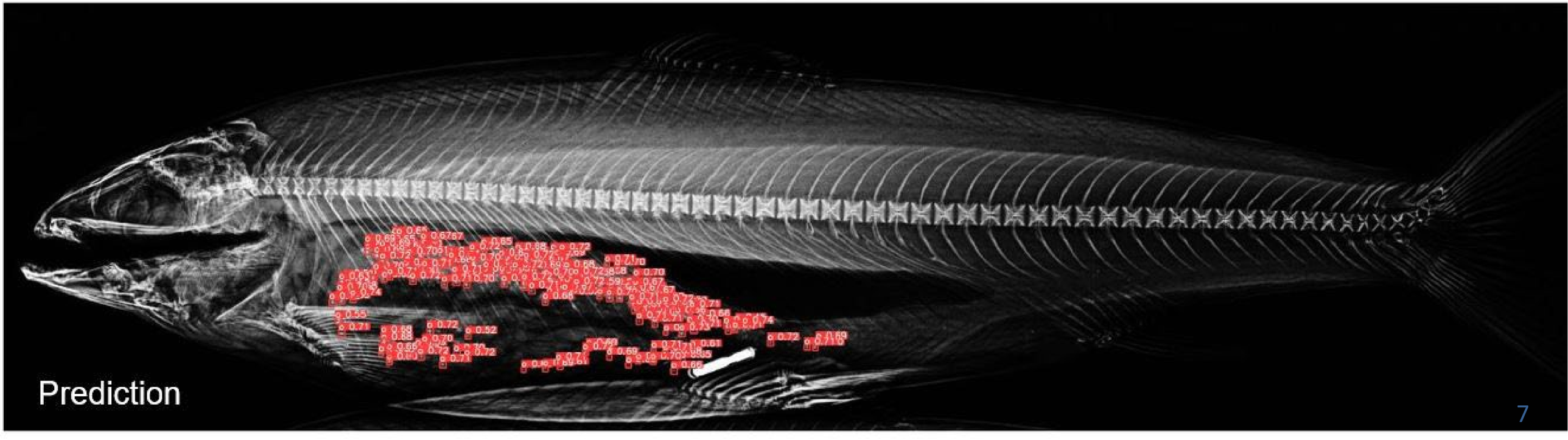
YOLO “You Only Look Once”

- A fast, efficient and real-time object detection algorithm.
- Pre-trained models with transfer learning capabilities.
- Works by predicting bounding boxes in a single pass.



https://techworldaj.blogspot.com/2018/03/getting-started-with-yolo-object.html


Original


Prediction

Statistical Analysis

The following mixed linear models are used for genetic analysis

Genetic parameters model

Restricted maximum likelihood (REML)

$$Y_{ijk} = \mu + s_i + t_j + g_k + e_{ijk}$$

GWAS model

Mixed linear model association- Leave one chromosome out (MLMA-LOCO) approach

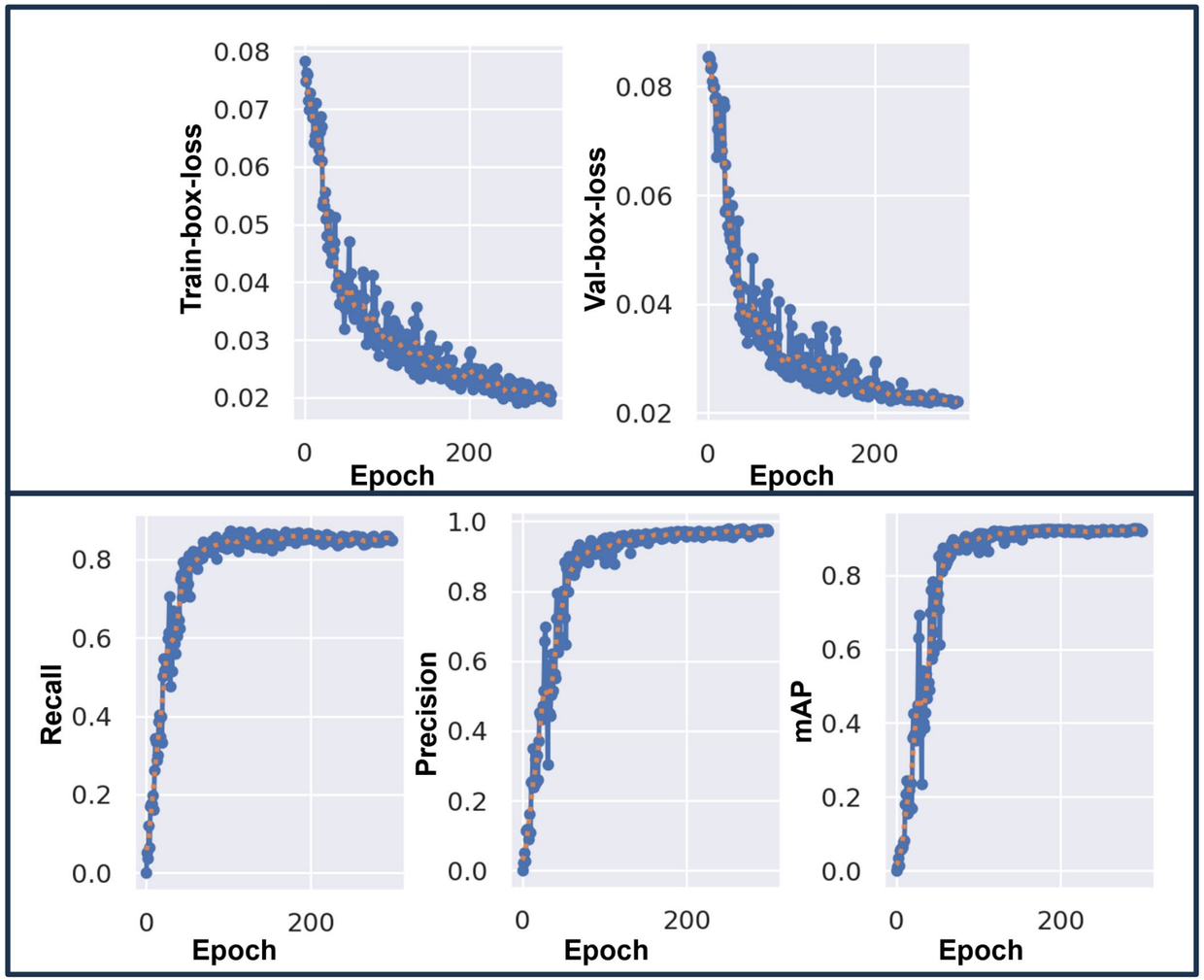
$$Y = \mu + X\alpha + Zu + e$$

R studio, GCTA and **DMU** software were used for all analysis.

Results

Model performance

Trainning Metrics



External validation

Set	No. of fish	R^2	RMSE	Slope
Train	60	**0.99**	4.23	1.02
Valid	20	**0.99**	9.34	1.04
Test	10	**0.99**	5.14	1.02

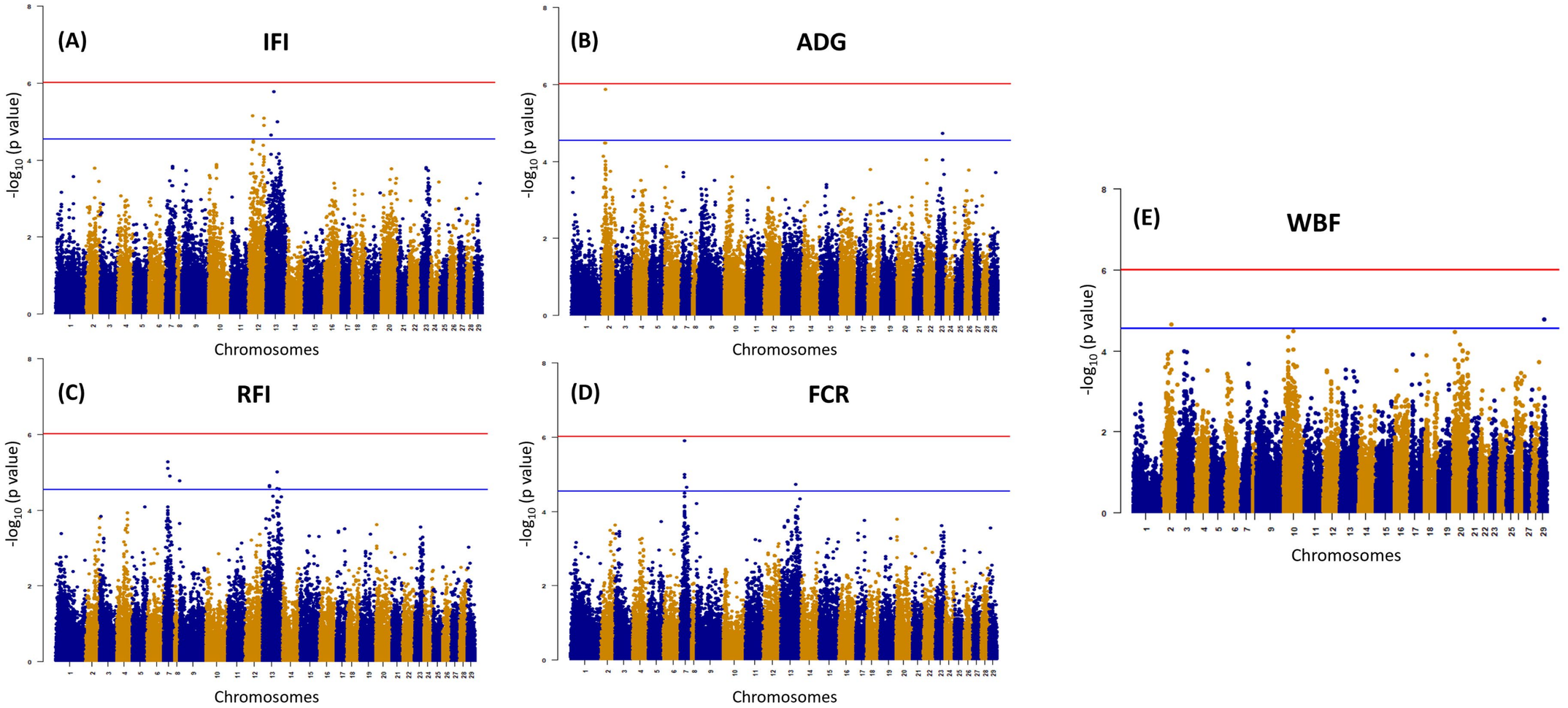
Genetic parameters

Trait	Time	Heritability
IFI	1	0.20 ± 0.05
	2	0.35 ± 0.07
	3	0.50 ± 0.07
ADG	1	0.48 ±0.07
	2	0.44 ±0.06
	3	0.55 ±0.06
RFI	1	0.11 ±0.05
	2	0.16 ±0.07
	3	0.17 ±0.11
FCR	1	0.09 ±0.04
	2	0.08 ±0.04
	3	0.23 ±0.06
WBF	3	0.61 ±0.06

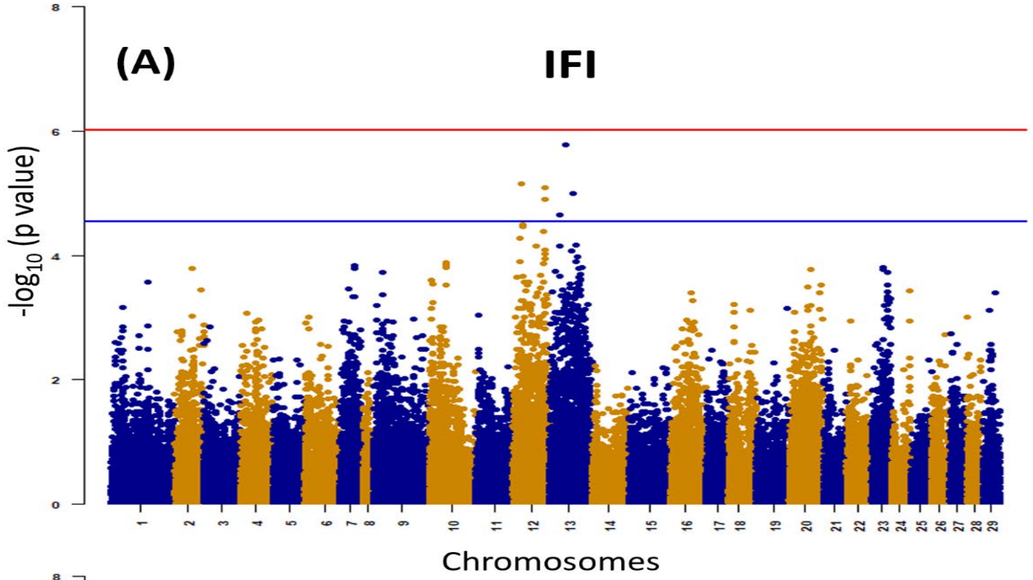
Correlations

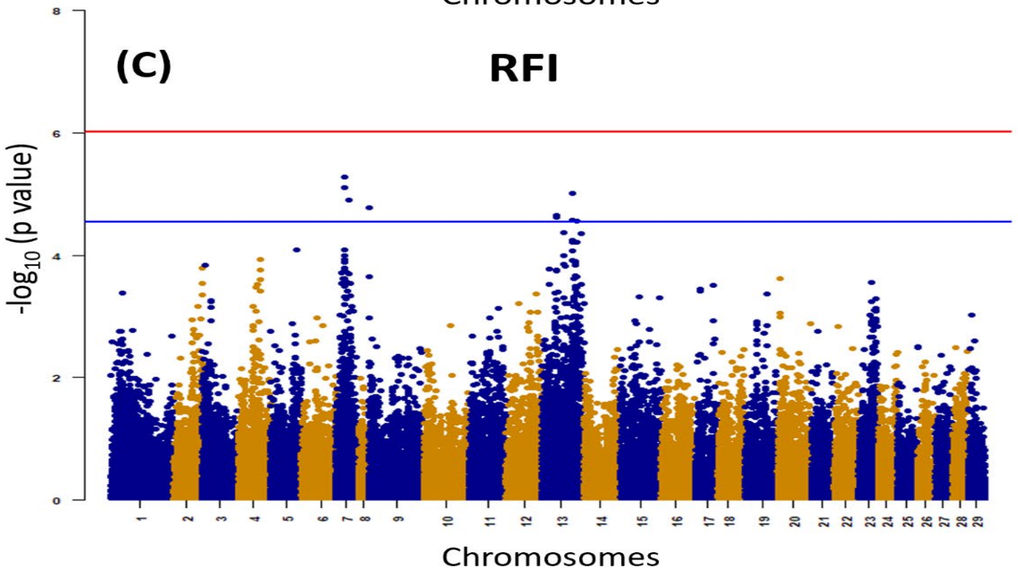
		Genetic correlations				
Phenotypic correlations	Heritability	$\overline{IFI}$	$\overline{DWG}$	$\overline{RFI}$	$\overline{FCR}$	WBF
	$\overline{IFI}$	**0.46 ± 0.06**	0.95 ± 0.02	0.57 ± 0.13	0.66 ± 0.11	0.52 ± 0.09
	$\overline{DWG}$	0.79	**0.53 ± 0.06**	0.28 ± 0.18	0.38 ± 0.17	0.64 ± 0.07
	$\overline{RFI}$	0.61	0.01	**0.14 ± 0.05**	0.99 ± 0.005	-0.10 ± 0.19
	$\overline{FCR}$	0.60	0.001	0.98	**0.15 ±0.05**	-0.01 ± 0.18
	WBF	0.45	0.63	-0.10	-0.08	**0.61 ±0.06**

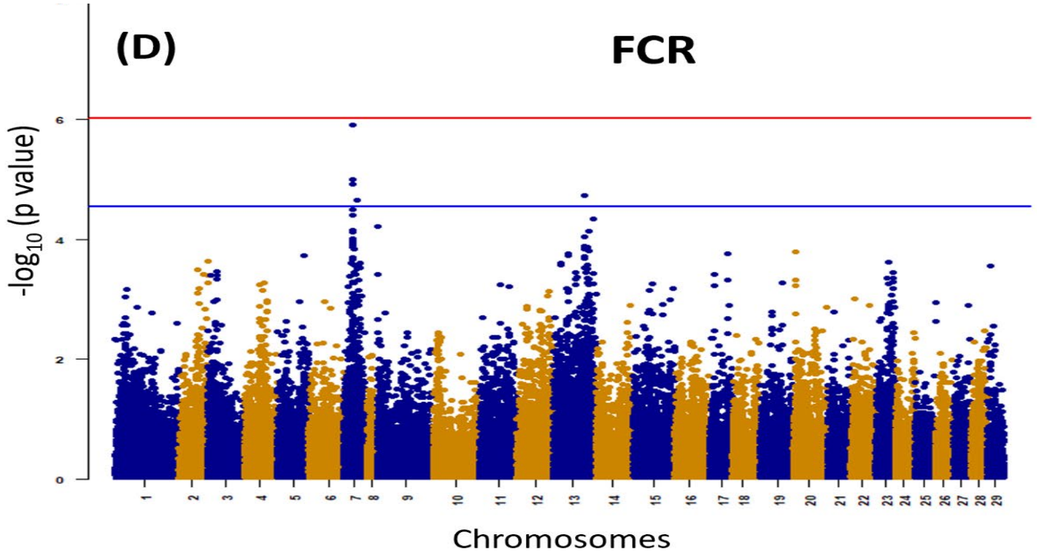
GWAS Results



GWAS Results







Gene identification and functional enrichment analysis

The **33 candidate genes** were identified within the **±50 kb** region of the top SNPs using the **Ssal_v3.1** reference Salmo Salar genome.

Genes are involved with cellular growth (*orp1, ZNF79, UPRT*) dietary intake (*mGlurs8*), fatty acid and protein metabolism (*FAXDC2, UPRT, SNAT2, Acox3*), bioenergetics (*S100-A11, Sin-3b*), and neuronal development and signalling (*Zfn-d4, Foxr1, Shc1*).

Gene Ontology (GO) revealed several biological processes related to the metabolism of fatty acids were enriched with candidate genes identified for RFI and FCR.

Summary

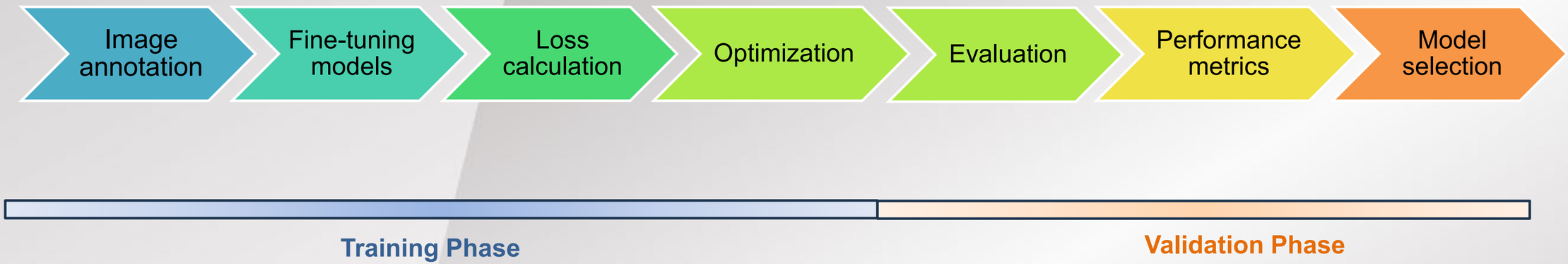
- X-ray imaging coupled with BeadDetect provides an accurate and non-invasive approach to phenotype IFI in fish
- Moderate to high heritabilities estimated for FE-related traits signify the potential for genetic improvement.
- Variability in genetic correlations across FE-related traits reflects shared and distinct genetic influence.
- GWAS showed the polygenic nature of the studied traits, supporting genomic selection for improvement.

✉ Take home message

Feed efficiency: measurable and heritable

Thank you so much for listening carefully …

Deep learning for bead detection



Genetics parameters

Trait	Time	Genetic variance	Residual variance	Heritability
IFI	1	0.02	0.06	0.20 ± 0.05
	2	0.10	0.18	0.35 ± 0.07
	3	0.29	0.29	0.50 ± 0.07
ADG	1	0.06	0.06	0.48 ±0.07
	2	0.13	0.16	0.44 ±0.06
	3	0.20	0.16	0.55 ±0.06
RFI	1	0.01	0.03	0.11 ±0.05
	2	0.02	0.11	0.16 ±0.07
	3	0.03	0.16	0.17 ±0.11
FCR	1	0.01	0.02	0.09 ±0.04
	2	0.01	0.02	0.08 ±0.04
	3	0.01	0.02	0.23 ±0.06
WBF	3	0.61	0.38	0.61 ±0.06