Multi-Trait Breeding Value–Based Selection and Prediction of Genetic Gain under Alternative Breeding Scenarios in Common Carp (*Cyprinus carpio*)

GRÓ · FTP
Fisheries Training Programme

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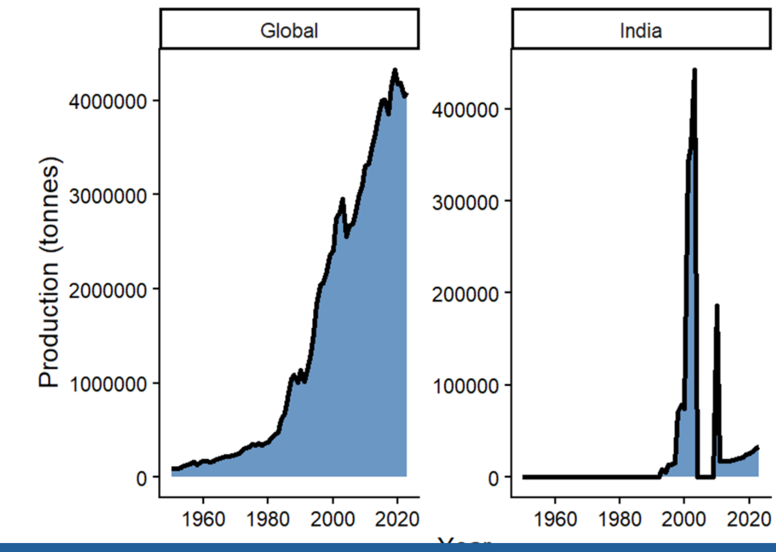
Research background

- Selective breeding program of common carp is conducted at ICAR-CIFE, Mumbai, India. The production environment is inland saline.
- Common carp tolerate low salinity (8 ppt) and a wide temperature range (3-35 °C). Barren saline areas are a potential aquaculture resource.
- The breeding objective is to develop a fast-growing, salinity-resilient strain suitable for inland saline aquaculture.
- The breeding data constitutes a multi-trait, multi-environment dataset; a multi-trait Best Linear Unbiased Prediction (BLUP) approach is appropriate.
- Stochastic simulations will predict best alternative breeding scenario for sustainable breeding (e.g., number and size of families).



Methodology

Breeding structure

Gen	Year	Sires	Dams	Families	Progeny
Second	2023	77	96	96	2291
	2024	277	326	326	4010
Total	2	354	422	422	6301

Estimation of (co)variance components

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_{as}\mathbf{a}_s + \mathbf{Z}_{fs}\mathbf{f}_s + \mathbf{Z}_{ps}\mathbf{p}_s + \mathbf{e}$$

where:

- $\mathbf{y}$ is the vector of phenotypic observations
- $\mathbf{b}$ is the vector of fixed effects
- $\mathbf{a_s}$ additive genetic effects interacting with salinity environments
- $\mathbf{f_s}$ full-sib effects interacting with salinity
- $\mathbf{p_s}$ pond effects interacting with salinity
- $\mathbf{e}$ is the vector of residual effects for each salinity
- $\mathbf{X}$, $\mathbf{Z_{as}}$, $\mathbf{Zf_s}$, and $\mathbf{Z_{ps}}$ are incidence matrices relating observations to respective effects

$$\mathbf{a}_s \sim N(0, \mathbf{G}_{as} \otimes \mathbf{A})$$

$$\mathbf{p}_s \sim N(0, \mathbf{I}_{p(s)}\sigma^2_{P(s)})$$

$$\mathbf{f}_s \sim N(0, \mathbf{I}_f \otimes \mathbf{f}_s)$$

$$\mathbf{e} \sim N(0, \mathbf{I} \otimes \mathbf{R}_s)$$

$$h^2_s = \frac{\sigma^2_{A,s}}{\sigma^2_{A,s} + \sigma^2_{F,s} + \sigma^2_{P,s} + \sigma^2_{E,s}}$$

$$r_g = \frac{\sigma_{A,ij}}{\sqrt{\sigma^2_{A,i}\sigma^2_{A,j}}}$$

Multi-trait Selection Index

$$I = \sum_{i=1}^{m} w_i \hat{A}_i$$

where:

- I is the aggregate genotype
- $\hat{A}_i$ is the estimated breeding value
- w_i is the economic weight
- m is traits in the breeding objective

Prediction of genetic response

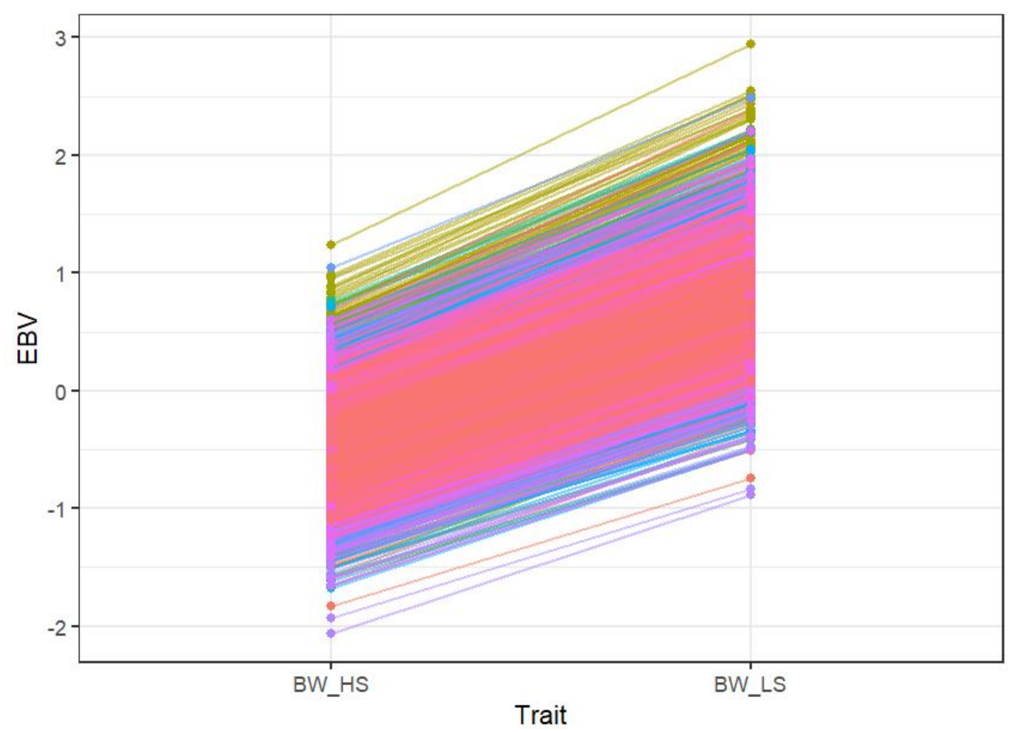
$$\Delta G = i \times r_{IH} \times \sigma_{A,H}$$

where:

- i is selection intensity,
- r_{IH} is index accuracy,
- $\sigma_{A,H}$ is additive genetic standard deviation

Simulation of alternative breeding

Scenarios/Parameters	1	2	3	4
No families/generation	250	125	85	65
Mating	2	2	2	2
Within family	10	20	30	40
Selected from family	4	4	4	4
Generation	10	10	10	10
Replication	10	10	10	10
Bulmer	3	3	3	3
Top males	400	200	136	105
Top females	500	250	170	130

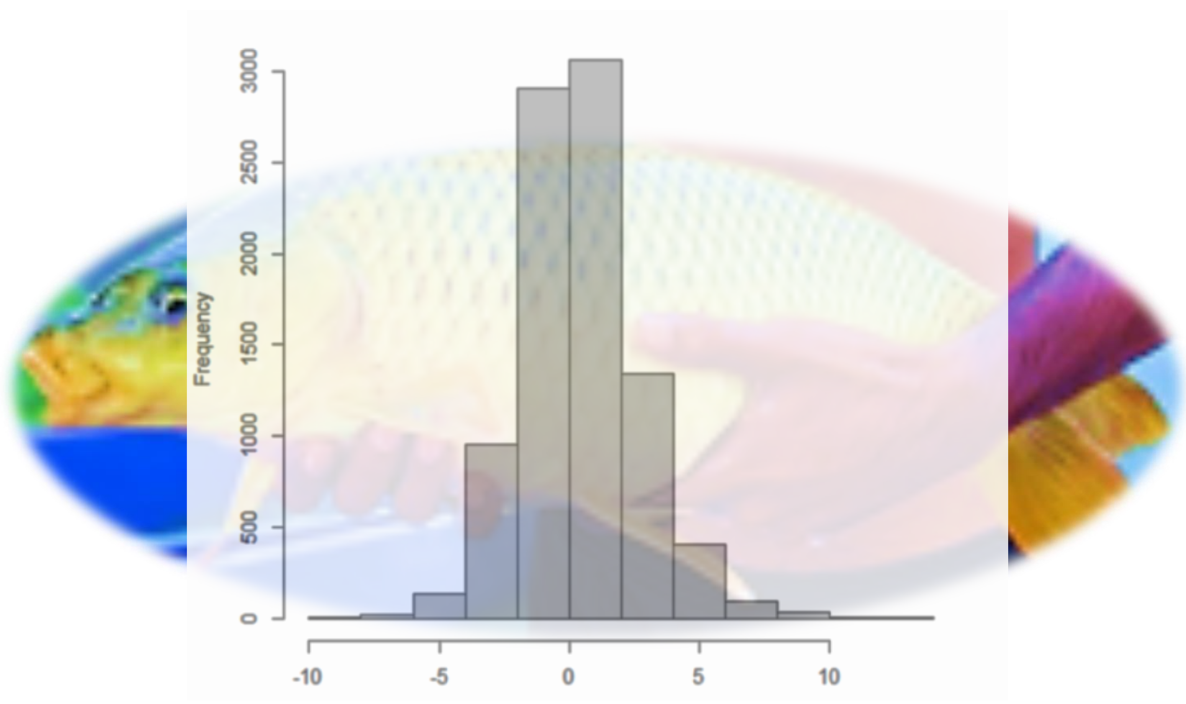


EBVs for BW across salinities

Results

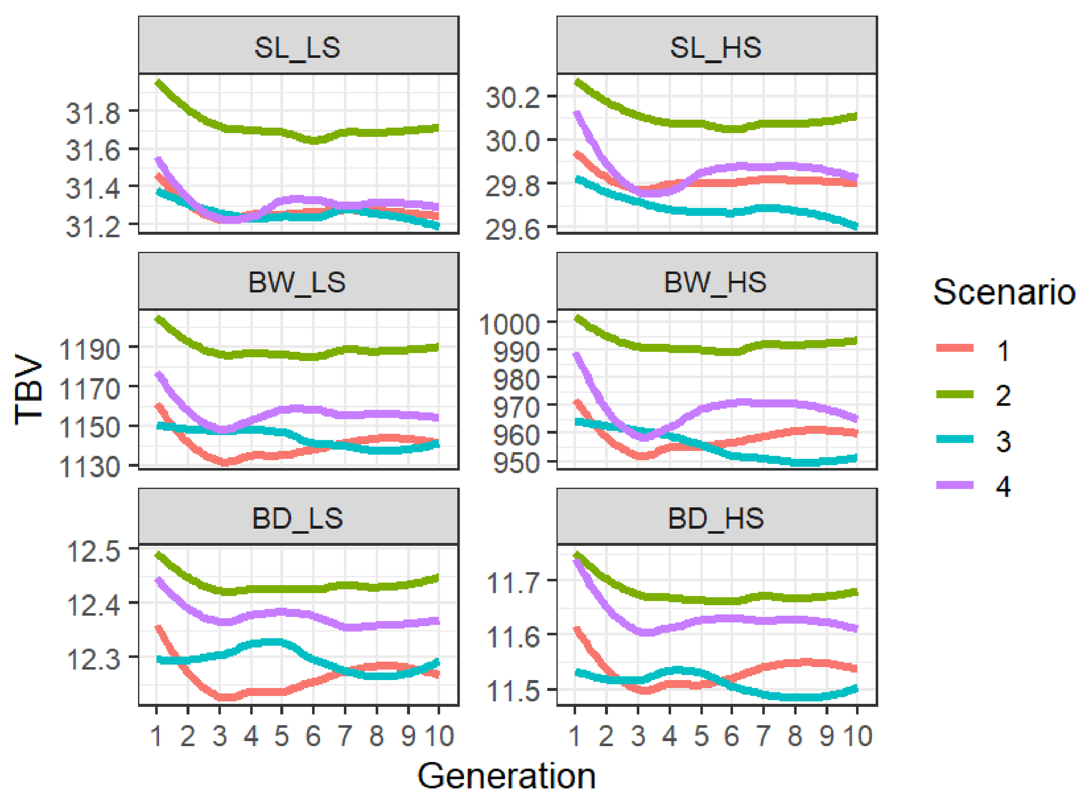
Descriptive statistics

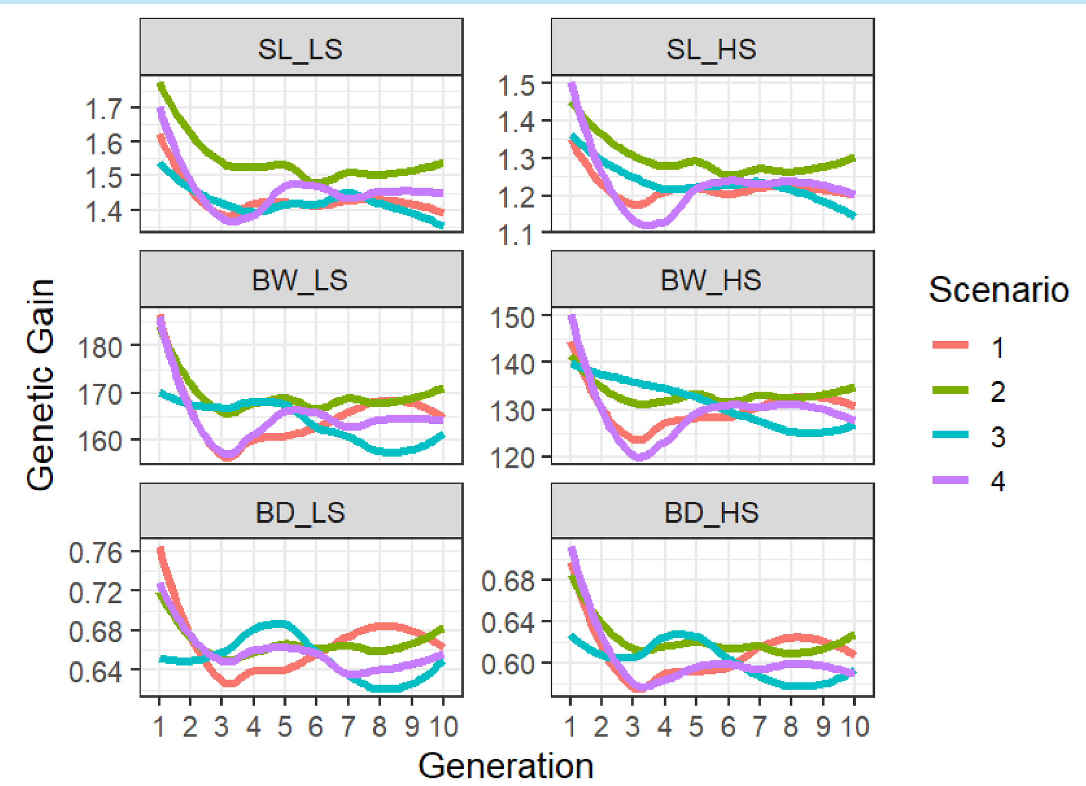
Salinity	LS (2-4 ppt)			HS (6-8 ppt)		
Traits	BW(g)	SL(cm)	BH(cm)	BW(g)	SL(cm)	BH(cm)
Mean	998.1	30	11.7	842.8	28.7	11.1
SD	317.4	3.1	1.3	295.2	3.1	1.5
CV (%)	31.8	10.4	11.5	35	10.8	13.5
Min	306	20.2	8.1	136	14.5	5.7
Max	2748	45.1	17.5	2725	42.3	17.2
N	2639	2639	2637	2373	2373	2372



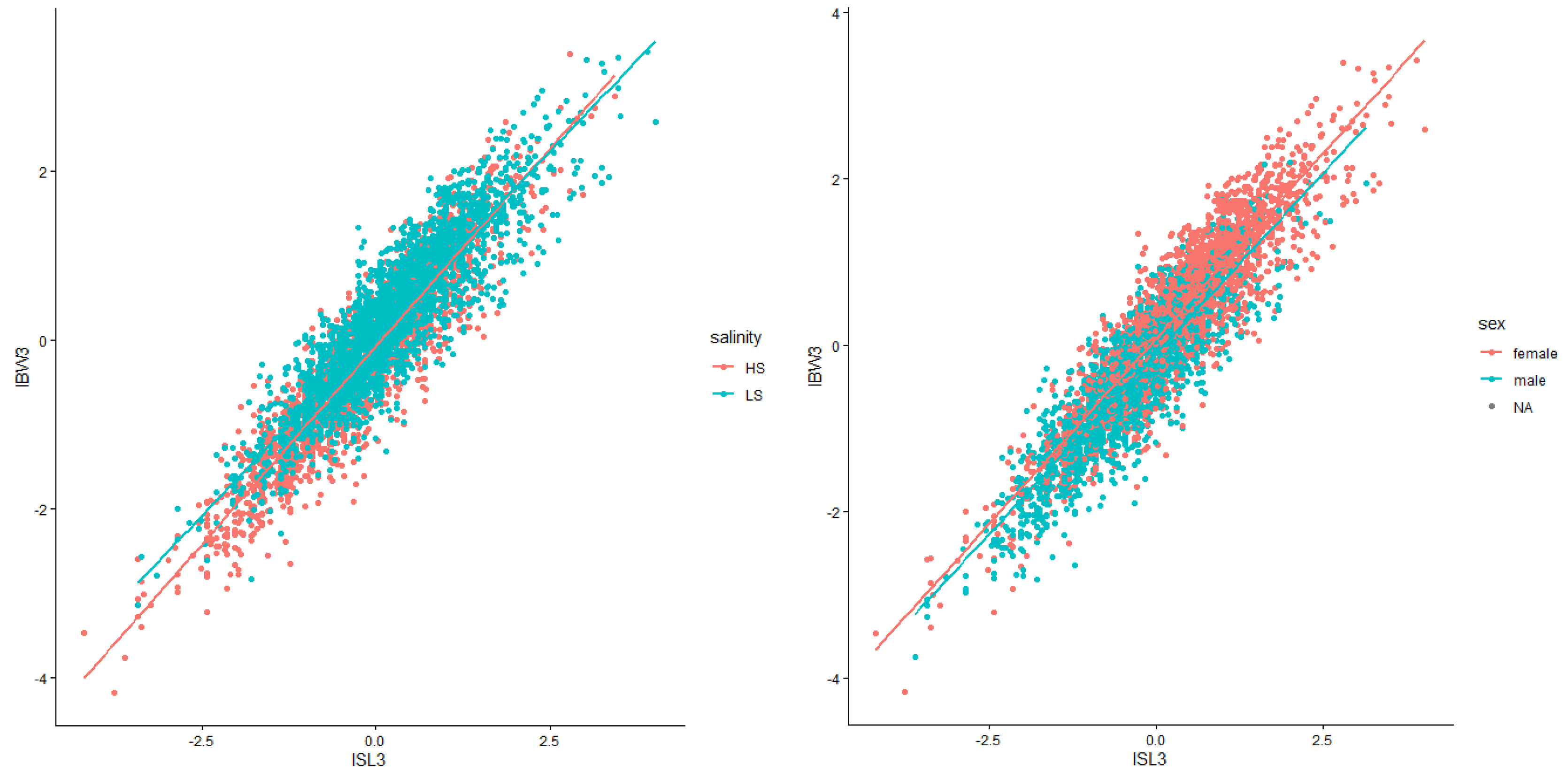
Distribution of multi-trait BLUP

- The multi-trait BLUP EBV had accuracy of 0.72.
- The theoretical response to aggregate genotype selection was predicted to be 4.25 units.





Alternative breeding scenario 2: True breeding value and genetic gain trend for multi-traits across 10 generations



Relationship of body weight and standard length across salinity and sex

Heritability (h²), pond variance (c²), full-sib effect (f²) and residual variances (r²)

	BW_HS	SL_HS	BH_HS	BW_LS	SL_LS	BH_LS
h^2	0.38 ± 0.11	0.44 ± 0.11	0.36 ± 0.11	0.52 ± 0.11	0.52 ± 0.1	0.57 ± 0.1
c^2	0.02 ± 0.02	0.02 ± 0.02	0.007 ± 0.007	0.09 ± 0.07	0.06 ± 0.04	0.04 ± 0.03
f^2	0.12 ± 0.05	0.09 ± 0.04	0.14 ± 0.05	0.08 ± 0.04	0.09 ± 0.04	0.07 ± 0.04
r^2	0.45 ± 0.07	0.43 ± 0.07	0.47 ± 0.07	0.29 ± 0.06	0.31 ± 0.06	0.30 ± 0.06

Conclusion

- The growth traits exhibited high heritability.
- High r_g is observed for traits across salinities indicating low G x E.
- Accuracy of multi-trait EBV is 0.72, thus, better selection decision.
- Aggregate genetic gain of +4.25 index units is predicted.
- Breeding scenario 2 is recommended for sustainable breeding.

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