

➤ Consequences of ignoring GxE interactions when estimating genetic parameters

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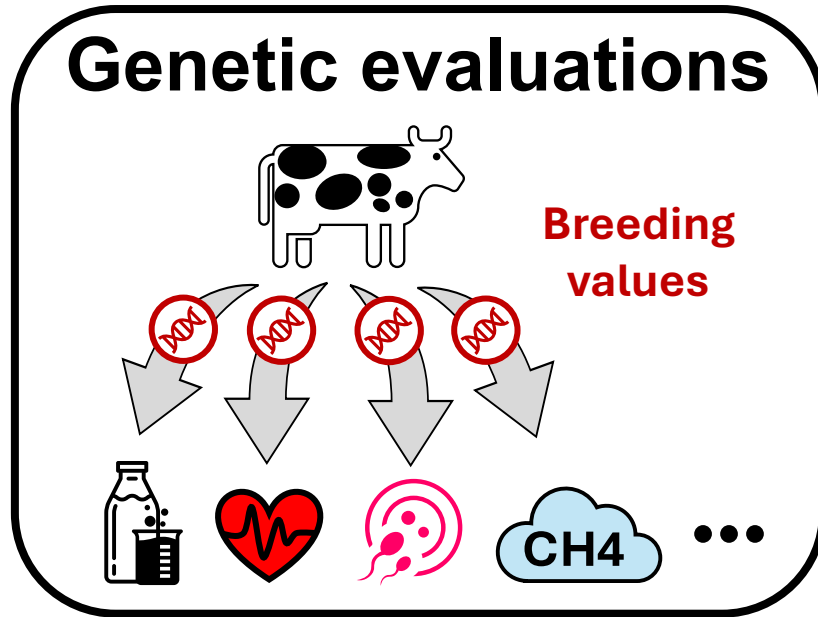
⁷Viking Genetics, Denmark



Introduction

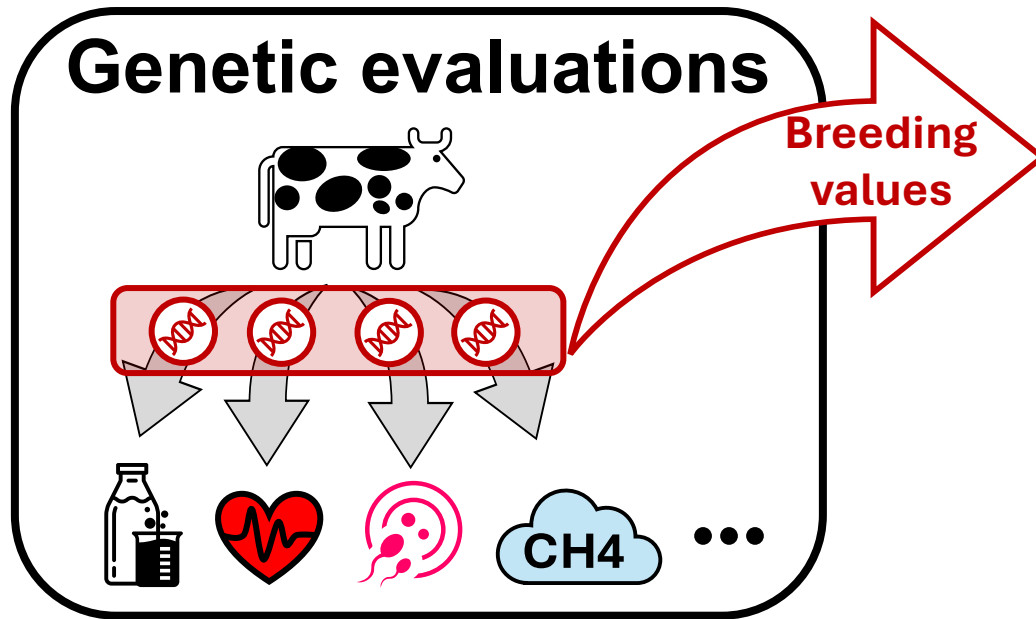
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➤ Breeding program:



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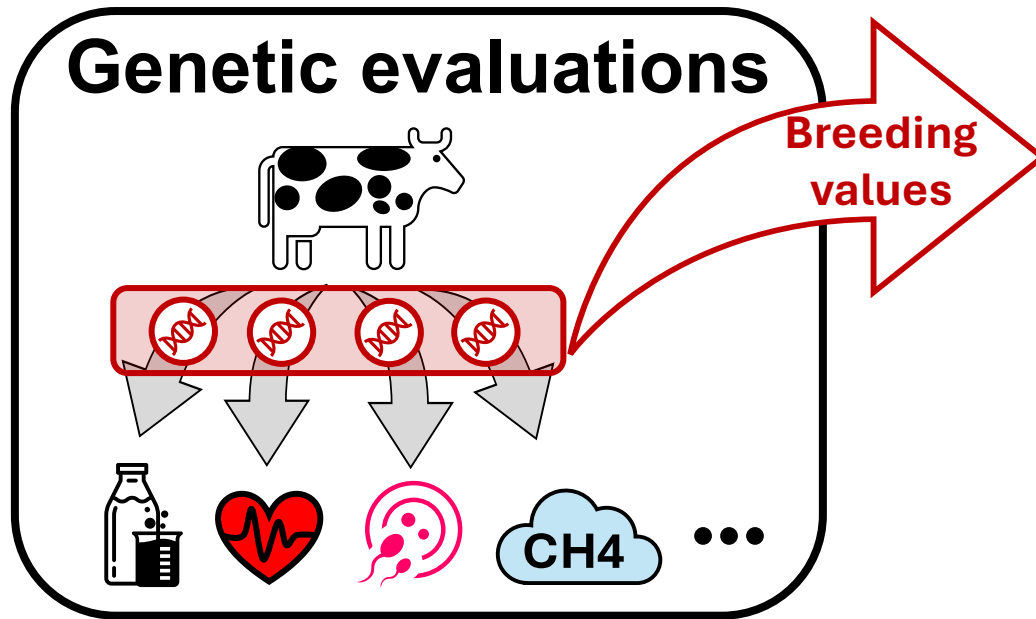


Selection index

$$SI = w_1 g_1 + w_2 g_2 + \dots + w_k g_k$$

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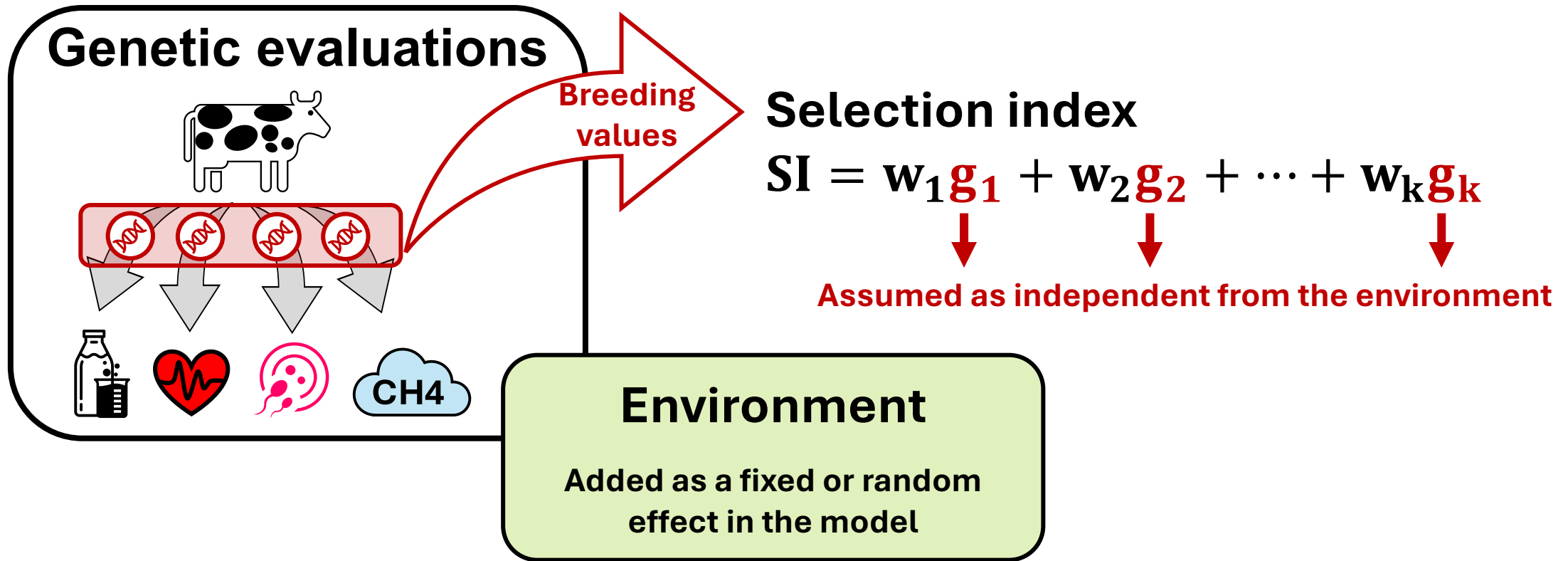
Selection index

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Assumed as independent from the environment

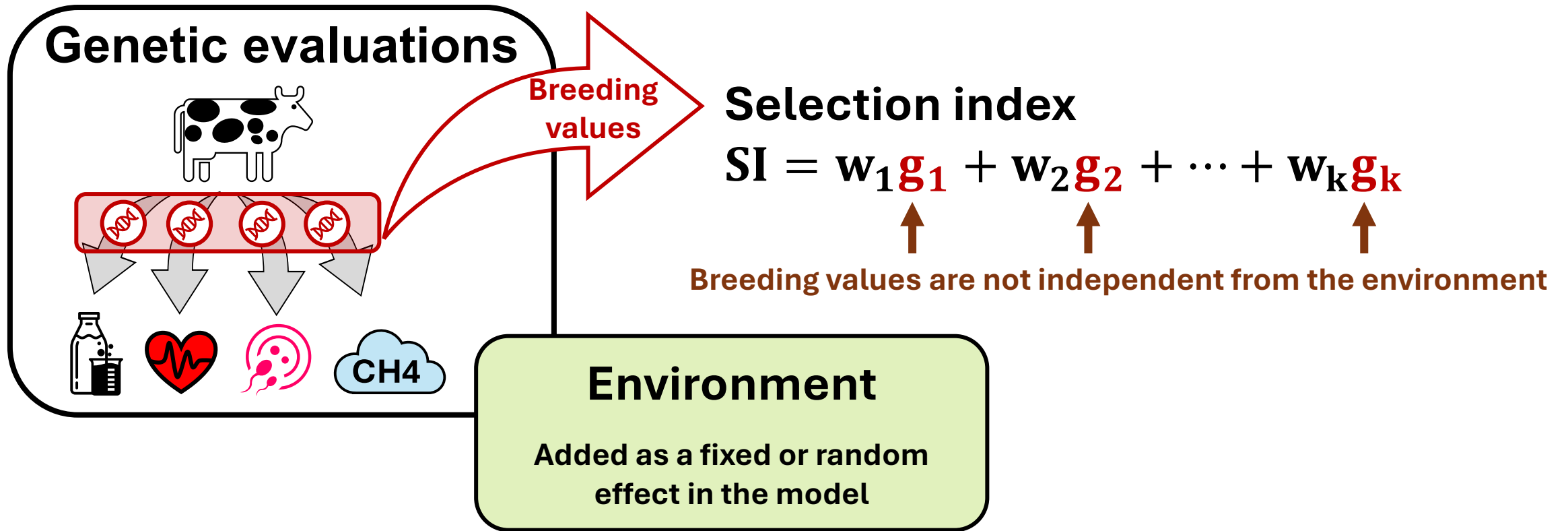
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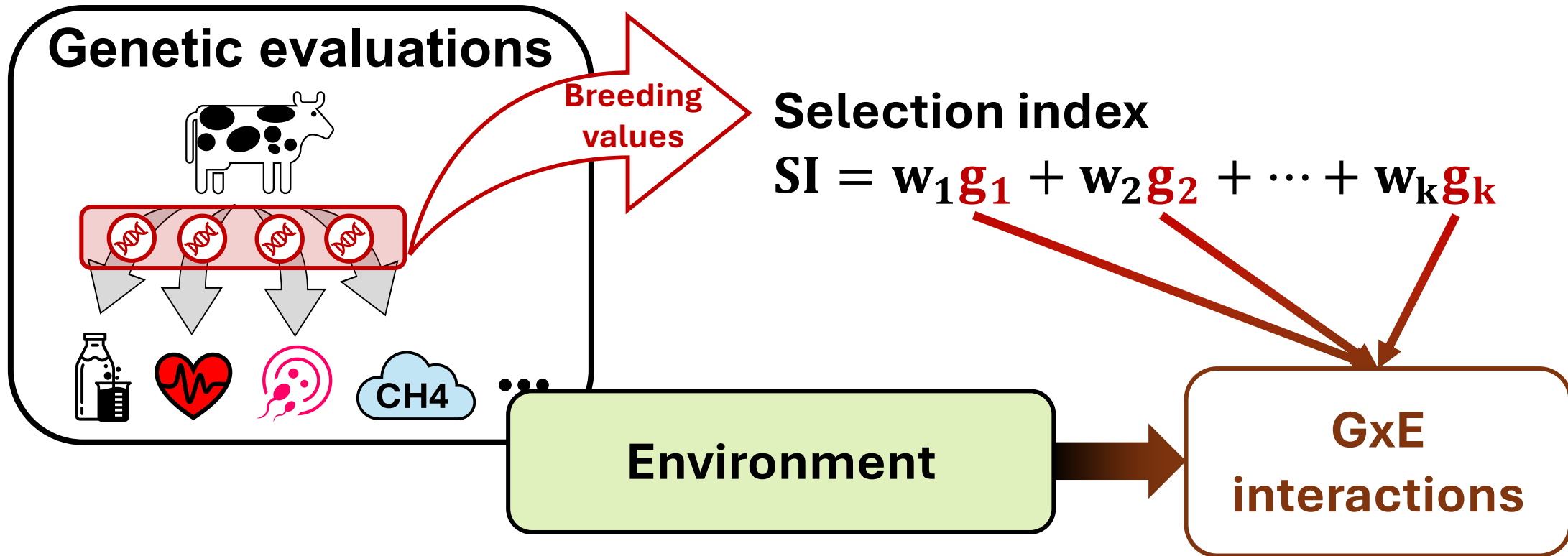
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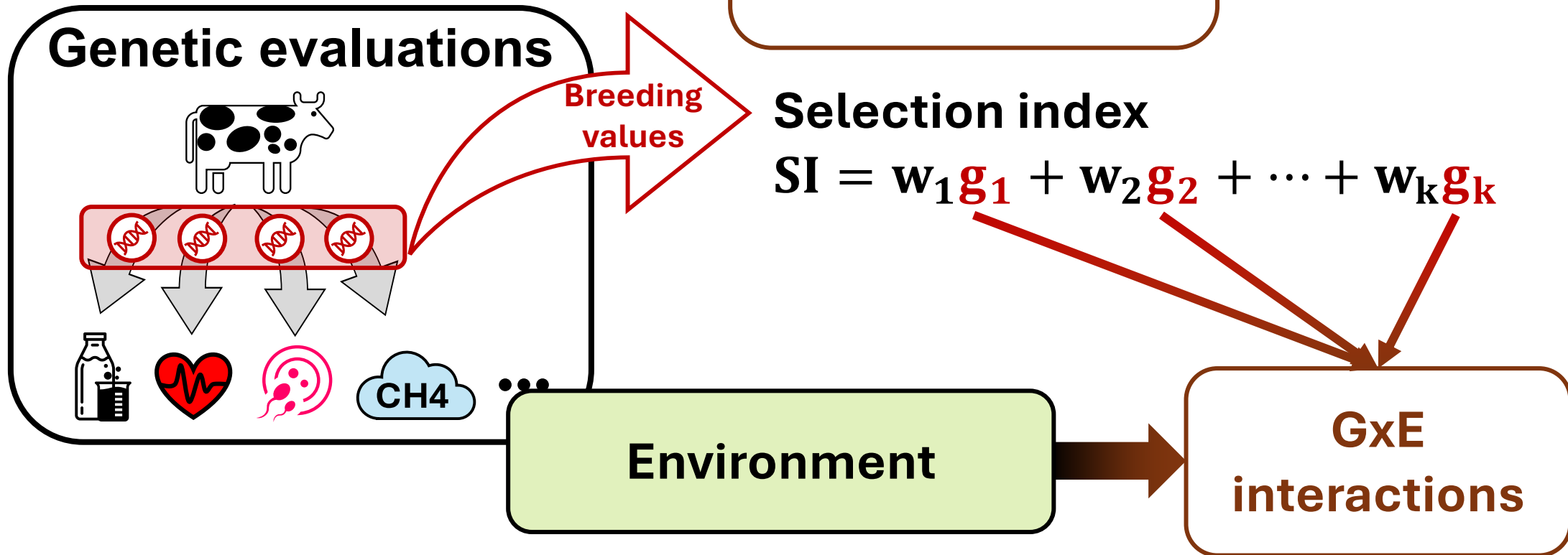
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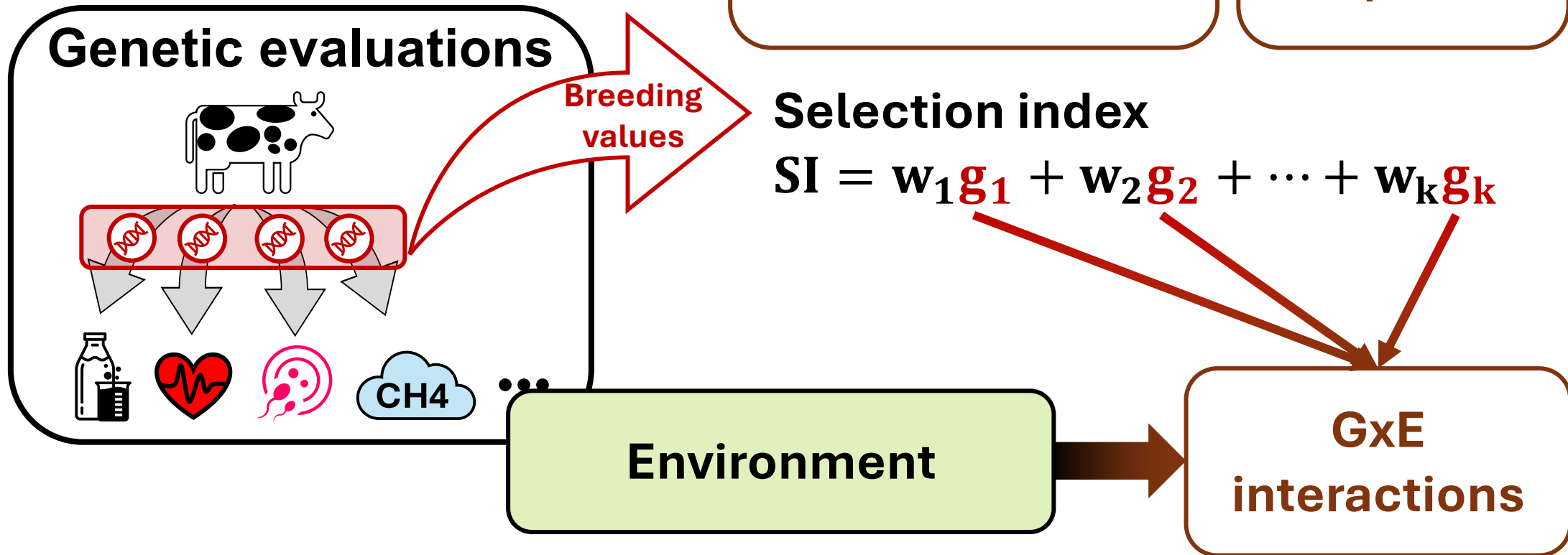
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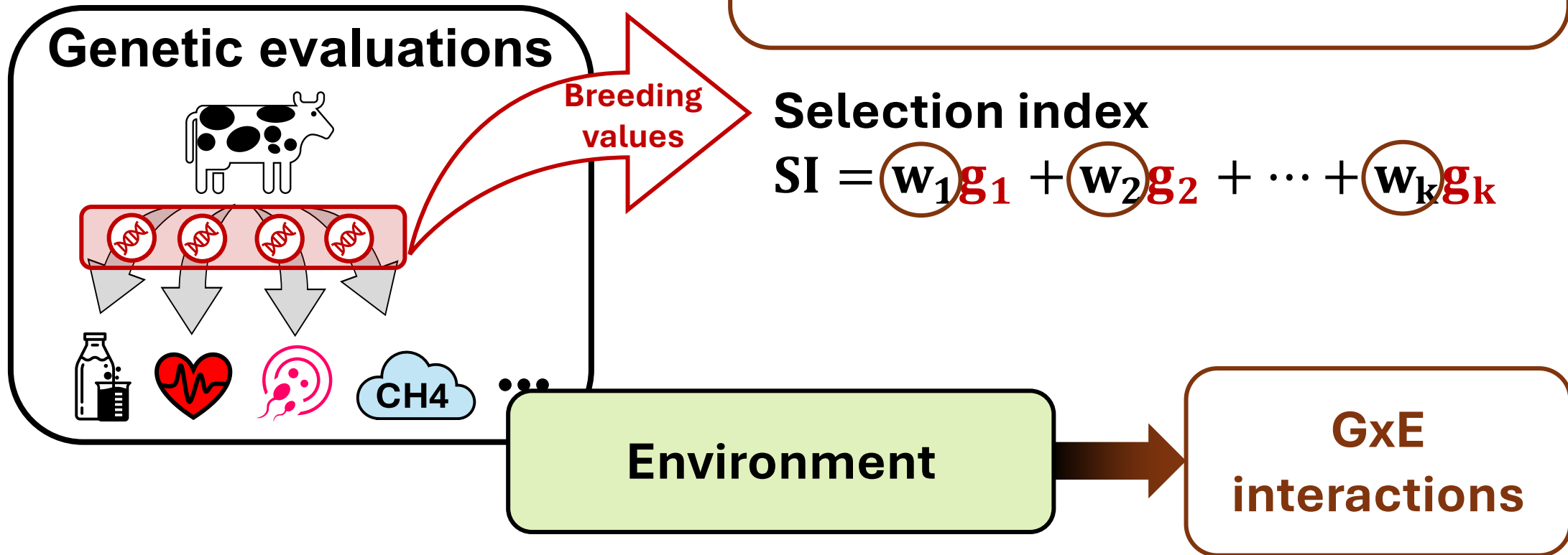
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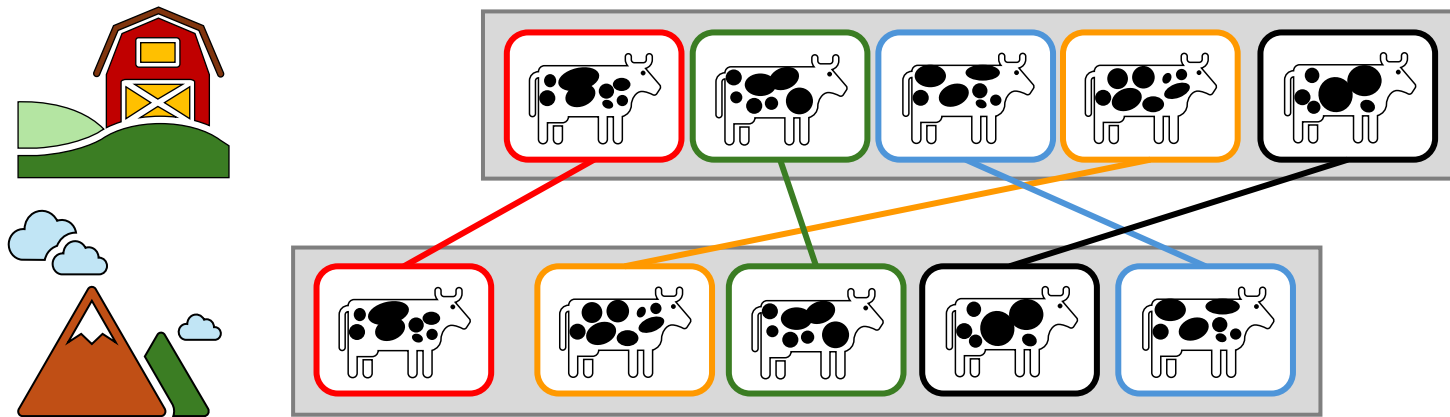
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GxE interactions

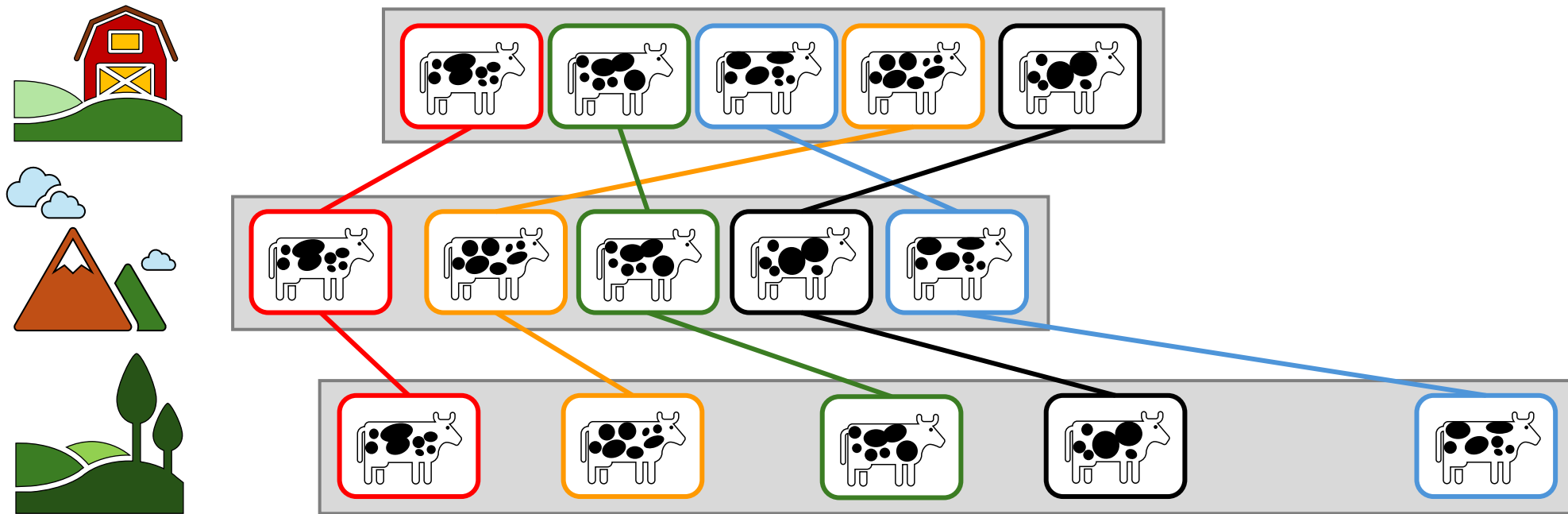
GxE interactions

- Re-ranking of breeding values per environment



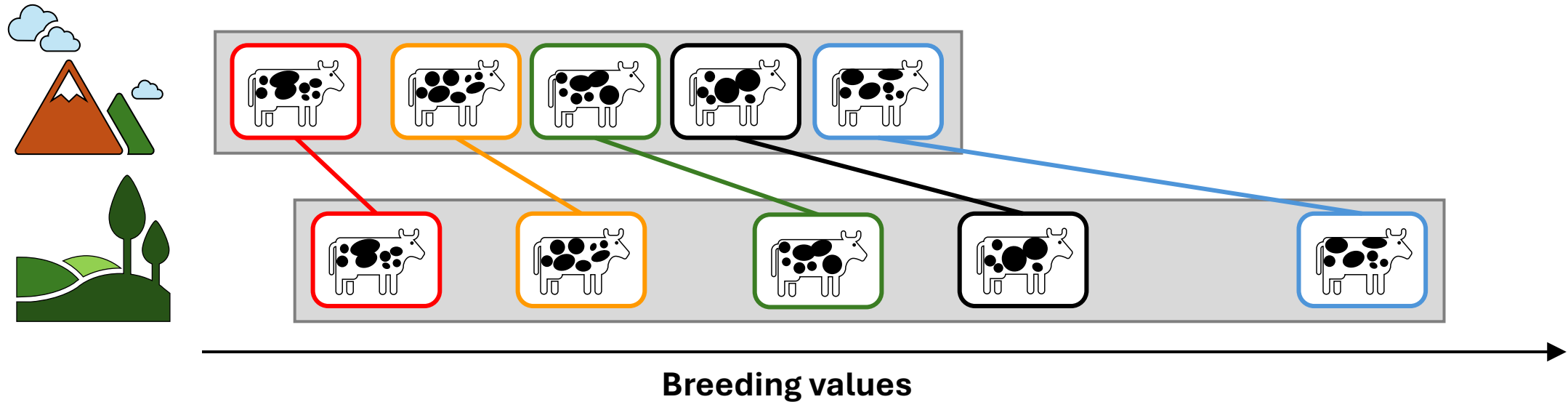
GxE interactions

- Re-ranking of breeding values per environment
- Differences of variance components per environment



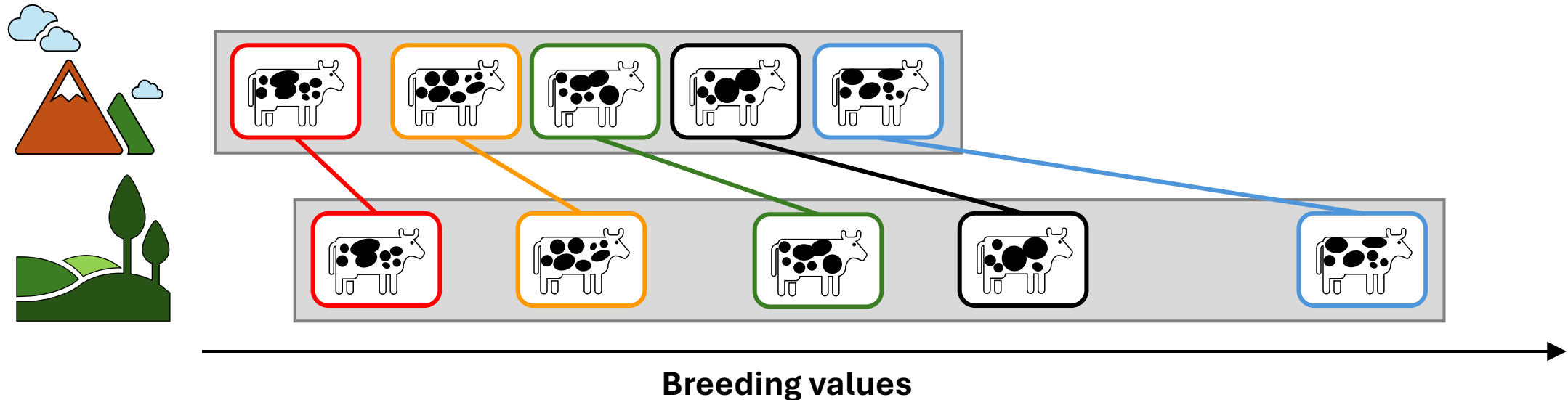
GxE interactions

➤ Consequences of GxE for individual traits



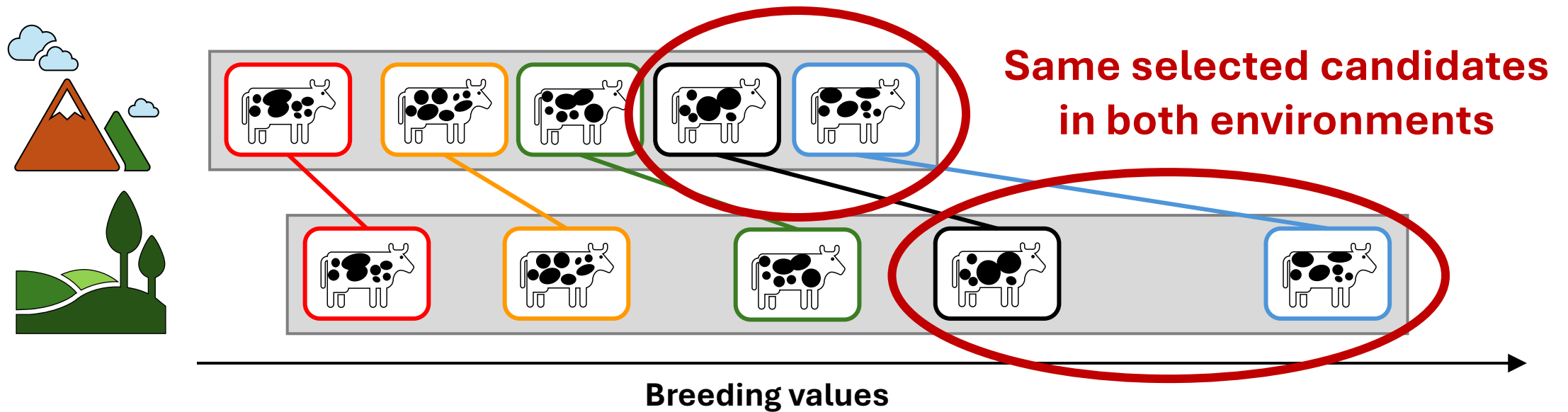
GxE interactions

- Consequences of GxE for individual traits
 - Often, none or very little re-ranking of breeding values is observed



GxE interactions

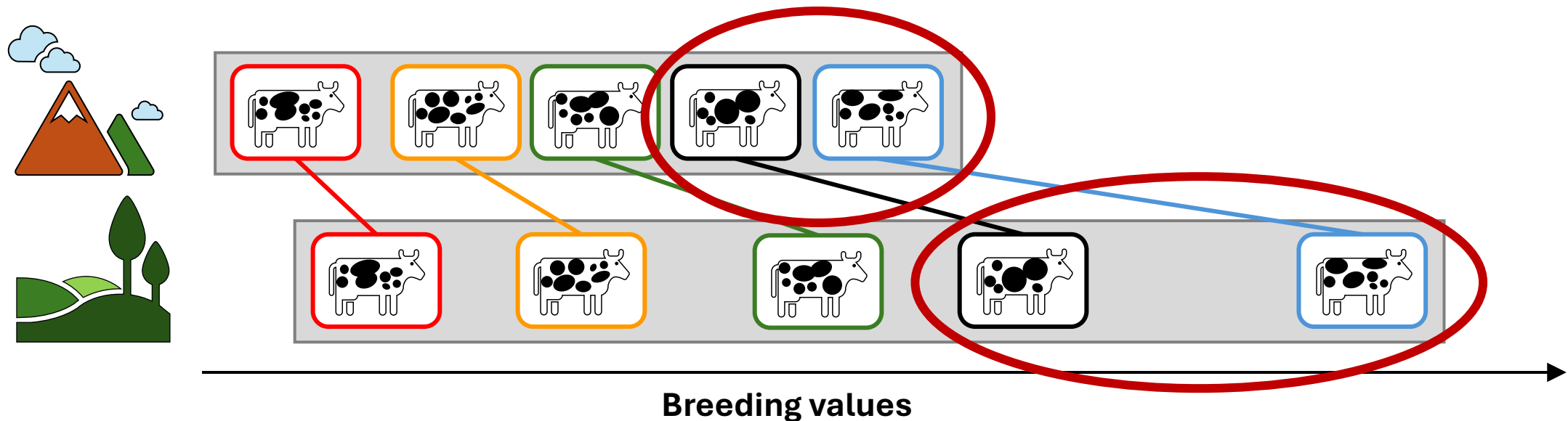
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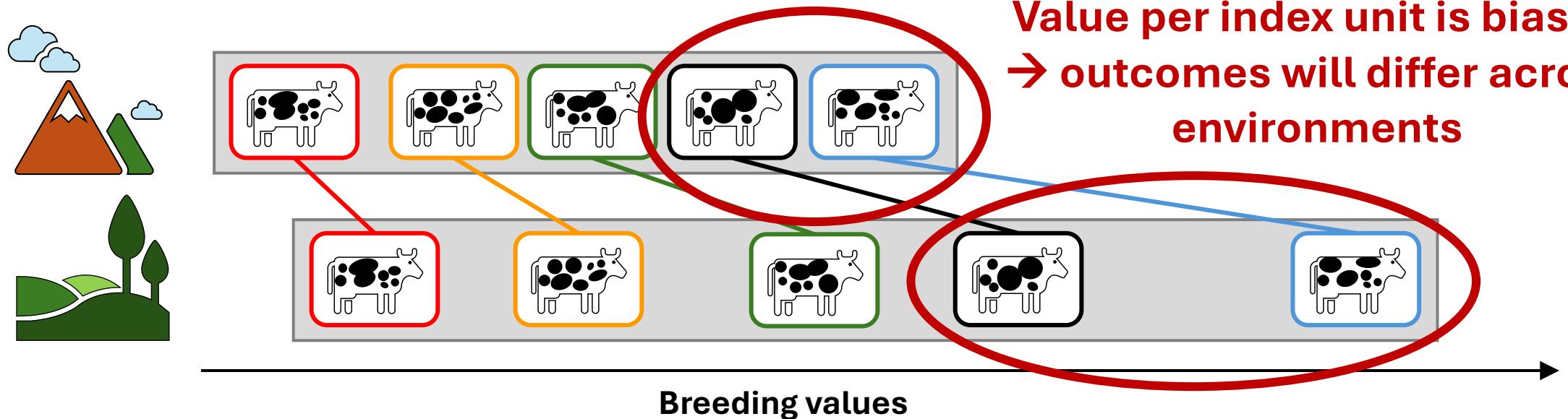


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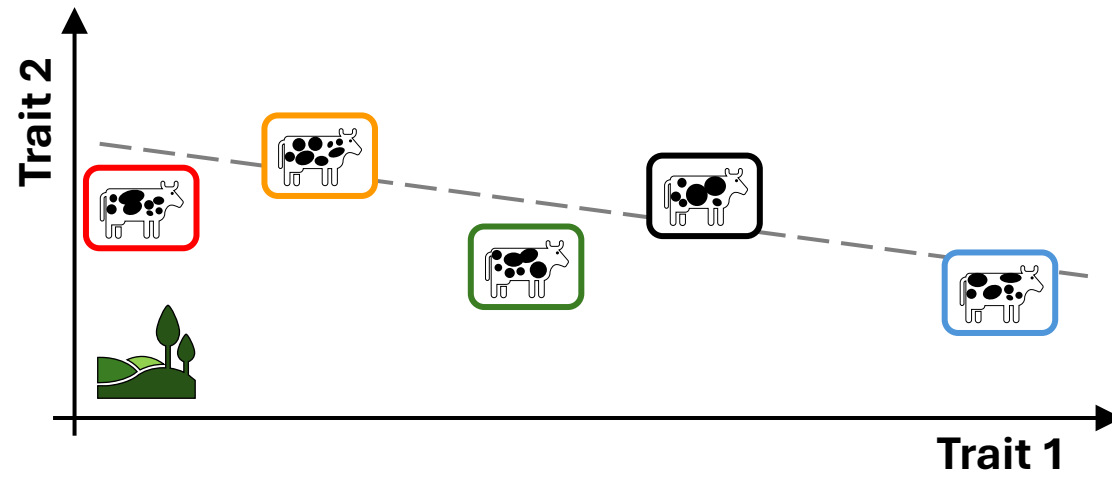
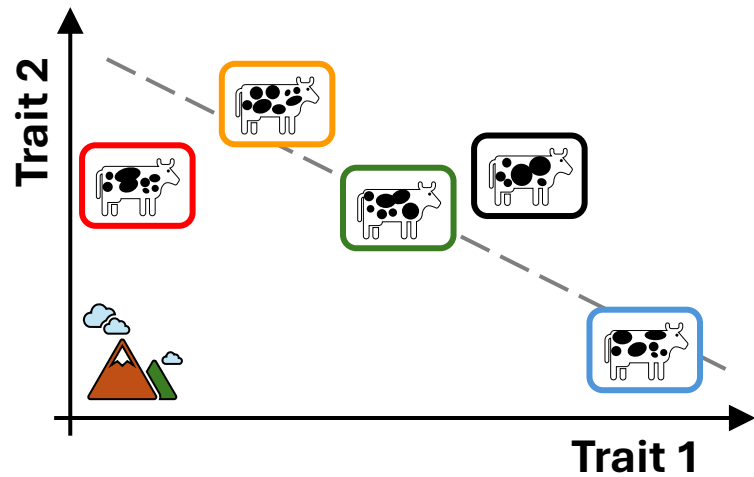
BUT...

**Value per index unit is biased
→ outcomes will differ across environments**



GxE interactions

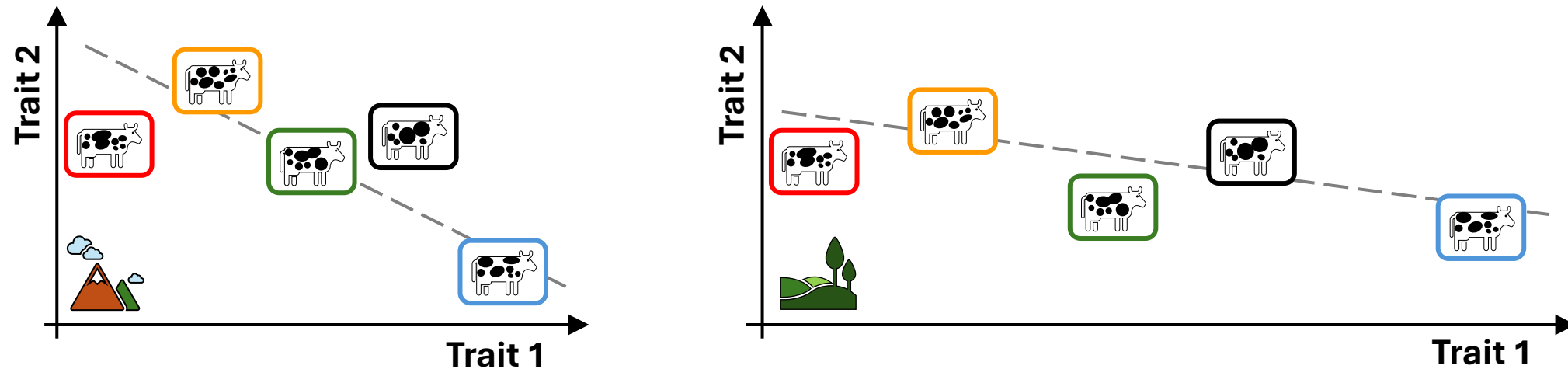
- Consequences of GxE for multiple traits altogether



GxE interactions

➤ Consequences of GxE for multiple traits altogether

- Changes in genetic variances and correlations will have a direct impact on the weights of the selection index ($SI = w_1g_1 + w_2g_2 + \dots + w_kg_k$)



GxE interactions

➤ Consequences of GxE for multiple traits altogether

- Changes in genetic variances and correlations will have a direct impact on the weights of the selection index ($SI = w_1g_1 + w_2g_2 + \dots + w_kg_k$)
- Selection index is more likely to present re-ranking of selection candidates



GxE interactions

➤ Consequences of GxE for multiple traits altogether

- Changes in genetic variances and correlations will have a direct impact on the weights of the selection index ($SI = w_1g_1 + w_2g_2 + \dots + w_kg_k$)
- Selection index is more likely to present re-ranking of selection candidates

Different selected candidates in each environment!



GxE interactions

- Ignoring GxE interactions still ensures average genetic progress
- Environments out the average/optimal → lower response to selection
- **What about the variance components we estimate?**

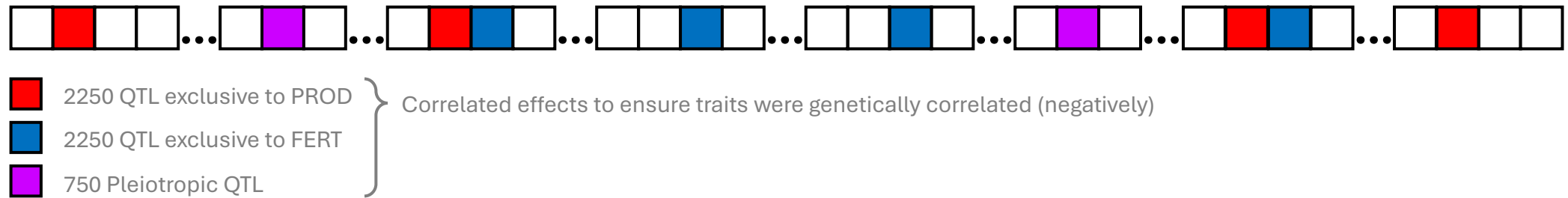
Simulation study

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 - Genomic data (50k SNPs)



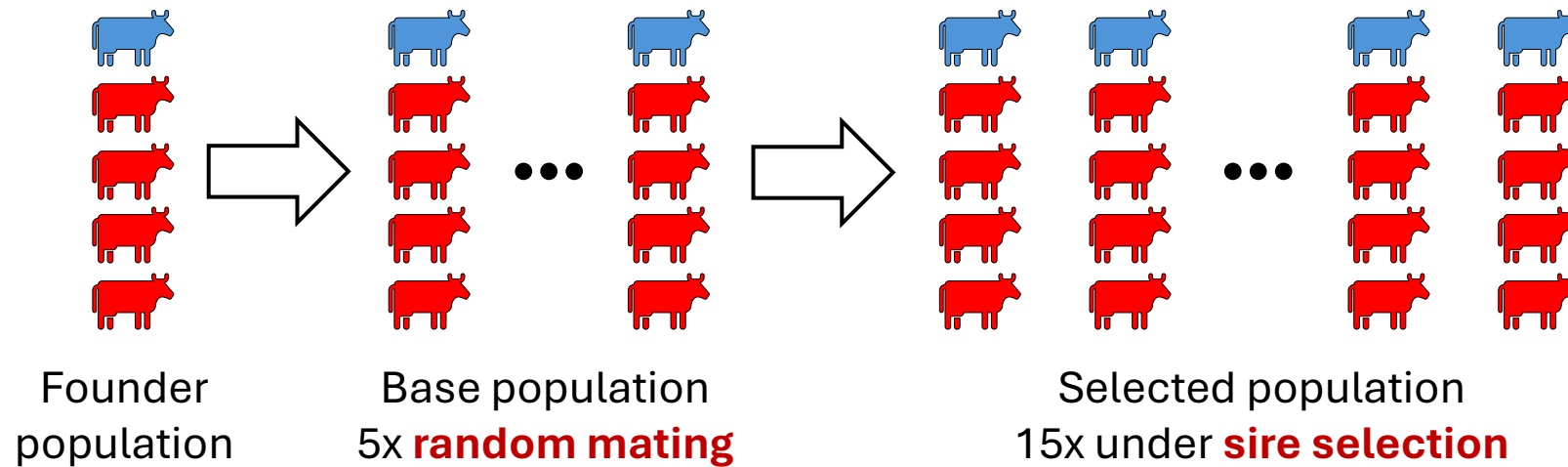
Simulation study

- Two traits representing production (PROD) and fertility (FERT)
 - Genomic data (50k SNPs)
 - Five environments, from **most favorable to most unfavorable** for both traits
 - Phenotypic means gradually decreased
 - Trade-off became stronger

Simulation parameters based on the reported for the French Montbeliarde dairy cattle, associated to temperature-humidity index
Vinet et al. Genet Sel Evol 56, 23 (2024). <https://doi.org/10.1186/s12711-024-00889-4>

Simulation study

- Two traits representing production (PROD) and fertility (FERT)
 - Genomic data (50k SNPs)
 - Five environments, from most favorable to most unfavorable for both traits
 - Founder + 20 generations with 2000 new individuals per generation



Full details of simulation and selection scheme will be found on the Interbull Bulletin

Selection scenarios

Selection scenarios

➤ Traditional selection

➤ Breeding values estimated without accounting for any GxE interactions

➤ $SI_0 = (w/\sigma_{g\text{PROD}})g_{\text{PROD}} + [(1 - w)/\sigma_{g\text{FERT}}]g_{\text{FERT}}$

$w = 0.8$

Selection scenarios

➤ Traditional selection

➤ Breeding values estimated without accounting for any GxE interactions

$$SI_0 = w g_{\text{PROD}} / \sigma_{g_{\text{PROD}}} + (1 - w) g_{\text{FERT}} / \sigma_{g_{\text{FERT}}}$$

$$w = 0.8$$

➤ Environment-customized selection

➤ Breeding values estimated accounting for GxE interactions

$$SI_\gamma = w_\gamma g_{\text{PROD}\gamma} / \sigma_{g_{\text{PROD}\gamma}} + (1 - w_\gamma) g_{\text{FERT}\gamma} / \sigma_{g_{\text{FERT}\gamma}}$$

applied to each environment $\gamma = 1, 2, 3, 4, 5$

Each w_γ were defined to ensure the same ratio of expected genetic progress from SI_0

$$q = \frac{[w + (1-w) \times \rho \sigma_{g_{\text{PROD}}}]}{[(1-w) + w \times \rho \sigma_{g_{\text{FERT}}}]} \approx 0.23$$

$$w_1 \approx 0.80$$

$$w_2 \approx 0.76$$

$$w_3 \approx 0.78$$

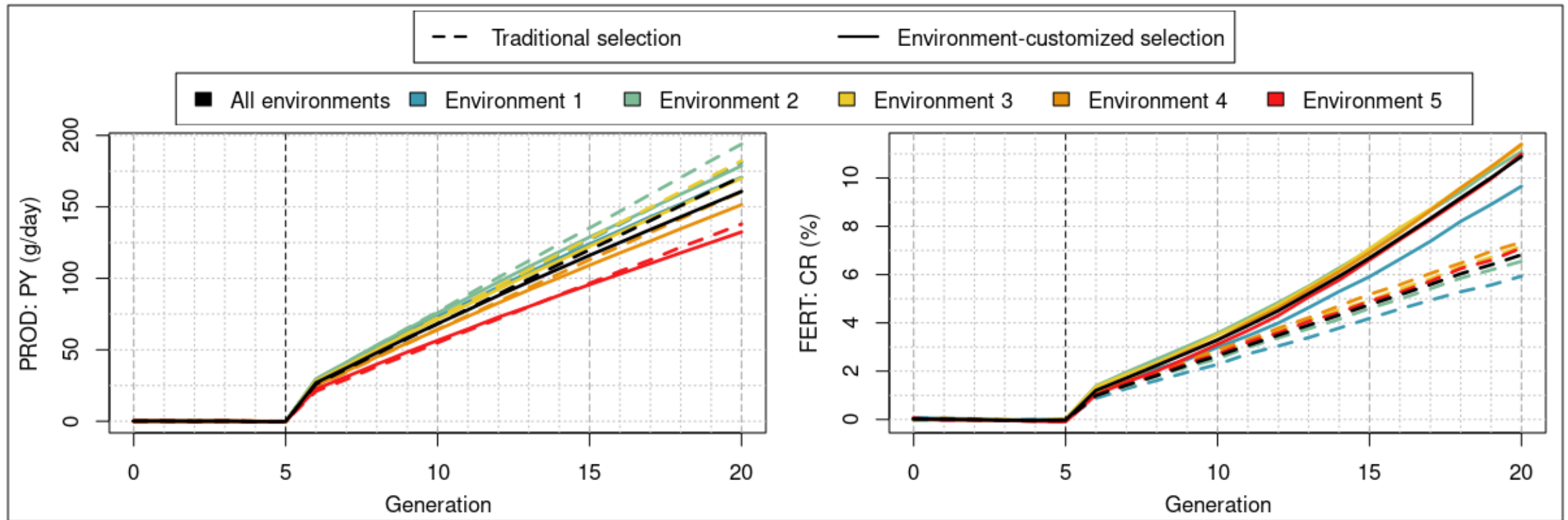
$$w_4 \approx 0.80$$

$$w_5 \approx 0.82$$

Genetic progress

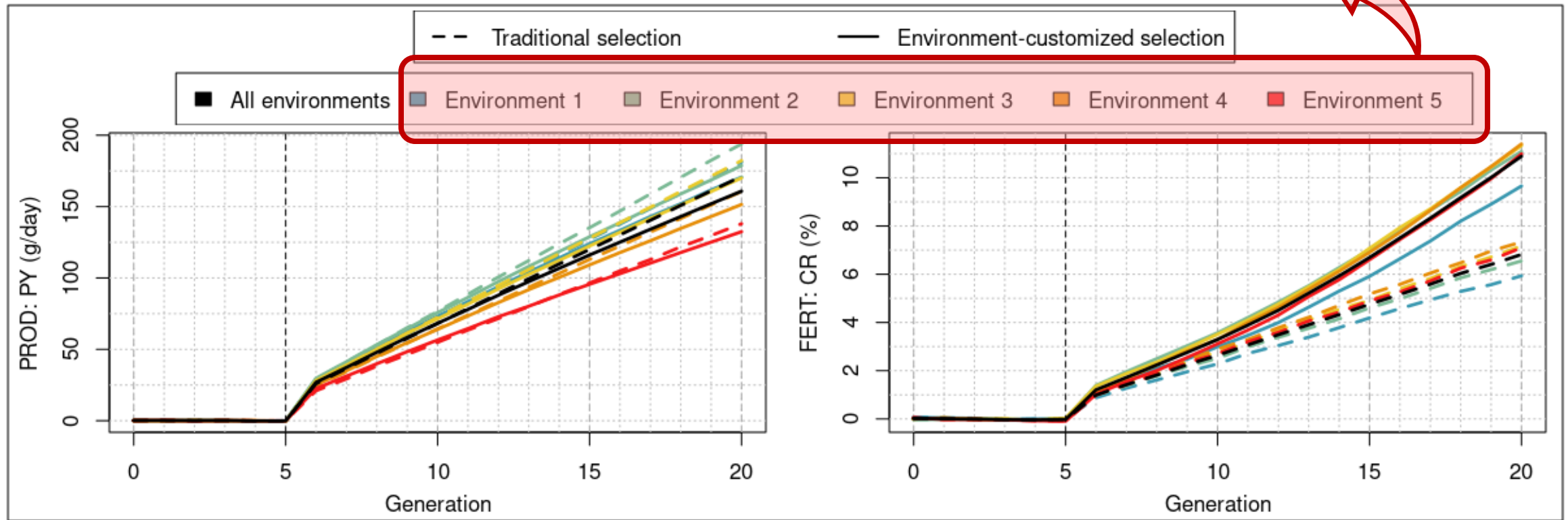
Genetic progress

Results presented are from 100 replicates of each selection scenario



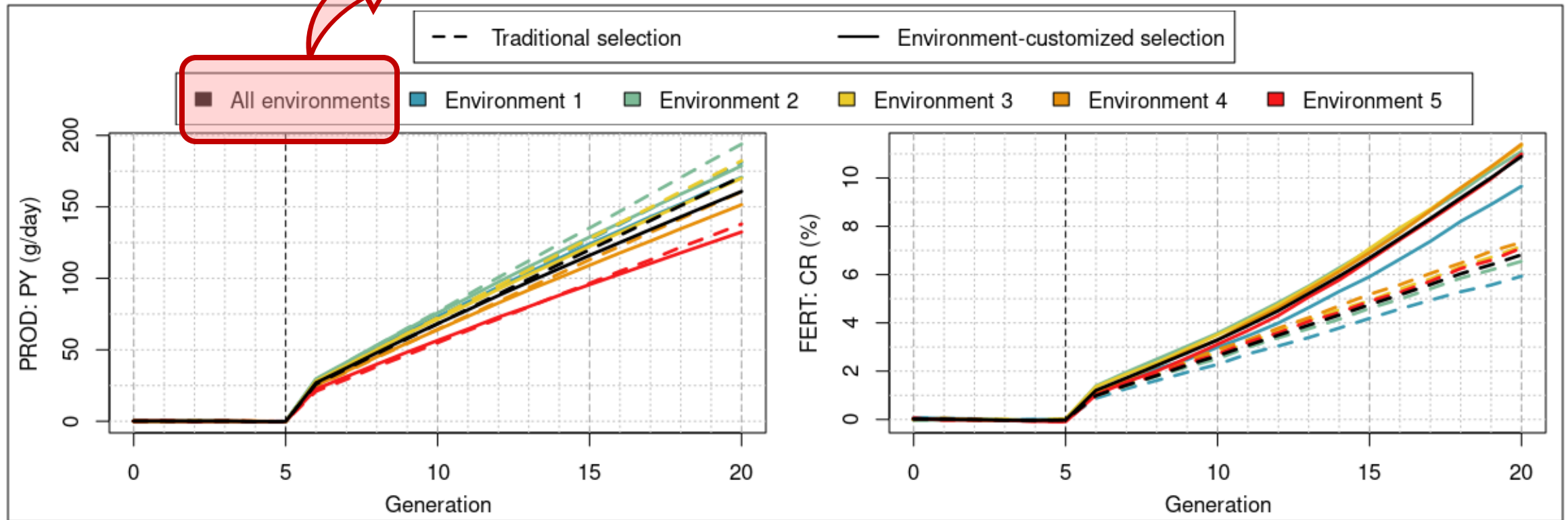
Genetic progress

True genetic progress observed per environment

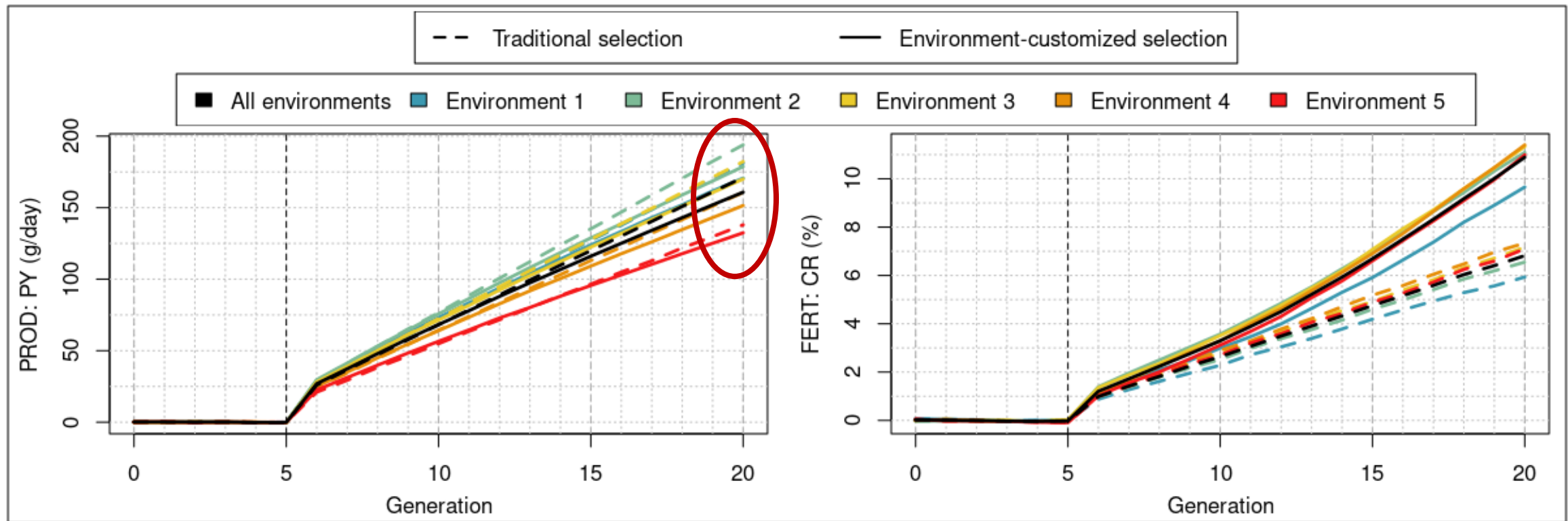


Genetic progress

Genetic progress from evaluation over all generations, disregarding GxE

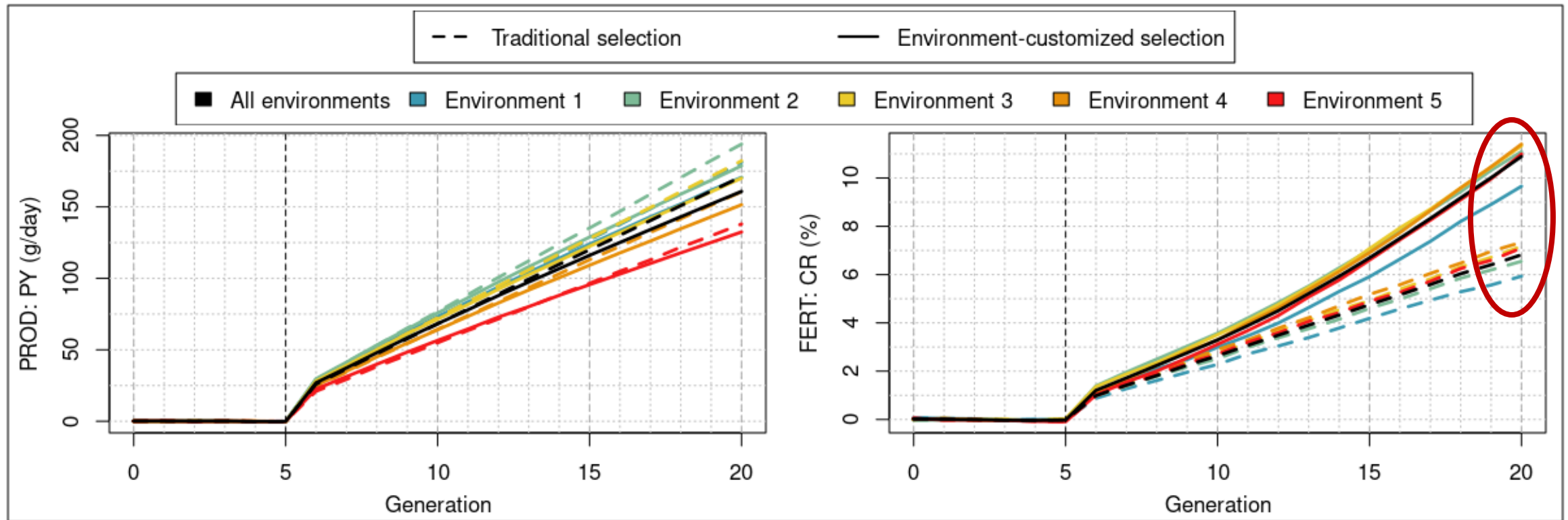


Genetic progress



No significant differences between selection scenarios for PROD

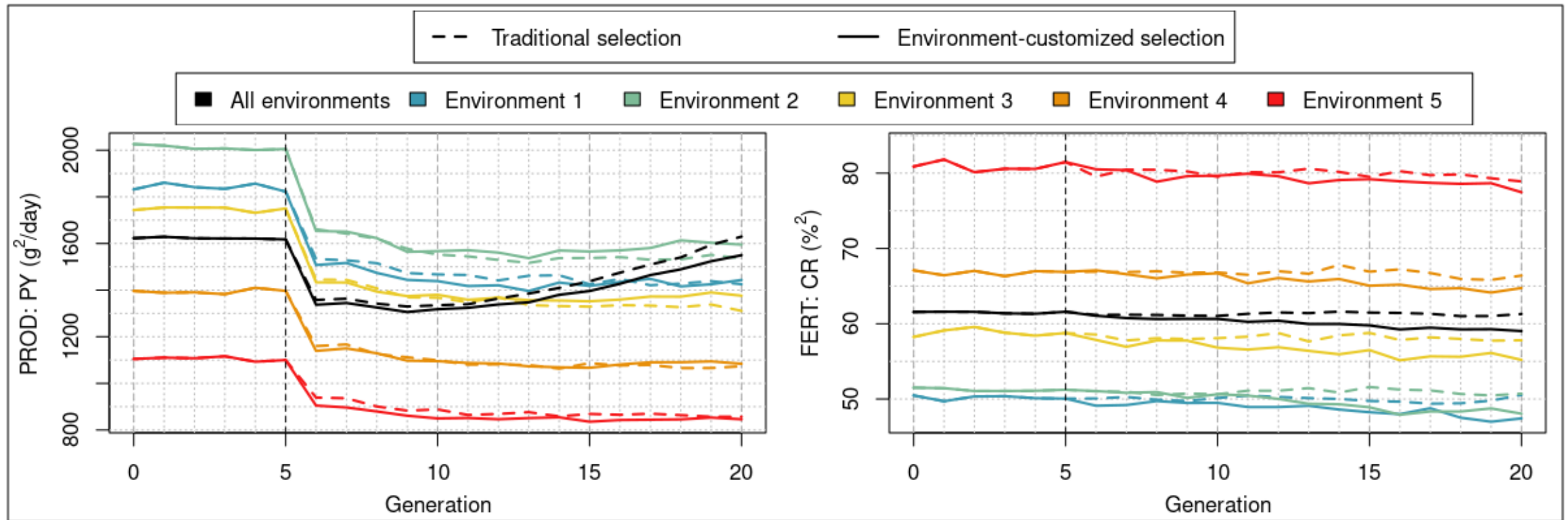
Genetic progress



Great benefit of environment-customized selection for FERT !

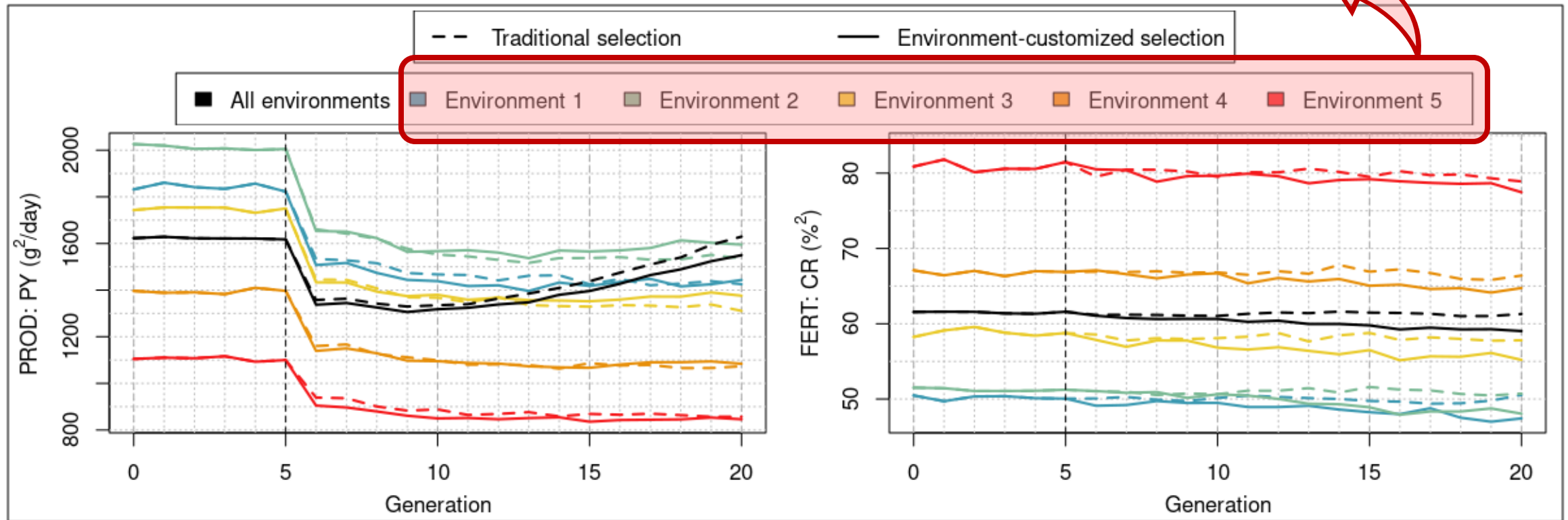
Variance Components

Genetic variances



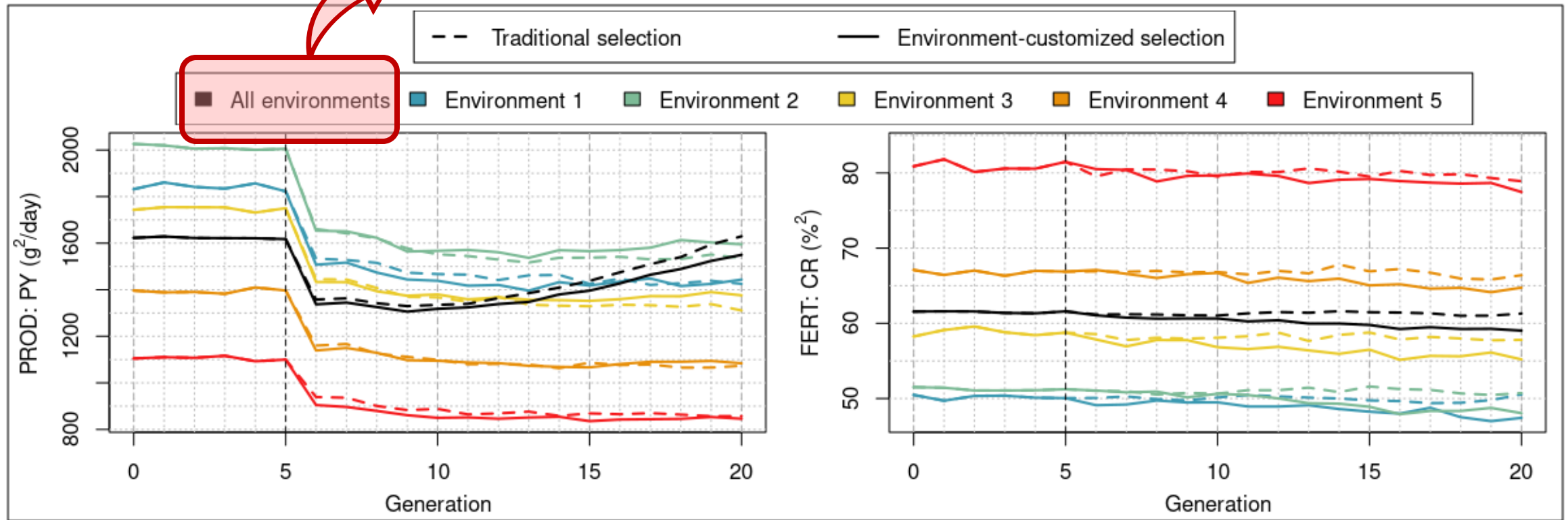
Genetic variances

True genetic variances observed per environment

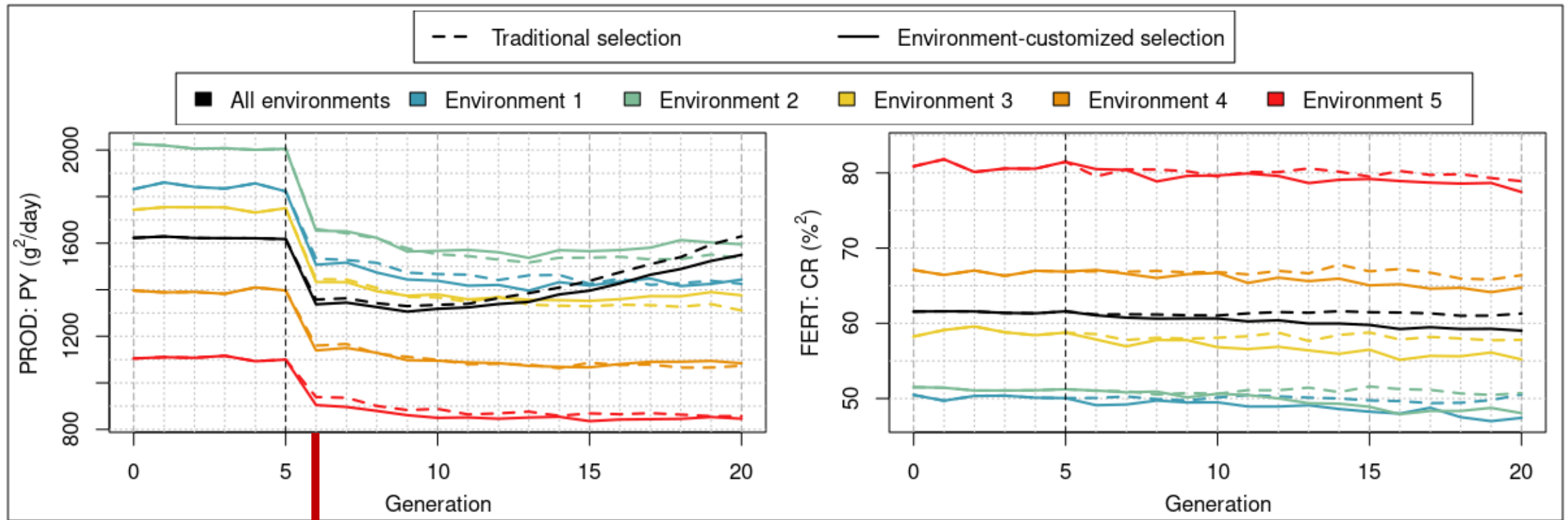


Genetic variances

Genetic variances estimated with data up to each generation, disregarding GxE

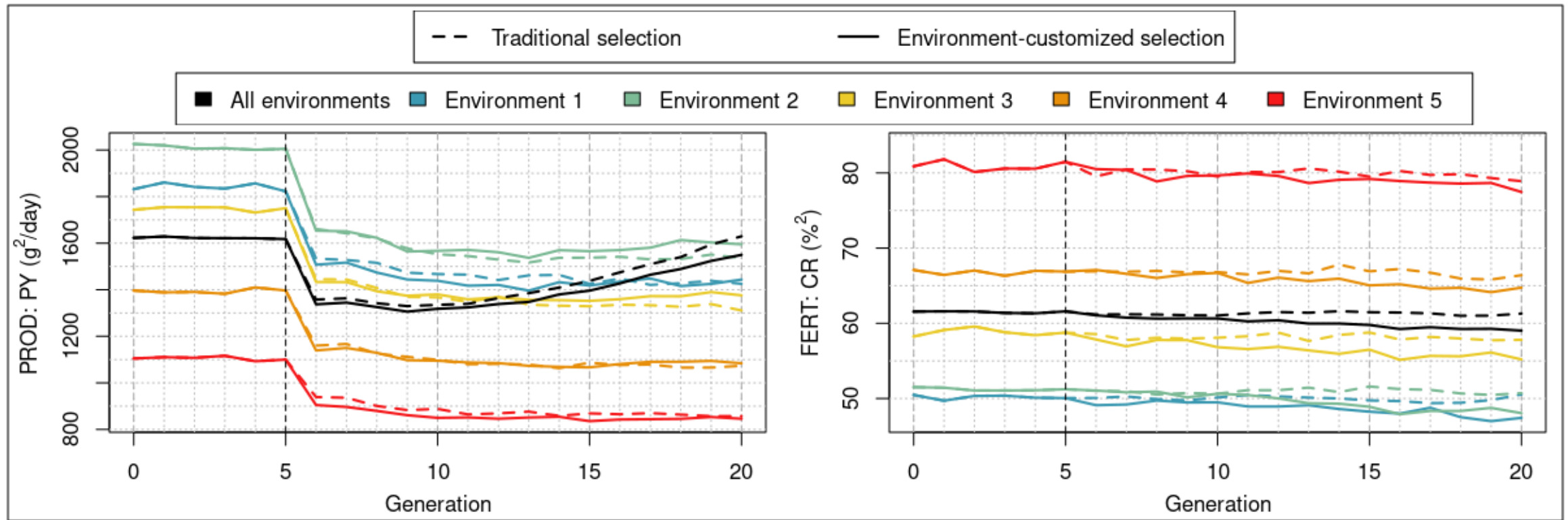


Genetic variances



First generation under selection

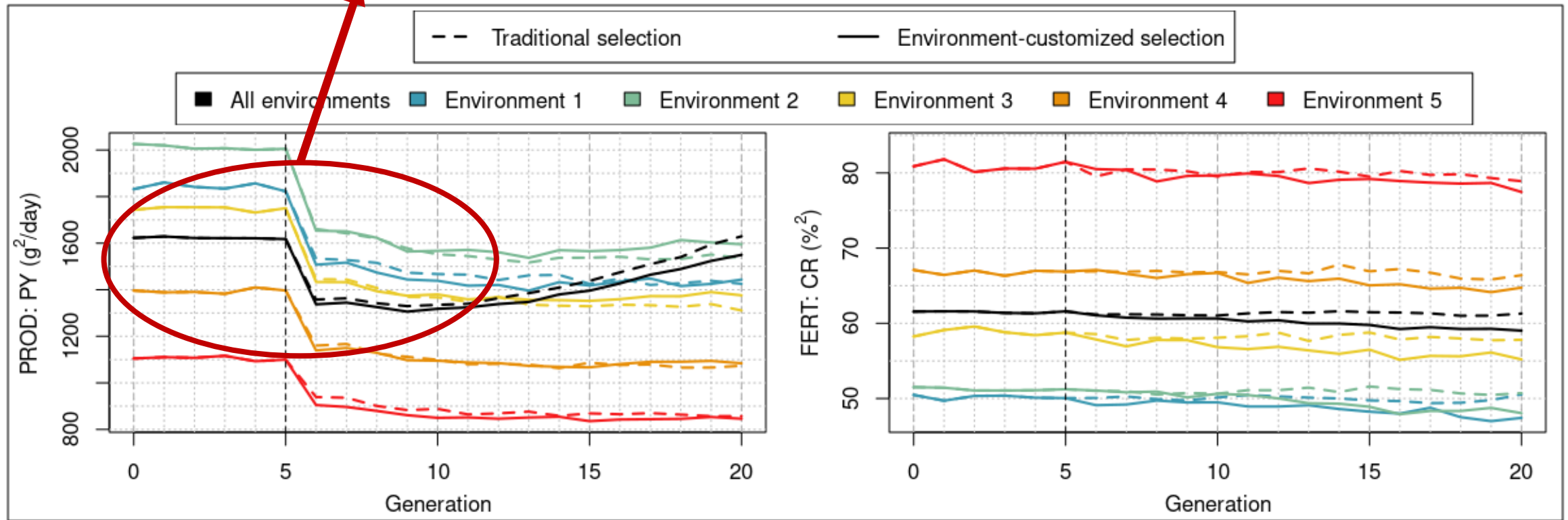
Genetic variances



No big difference of true σ_{g1}^2 between selection scenarios

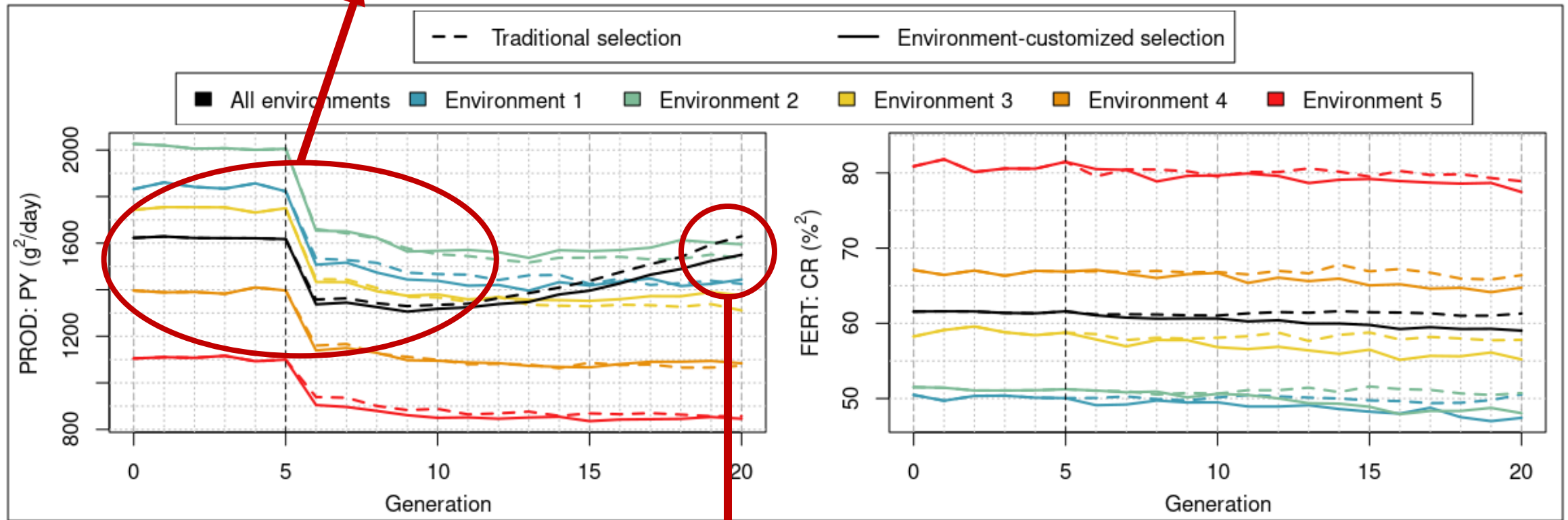
Genetic variances

$\sigma^2_{g_{PROD}} \approx$ average of environments



Genetic variances

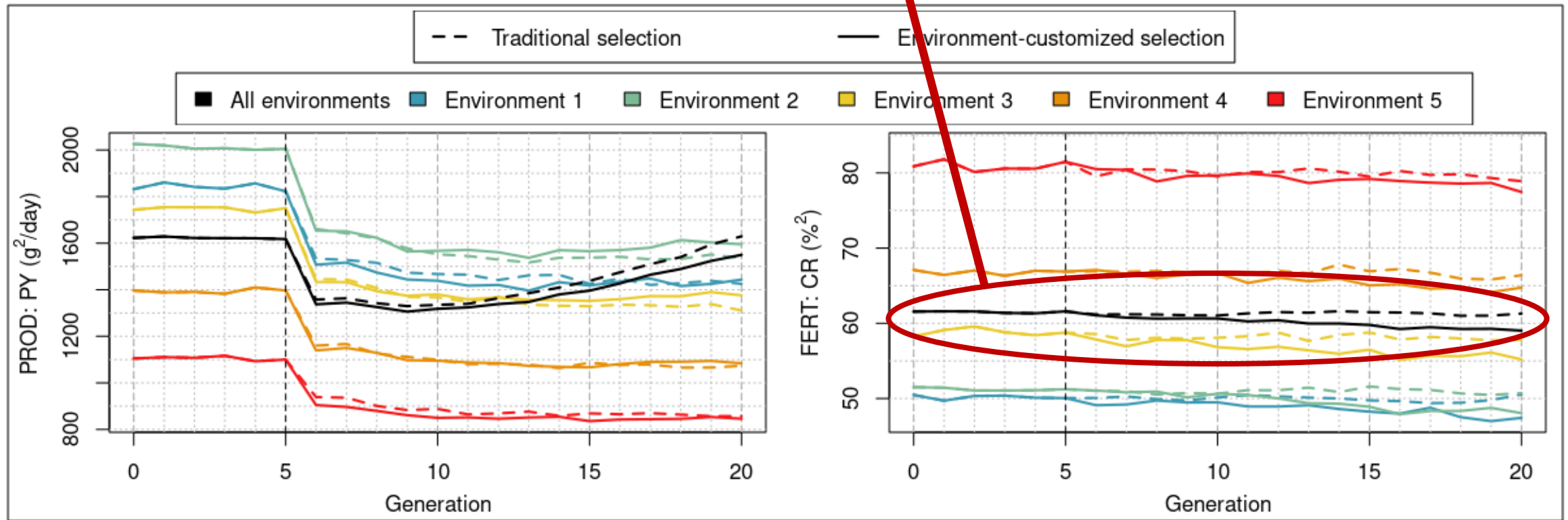
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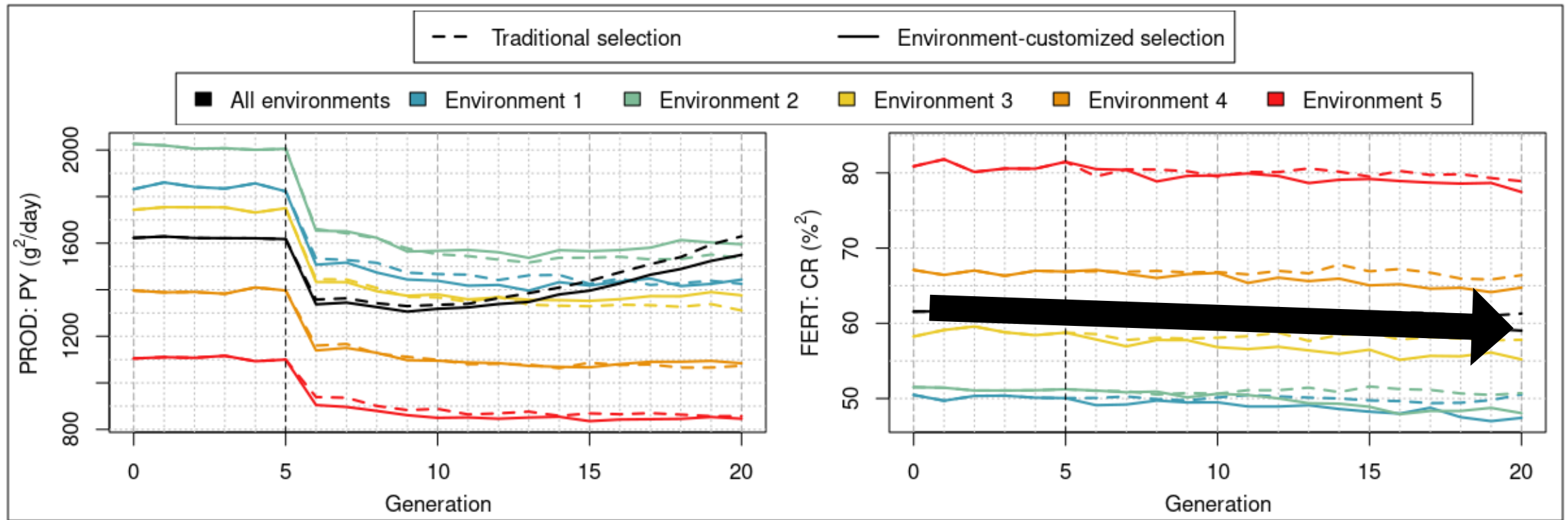
$\sigma_{g_{PROD}}^2$ approaches values of most favorable environments

Genetic variances

$\sigma_{gFERT}^2 \approx$ average of environments
(low h^2 and weight of selection)

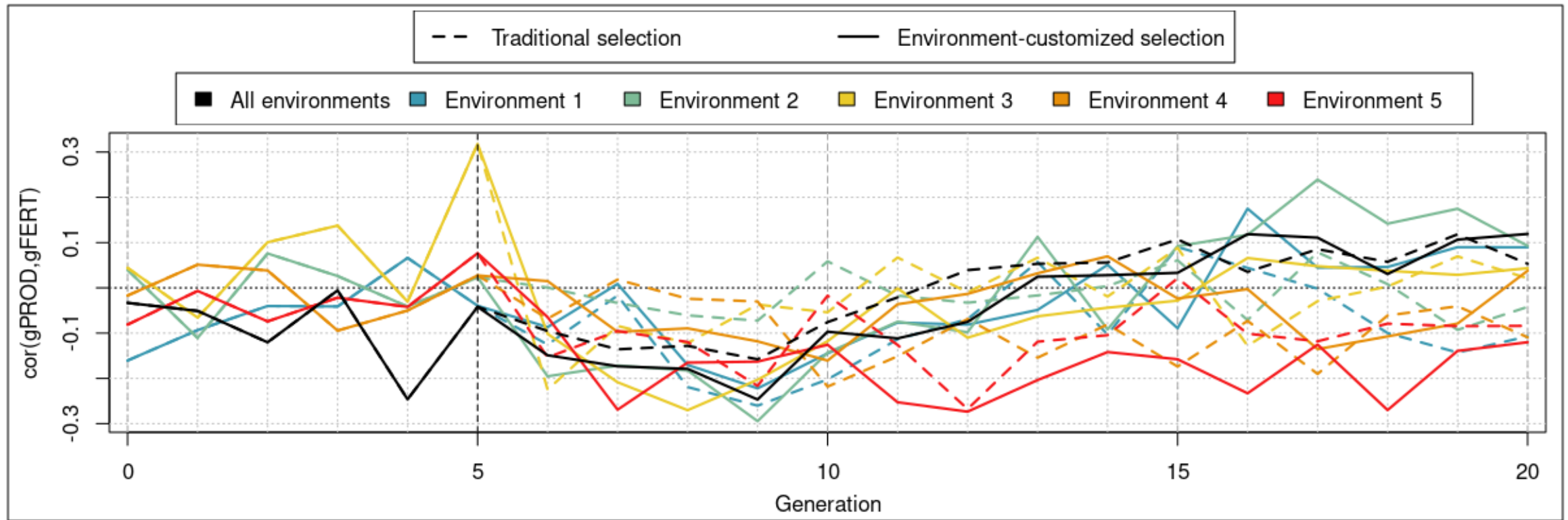


Genetic variances



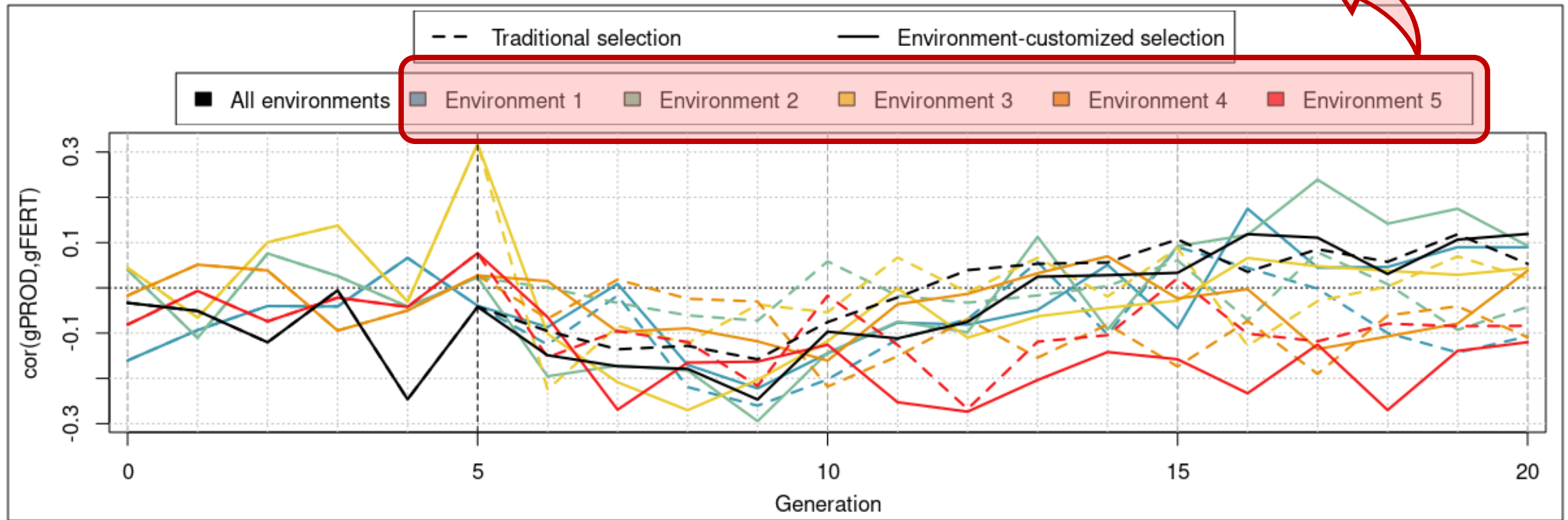
**Slow tendency to approach σ_{GFERT}^2
of most favorable environments?**

Genetic correlations



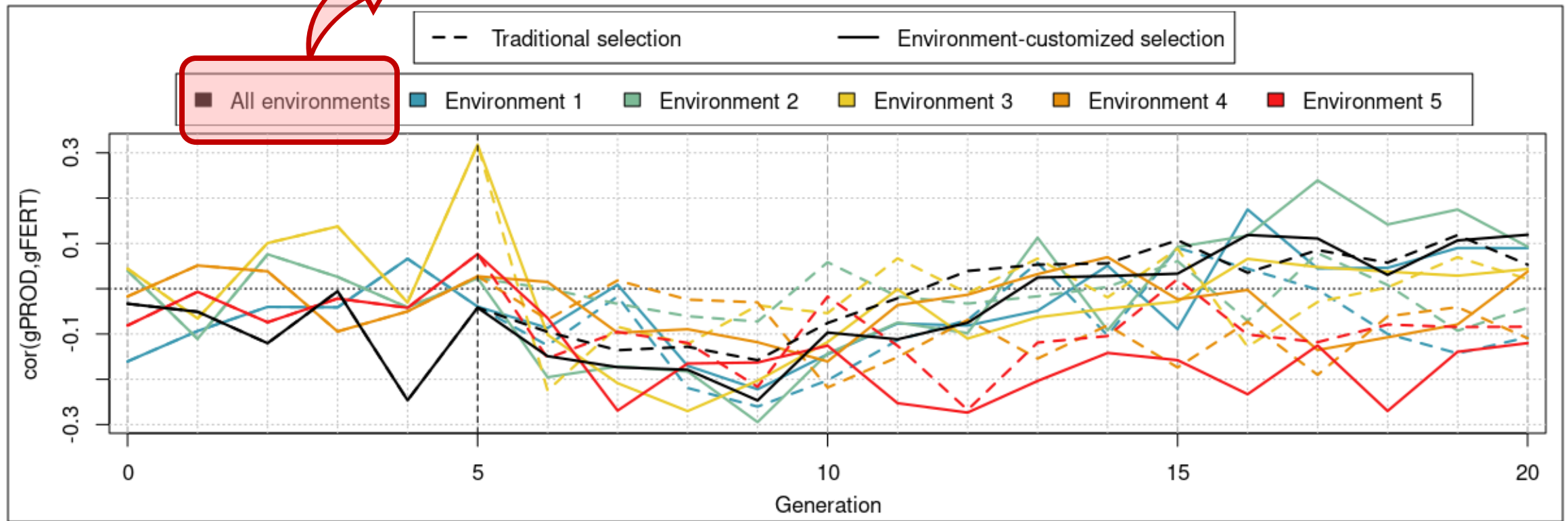
Genetic correlations

True genetic correlations observed per environment



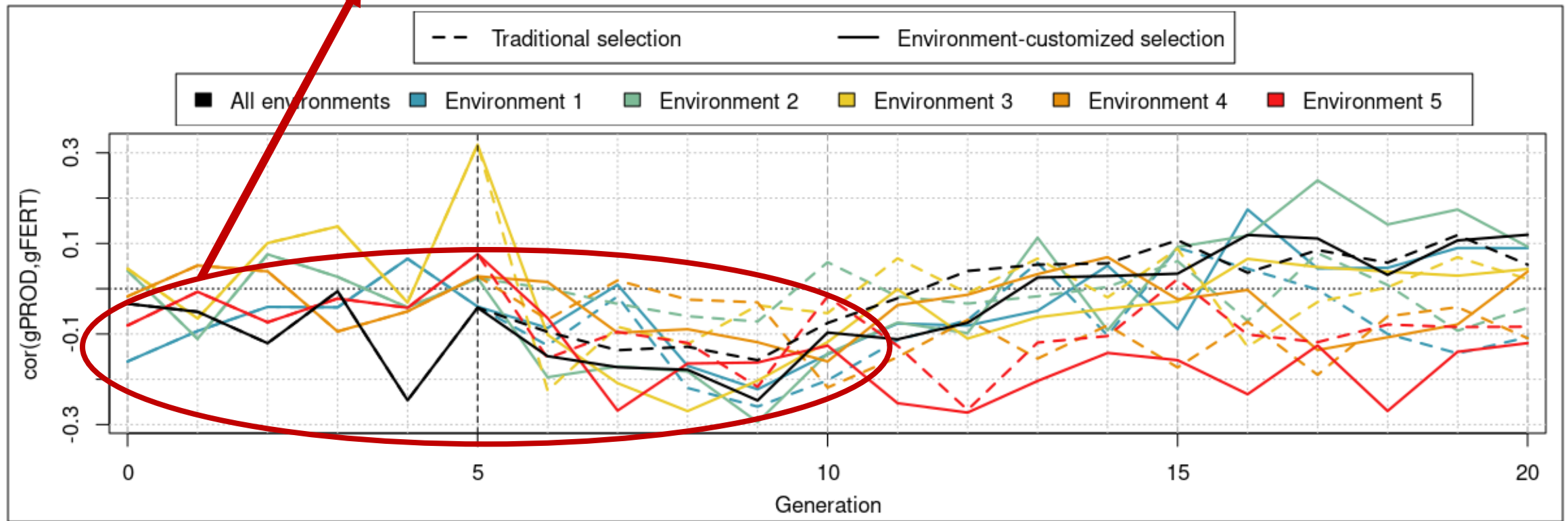
Genetic correlations

Genetic correlations estimated with data up to each generation, disregarding GxE



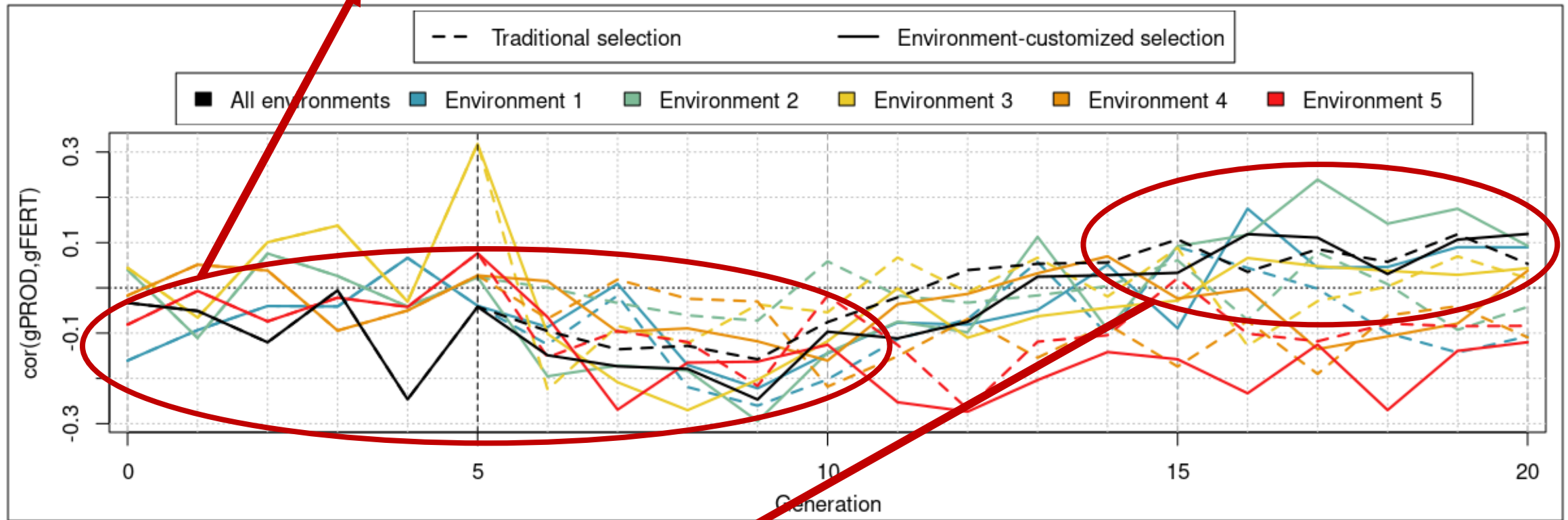
Genetic correlations

$\rho_{\text{PROD,FERT}} \approx \text{average of environments}$



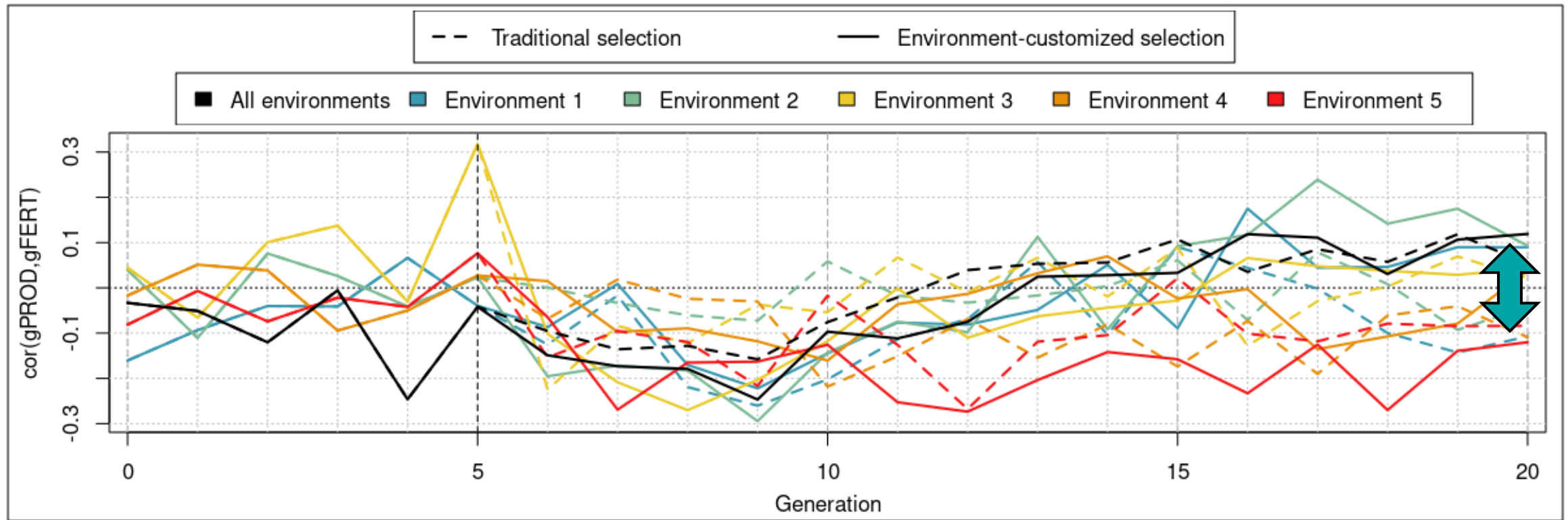
Genetic correlations

$\rho_{\text{PROD,FERT}} \approx \text{average of environments}$



$\rho_{\text{PROD,FERT}}$ approaches values of most favorable environments under environment-customized selection

Genetic correlations



Apparent difference of true ρ between selection scenarios on the most favorable environments

Take home messages

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→ Climate (THI and other indicators)
Farming practices
Barns conditions
Feed
Sanitary environment
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GxE interactions are also perceived (and often mostly) through variance components (σ_g^2 and ρ)

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**Average variance component estimates may not represent correctly the reality in each environment
→ wrong breeding decision**

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**Poster
Silja Beerling**

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**Thank
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