The impact of non-additive effects on the genetic correlation between populations

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Genetic correlation between populations (r_g)

A

B

GxE

GxG

$$r_g \equiv \frac{cov(\alpha_A, \alpha_B)}{\sigma_{\alpha_A} \sigma_{\alpha_B}}$$

r_g
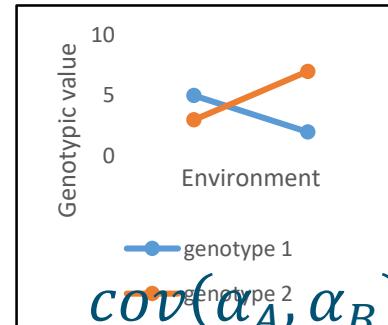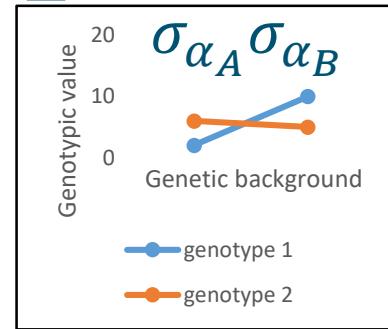
Example of GxG - Epistasis

	AA	**Aa**	**aa**
BB	2.4	1.2	0
Bb	1.2	1.2	1.2
bb	0	1.2	2.4

Average effect (α) of locus A, depends on p of B

How do *dominance* and *epistasis* affect the genetic correlation between populations (r_g)?

- Type of non-additive effects

- Size of non-additive effects

- Divergence between populations

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Objective

Study effect of dominance and epistasis on r_g

- Simulate 2 livestock populations
    - Separated for 50 generations
        - Population A <u>selected</u>
        - Population B <u>drift</u>

- Simulate dominance or epistasis
    - Vary <u>effect size</u> and <u>number of interactions</u>

Genetics of the trait

500 QTL	5 genetic models	3 non-additive effect sizes
Additive effects	■ Dominance	■ Small (realistic)
$a \sim Normal(0,1)$	■ Epistasis (4 models)	■ Intermediate
		■ Large

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Epistatic models

a. Additive x additive (E_{AA})

		genotype locus l		
		YY	Yy	yy
genotype locus k	WW	2	1	0
	Ww	1	1	1
	ww	0	1	2

b. Dominance x dominance (E_{DD})

		genotype locus l		
		YY	Yy	yy
genotype locus k	WW	0	1	0
	Ww	1	1	1
	ww	0	1	0

c. Complementary (E_C)

		genotype locus l		
		YY	Yy	yy
genotype locus k	WW	1	1	0
	Ww	1	1	0
	ww	0	0	0

d. Multiplicative (E_M)

		genotype locus l		
		YY	Yy	yy
genotype locus k	WW	4	2	0
	Ww	2	1	0
	ww	0	0	0

Each locus involved in 5 interactions

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Results

# Impact of genetic model and effect size

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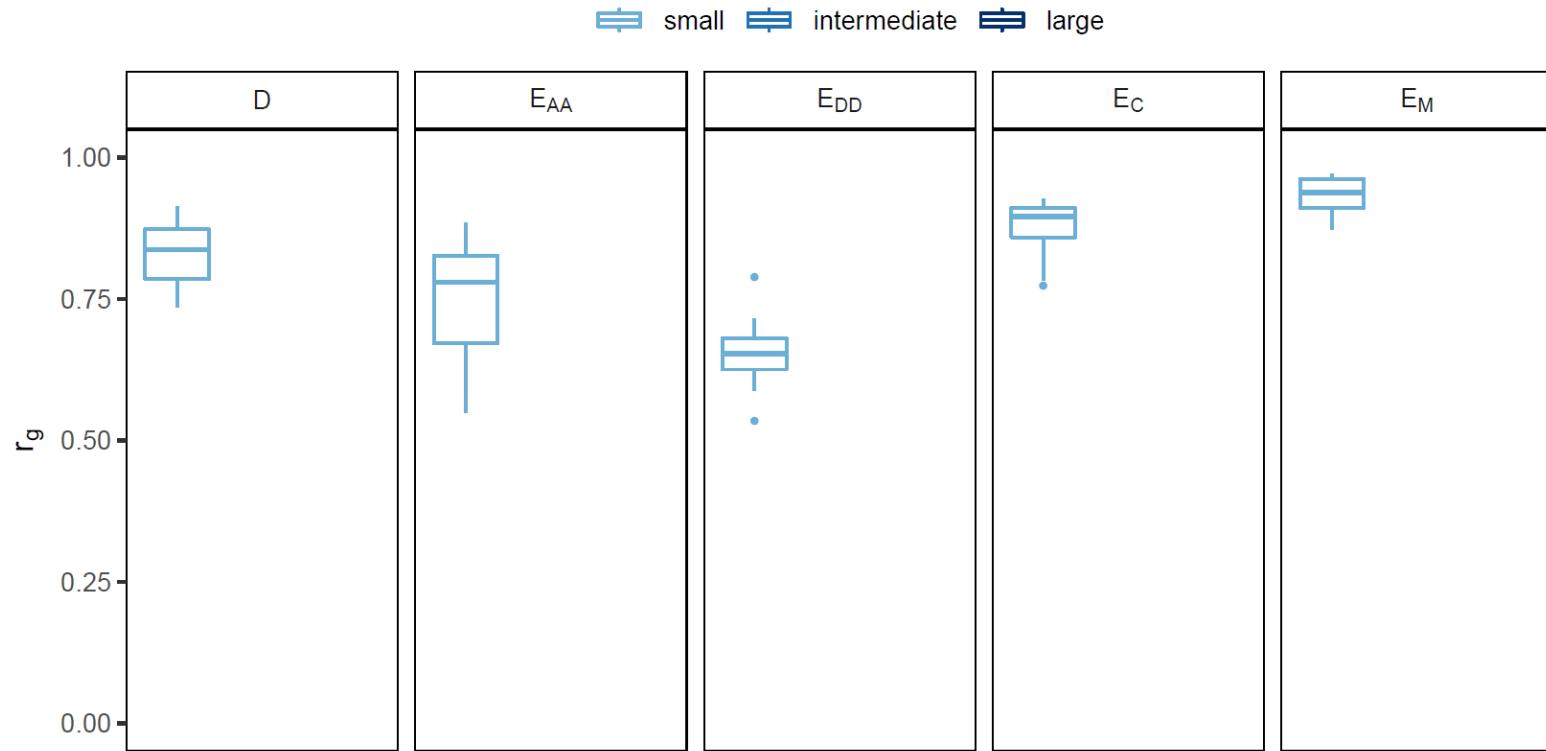
Effect of N interactions per locus

5 interactions with "large" effect

100 interactions with "small" effect

Similar effects of

- **Magnitude**

- **N interactions/locus**

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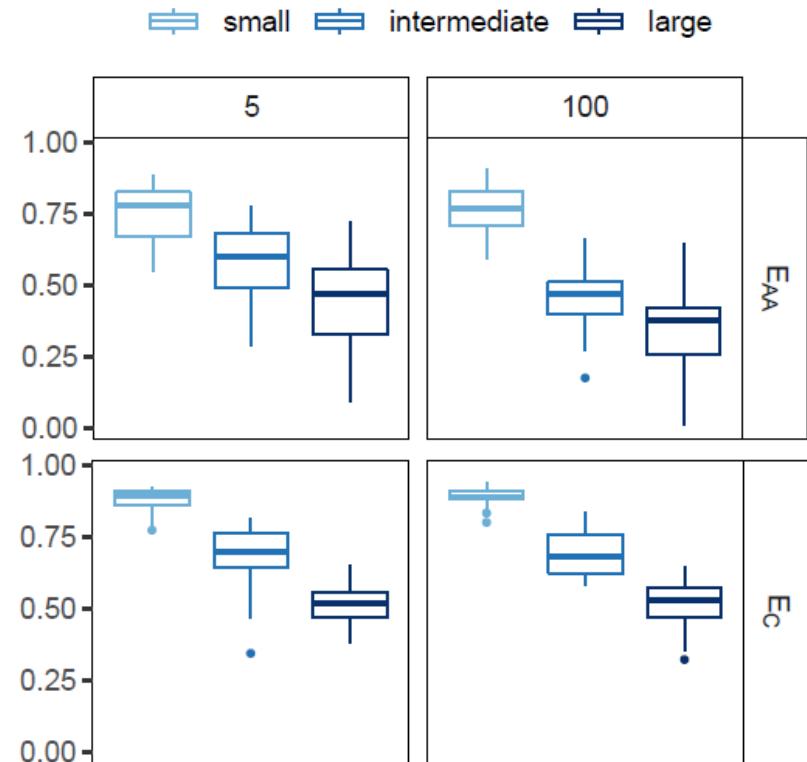
Limit to r_g?

## Massive dominance and epistatic effects (x100)

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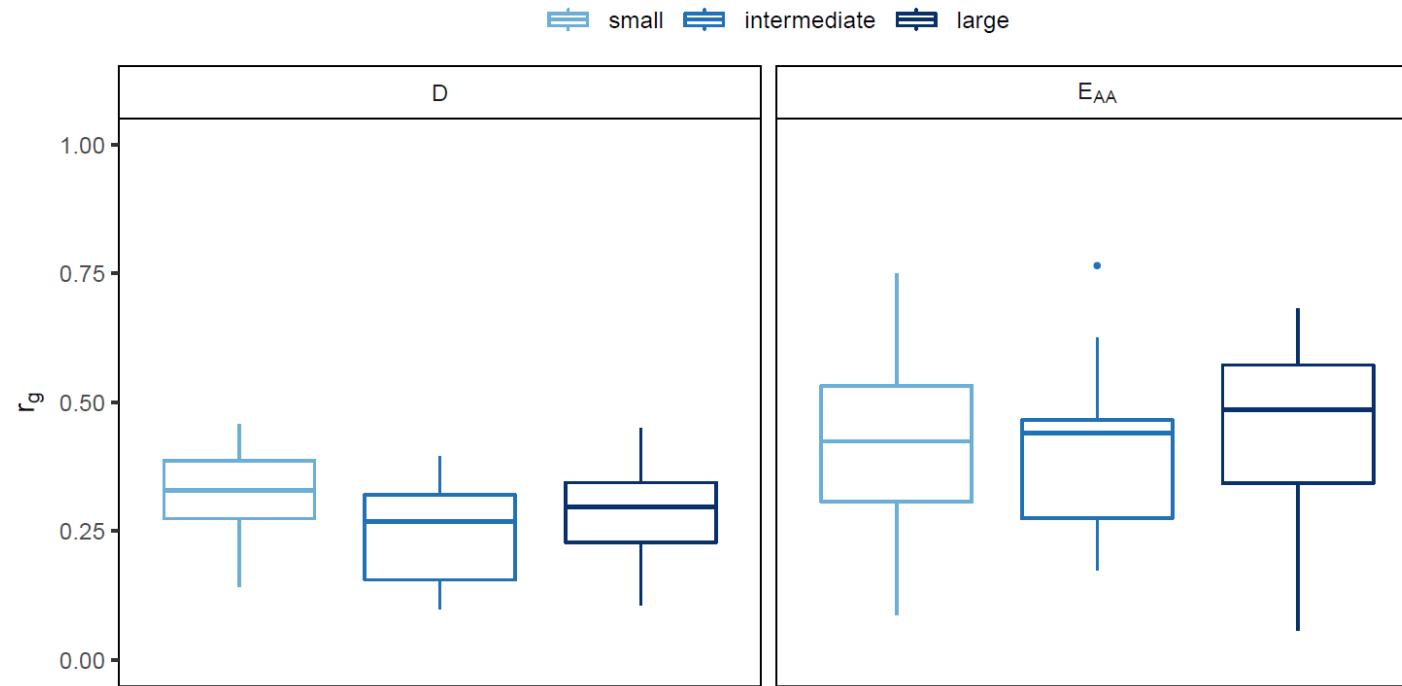
No effect of increasing effect size?

Increase in effect size or N interactions also changes the scale of α

$$r_g = \frac{cov(\alpha_A, \alpha_B)}{\sigma_{\alpha_A} \sigma_{\alpha_B}}$$

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Take-home message

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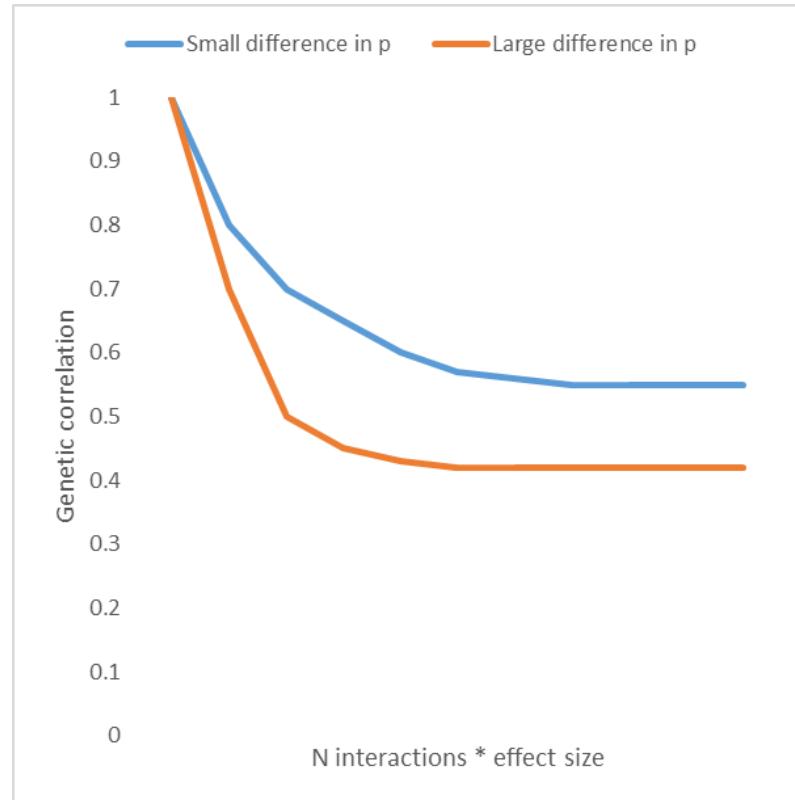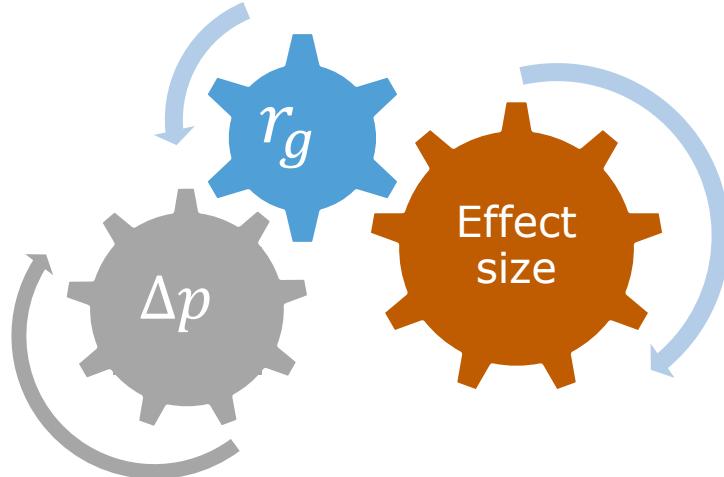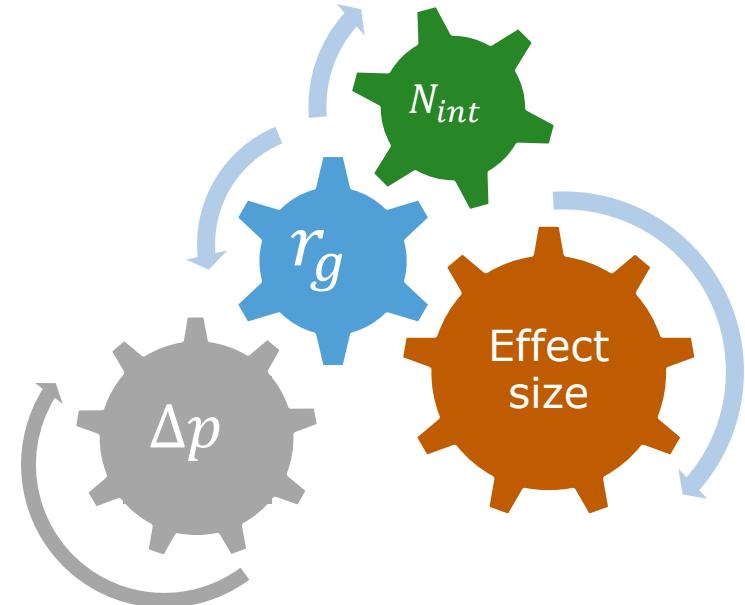
Conclusions

- $r_g < 0.8$ unlikely to be due to dominance alone
  - Dominance variance is usually small

- r_g depends on
  - population divergence (Δp)
  - size dominance effects
  - size epistatic effects * N interactions

- Differences in allele frequency may limit r_g

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scenario	Effect size	VA	VD	VI
D	Small	0.924	0.076	0.000
	Intermediate	0.511	0.489	0.000
	Large	0.198	0.802	0.000
E_{AA}	Small	0.997	0.000	0.003
	Intermediate	0.988	0.000	0.012
	Large	0.969	0.000	0.031
E_{DD}	Small	0.694	0.303	0.004
	Intermediate	0.347	0.637	0.016
	Large	0.152	0.813	0.035
E_C	Small	0.947	0.051	0.001
	Intermediate	0.737	0.250	0.013
	Large	0.471	0.511	0.017
E_M	Small	0.999	0.000	0.001
	Intermediate	0.995	0.000	0.005
	Large	0.989	0.000	0.011

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