Tracing Homoeolog Expression Bias Inheritance in wheat

Marek Glombik

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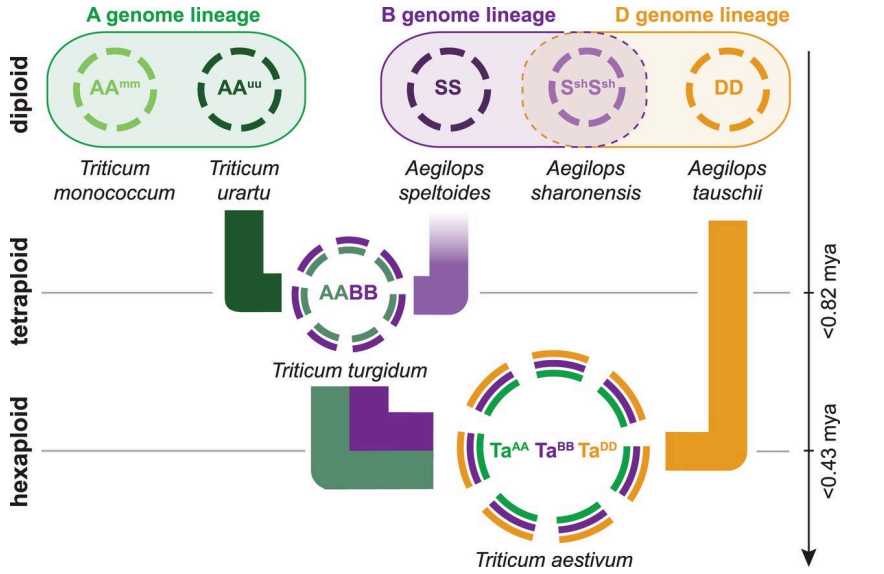
Plant and Animal Genome conference, San Diego, US

Biotechnology and Biological Sciences Research Council
John Innes Centre
Unlocking Nature's Diversity
@GlombikM

Wheat genome

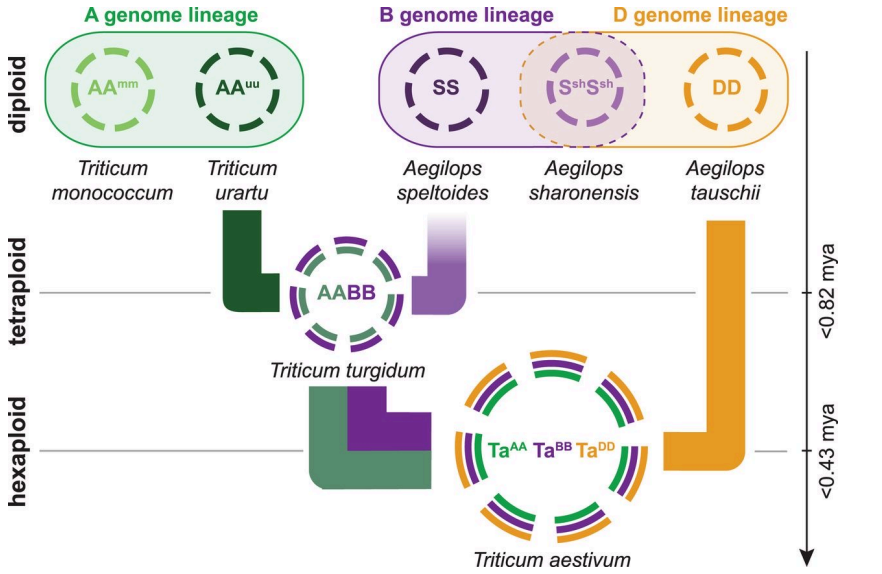
- Allohexaploid – three subgenomes (**A**, **B**, **D**)



IWGSC, et al. (2014)

Wheat genome

- Allohexaploid – three subgenomes (**A**, **B**, **D**)
- Over 53,000 genes have 1:1:1 correspondence across subgenomes = ***triad***
- Corresponding genes = ***homoeologs***



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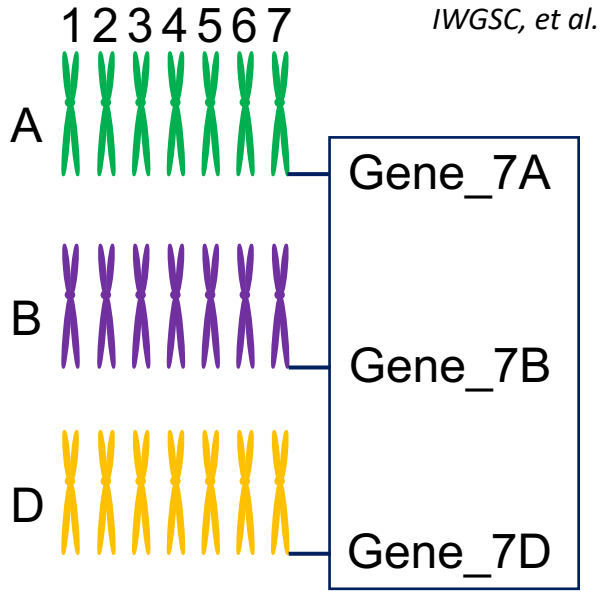
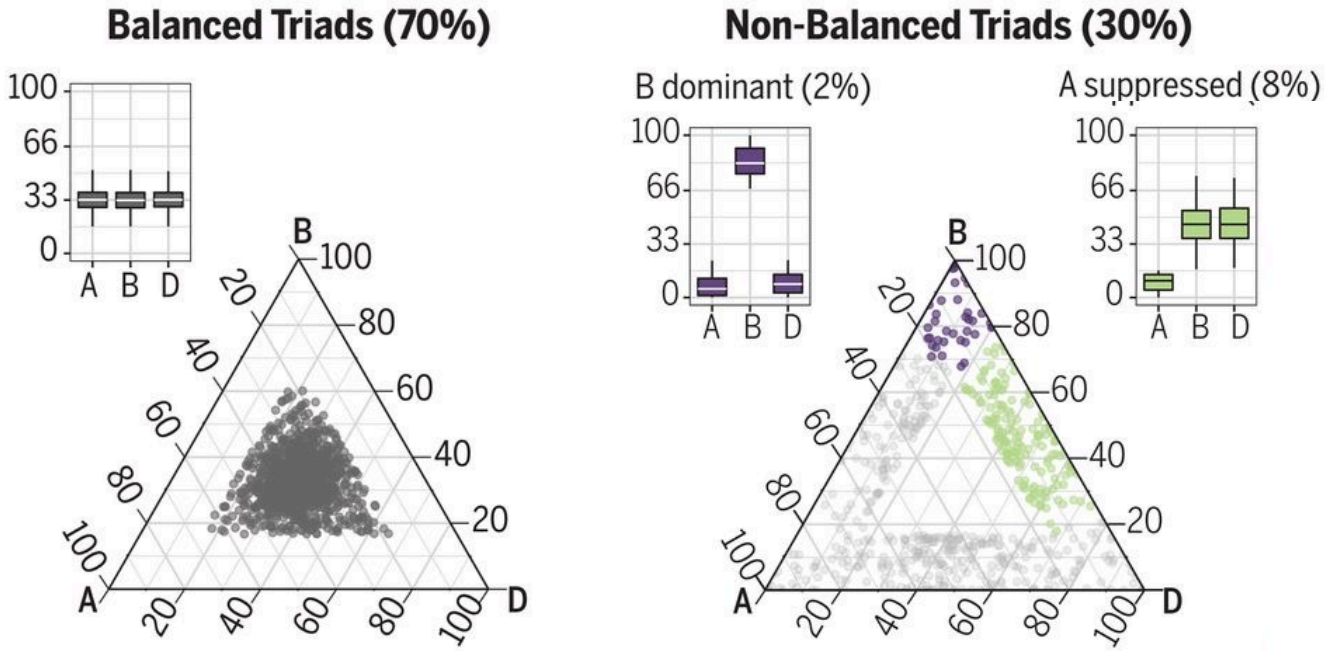


Wheat transcriptome

- 70 % of triads display balanced expression (no Homoeolog Expression Bias - HEB)



Ramírez-González, R. H., Borrill, P. et al. (2018)

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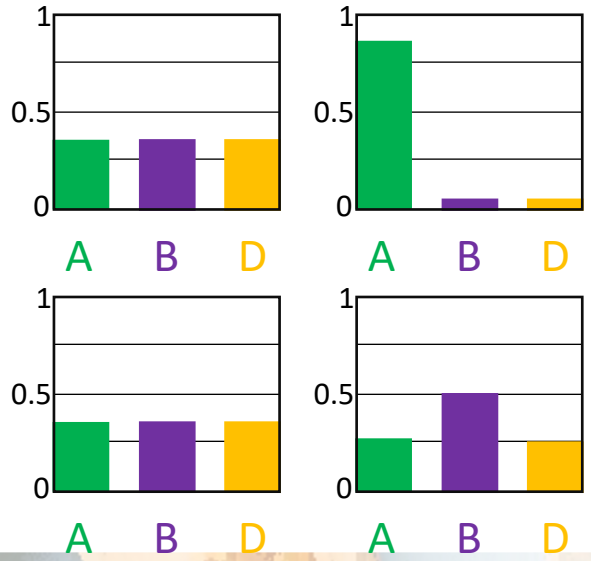

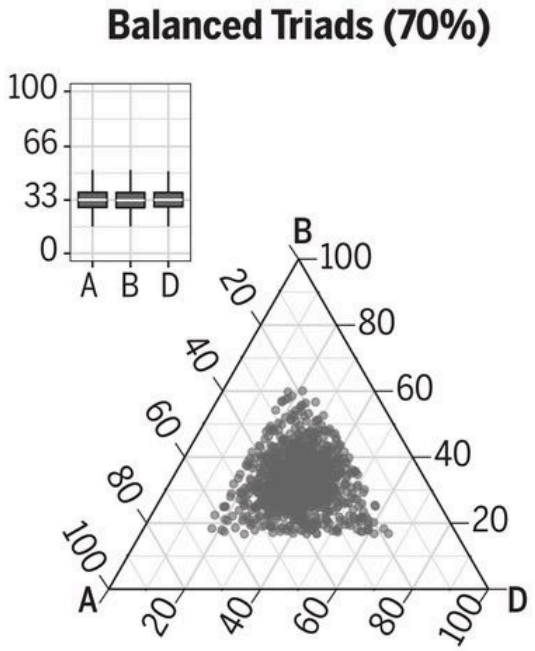

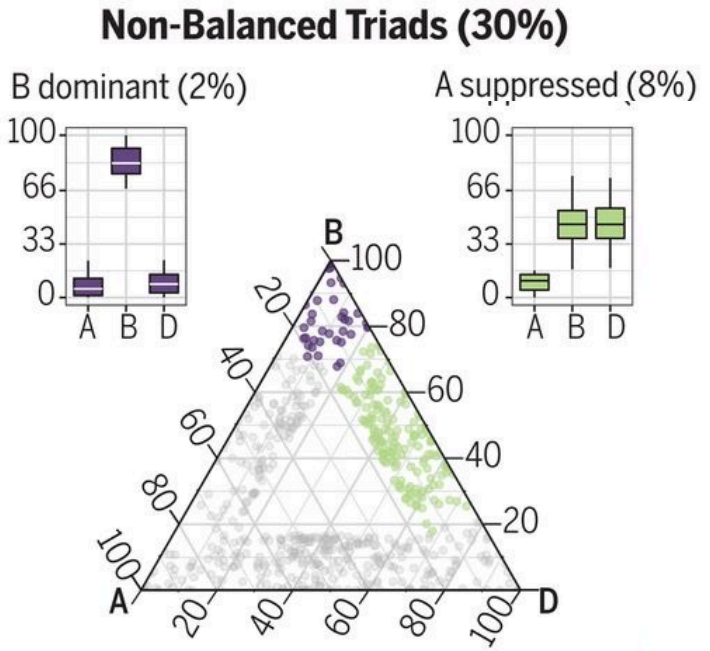

Ramírez-González, R. H., Borrill, P. et al. (2018)

Variety X

Variety Y

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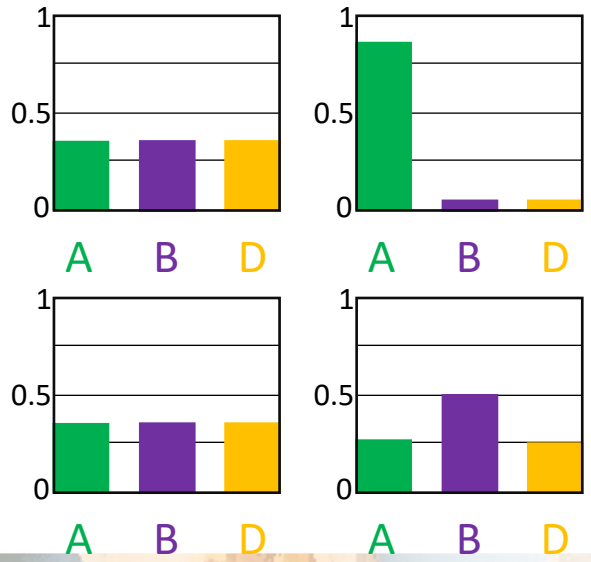

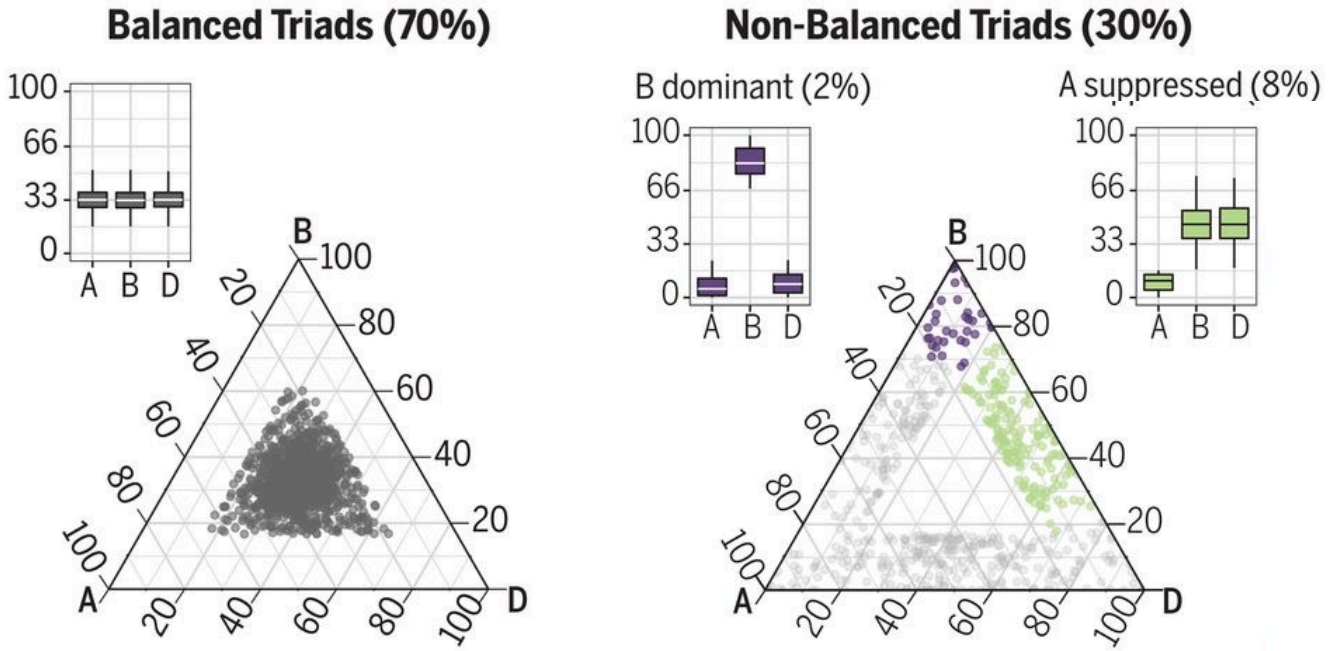

Ramírez-González, R. H., Borrill, P. et al. (2018)

Variety X

x

Variety Y

Progeny?

Paragon (W10074 PF-1) x Charger (WPxCHA 10001)

Paragon (W10074 PF-1) x Watkins (WATDE0228 PF-1)

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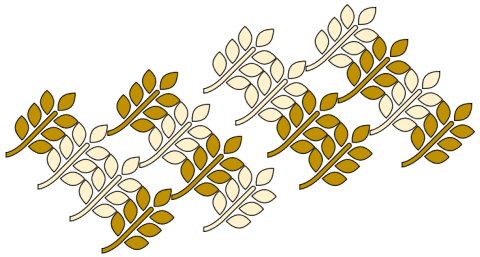
Paragon (W10074 PF-1) x Charger (WPxCHA 10001)



50 F_6 lines

6th generation of single seed descent

Paragon (W10074 PF-1) x Watkins (WATDE0228 PF-1)

50 F_6 lines

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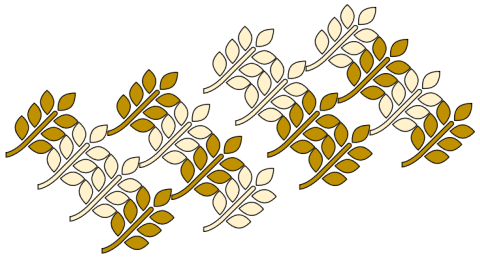

50 F_6 lines

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Leaf tissue 14-day old seedlings

Leaf tissue 14-day old seedlings

RNA-sequencing

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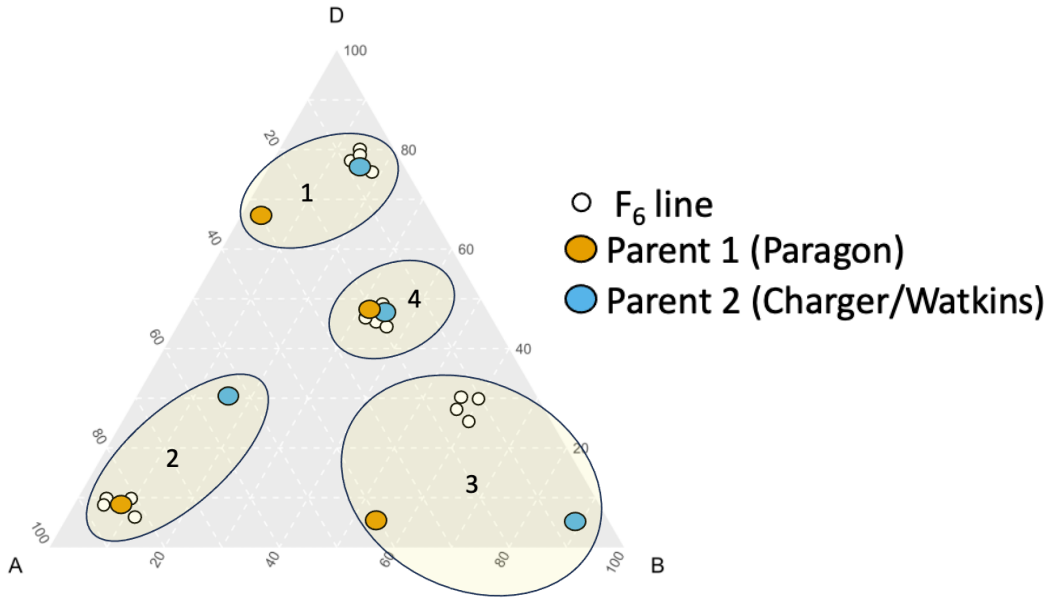
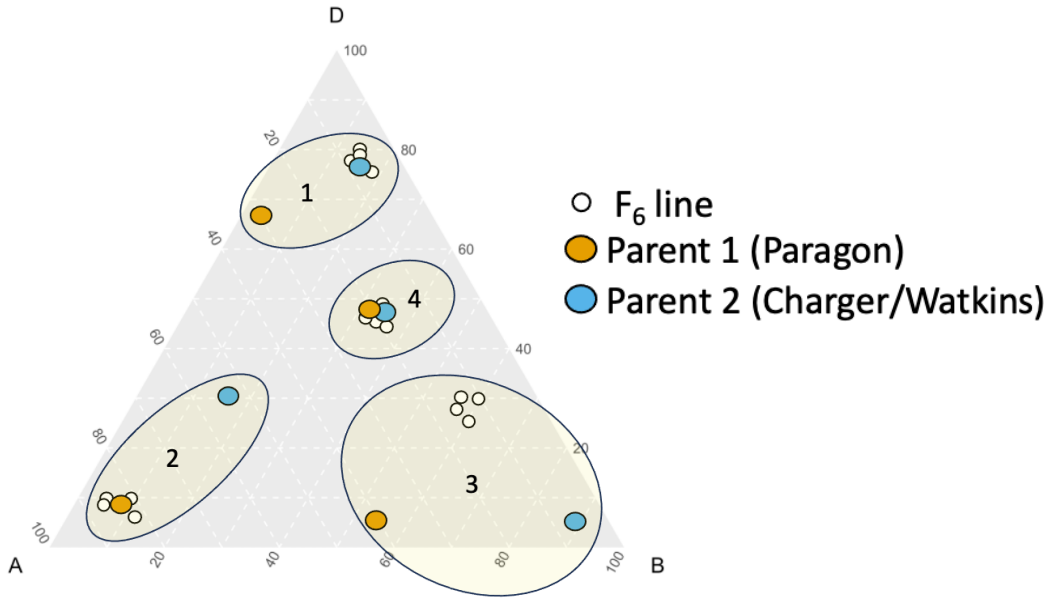
HEB analysis



HEB analysis

- Bias distance – relative distance between F_6 line HEB and parental HEB



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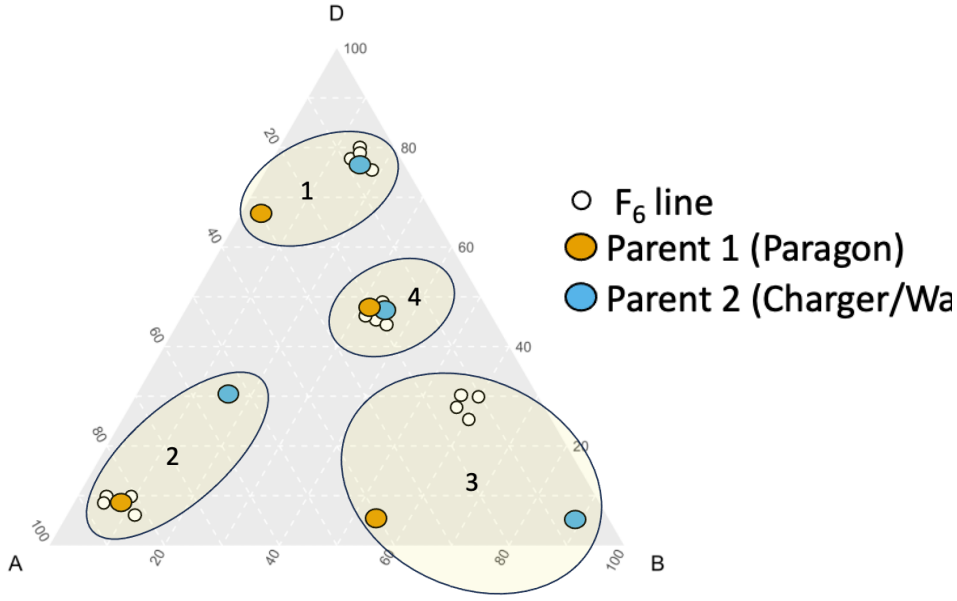
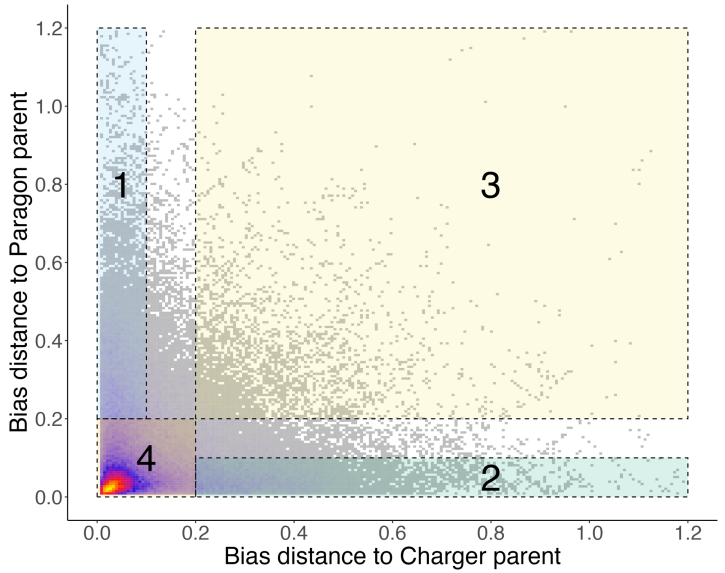
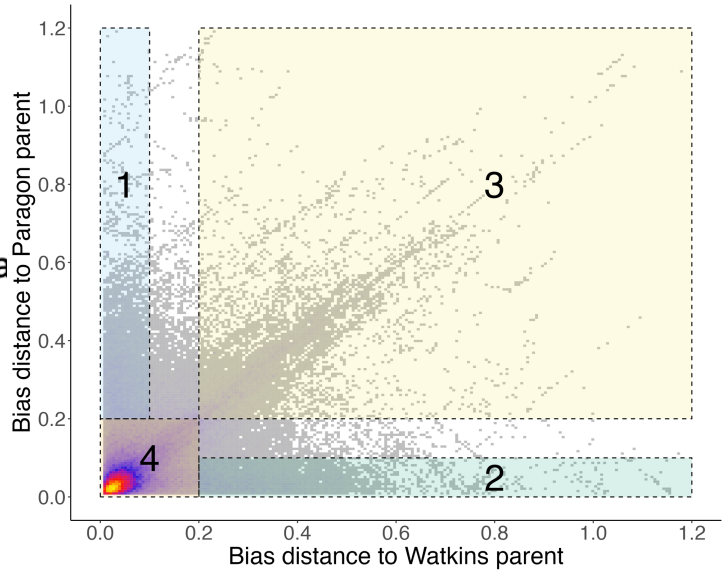




PxC



PxW

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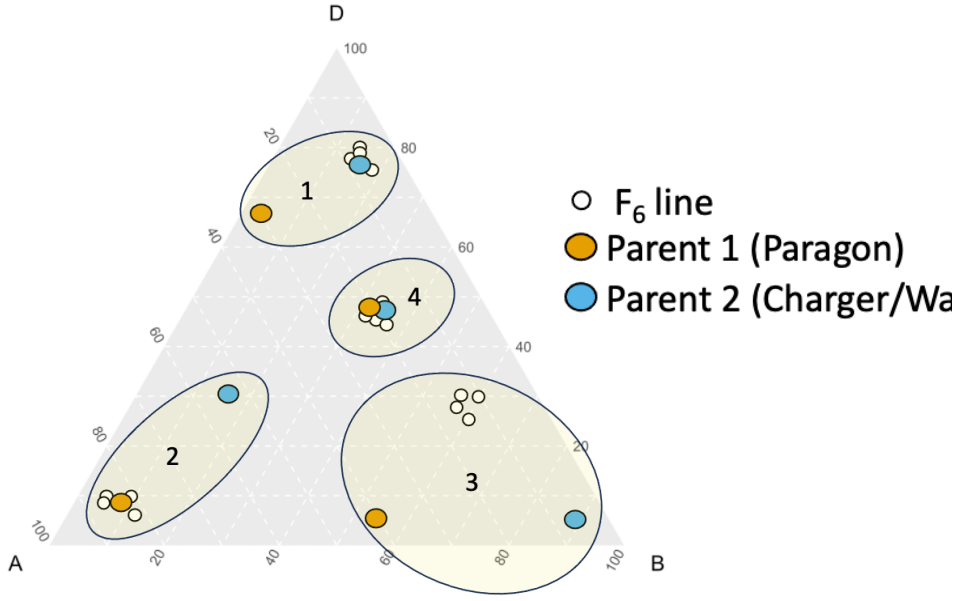
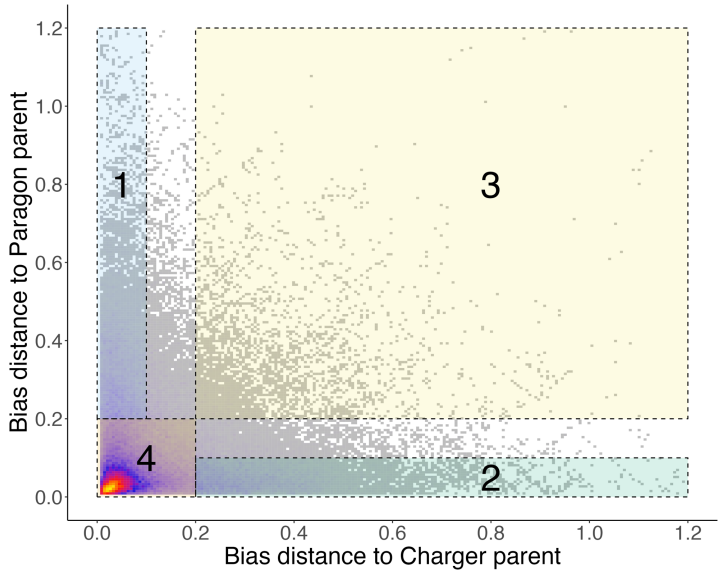
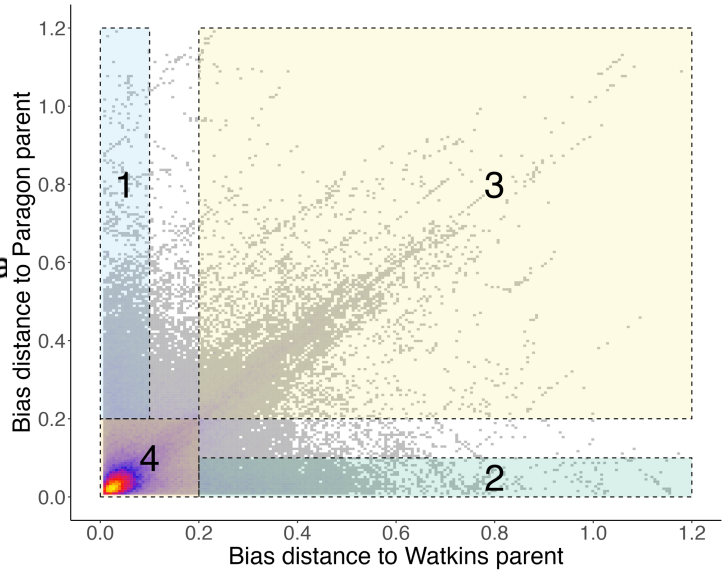
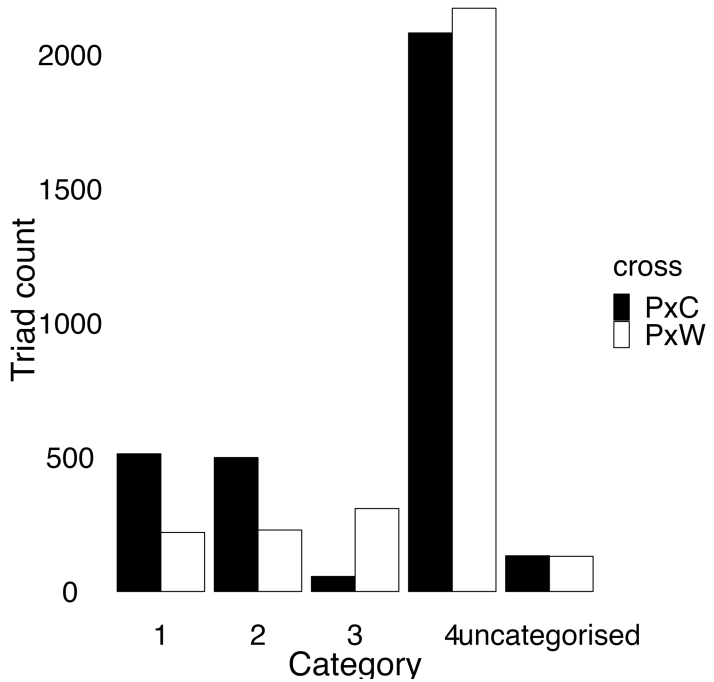
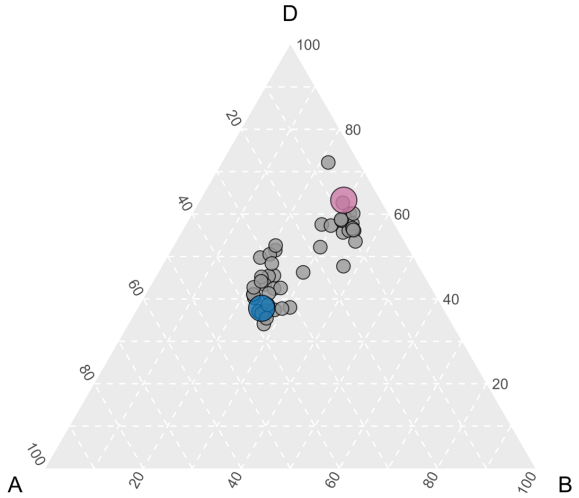
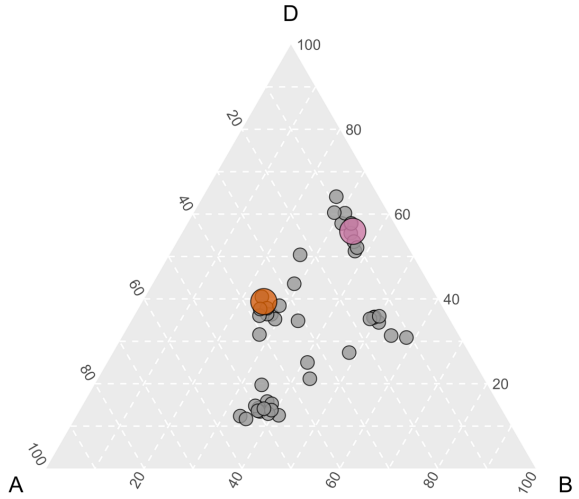









D
A
B
100
80
60
40
20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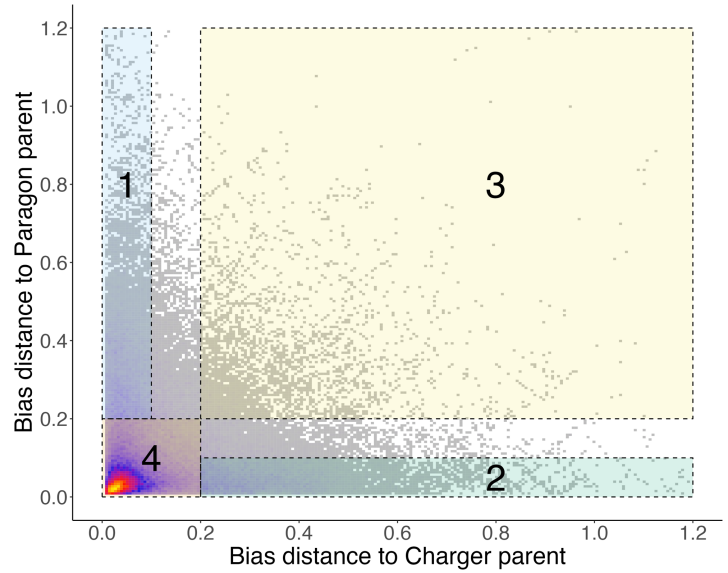
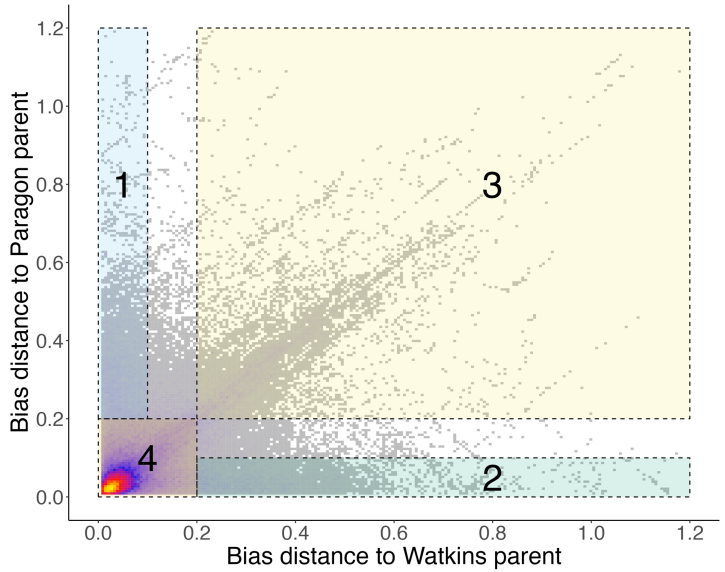
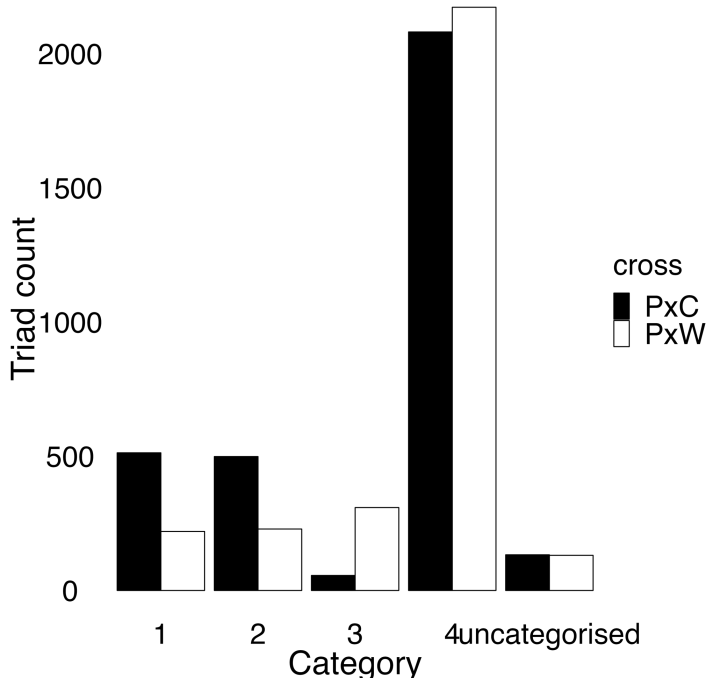
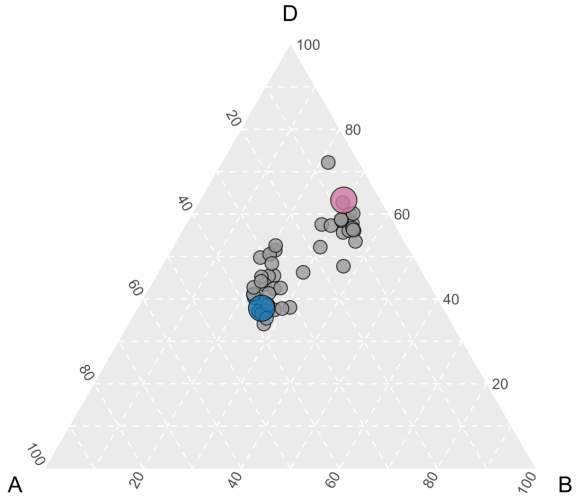

Bias distance to Paragon parent
Bias distance to Charger parent
1
2
3
4
0.0
0.2
0.4
0.6
0.8
1.0
1.2


Bias distance to Paragon parent
Bias distance to Watkins parent
1
2
3
4
0.0
0.2
0.4
0.6
0.8
1.0
1.2

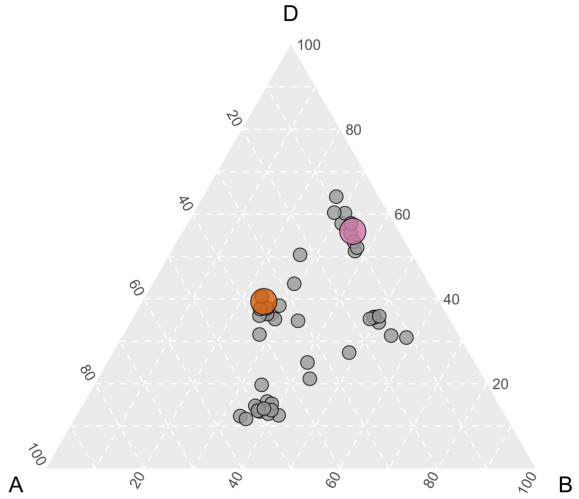
PxC

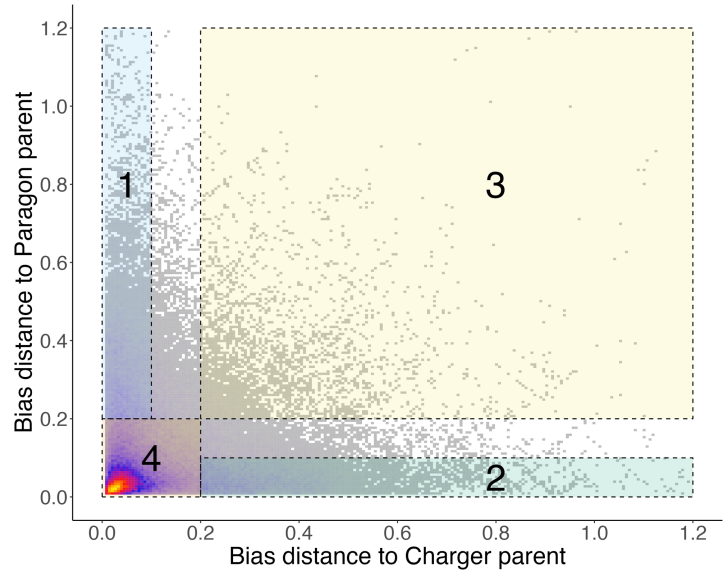
PxW

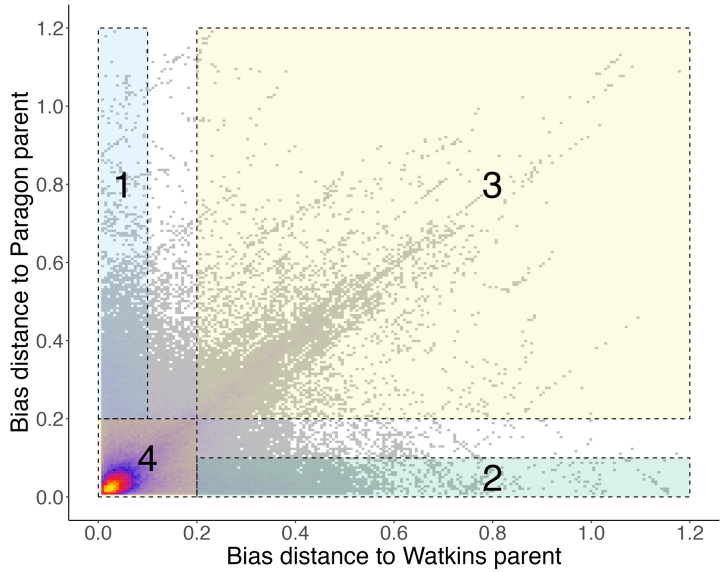

Triad count
Category
cross
PxC
PxW
0
500
1000
1500
2000
1
2
3
4uncategorised



Link to genotype?

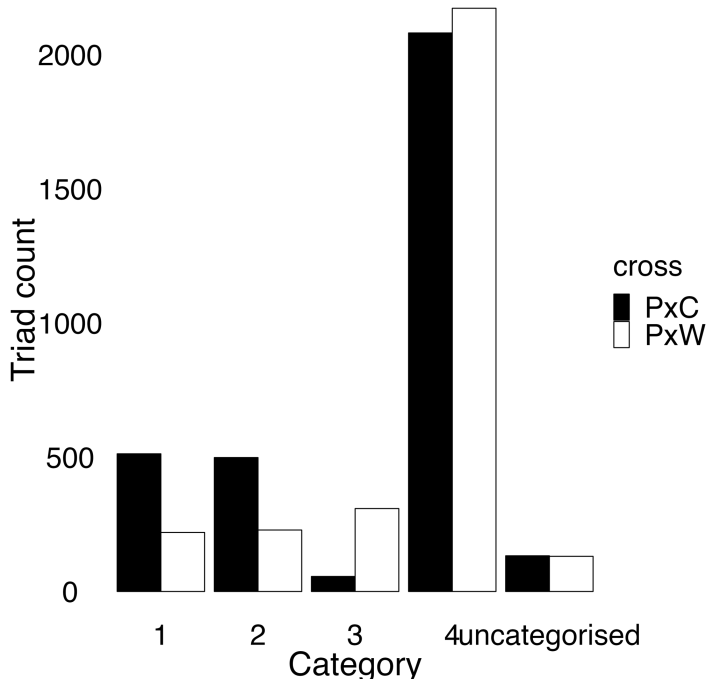






PxC

PxW



Association between a SNP and gene expression

- eQTL analysis

Association between a SNP and gene expression

- eQTL analysis
- **7 957** SNPs in **3 080** genes **PxC**
- **5 538** SNPs in **2 059** genes **PxW**

Association between a SNP and gene expression

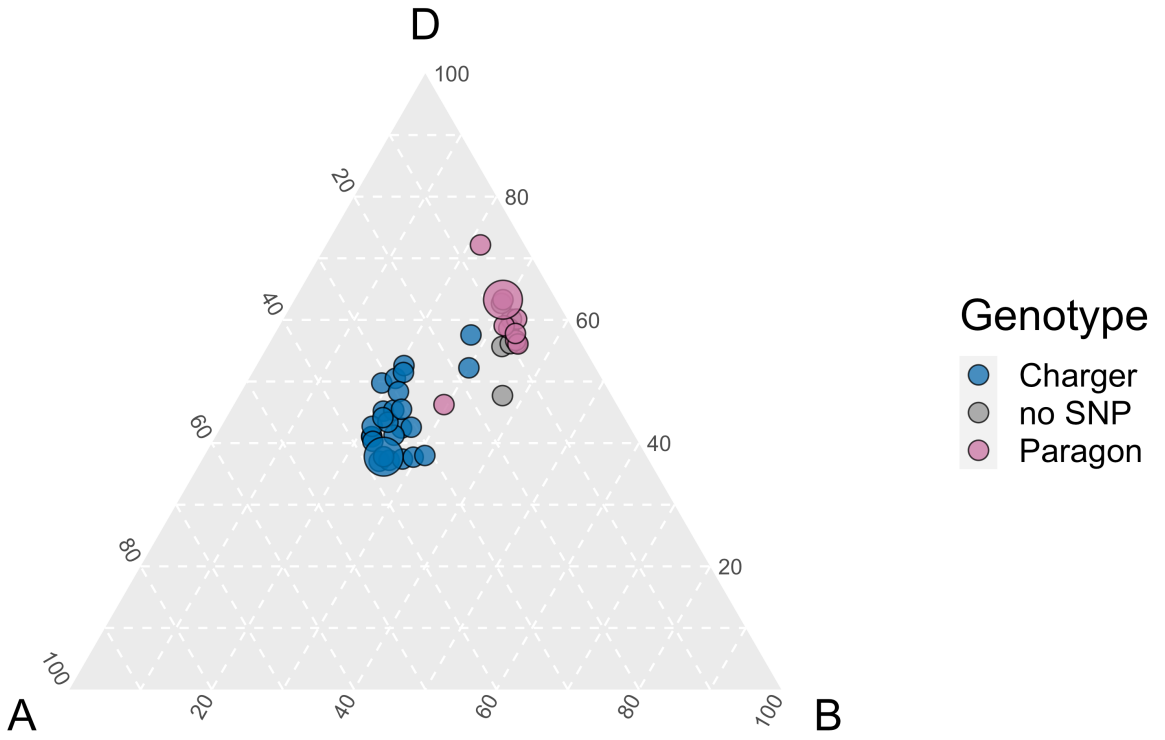
- eQTL analysis
- **7 957** SNPs in **3 080** genes **PxC**
- **5 538** SNPs in **2 059** genes **PxW**

- **512** triads in **PxC – 75 %**
- **76** triads in **PxW – 54 %**

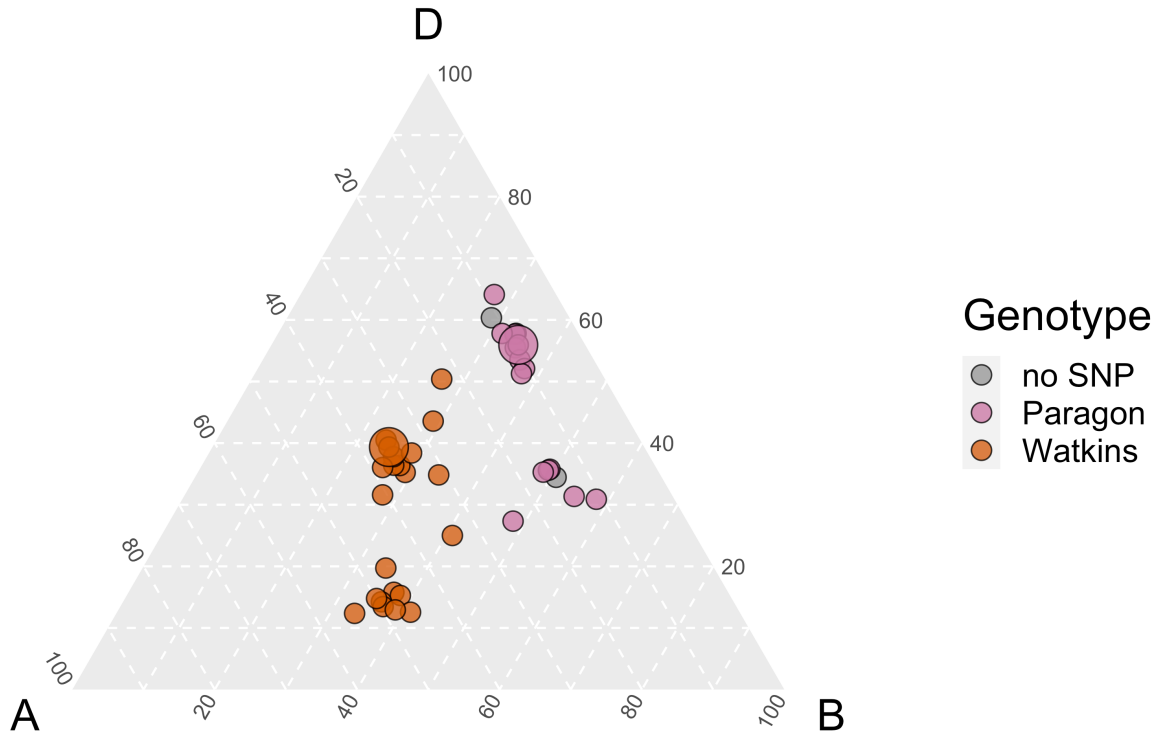
Connected to HEB analysis based on bias distance calculations

Association between a SNP and gene expression

PxC



PxW



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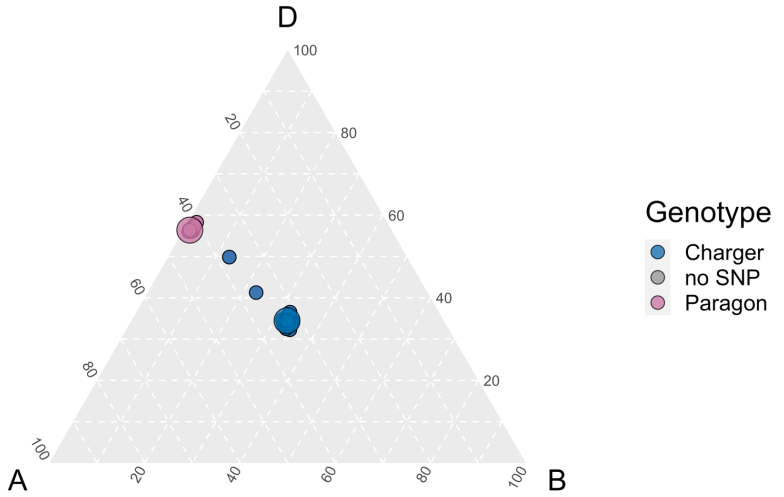
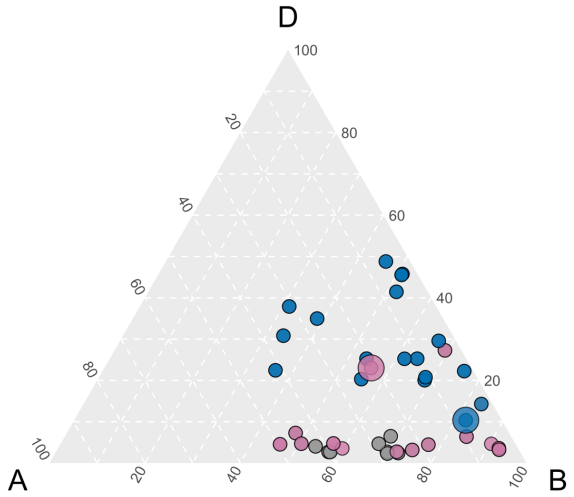


Genotype
- Charger
- no SNP
- Paragon

PxC



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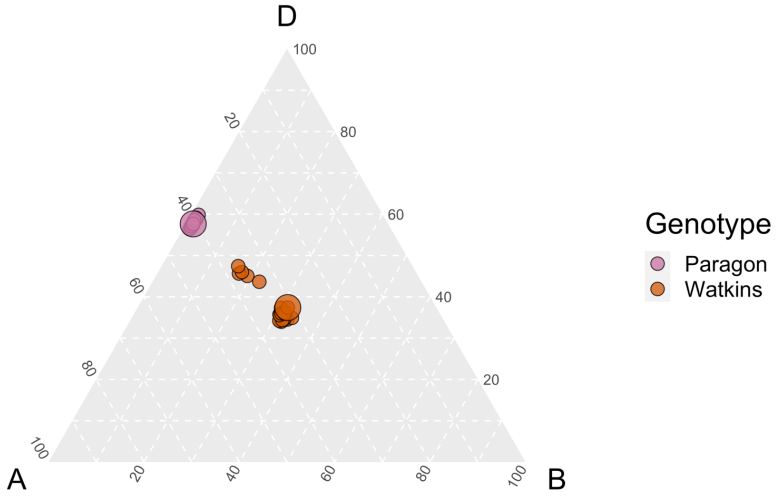

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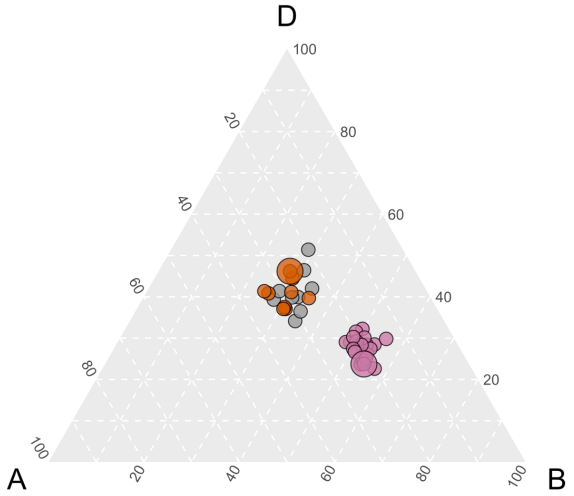
PxW



Genotype
- no SNP
- Paragon
- Watkins

Take home message

- HEB in wheat is partially linked to genotype
- Crossing wheat varieties may lead to a myriad of triad expression patterns that can highly differ from parental lines and potentially influence trait expression

Acknowledgement

Borrill Lab
Philippa Borrill
Sam Burrows
Catherine Evans
Arunkumar Ramesh

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