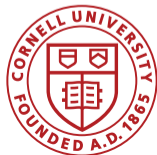


# Homeologous Epistasis in Wheat: The Search for an Immortal Hybrid

Nicholas Santantonio,  
Jean-Luc Jannink and Mark Sorrells

Cornell University

January 11, 2020



# Mac Key 1970

*Hereditas* 66: 165—176 (1970)

## Significance of mating systems for chromosomes and gametes in polyploids

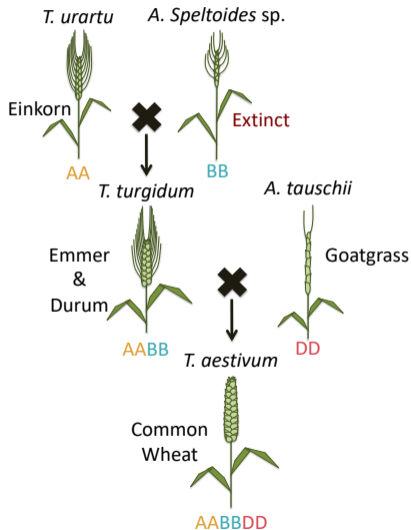
JAMES MAC KEY

*Department of Genetics and Plant Breeding, Agricultural College of Sweden, Uppsala<sup>1</sup>*

(Received August 10, 1970)

- ▶ Evolutionary “balance between new-creating and preserving forces.”
- ▶ Maintain “homozygosity and heterozygosity ... at different homoeologous loci.”
- ▶ Allopolyploids preserve through selfing (homo), while maintaining allelic diversity (homeo)

# Evolution of allohexaploid wheat



## *Triticum*

- ▶ Fertile Crecent
- ▶ Neolithic revolution
- ▶ AA × BB ~ 0.5 Mya

## *Aegelops*

- ▶ early speciation from *Triticum* (A × B)
- ▶ AABB × DD ~ 10,000 ya

# Allohexaploid wheat

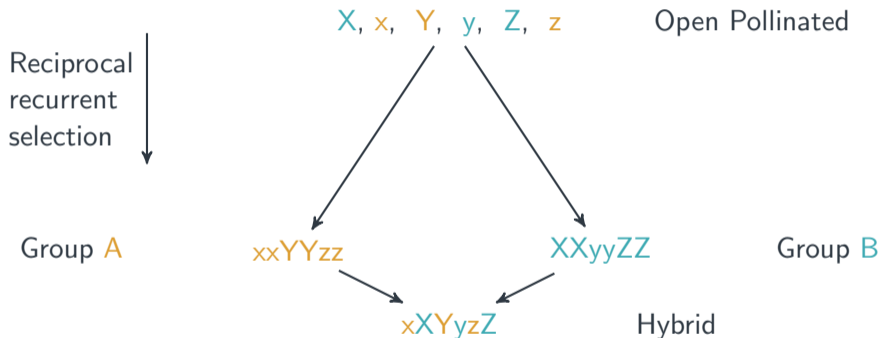


## Allopolyploid

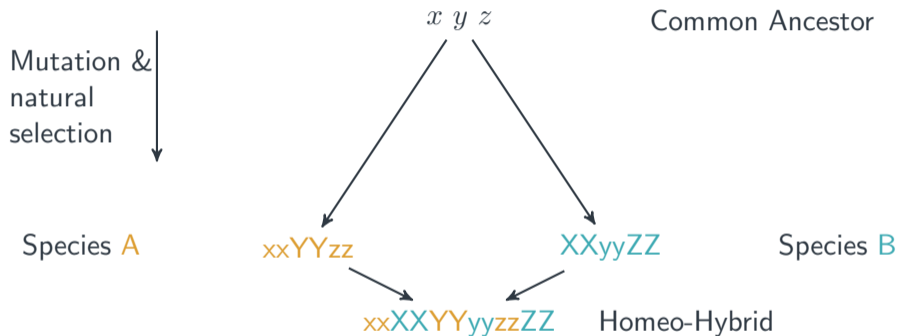
- ▶ **Very difficult to assemble a genome**
  - ▷ Thank you IWGSC! (and for prepublication access!)
- ▶ Disomic inheritance
  - ▷ no crossover across homeologous chromosomes
- ▶ Autogamous
  - ▷ self-pollinated (outcrossing < 1%)
- ▶ Allelic diversity preserved across subgenomes
  - ▷ Most genes have three divergent copies!

Is wheat an immortalized hybrid?

# Hybrid generation



# Allopolyploid formation



homeoallelic interactions? (homeologous epistasis)

With markers and RefSeq, we can now ask this question!

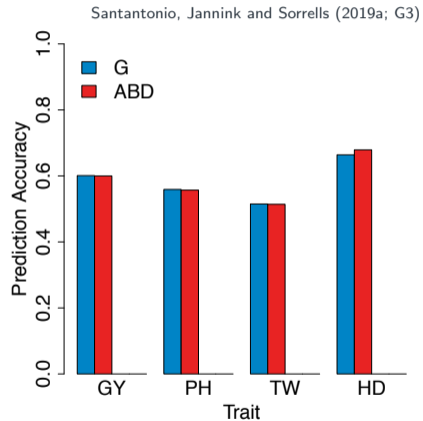
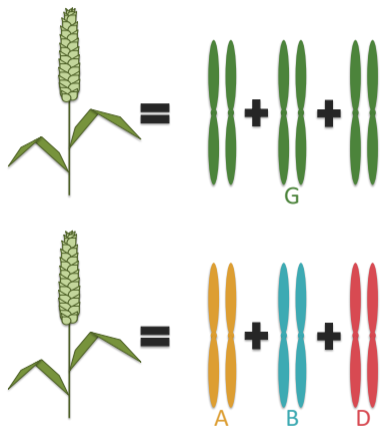
# Cornell Winter Wheat Master Population



## Cornell winter wheat breeding population

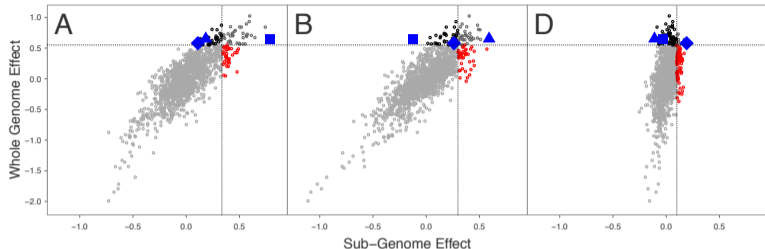
- ▶ 8,692 phenotypic records
  - ▷ 1,447 lines
  - ▷ 26 NY trials
  - ▷ 10 years (2007 - 2016)
  - ▷ 2-3 locations / year
  - ▷ 11,604 GBS markers
- ▶ 4 traits
  - ▷ Grain Yield (GY)
  - ▷ Test Weight (TW)
  - ▷ Heading Date (HD)
  - ▷ Plant Height (PH)
- ▶ Align markers to RefSeq v1.0
  - ▷ separate markers by subgenome
  - ▷ calculate genetic covariance for each subgenome:  $\mathbf{K}_A$ ,  $\mathbf{K}_B$  and  $\mathbf{K}_D$
  - ▷ estimate subgenome breeding values

# Can predict subgenome breeding values





## GY Grain Yield

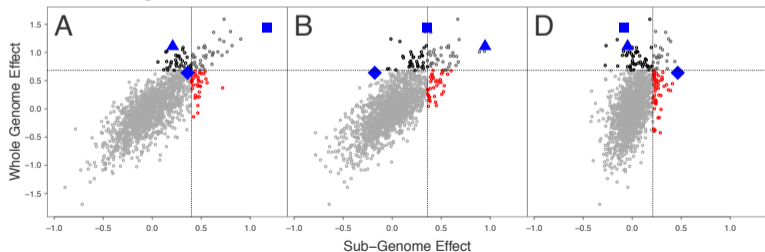


■ best A  
 ▲ best B  
 ◆ best D

► Best individuals don't have the best subgenomes

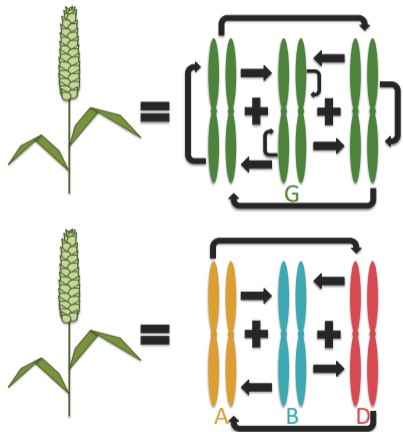
► Can select parents with complementary subgenomes

## TW Test Weight



Santantonio, Jannink and Sorrells (2019a; G3)

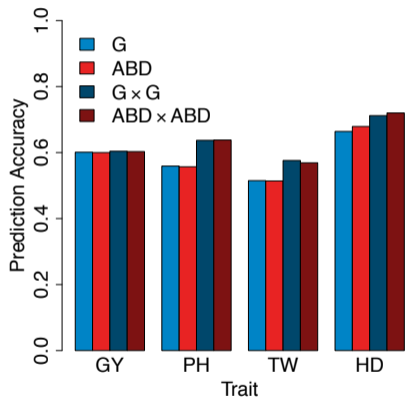
# Subgenome interactions aid genomic prediction



Hadamard product  
for epistatic  
covariance  
 $K_G \odot K_G$

$K_A \odot K_B$   
 $K_A \odot K_D$   
 $K_B \odot K_D$

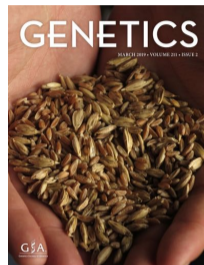
Santantonio, Jannink and Sorrells (2019a; G3)



Suggests all epistasis is homeologous?

# Two-Locus Epistasis

Santantonio, Jannink and Sorrells (2019b; Genetics)



Consider the two locus model (from Hill et al. 2008):

$$E[y] = \mu + B\alpha_B + C\alpha_C + BC(\alpha\alpha)_{BC}$$

Additive  $\times$  Additive

	<i>CC</i>	<i>cc</i>
<i>BB</i>	$2a$	$0$
<i>bb</i>	$0$	$2a$

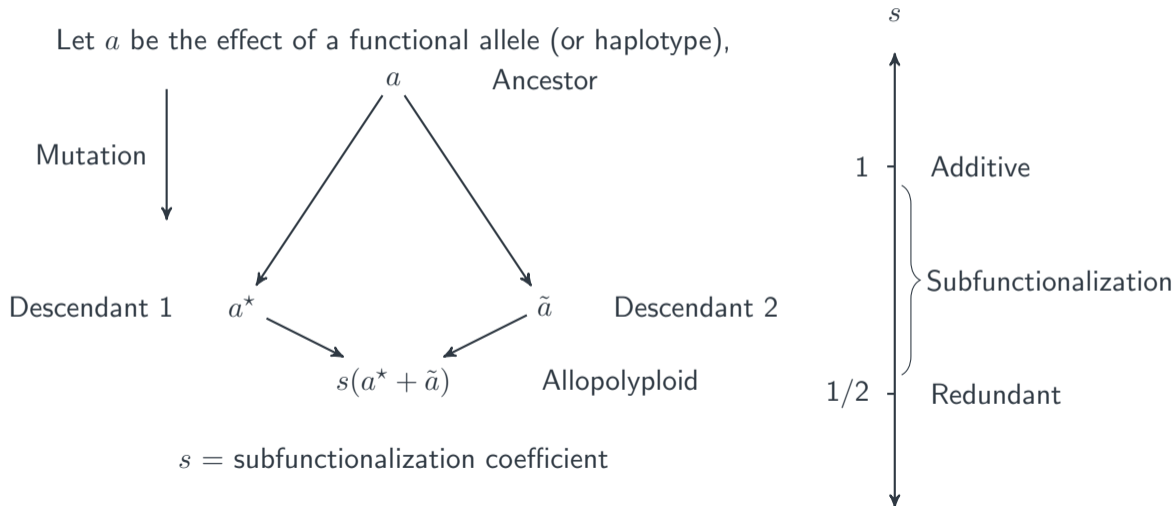
Duplicate Factor

	<i>CC</i>	<i>cc</i>
<i>BB</i>	$a$	$a$
<i>bb</i>	$a$	$0$

Subfunctionalization

	<i>CC</i>	<i>cc</i>
<i>BB</i>	$s(a^* + \tilde{a})$	$a^*$
<i>bb</i>	$\tilde{a}$	$0$

# Subfunctionalization Epistasis



Caledonia × NY8080

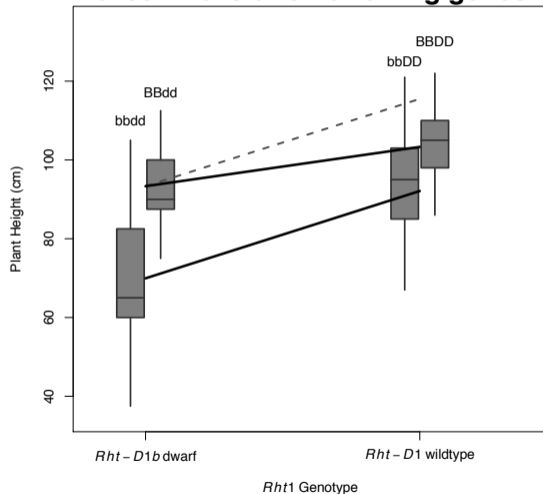
*Rht-B1* × *Rht-D1*

- ▶ 158 RILs
- ▶ Segregating for two homeologous dwarfing genes

Subfunctionalization of Dwarfing Genes

- ▶  $1 + 1 \neq 2$
- ▶ functional redundancy

## Interaction of markers near Green Revolution dwarfing genes



Caledonia × NY8080

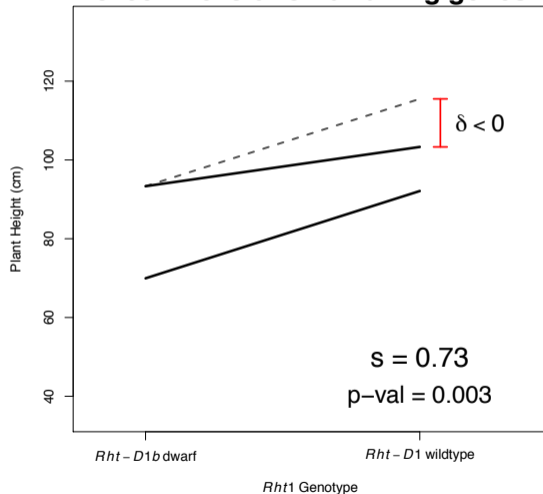
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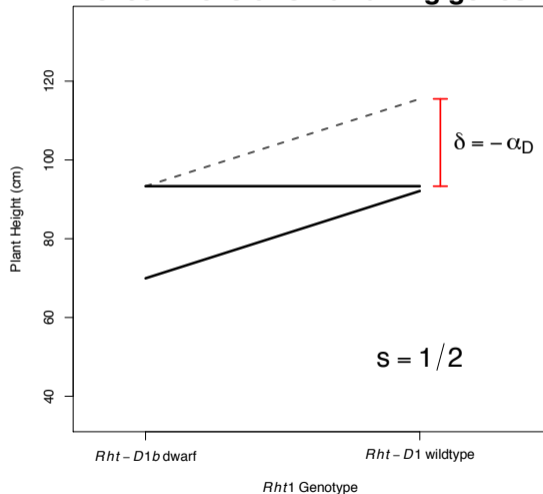
Caledonia  $\times$  NY8080  
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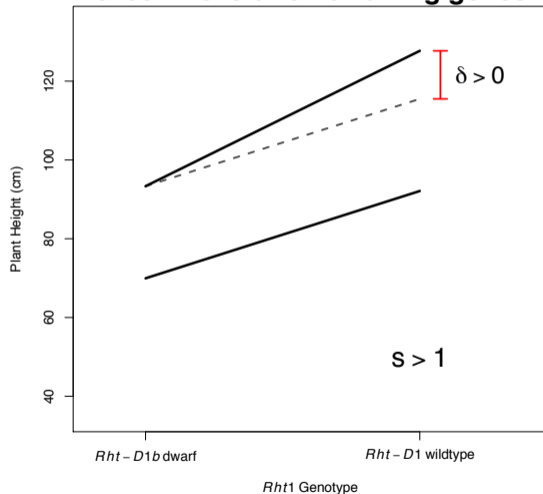
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Subfunctionalization of Dwarfing Genes

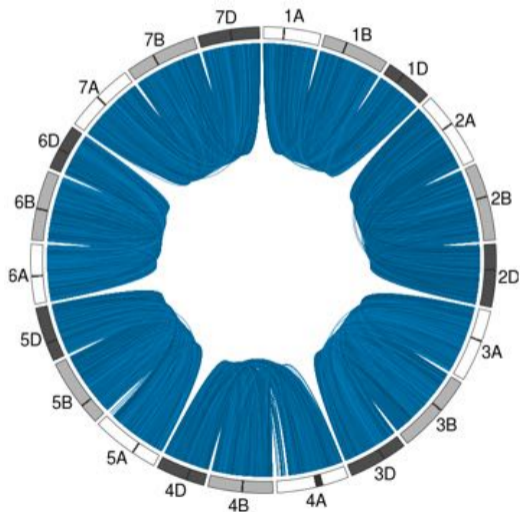
- ▶  $1 + 1 \neq 2$
- ▶ functional redundancy

## Interaction of markers near Green Revolution dwarfing genes





# Homeoallelic Marker Sets



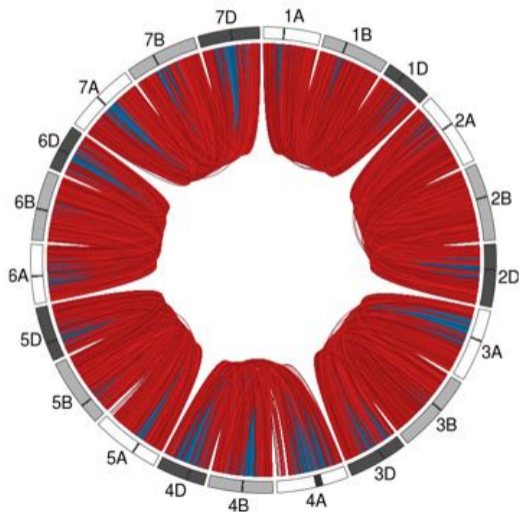
## IWGSC RefSeq v1.0 genome

- ▶ 110,790 coding sequences
- ▶ Align CDS to self

## Alignments

- ▶ 24,695 singletons, 20,319 multi-align
- ▶ 23,796 homeologous gene sets
  - ▷ 18,184 triplicates
  - ▷ 5,612 duplicates
  - ▷ ~ 60% gene space

# Homeoallelic Marker Sets



## IWGSC RefSeq v1.0 genome

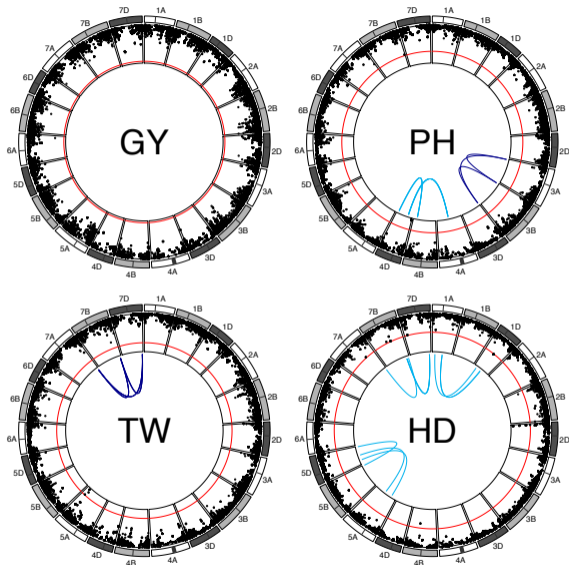
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## Anchor closest GBS marker

- ▶ 10,172 marker sets
  - ▷ 6,142 triplicates
  - ▷ 3,985 duplicates

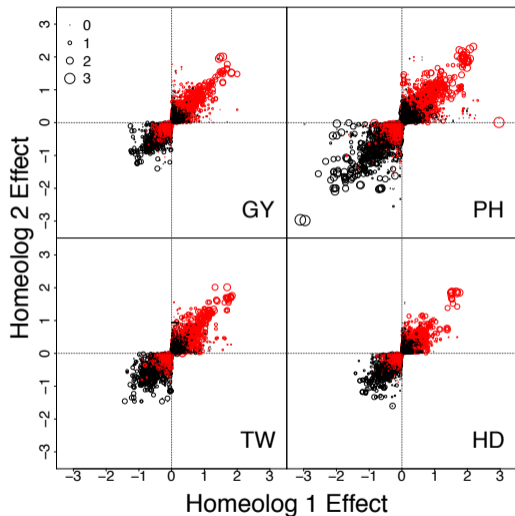


### Additive GWAS

- ▶ Few large effect QTL
- ▶ But high prediction accuracy
  - ▷ Many small effect loci

### Homeologous Epistasis GWAS

- ▶ Few large effect interactions
- ▶ Pattern genome-wide?
- ▶ Increase in prediction accuracy?



### Additive vs 2-way Interactions

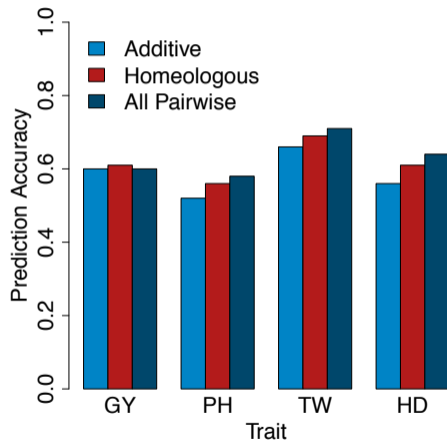
- ▶ Negative trend
- ▶  $\frac{1}{2} < d < 1$
- ▶ “less than additive”

### Subfunctionalization

- ▶ redundant function

# Homeologous interactions explain much of non-additive genetic signal

- ▶ How much non-additive genetic signal is explained by homeologous interactions?
- ▶ ~ 60-75%



# Summary of Homeoallelic Epistasis



Homeoallelic interactions tend to be less than additive

- ▶ Suggests global subfunctionalization of homeologous orthologs

Homeoallelic pairs explain more than half of the non-additive genetic signal

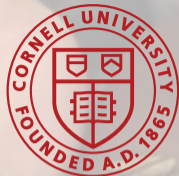
- ▶ GY not affected, too polygenic to detect?

Opportunity to fix advantageous homeoallelic pairs

- ▶ Establish heterozygosity across subgenomes
- ▶ Immortalize through inbreeding



**Allopolyploids are not diploids.**



## Co-Authors

- ▶ Mark Sorrells
- ▶ Jean-Luc Jannink

## Small Grains

- ▶ David Benscher
- ▶ Amy Fox
- ▶ Jesse Chavez
- ▶ James Tanaka

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- ▶ Lisa Kissing Kucek
- ▶ Lynn Veenstra
- ▶ Itaraju Brum
- ▶ Uche Godfrey Okeke
- ▶ Marnin Wolfe
- ▶ Roberto Lonzano Gonzalez

USDA National Needs Fellowship (2013-2016)

