Pyramiding of target alleles

PhD students’ Summer Seminar 2014

Wolfgang Link

Die Marktplatzpyramide in Karlsruhe

“**Genomic selection** is **revolutionizing** both animal and **plant breeding**”

Genomic selection in plant breeding: from theory to practice. Jannink, 2010.
Briefings in Functional Genomics 9, 166-177.

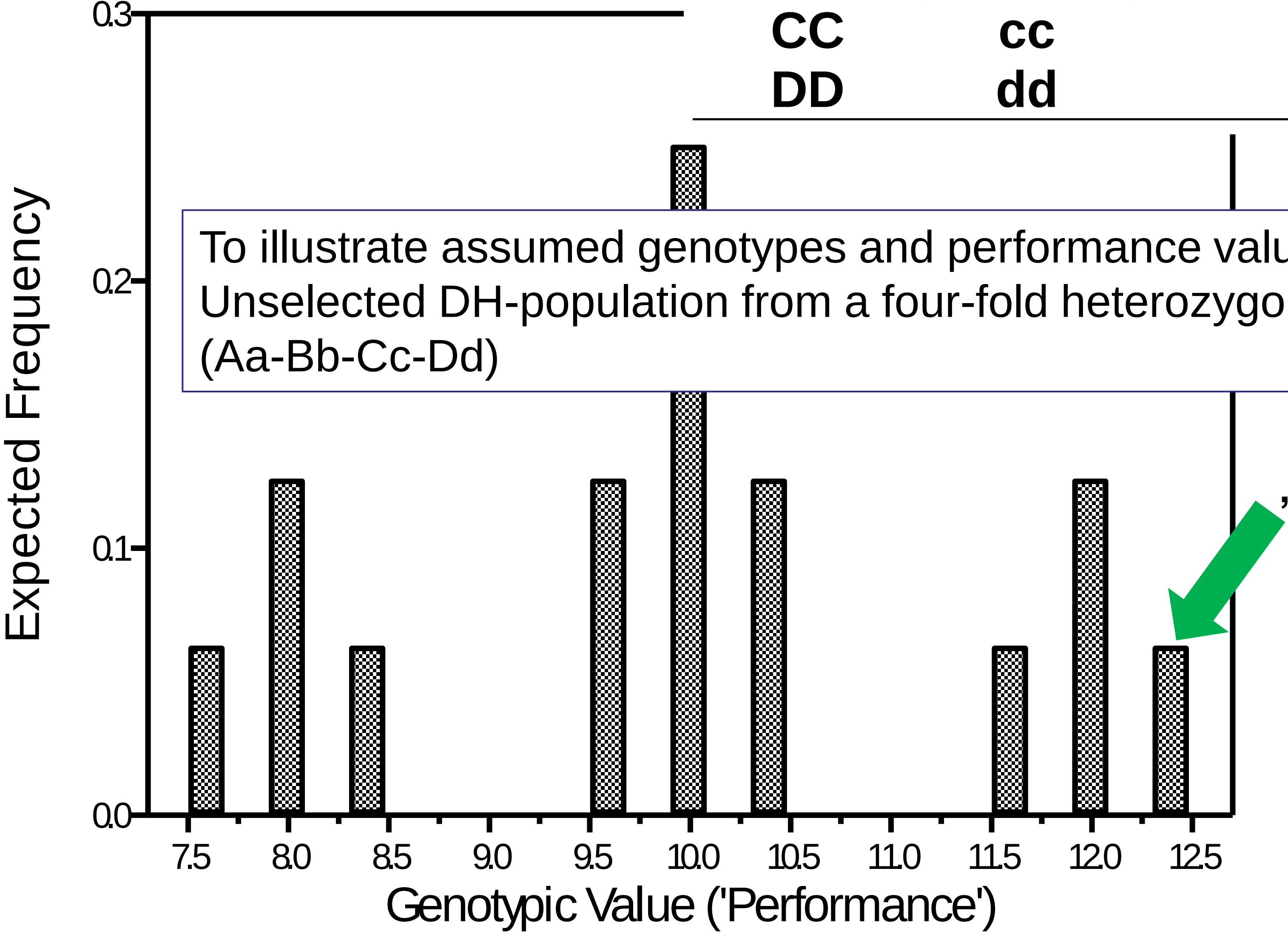
I intend to remind us that:

- In spite of same Breeding Value, outcome may be different (… if you look for ‘best’ genotype);
- When planning a cross, genotypic values may deceive you; detailed consideration of genes may be needed;

And I intend to show a ‘real’ example of marker-assisted pyramiding of alleles

First item

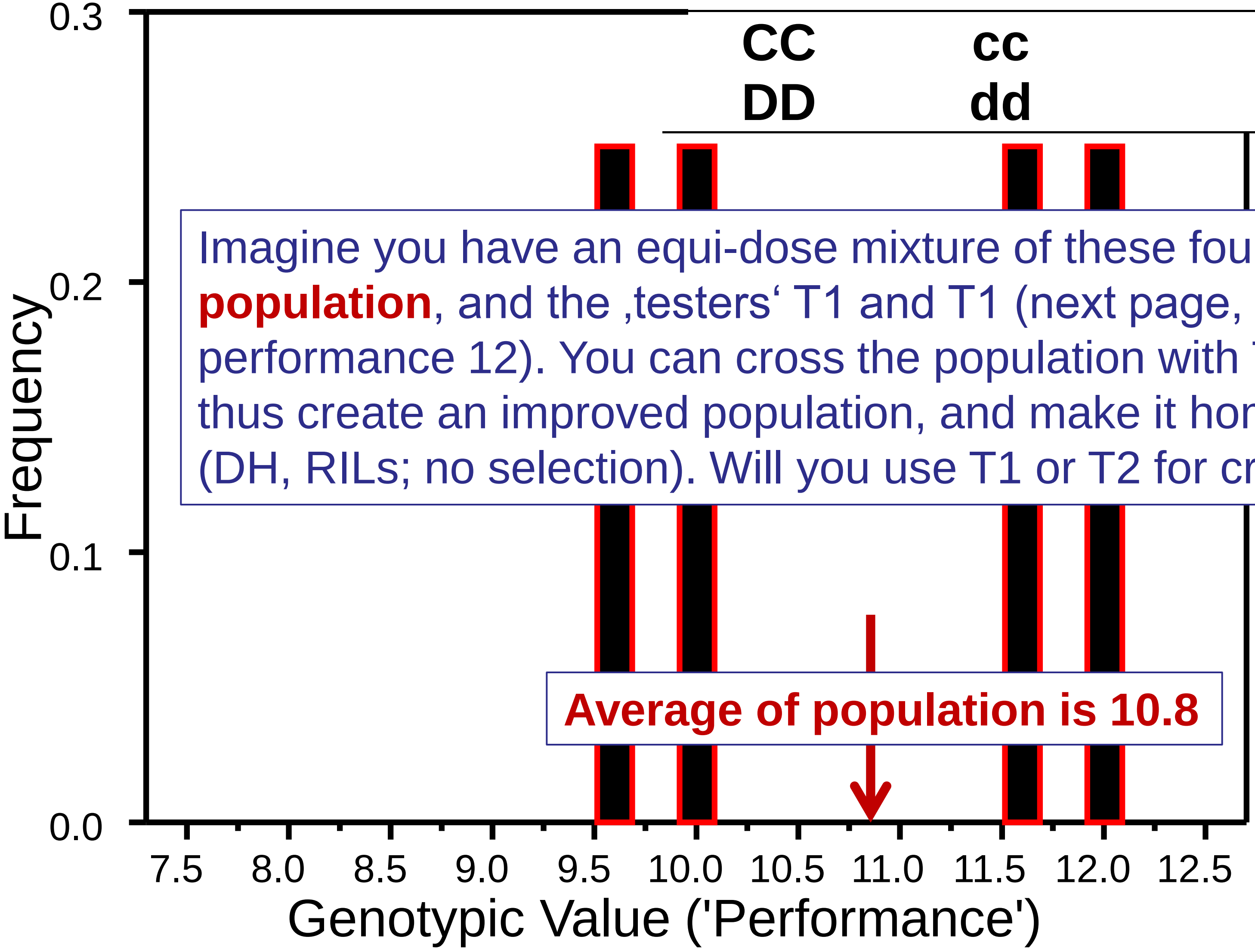
Genotype		Additive effect ‘a’
AA	aa	0.2
BB	bb	0.2
CC	**cc**	**1.0**
DD	**dd**	**1.0**



To illustrate assumed genotypes and performance values:
Unselected DH-population from a four-fold heterozygous F1
(Aa-Bb-Cc-Dd)

‚Best DH‘
AA-BB
CC-DD

Genotype		Additive effect ‘a’
AA	aa	0.2
BB	bb	0.2
CC	**cc**	**1.0**
DD	**dd**	**1.0**



Imagine you have an equi-dose mixture of these four lines as **population**, and the ‚testers‘ T1 and T1 (next page, both with performance 12). You can cross the population with T1 and T2, thus create an improved population, and make it homozygous (DH, RILs; no selection). Will you use T1 or T2 for crossing?

Average of population is 10.8

Homozygous genotypes at four unlinked loci & corresponding ‘performances’. Average ‘performance’ of all homozygotes is 10.0

		DD		dd	
		BB	bb	BB	bb
CC	AA	12.4	**12.0**	10.4	10.0
	aa	**12.0**	11.6	10.0	9.6
cc	AA	10.4	10.0	8.4	8.0
	aa	10.0	9.6	8.0	7.6

Genotype		Additive effect ‘a’
AA	aa	0.2
BB	bb	0.2
CC	**cc**	**1.0**
DD	**dd**	**1.0**

Genotypes and ‘performance’ of two ‘testers’ and of **population**

T1		T2		**Population**		Additive effect ‘a’
Genot.	Perf.	Genot.	Perf.	Genotypes	Perf.	
AA	12.0	aa	12.0	aa	**10.8**	0.2
bb		**BB**		**BB** bb 1:1		0.2
CC		**CC**		**CC**		1.0
DD		**DD**		**DD** dd 1:1		1.0

DH/RIL-offspring of ‘T1 x Population’ and of ‘T2 x Population’

T1 x Population				T2 x Population			
Genotypes			Perf.	Genotypes			Perf.
AA	aa	1:1	**11.4**		aa	-	**11.4**
BB	bb	1:3		**BB**	bb	3:1	
CC		-		**CC**		-	
DD	dd	3:1		**DD**	dd	3:1	

Min-Max: 9.6 - **<u>12.4</u>**

Min-Max: 9.6 – 12.0

Breeding value of testers is **11.4** – **10.8** = 0.6

Genotypes and ‘performance’ of two ‘testers’ and of population

T1		T2		Population				Additive effect ‘a’
Genot.	Perf.	Genot.	Perf.	Genotypes			Perf.	
AA	12.0	aa	12.0	aa			**10.8**	0.2
bb		**BB**		**BB**	bb	1:1		0.2
CC		**CC**		**CC**				1.0
DD		**DD**		**DD**	dd	1:1		1.0

DH/RIL-offspring of ‘T1 x Population’ and of ‘T2 x Population’

T1xPopulation				T2xPopulation			
Genotypes			Perf.	Genotypes			Perf.
AA	aa	1:1	**11.4**	aa		-	**11.4**
BB	bb	1:3		**BB**	bb	3:1	
CC		-		**CC**		-	
DD	dd	3:1		**DD**	dd	3:1	
Min-Max: 9.6 - **12.4**				Min-Max: 9.6 – 12.0			

Same **Breeding Value** of the two testers => same improvement of population; But not same ‚best‘ genotype, because testers ‚complement‘ the population differently: **Genes Count**!

Second item

Homozygous genotypes at four unlinked loci & corresponding ‘performances’. Average ‘performance’ of all homozygotes is 10.0

		DD		dd	
		BB	bb	BB	bb
CC	AA	12.4	12.0	10.4	10.0
	aa	12.0	11.6	10.0	**9.6**
cc	AA	10.4	10.0	**8.4**	8.0
	aa	10.0	**9.6**	8.0	7.6

You use a three-way cross to breed a superior **barley**.
Performances are:
P1 = 8.40, **P2 = 9.60**, **P3 = 9.60**.
How to cross?

Expected performance of DH-offspring from:

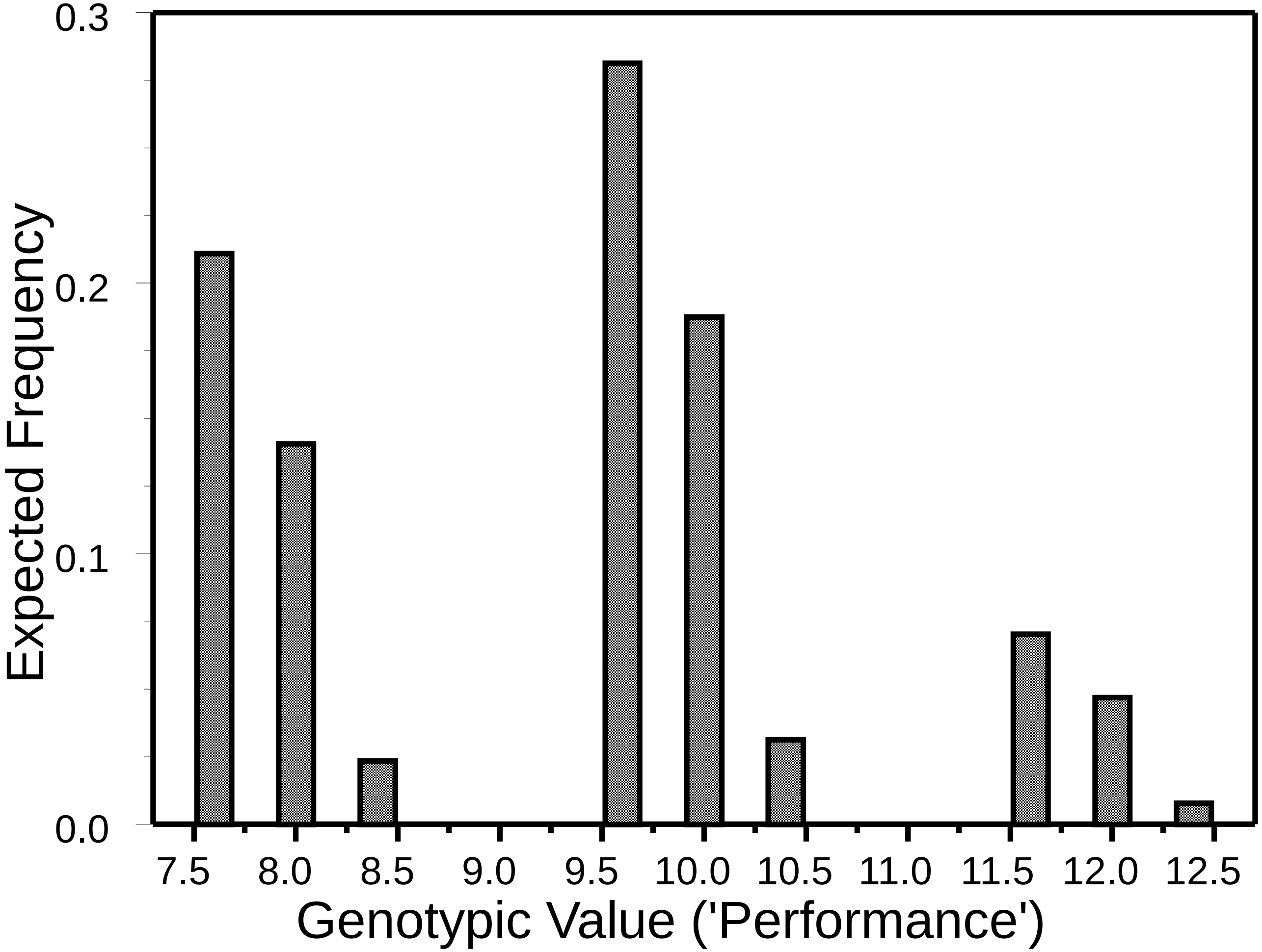
I (**P1** x P2) x P3 = ¼(**8.4**) + ¼(9.6) + ½ (9.6) = 9.3
II (**P1** x P3) x P2 = ¼(**8.4**) + ¼(9.6) + ½ (9.6) = 9.3
III (P2 x P3) x **P1** = ¼(9.6) + ¼(9.6) + ½ (**8.4**) = **9.0**

So, you choose the first or second option. Well …;
You take the average performance of the offspring as criterion.

What about the best single offspring that segregates from these crosses?

I (**P1** x P2) x P3 = ¼(**8.4**) + ¼(9.6) + ½ (9.6) = 9.3

II (**P1** x P3) x P2 = ¼(**8.4**) + ¼(9.6) + ½ (9.6) = 9.3

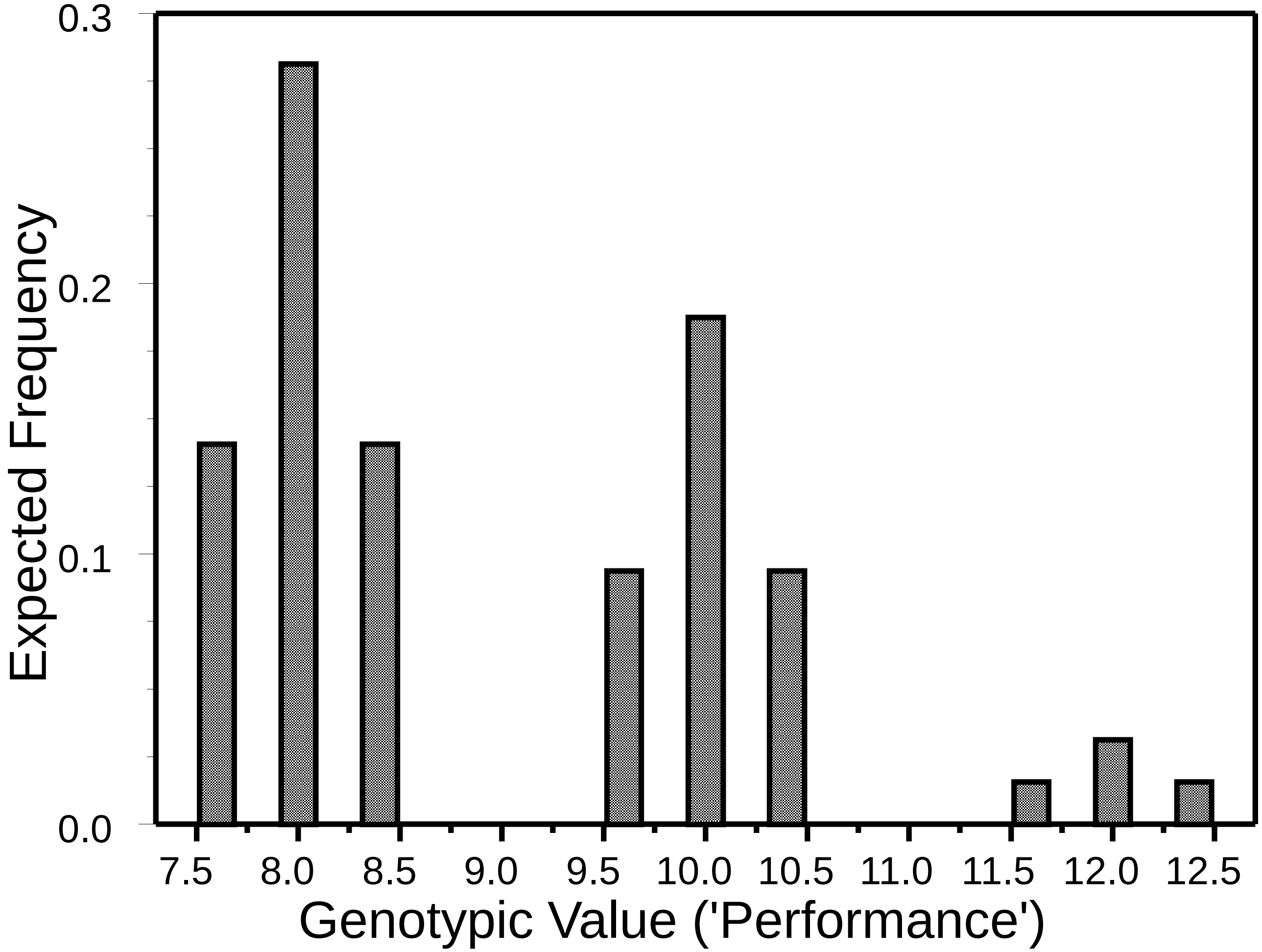


Average is 9.3

Best one is 12.4

Frequency of
‚best‘ is 1/128

III (P2 x P3) x **P1** = ¼(9.6) + ¼(9.6) + ½ (**8.4**) = **9.0**



Average is 9.0

Best is 12.4

Frequency of ‚best‘ is 1/64

How come?

Frequency of ‚best‘

I

P1			P2			P3	
Gen.	Value		Gen.	Value		Gen.	Value
AA	**8.4**	X	aa	9.6	X	aa	10.4
BB			bb			bb	
cc			CC			cc	
dd			dd			DD	

$(\tfrac{1}{4})^2 \ (\tfrac{1}{4})^1 \ (\tfrac{1}{2})^1 = 1/128$

II

P1			P3			P2	
Gen.	Value		Gen.	Value		Gen.	Value
AA	**8.4**	X	aa	10.4	X	aa	10.4
BB			bb			bb	
cc			cc			CC	
dd			DD			dd	

$(\tfrac{1}{4})^1 \ (\tfrac{1}{4})^2 \ (\tfrac{1}{2})^1 = 1/128$

III

P2			P3			**P1**	
Gen.	Value		Gen.	Value		Gen.	Value
aa	10.4	X	aa	10.4	X	AA	**8.4**
bb			bb			BB	
CC			cc			cc	
dd			DD			dd	

$\boxed{(\tfrac{1}{4})^1 \ (\tfrac{1}{4})^1 \ (\tfrac{1}{2})^2 = 1/64}$

I
or
II

P1			P2			P3	
Gen.	Value		Gen.	Value		Gen.	Value
AA	**8.4**	X	aa	9.6	X	aa	10.4
BB			bb			bb	
cc			CC			cc	
dd			dd			DD	

Frequency of ‚best‘

$(\frac{1}{4})^{2}\ (\frac{1}{4})^{1}\ (\frac{1}{2})^{1} = 1/128$

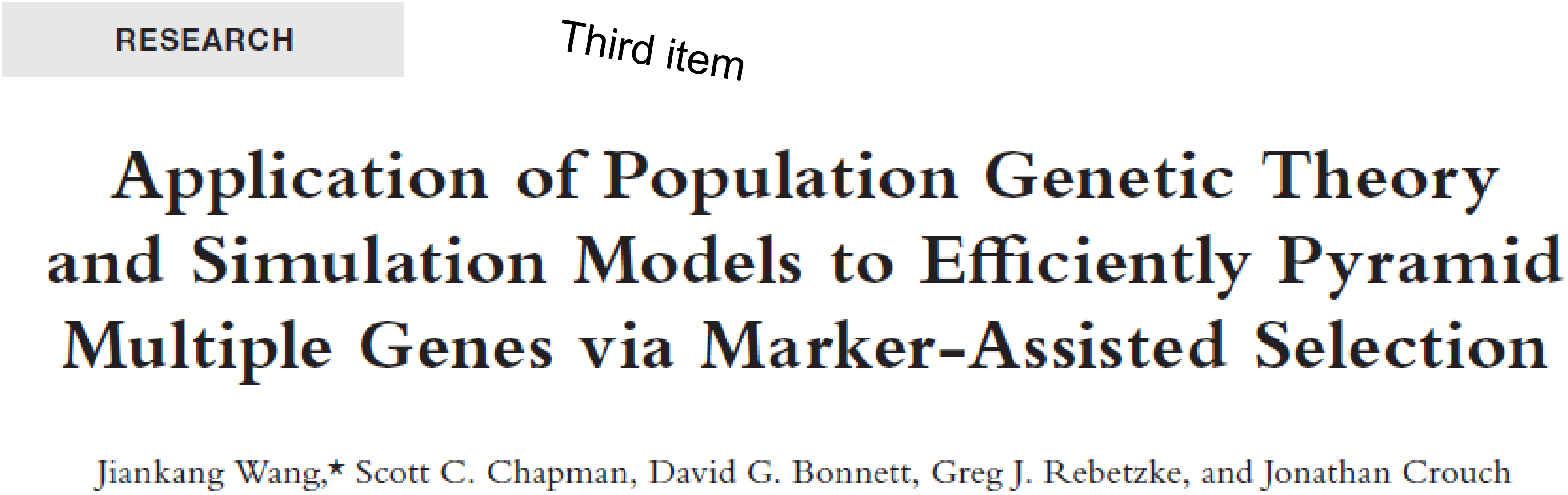
III

P2			P3			**P1**	
Gen.	Value		Gen.	Value		Gen.	Value
aa	10.4	X	aa	10.4	X	AA	**8.4**
bb			bb			BB	
CC			cc			cc	
dd			DD			dd	

$\boxed{(\frac{1}{4})^{1}\ (\frac{1}{4})^{1}\ (\frac{1}{2})^{2} = 1/64}$

To maximize the frequency of best genotype in a segregating familiy, it may not be enough to know the parents‘ genotypic or breeding value but it may be necessary to consider the details, such as gene number, complementation of genes (and linkage and allele phase ...)

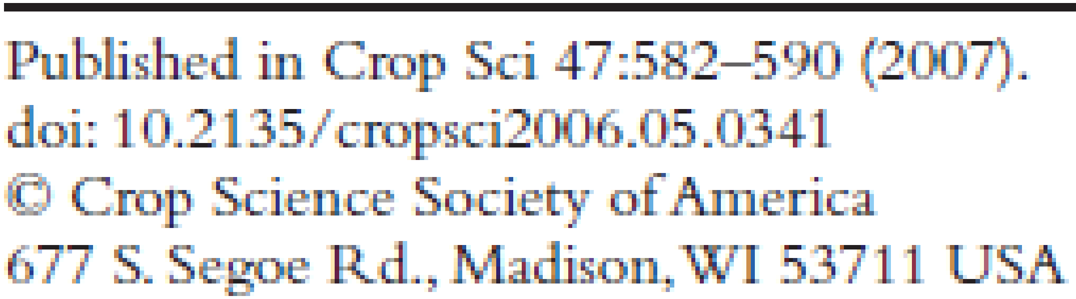
Third item



RESEARCH

Application of Population Genetic Theory and Simulation Models to Efficiently Pyramid Multiple Genes via Marker-Assisted Selection

Jiankang Wang,* Scott C. Chapman, David G. Bonnett, Greg J. Rebetzke, and Jonathan Crouch



Published in Crop Sci 47:582–590 (2007).
doi: 10.2135/cropsci2006.05.0341

677 S. Segoe Rd., Madison, WI 53711 USA

Nine loci, their locations, the genotype for the three parents and the target alleles. Wang et al., 2007. Crop Science 47, 582-590.

Gene / Locus	**Rht-B1**	**Rht-D1**	**Rht8**	**Sr2**	**VPM**	**Cre1**	**Glu-B1**	**Glu-A3**	**tin**	Number of target alleles
Chromosome	4BS	4DS	2DL	3BS	7DL	2BL	1BL	1AS	1AS	
Marker type	Codominant				Dominant		Codominant			
Distance (cM)	0.0		0.6	1.1	0.0				0.8	
Target alleles	Rht-B1**a**	Rht-D1**a**	**R**ht8	**S**r2	**V**PM	**C**re1	Glu-B1**i**	Glu-A3**b**	**t**in	
	Dwarfing			Rust		Nematode	Quality		Tiller	
Rht-B1b, Rft-D1b reduce plant height & coleoptile length: unfavorable under drought **R**ht8 reduces plant height without reducing coleoptile length: favorable under drought										
HM14BS	**a**	**a**	**R**	s	v	c	a	e	T	**3**
Silverstar+tin	b	**a**	r	s	v	**C**	**i**	c	**t**	**4**
Sunstate	**a**	b	r	**S**	**V**	c	**i**	**b**	T	**5**

Nine loci, their locations, the genotype for the three parents and the target alleles. Wang et al., 2007. Crop Science 47, 582-590.

HM14BS	a	a	R	s	v	c	a	e	T	3
Silverstar+tin	b	a	r	s	v	C	i	c	t	4
Sunstate	a	b	r	S	V	c	i	b	T	5
Segregation 3-way F1	1:1	-	1:1	-	-	1:1	1:1	-	1:1	3.125%
MAS in 3-way F1	aa	ab	Rr	Ss	Vv	Cc	ii	bc be	tT	
	½	-	½	-	-	½	½	-	½	
Segregation 3-way F2	-	1:2:1	1:2:1	1:2:1	1:2:1	1:2:1	-	1:2:1	1:2:1	3.96%
MAS in 3-way-F2 (‘enrichment’)	aa	ab aa	RR	Ss SS	Vv VV	Cc CC	ii	bc/e bb	tT tt	
	-	¾	¼	¾	¾	¾	-	Repulsion 3cM		
DHs derived from enriched F2	-	⅔	-	⅔	⅔	⅔	-			1.60%
	aa	aa	RR	SS	VV	CC	ii	bb	t t	

Nine loci, their locations, the genotype for the three parents and the target alleles. Wang et al., 2007. Crop Science 47, 582-590.

Gene / Locus	**Rht-B1**	**Rht-D1**	**Rht8**	**Sr2**	**VPM**	**Cre1**	**Glu-B1**	**Glu-A3**	**tin**	
Chromosome	4BS	4DS	2DL	3BS	7DL	2BL	1BL	1AS	1AS	Number of target alleles
Marker type	Codominant				Dominant		Codominant			
Distance (cM)	0.0		0.6	1.1	0.0				0.8	
Target alleles	Rht-B1**a**	Rht-D1**a**	**R**ht8	**S**r2	**V**PM	**C**re1	Glu-B1**i**	Glu-A3**b**	**t**in	
	Dwarfing			Rust		Nematode	Quality		Tiller	
Rht-B1b, Rft-D1b reduce plant height & coleoptile length: unfavorable under drought **R**ht8 reduces plant height without reducing coleoptile length: favorable under drought										
HM14BS	**a**	**a**	**R**	s	v	c	a	e	T	**3**
Silverstar+tin	b	**a**	r	s	v	**C**	**i**	c	**t**	**4**
Sunstate	**a**	b	r	**S**	**V**	c	**i**	**b**	T	**5**
Segregation 3-way F1	1:1	-	1:1	-	-	1:1	1:1	-	1:1	3.125%
MAS in 3-way F1	**aa**	ab	**R**r	**S**s	**V**v	**C**c	**ii**	**b**c **b**e	**t**T	
	½	-	½	-	-	½	½	-	½	
Segregation 3-way F2	-	1:2:1	1:2:1	1:2:1	1:2:1	1:2:1	-	1:2:1	1:2:1	3.96%
MAS in 3-way F2 ('enrichment')	**aa**	**a**b **aa**	**RR**	**S**s **SS**	**V**v **VV**	**C**c **CC**	**ii**	**b**c/e **bb**	**t**T **tt**	
	-	¾	¼	¾	¾	¾	-	Repulsion 3cM		
DHs derived from 'enriched' F2	-	⅔	-	⅔	⅔	⅔	-			1.60%
	aa	**aa**	**RR**	**SS**	**VV**	**CC**	**ii**	**bb**	**t t**	

Minimum population size to get at least one with 99% probability

$N_{min} = 146$

$N_{min} = 114$

$N_{min} = 286$

“**Genomic selection** is **revolutionizing** both animal and **plant breeding**”

Genomic selection in plant breeding: from theory to practice. Jannink, 2010.
Briefings in Functional Genomics 9, 166-177.

I intended to remind us that:

- In spite of same Breeding Value, outcome may be different (… if you look for ‘best’ genotype);
- When planning a cross, genotypic values may deceive you; detailed consideration of genes may be needed;

And I showed a ‘real’ example of marker-assisted pyramiding of alleles

Foto from visit at IAV, Rabat

Thank you for attention

P2			P3			P1	
Gen.	Value		Gen.	Value		Gen.	Value
aa bb CC dd	10.4	X	aa bb cc DD	10.4	X	AA BB cc d	8.4

Frequency of ,best‘
$(\frac{1}{4})^1 (\frac{1}{4})^1 (\frac{1}{2})^2 =$ **1/64**

How many offspring individual do you need to be – say – **99%** ,sure‘ to have on of these ,best‘ in your offspring family?

I mean, if you just take N=64 you may not be sure to get the expected **1 out of 64**!

If you take one offspring, the probability to NOT HAVE the best one is **63/64**.

If you take 44 offspring, the probability to NOT HAVE at least one best is [**63/64**]^{44} =0.50.

How many do you need to bring this to <0.01?

Probability to not have at least one best <0.01?

N= log(**0.01**) / log(**63/64**) = 293