This is a list with ~statements which are wrong. It is meant as motivation to ponder about ‘what is wrong here’. wlink@gwdg.de Juni 2019

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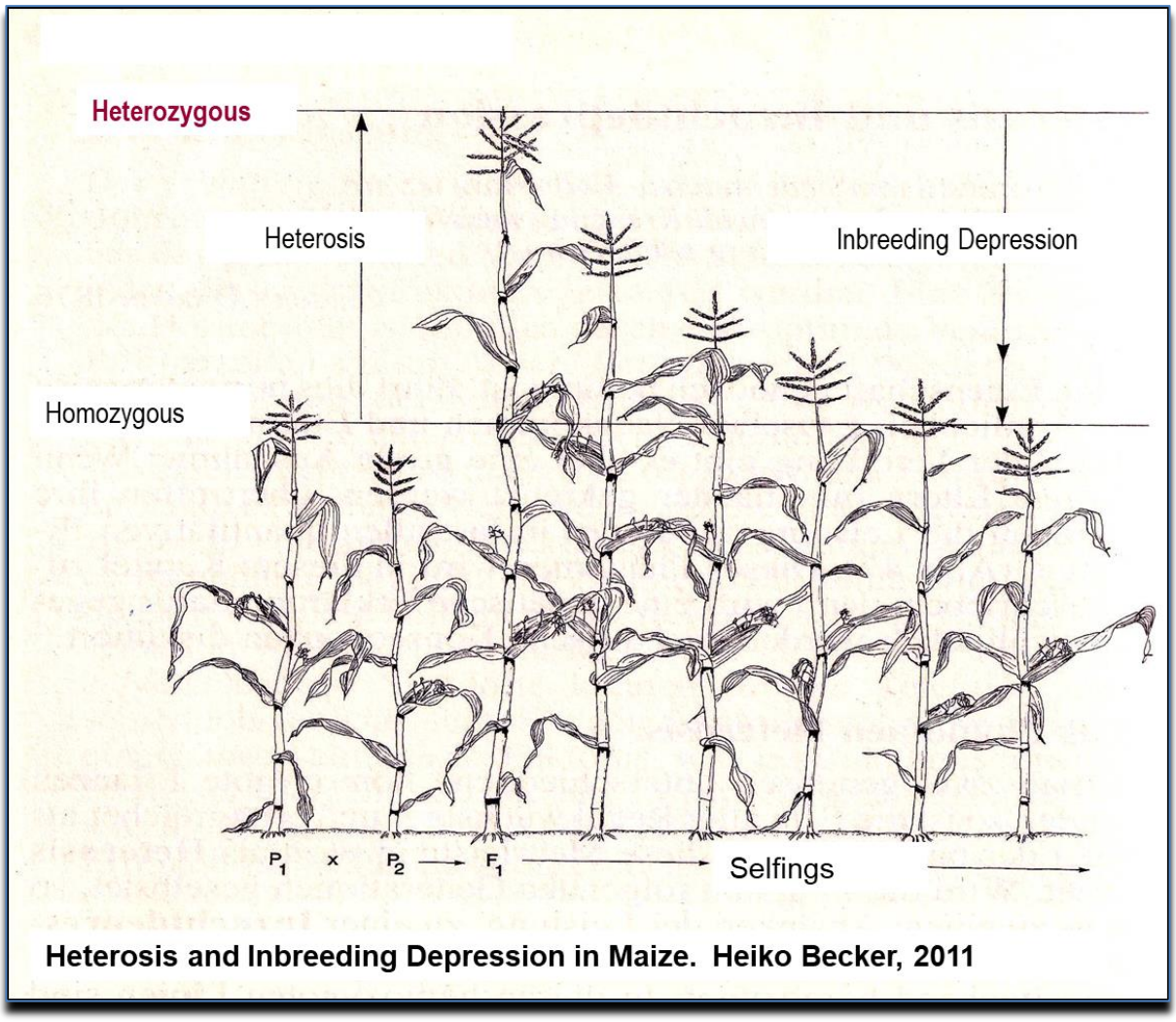

Heterosis and Inbreeding Depression in Maize. Heiko Becker, 2011

HETEROSIS IN DIPLOID CULTIVARS

In a diploid species with two alleles at a locus, the average heterosis of a cross is greatest for a single-cross hybrid due to the occurrence of the greatest possible

On the heterosis of single-cross, three-way cross and four-way cross hybrids

number of loci with a dominant allele. For example, the mating of the inbreds *AABBccdd* × *aabbCCDD* results in single-cross individuals with a dominant allele at each locus, *AaBbCcDd*. Dominant alleles at each of the four loci for all single-cross individuals provide the highest average performance for the cross.

A three-way hybrid is produced by the mating of a single-cross hybrid to a third inbred parent. The average heterosis expressed by the three-way hybrid

Walter R. Fehr, Principles of Cultivar Development, Volume 1. Theory and Technique. 1991. Page 148.

the three-way than in the single cross. Consider the mating of the single cross *AaBbCcDd* with the inbred *AABBccdd*. The genotypes of the hybrid progeny are *A__B__CcDd*, *A__B__Ccdd*, *A__B__ccDd*, *A__B__ccdd*. Because of the occurrence of homozygous recessive loci in some of the progeny, the frequency of loci with dominant alleles and the average heterosis in the three-way cross is less than in the single cross.

In a double-cross hybrid formed by mating two single crosses, the average frequency of loci with a dominant allele and average heterosis would be less than in a three-way hybrid. Consider the mating of two single crosses with identical genotypes, *AaBbCcDd* × *AaBbCcDd*. Homozygous recessive alleles at one or more loci in some of the progeny of this mating would reduce the average heterosis of the cross.


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4. Heterosis in F_2 is half as large as heterosis in F1
5. F_2 is 50% heterozygous and 50% homozygous
6. The more the parents were inbred, the higher is heterosis of their hybrid
7. 4way crosses yield less than 2way crosses
8. The advantage of hybrid cultivars is their heterosis
9. Interspecific hybrids are sterile if parents differ in chromosome number
10. Backcrossing is mainly a strategy to introduce monogenic features (such as resistance). It can be applied in line, clone, hybrid, population breeding.
11. After transforming (GMO) a fair number of different genotypes and making them homozygous for the trans-gene (e.g. sunflower lines, herbicide resistance), one can create from them a diverse (synthetic) population which is stable and homogenous for this feature.
12. Triticale (such as the cultivar 'Tulus') is a cross between wheat (*T. aestivum*) and rye (*S. cereale*)
13. If a chromosome does not show recombination at 25% of its length (e.g. near centromere), and has e.g. 100cM mapping length, then at about 25cM no markers can be placed.
14. You mutagenize seed (corn, canola; M0), and if one plant then has the mutation (M1); and the mutation is recessive and has no consequence for gamete viability. And you self-fertilize the M1-plant. Then in F2 you expect the Mendelian 1 : 3 segregation for the mutant vs. wild-type phenotype
15. The higher the number of genes that contribute to the genetic variation of a trait, the larger the genetic variance tends to be
16. The higher the number of genes that contribute to the genetic variation of a trait, the smaller the genetic variance tends to be

17. Whether you take L locations and Y years as factors in your linear model or you model this as L x Y 'environments' in your linear model, for the heritability (broad sense) this does not make a difference
18. ●Drift causes inbreeding ●Inbreeding reduces dominance variance and increases additive variance hence ●Drift increases additive variance
19. Selection exploits diversity, hence variance. Selection reduces the genetic variance, it cannot increase the genetic variance.
20. In HWE, via random mating, only the additive effects are inherited ($\alpha 1$, $\alpha 2$, α). These are the statistical, hence average effects of the alleles. The dominance deviations ("SCA") of individuals have thus heritability of zero in a HWE population.
21. The larger the impact of the different locations and years etc. on the trait, the smaller is heritability (broad sense)
22. You need at least data from 2 environments to estimate h^2 of a genotype
23. Random mating is 'random mating of male and female gametes', this is true in animals and in plants
24. The genetic coefficient of co-ancestry (consanguinity, genetic relationship) on an individual to itself is r=1
25. Based on CMS, one can well produce seed of 2way, 3way and 4way hybrids (e.g. in sunflower, corn, canola)
26. Hybrid cultivars show a 'dead-end' feature. They 'biologically' block farmers' rights and breeders' rights
27. If in resistance A (e.g. rust) four genes code for the relevant metabolic steps (enzymes) and in resistance B (mildew) two genes, then the Mendelian segregation pattern for A must be more complicated (1:2:1; 9:3:3:1; etc.) than for B
28. Homozygous parents do not transfer their 'personal' homozygosity into their crossbred offspring, as obvious in DH-based hybrid breeding

29. Crossing a number of inbred lines e.g. in a diallel pattern means genetically recombining them
30. By calculating means across replicates, we can eliminate the effect of soil heterogeneity and the effect of competition among neighbors (different plant heights)
31. Most mutant alleles are inherited in a recessive way
32. *Triticum monococcum* was one of the parents (A-genome) of our modern wheat
33. A selection intensity of 1% can cause risk of drift
34. Faba bean breeders exploit the linkage between hilum colour and Vicine content. White hilum colour is used to select for low Vicine (marker-assisted selection, morphological marker). Hence, one could exploit this and screen genebank accessions for hilum colour, easy to do, and thus find very many genetically diverse low-Vicine types.

35. 2/3 = 0.67
36. If you test for 1:3 (χ^2-test), you have 1df, and the tabulated value for P=5% is 3.841. If you find a value of less than this, then you can statistically accept the hypothesis of mongenic dominant-recessive inheritance
37. The 'variance component of genotypes' is an estimate of the genetic variance (basis: series of field tests with a fixed set of genotypes). You can take this variance as estimator of the variance among the true genotypic values of your candidates.
38. A phenotypically <u>superior</u> candidate has the same probability to be impacted by a positive (or negative) GxE interaction as a phenotypically <u>inferior</u> candidate.

39. If you have tested your N=12 candidates in three environments for yield and resistance, then you should calculate the breeding-relevant correlation between yield and resistance from 3 x 12 = 36 data pairs (results), because this gives you more degrees of freedom when testing the correlation for significance
40. Exotic germplasm typically has more unfavorable QTL than adapted germplasm
41. If your DNA-markers are not mapped, then you cannot check their usefulness for MAS, neither via biparental QLT-mapping nor via GWAS
42. If you find a very clear, highly significant marker in you search for QTL, then this marker can directly applied in breeding (MAS)
43. If applying a FDR of <10% (Benjamini, Hochberg, 1995), then the highest hit (marker) can be termed causative marker
44. The markers which you find significant suffer from the uncertainty of being estimated stronger-than-true or weaker-than-true. This error is symmetrical and, on average, is balanced
45. To find the position of your candidate gene quite precisely you must employ very many markers. In a genome of 1400cM length (*Vicia faba*) you should at least employ [1.400cM / 0.1cM] = 14.000 markers, this means you need to use at least a 14K chip
46. The higher the ratio of root-mass/shoot-mass, the higher is the drought-stress tolerance of a genotype