CHISINAU, MOLDOVA
Institute of Genetics and Physiology of Plants

The genetic of kernel set in one of the maize hybrids

--Mikhailov, ME

The double haploid lines derived from MK01 x A619 maize hybrid show the very large spectrum of kernel set. About 10 lines from 45 are characterized by full ears (as MK01 parent), 1-2 lines have empty or near empty (few kernels on ear) cobs, the other lines are intermediate (see Fig.1). This phenomenon is not due to meiotic aberrations, because artificial pollination produces normal full ears for all these lines. It appears this is due to difficult outlet of silk from ear. This feature is clearly inherited from A619 parent line, which shows the mean kernel set 70-90% at different years (if we take a full ear as 100%). The hybrid MK01 x A619 is characterized by full ears, as the parent MK01.

To investigate the genetic control of this phenomenon, we have chosen the worst double haploid lines – DH12-00 and derived from it the analyzing crosses (MK01xDH12-00) x DH12-00 and (A619xDH12-00)xDH12-00. In 2009 the 79 plants of first cross and the 79 plants of second cross were tested, in 2011 – 47 and 50, respectively. In the first cross the clear bimodal distribution for kernel set was observed. This suggests the small number of genetic factors that control this trait and differ in MK01 and DH12-00 lines. The A619 and DH12-00 lines should be distinguished by larger number of genes.

To evaluate and eliminate the environmental variation, the selfed progeny of these crosses were tested (Table 2). The genetic variance obtained was used for estimation of number of genetic factors influencing kernel set. Number of factors was estimated by the formula Castle-Wright modified to our case:

$$n = \frac{(2+\beta)^2}{64\,\sigma_g^2} \ .$$

Mean degree of dominance β was calculated as

$$\beta = \frac{KS(PxDH12{-}00) - (KS(P) + KS(DH12{-}00))/2}{KS(P) - KS(DH12{-}00)}$$

where KS is mean kernel set of genotype given in brackets, P is MK01 or A619.

These results, likely, suggest that variation between double haploid lines for kernel set caused by two recessive mutation of A619 line preventing outlet of silk from ear. In the A619 line these mutations do not act in full as they are compensated by several (5-7) semi dominant suppressors. In a recombinant progeny this compensatory gene complex breaks down, allowing the full action of mutation until almost empty ears in some genotypes, including selected for analyzing crosses the DH12-00 line.

Table 1. Mean kernel set in 2011

Genotype	Mean kernel set, %
MK01	99.8±0.2
A619	82.5±4.5
MK01xA619	99.9±0.1
DH12-00	0.8±0.3
MK01xDH12-00	88.7±3.7
A619xDH12-00	60.4±7.0
(MK01xDH12-00)xDH12-00	39.7±5.6
[(MK01xDH12-00)xDH12-00]⊗	33.6±4.6
(A619xDH12-00)xDH12-00	17.9±4.8
[(A619xDH12-00)xDH12-00]⊗	11.6±1.7

Table 2. Variances of kernel set and estimation of number of genetic factors

Parameter	[(MK01xDH12-00) x DH12-00]⊗	[(A619xDH12-00) x DH12-00]⊗
Number of families	27	46
σ^2 between families	661.58	127.65
σ^2 environmental	58.33	22.11
σ^2 genetic	603.26	105.54
Mean degree of dominance	0.78	0.46
Number of genetic factors	2.0±0.6	6.0±1.3

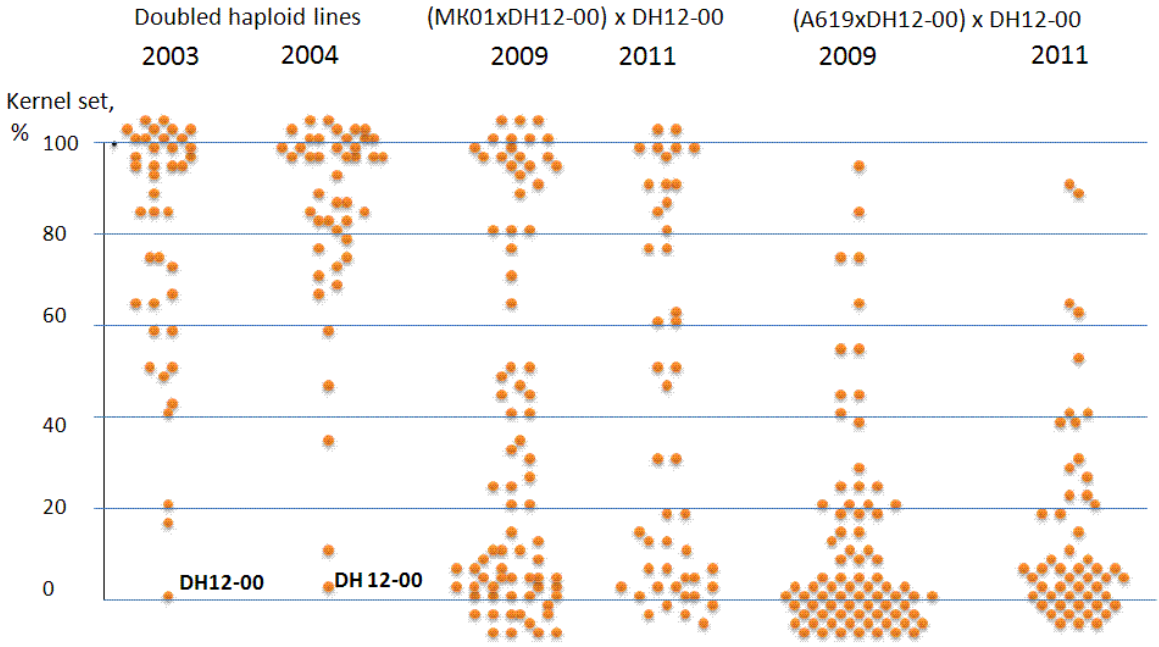

Fig.1. The genetic distribution of some populations for kernel set
Comment. Some of the points with coordinates 0 and 100 are located below 0 and above 100