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Combinative properties of maize double haploids

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The combinative capacity of the double haploid (DH) lines derived from the maize hybrids MK01 x A619 and Rf7 x Ku123 has been tested. In DH lines genes from both the parents are combined at random, so their combinative capacity varies and depends on number of favorable alleles obtained from each parent.

We tested combinative capacity of grain yield in DHxP crosses. This calculated parameter was used for analysis:

$$C(P_1) = \frac{M(DHxP_2) - M(P_2)}{M(F_1) - M(P_2)}$$

where M is grain yield of the genotype indicated in brackets. Grain yield of parents and F_1 was as follow (gm/plant at the density 4/m²):

2010 year: MK01 - 100.8±5.6, A619 - 22.4±4.4, MK01xA619 - 181.6±5.4

2011 year: Rf7 - 105.6±5.2, Ku123 - 76.7±3.4, Rf7xKu123 - 191.9±4.2.

We name the $C(P_1)$ parameter as combinative capacity of the DH line relatively the P_1 parent. It shows the increase in grain yield which gives the DH line compared with increase, which gives the P_1 line (in crosses with the same line P_2). The value of $C(P_1)$ depends on the number of favorable alleles inherited by DH line from P_1 . The distribution of the DH lines by values of C is shown in Fig.1-4. The general statistics are given in Table.

In the absence of non allelic interactions (additive-dominant model) C should be distributed symmetrically about the value of 0.5. In fact, only $C(Ku123)$ is distributed symmetrically, otherwise C are less than 0.5, and in two cases significantly (see Table). This suggests significant role of non allelic interactions of complementary type between the favorable alleles of the lines MK01 and Rf7.

Non allelic interactions are not significant in the case of A619 and absent in the case of Ku123. Apparently, in these cases gene effects are summarized to additive-dominant model.

In Fig.1-4 the differences in the excess are clearly visible. The distributions of $C(MK01)$ and $C(Rf7)$ have the sharp peaks. In the distributions of $C(A619)$ and $C(Ku123)$ the peaks are less expressive. Sharpness of the peak should depend on the number of genetic factors affecting C . The more genetic factors, the sharper the peak. The number of genetic factors can be estimated from Castel-Wright. In our case, it looks like this:

$N = 0.25 / (\sigma^2 - e^2)$, where N is number of genetic factors, σ^2 is variance of C , e^2 is mean square error of partial value of C .

The estimations are given in Table. Under the assumption that the degree of dominance is equal to 1, these estimations mean the number of favorable alleles (or groups of linked alleles) in the corresponding line, responsible for heterosis of grain yield in crosses.

In both the studied hybrids the same phenomenon is observed. More productive parent has more alleles influencing heterosis, and significant non allelic interactions appear between them. In less productive parent number of favorable alleles is smaller and non allelic interactions between them are less significant or absent.

Table. Relative combinative capacity of DH lines

Hybrid	Parameter	Number of DH lines	Mean C	Standard deviation of C	Mean error of partial C	Estimated number of genetic factors
MK01 x A619	$C(MK01)$	41	0.387±0.021***	0.135	0.059	16
	$C(A619)$	42	0.442±0.030	0.192	0.101	9
Rf7 x Ku123	$C(Rf7)$	26	0.378±0.027***	0.137	0.049	15
	$C(Ku123)$	25	0.489±0.044	0.220	0.096	6

*** Difference from 0.5 is significant at $P < 0.001$

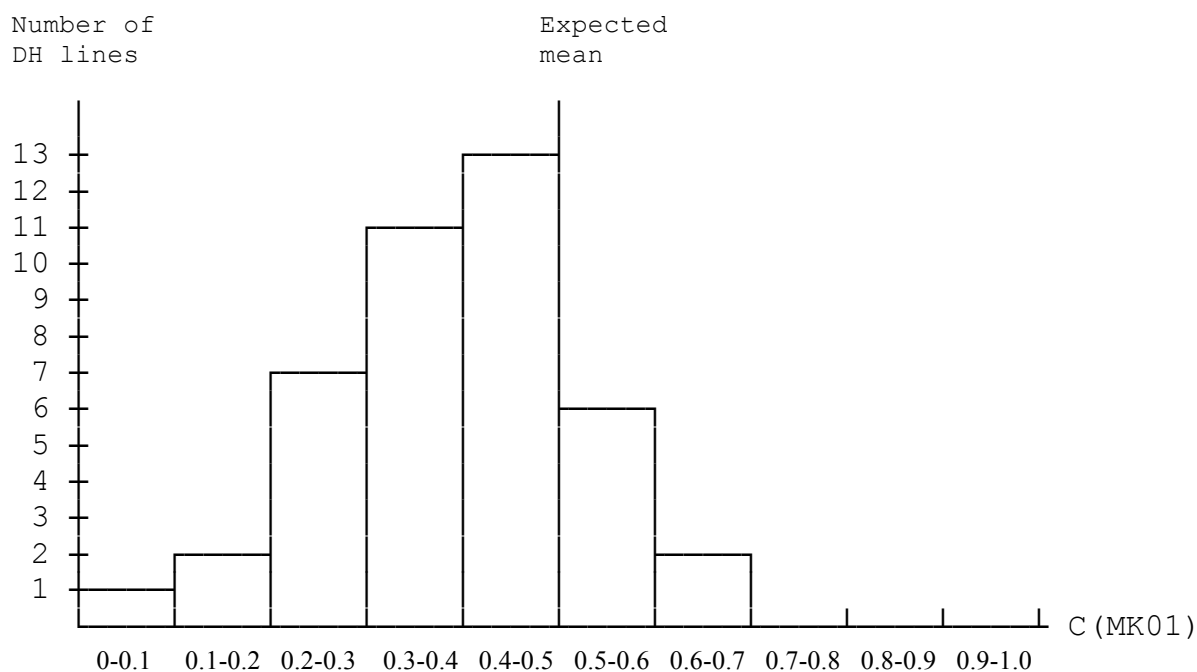


Fig.1. Distribution of DH lines from combinative capacity relatively MK01 (in crosses with A619)

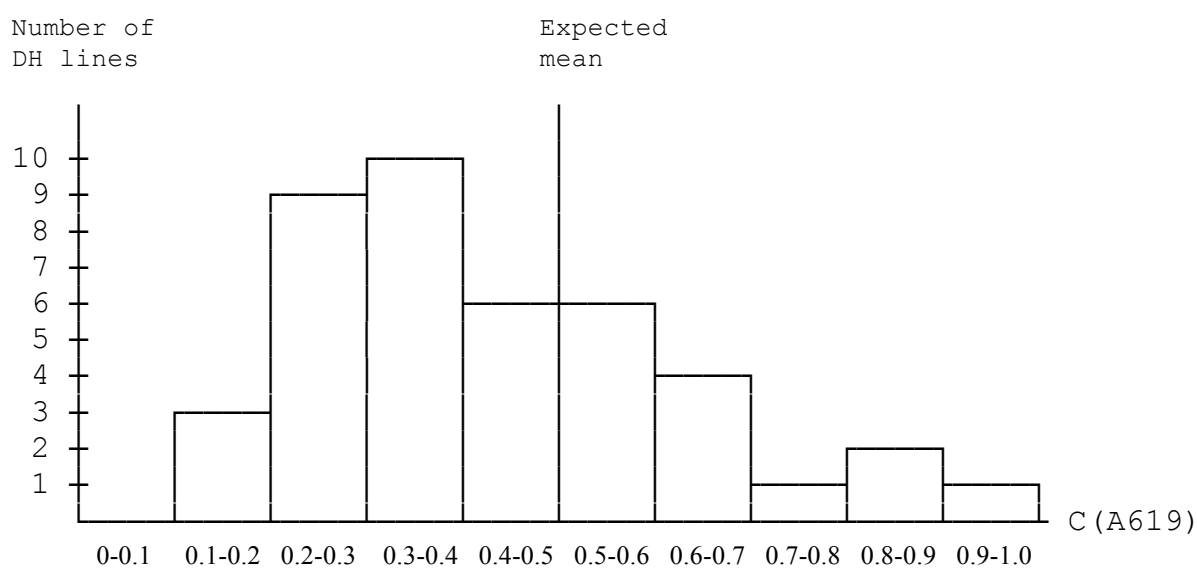


Fig.2. Distribution of DH lines from combinative capacity relatively A619 (in crosses with MK01)

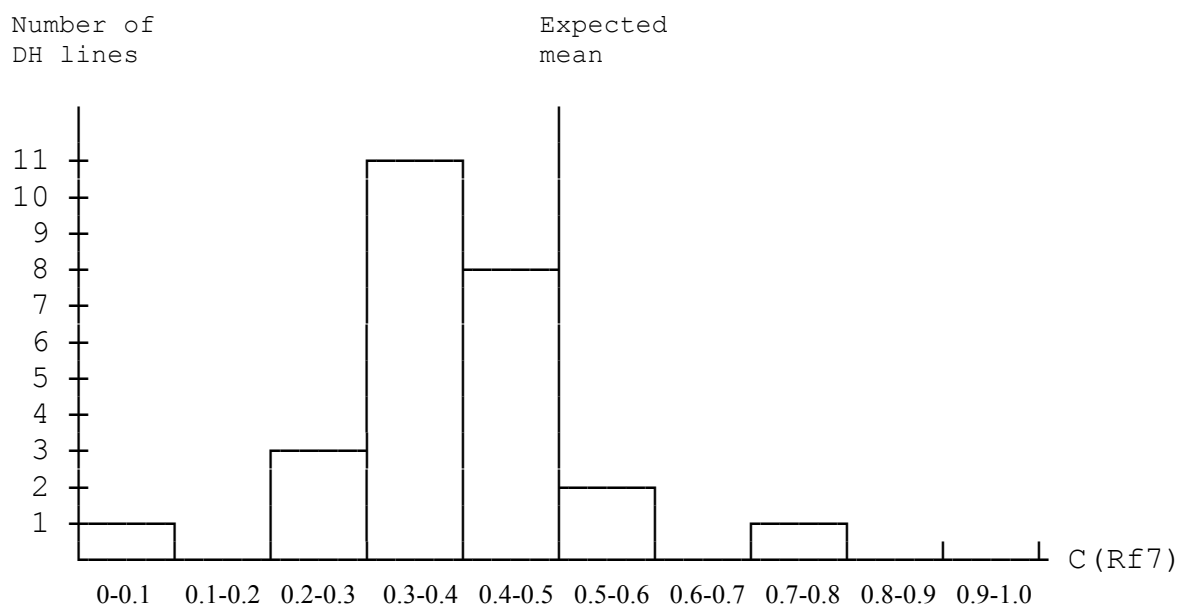


Fig.3. Distribution of DH lines from combinative capacity relatively Rf7 (in crosses with Ku123)

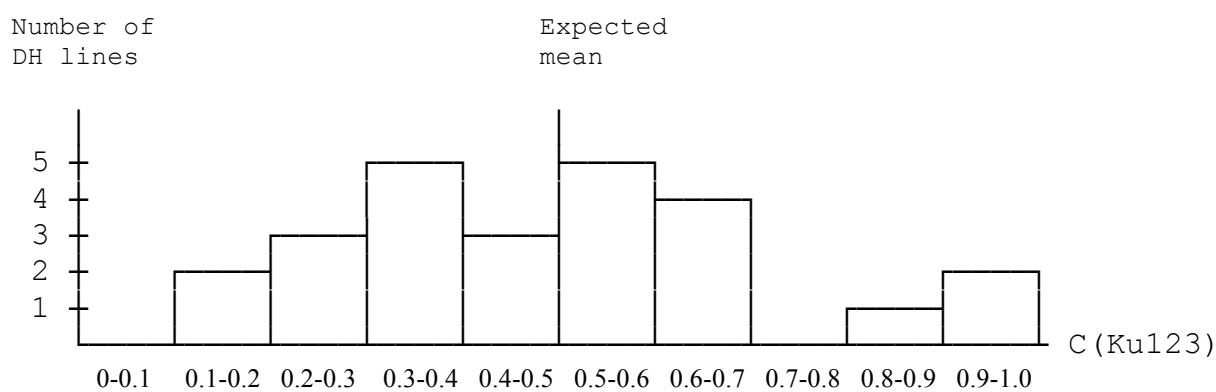


Fig.4. Distribution of DH lines from combinative capacity relatively Ku123 (in crosses with Rf7)