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ENDOSPERM DEVELOPMENT GENE IN THE SHORT ARM OF CHROMOSOME 9 IN MAIZE (*Zea mays* L.)[1]

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LIN (*2*) observed a reduction in kernel size associated with endosperms hypoploid for varying amounts of 10L and suggested that a gene or genes necessary for normal endosperm development are present in 10L. Utilizing a set of B-10L translocations with breakpoints in different regions of 10L, Lin was able to locate these genes. For each translocation, Kernel weight was obtained for the hypoploid and euploid sibs. The data indicate that there are at least four genes affecting endosperm development in the long arm of chromosome 10. Three of these are clustered in the proximal region, while a fourth with minor effects is located in the distal region of 10L.

Using the TB-1b and TB-la translocations as the pollen parent, ROMAN and ULLSTRUP (*6*) found that hypoploid for most of 1S, coming from nondisjunction of the B^1 chromosome of the TB-1b translocation, and for the distal portion of 1L in the case of TB-1a resulted in kernels of reduced size and weight. Although the size of the deficient segment is about the same in TB-1a and TB-1b, the difference in kernel weight between the sib hypoploid and euploid kernels was greater for TB-1a than for TB-1b.

BIANCHI *et alii* (*1*) reported that kernels hypoploid for more than half of 4S, coming from crosses using TB-4 as the pollen parent, had only two-thirds of the weight of normal sibs. However, the hypoploid kernels were sugary in phenotype and sugary kernels have a slightly reduced development so the presence of genes affecting endosperm development in 4S is questionable. In their studies with

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TB-9b, where the breakpoint in chromosome 9 is in the short arm between the *Bz* and *Wx* loci, hypoploid kernels were not smaller.

Thus, some chromosome regions carry genes necessary for normal endosperm development and others do not. It is not the amount but the quality of the deleted chromatin that determines whether or not endosperm development is affected.

Since B chromosomes induce breaks in knob-bearing chromosomes-«high-loss phenomenon» (*5*) — and the breaks can occur anywhere between the knob and the centromere (*3*), the deficient chromosomes produced by the «high-loss phenomenon» were utilized to test for the presence of genes controlling endosperm development in the short arm of chromosome 9 (9S).

Material and methods. The high-loss strain used in this experiment had several B chromosomes and chromosome 9 carried a large knob terminating the short arm (9S). Kernels derived from the pollination of *c* tester plants by a high-loss line with the dominant *C* allele were scored for colored aleurone (no loss: presence of the dominant *C* allele) and colorless aleurone (loss of *C* coming from breaks proximal to the *C* locus). For each ear, the two groups of kernels were weighed and the average weight of individual kernels was determined. The mosaic *C-c* kernels, arising from breaks in chromosome 9 between *C* and the terminal knob, were not included. Since about 90% of the breaks in 9S, induced by B's, area at or close to the centromere (*4*), a comparison of the weights of *C* and *c* kernels reveals whether or not the missing 9S segments in colorless kernels carry any gene (s) needed for normal endosperm development.

Results and discussion. Table 1 gives the average weight per kernel in the *C* and *c* classes in four groups of ears varying in genetic backgound. The four groups of ears gave very consistent results. There is no doubt that deletion of 9S is associated with reduction in kernel size of nearly 20%. Thus, at least one gene for normal endosperm development is located in 9S.

An attempt was made to determine the specific region of 9S carrying this gene or genes. Weight per kernels was determined for three classes of kernels, identifiable by endosperm phenotype, which were derived from breaks at different positions in 9S. These included the *C-c;Wx-wx* kernels from breaks distal to *C*, followed by the bridge-breakage-fusion cycle; the *c Wx-wx* kernels from breaks between *C* and *Wx* followed by a bridge-breakage-fusion cycle, and the *c wx* kernels from breaks proximal to *wx* producing deletions including the *C* and *Wx* loci.

In kernels exhibiting chromatin loss, taken from 29 ears, the average weight in grams per kernel was 0.174 for the *C-c;Wx-wx*; 0.145 for the *c Wx-wx*; and, 0.144 for the *c wx* class. These results indicate that the gene(s) is located between *C* and *Wx*; however, this cannot be taken as the definitive location, because of the low frequencies of *c Wx-wx* and *C-c;Wx-wx* kernels. There are good grounds for excluding the gene from the distal part of 9S: the *C-c* kernels were as large and as heavy as sib kernels with no loss. Moreover, the results of BIANCHI *et alii* (*1*) with the TB-9b translocation, where the breakpoint in 9S is between the *Bz* and *Wx* loci, showed no reduction in kernel weight for the hypoploid compared to the euploid kernels.

RESUMO

Os cromossomos B, em milho, induzem quebras em cromossomos do complemento regular portadores de «knobs». As quebras, embora não ocorram ao acaso, podem verificar-se em qualquer ponto entre o centrômero e o «knob».

Deficiências produzidas pelos cromossomos B foram utilizadas para testar a

TABLE 1 - Weight of *C* (normal) and *c* (hypoploid) kernels derived from the pollination of *c* testers by high-loss lines homozygous for *C*

	Number of ears	Number of Kernels		Weight/Kernel (g.)		c/C x 100
		C	c	C	c	
1.	20 ears	4356	794	0.2658	0.2177	81.9%
2.	11 ears	6577	1208	0.2706	0.2212	81.7%
3.	11 ears	2356	311	0.1721	0.1443	83.8%
4.	30 ears	4929	643	0.1708	0.1430	83.7%
	72 ears	18216	2956	0.2297	0.1901	82.7%

presença de gene que controla o desenvolvimento do endosperma, no braço curto do cromossomo 9.

Sementes com um cromossomo 9 deficiente para todo ou quase todo o braço curto apresentaram redução de 20% no peso, quando comparadas com outras, da mesma espiga, com o complemento cromossômico normal. Isto evidencia a presença de pelo menos um gene necessário para o desenvolvimento normal do endosperma, localizado no braço curto do cromossomo 9. Testes preliminares indicaram que o referido gene se localiza entre os genes *Wx* e *C*, o que corresponde, citologicamente, ao segmento compreendido entre as posições 0,5 e 0,75.

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