In the above tabulation it is evident that chromatin elimination during embryo sac formation will lead to deficient endosperms much less frequently than to deficient embryos. In order to more accurately assess the occurrence of loss in the megaspore mitoses, crosses were made using plants of the high-loss line with knobbed chromosomes 3 carrying the dominant $\underline{Gl}_6$, $\underline{Lg}_2$, and $\underline{A}_1$ alleles as the female parent in crosses with gl lg a pollen. The recessive gl and lg alleles produce glossy and liguleless seedlings, respectively, when homozygous or hemizygous. These high-loss plants gave from 10-12 percent of A loss when used as the pollen parent but produced no kernels with colorless endosperm when used as the egg parent. In a population of over 4000 from crosses with high-loss plants as the female parent, all of the F_1 kernels were colored and no F_1 sporophytes were found exhibiting the recessive gl, lg, or a phenotypes expected following elimination of part or all of chromosome 3--i.e., there were no deficient embryos. Our conclusion that B-chromosome induced loss of knobbed A chromosomes is restricted to the second microspore division and does not take place during embryo sac development is confirmed by these more exacting tests.

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1. Intraspecies variation of ribosomal gene redundancy in Zea mays.

Ribosomal genes in eukaryotes are highly redundant. Considerable variation in the level of rDNA cistron redundancy among species has been reported but it seems to be generally accepted that intraspecies variability in redundancy level is small. Ribosomal DNA variation as a result of natural variation, mutation, deletions, or duplications has been reported for a few species (3, 6, 7, 9, 10).

While examining the question of rDNA arrangement at the nucleolar organizer region (NOR) and differential activity and competition of the

NOR or NOR portions in translocated stocks (translocation through the NOR) in maize, it was necessary to establish the base level of rDNA redundancy. In these studies we noted that a variation in the levels of rDNA redundancy existed in the different maize stocks. The first report on the number of rRNA genes and the localization of rDNA cistrons at the NOR in maize and higher plants was published by Phillips et al. (7). Ingle et al. (4) later reported a different level of DNA-rRNA hybridization for maize. The saturation hybridization levels for maize reported by the two laboratories are 0.37%, 0.26% (7) and 0.27% (4).

The differences in the percent of rDNA in maize reported by Phillips and Ingle may be attributed to differences in hybridization techniques or to differences in DNA values used to determine the genome size. However, our experimental data supports the hypothesis that the number of rDNA cistrons is not constant in maize but varies from one strain to another. Since our results (Table 1) coincide with results reported by the two different laboratories plus additional values, we feel that such variations are not due to technique differences or other factors, but are real variations in genetically controlled gene redundancy.

Table 1

Number of rRNA genes of different inbred strains of maize (Zea mays)

Strain	% DNA hybridized at saturation	rRNA genes/2C[1]
FS (hybrid)	0.391	1.82×10^4
432	0.360	1.68×10^4
Black Mexican, no B's	0.358	1.67×10^4
Black Mexican + 4 B's[2]	0.314	
Black Mexican corrected	0.358	1.67×10^4
KYS	0.339	1.57×10^4
W22	0.254	1.18×10^4

1. 15.5×10^{-12} g/2C cell (McLeish and Sunderland, 1961).
2. B chromosome 3.8% (Ayonoadu and Rees, 1971).

We examined the variation in redundancy levels of rDNA cistrons in several inbred lines of maize by molecular DNA-rRNA hybridization. The assay consists of saturation hybridization of ^{32}P-labeled, MAK purified maize rRNA with MAK purified DNA from nuclei (8). Hybridization was carried out on millipore filters; the amount of DNA per filter was determined by HCl extraction after counting (2). The results shown on Table 1 are based on the mean value of at least four separate extractions and four separate hybridization experiments. All hybridization results are reported as percent of nuclear DNA which hybridizes with rRNA.

The amount of nuclear DNA which hybridizes with rRNA in the different inbred lines examined, varied from 0.254% to 0.391%; the stock with the higher level having approximately 54% more rDNA cistrons than the line with the lower level. The number of rDNA cistrons per diploid genome thus ranges from 1.18×10^4 to 1.82×10^4.

Since our study utilizes strains with B chromosomes, it is necessary to correct for the additional DNA contributed by the B chromosome which is considered genetically inactive and not part of the normal genome. The Black Mexican strain with and without B chromosomes was used as control. Table 1 shows that the saturation level of Black Mexican strain without B chromosomes was 0.358% while saturation level of Black Mexican strain with four B chromosomes was 0.314%. Gene redundancy would appear to be different between the two strains. Each B chromosome contains approximately 3.8% of the DNA of the total genome (1). By making the correction for the four B chromosomes found in this strain, the saturation level changes from 0.314% to 0.358% per normal diploid genome. This shows that correction is possible and necessary in order to determine the normal diploid rDNA redundancy of strains with and without B chromosomes and that the level of redundancy may be genetically controlled since these strains have been maintained separate for some time.

In light of the range in rDNA cistron variation that exists in maize, it is important that the background level of redundancy be established for each inbred line that is used. In experiments using lines with B chromosomes or any form of aneuploidy, the base level of rDNA cistrons must be known, otherwise any variation from the normal would definitely

be altered if the background was not known or a different background used for its base level, e.g. 0.25% or 0.39%.

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