Table 1

Frequency of nucleoli dissociated from the organizer site at diakinesis in PMC's

	No. of spikelets studied	No. of PMC's examined	No. of PMC's showing dissociation		
			Wide apart	Slightly apart	Total
Inbred lines:					
Jhadgan	1	600	1	0	1
Gandasahi	8	4,790	0	0	0
Mahabirapur	10	8,956	0	0	0
Guali	6	2,240	0	0	0
Chheliguda	2	754	0	0	0
Hybrids:					
Ganga 101 (double-cross)	6	2,920	33	16	49
(105 X 101) X (115 X 111)	5	590	11	0	11
Kenduguda X Jhadgan	12	720	1	0	1

There are reasons to believe that the size of the nucleolus is directly proportional to its synthetic activity, particularly RNA and protein synthesis. Since the nucleoli dissociated from the organizer sites are often large, it is necessary to examine whether these cells and their nucleoli are more active in RNA/ protein synthesis, and whether this activity has any relationship to vigor. We are particularly interested to ascertain if synthetic activity can be used as a measure of combining ability of inbred lines. In case some kind of easy-to-detect morphological cellular manifestation (e.g. the nucleolar condition reported here) is related to synthetic activity and vigor, means would be provided for studying combining ability at the cellular level and thus to understand the cellular basis of the phenomenon.

B. K. Mohapatra
S. K. Sinha

3. <u>The nature of variation in some quantitative traits in terms of adaptation.</u>

The contention that heterozygosity would lead to developmental stability or homeostasis at least in outbreeding species has been examined by us in respect to several quantitative characters including different aspects of meiotic chromosomal behavior. These studies have revealed that heterozygosity *per se* may not ensure developmental homeostasis. But the phenomenon is more likely to be encountered in heterozygotes rather than homozygotes. Our interest in the study of phenotypic variation in inbred and single-cross hybrid maize (MNL 40:119-120) has been partly prompted by the opportunity that this study would provide to understand the biological significance of variation in different characters in terms of adaptation. By comparing the magnitude of variation in a large number of inbreds and hybrids it may be possible to ascertain whether (1) the variation in a particular trait is a reflection of developmental instability arising from 'accidents in development' and without having a role in adaptation, or (2) the variation has an adaptive significance so that it is a measure of 'developmental flexibility' arising in adapted individuals in response to the variable environment. In the present report we will refer to these as Type 1 and Type 2 variation, respectively. In case of characters showing Type 1 variation, the variance in hybrids (average of a number of hybrids) would be expected to be less than that in inbreds; and in case of traits showing Type 2 variation the reverse would hold good.

To begin with, we have focused attention on (1) seedling traits and (2) certain aspects of meiotic chromosomal behavior. We have purposely chosen the former in order that the experiments can be repeated as often as necessary and if required under varying conditions and thus the premise underlying the operational approach to understanding variation can be put to a rigorous test.

Tentative inferences regarding the nature of variation (Type 1 or 2) in several traits are indicated below (Table 1).

Table 1

Comparisons of phenotypic variances in inbreds and hybrids. (The figures represent average values of squared coefficients of variation)

	Inbreds*	Hybrids**	Remarks (Type 1/Type 2 variation)
(a) Seedling traits:			
Radicle length	2508	1114	Type 1
Average length of seminal roots	3924	1441	Type 1
Coleoptile length	519	304	Type 1
Mesocotyl length	1174	1460	Type 2?
Length of the first leaf	897	403	Type 1
Number of seminal roots	2029	956	Type 1
No. of vascular strands in radicle	218	247	??
(b) Chromosomal traits:			
Chiasma frequency per PMC at diak.	0.0012	0.0011	??
Sixth chromosome chiasma frequency (per PMC at diak.)	0.0141	0.0095	Type 1
Univalent frequency	0.3341	0.1715	Type 1

*Average of 6 inbreds in case of seedling traits; average of 4 in case of

chromosomal traits.
**Average of 6 hybrids (including reciprocal crosses) in case of seedling traits; average of four (including reciprocals) in case of chromosomal traits.

It is evident that for most of the traits studied the variation is due more to developmental instability rather than to adaptive changes. For three characters it is difficult even to make tentative inferences. Further work is in progress to detect characters exhibiting adaptive changes.

A. P. Rao
B. K. Mohapatra
S. K. Sinha

4. Evidence for genes controlling pollen grain development in chromosome 9 and an attempt at locating similar genes in other chromosomes.

A study of pollen grains segregating for waxy and starchy phenotypes in plants heterozygous for Inversion 9a has given the following picture regarding variability in shape and size associated with the two phenotypes (Table 1).

Table 1

Comparison of shape and size of grains segregating for Wx and wx in plants heterozygous for Inversion 9a

	% of grains of different shape		Size (in divisions of the ocular micrometer)	
	Spherical	Oval	diameter of spherical grains	length of oval grains
Starchy (Wx)	44	56	37.0	37.6
Waxy (wx)	72	28	33.6	37.0

It appears that a block of genes associated with spherical shape and small size are linked to the wx allele. A part of this block may be located in the inverted segment and another part may be close to the same gene but on the side opposite to the inverted segment so that these genes may be free to enter into recombination with the genes in the homologous segment linked to the Wx allele.

We are further studying the variation associated with the starchy-waxy phenotypes in plants heterozygous for T 6-9b as well as a few other translocations involving chromosome 9 marked by wx. It is hoped that this study, when completed, will reveal the distribution of genes controlling pollen grain development in segments of different chromosomes in the