

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 ( <u>Wx</u> )	44	$\frac{56}{28}$	37.0	37.6
Waxy ( <u>wx</u> )	<u>72</u>		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

vicinity of break points. The rationale of this analysis is but an extrapolation of Dobzhansky and Rhoades' approach for locating favorable dominant genes.

We are also planning to extend this analysis in order to locate, if possible, the components of the polygenic system controlling aspects of meicyote development.

S. K. Sinha  
A. T. Roy  
Bhabanty Mohanty

OSMANIA UNIVERSITY  
Hyderabad 7, A.P., India  
Department of Genetics

1. Protein and some amino acid composition of Indian hybrid maize.

The six leading hybrids Ganga-3, Ganga-101, Ganga safeed-2, Ranjit, Deccan hybrid, and high starch as well as the opaque-2 mutant have been analyzed for crude protein and for lysine, leucine, tryptophan, and methionine content. The hydrolysis of the protein was carried out for six hours in an autoclave in 2.5N NaOH in the case of tryptophan and 2.5N HCl in the case of the other amino acids. The amino acids were estimated microbiologically with Leuconostoc mesenteroides P-60 (Steele, B. F. et al, J. Biol. Chem. 177:533, 1949) in collaboration with the microbiology Section of the Nutritional Research Laboratory. The results are presented in Table 1.

Table 1  
(grams/16gms.nitrogen)

	<u>Lysine</u>	<u>Leucine</u>	<u>Tryptophan</u>	<u>Methionine</u>	<u>Crude protein</u> <u>(in per-</u> <u>centage)</u>	<u>Yield</u> <u>in</u> <u>Kg/Ha</u>
1) Opaque-2	5.92	8.00	0.55	1.74	9.97	
2) Ranjit hybrid	2.95	12.30	0.44	1.91	10.19	4500
3) Hi starch	2.76	12.95	0.39	1.88	10.47	4500
4) Ganga-3	3.50	13.50	0.43	2.24	9.60	4000
5) Deccan hybrid	3.52	13.15	0.53	2.36	7.96	4900
6) Ganga safeed-2	3.00	13.30	0.41	1.88	9.99	4500
7) Ganga-101	2.60	12.50	0.45	1.65	11.13	4100