3. A floury endosperm, high lysine locus on chromosome 10.

A floury endosperm mutant, which occurred spontaneously in a W22 $\underline{ACr}^g/\underline{ACr}^g$ stock, was analyzed for lysine content.* The floury mutant had 3.4 gms lysine per 100 gms protein, compared with 2.1 gms lysine/100 gms protein for the isogenic normal endosperm stock of W22. In the same analysis opaque-2 and floury-2 stocks gave values of 3.65 and 3.2 gms lysine/100 gms protein, respectively.

The floury mutant is linked with R on chromosome 10. Five separate estimates of the recombination value in $\underline{R}^r+/\underline{r}^g\underline{fl}$ plants are 23%, 26% (F_2 Data); and 22%, 24% and 26% (Backcross data). Linkage relations with other chromosome 10 markers are being determined.

*Performed by Dr. J. A. Ronalds,
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K. S. McWhirter

4. Measurement of gene effects by application of a mathematical model to triploid endosperm data.

Various models have been used by workers such as Hayman & Mather, Kempthorne & Cockerham to describe gene action and interaction for diploid genotypes. Data are available for endosperm tissue which gives sixteen triploid genotypes rather than the nine genotypes from diploids. The triploid data are used in this article for application of Cockerham's model. In the original diploid model, 9 orthogonal coefficients were used to provide each of 8 parameters which measured deviations from the mean value for the 9 genotypes. The triploid model has 16 orthogonal coefficients for each parameter, as shown in the columns of Table 1. The sixteen columns are headed by μ, the mean value of the 16 genotypes and the symbols for the 15 parameters which describe the gene action or deviation from the mean.

At the foot of each column are figures for these parameters derived from three sets of data. The sources of these data were:

1) K. S. McWhirter (1962). "A Phenotypic Comparison of Three Stippled Genes" M.G.C. N.L. 36:100-101.
2) Helm, J. L., V. L. Ferguson & M. S. Zuber (1969). "Interaction of Dosage Effects on Amylase Content of Corn at the Du and Wx loci" Hered. 60:259-260.

3) These data are derived from a maize stock in which the kernels vary in colour from yellow, through lemon, to white. This variation is due to the interaction of genes at the Y-y locus on chromosome 6 and genes at an independent, unknown locus, provisionally designated ly-iy.

The gene ly acts as a partially dominant inhibitor of the yellow colour produced by Y. The full yellow colour of Y when only iy is present is reduced to a lemon colour when ly is present. y gives a white or cream colour when only iy is present and the presence of ly changes the cream colour to pure white.

Genetic experiments were completed to prove that this system did in fact involve an interaction between genes at two independent loci. From a cob which carried yellow, lemon and white kernels in the ratio of 3Y:9L:4W the results shown in Table 2 were obtained.

A hexane extract of the maize kernels was used to give total carotenoid content in p.p.m. as a measure of yellow pigments. These data are recorded in Table 3.

The groups of figures in Table 3 are from two sources. Figures without brackets are the observed figures for the particular character, i.e., carotenoid content. Figures enclosed by brackets are obtained by summing the additive, dominance and interaction effects for a particular genotype. These additive, dominance and interaction effects are obtained from the parameters at the foot of Table 1 in the following manner.

Additive = α component for the particular gene, e.g., ly_α or Y_α

Dominance = $\beta+\delta$ components for a particular gene, e.g., $ly_\beta+ly_\delta$

Interaction = $\alpha\alpha+\beta\beta+\delta\delta+\alpha\beta+\beta\alpha+\alpha\delta$ etc. or the sum of all the interacting terms for the two genes.

For each genotypic value, the expected value (Figures in brackets Table 3) can be calculated by summing the term x orthogonal coefficient for that term and that genotype.

Using genotype ly_1ly_1ly YYY as an example.

Expected Value = $1x\mu+3x1ly_\alpha - 1x1ly_\beta+1x1ly_\delta+3xY_\alpha- 1x1ly_\beta+1x1ly_\delta$ ...$-1x1ly_\delta Y_\beta$

= 1x5.94+3x-1.72-1x-2.61+1x-0.38+3x1.42-1x0.79+1x0.04+9x-0.54-
3x-0.76-3x-0.14+1x-0.23+3x0.2-1x0.0+1x-0.03+3x-0.09-1x-0.08

= 3.97

Using this set of figures, the effects of the various components can be gauged with more accuracy than a subjective analysis will allow.

For example, the additive ly_α effect reduces yellow colour more than the Y_α effect increases colour.

Table 1

Orthogonal coefficients used with triploid data to determine the deviation from the mean value due to the fifteen parameters shown

Genotypes	μ	l_α	l_β	l_δ	Y_α	Y_β	Y_δ
lylyly YYY	1	3	-1	1	3	-1	1
" YYy	1	3	-1	1	1	1	-3
" Yyy	1	3	-1	1	-1	1	3
" yyy	1	3	-1	1	-3	-1	-1
lylyiy YYY	1	1	1	-3	3	-1	1
" YYy	1	1	1	-3	1	1	-3
" Yyy	1	1	1	-3	-1	1	3
" yyy	1	1	1	-3	-3	-1	-1
lyiyiy YYY	1	-1	1	3	3	-1	1
" YYy	1	-1	1	3	1	1	-3
" Yyy	1	-1	1	3	-1	1	3
" yyy	1	-1	1	3	-3	-1	-1
iyiyiy YYY	1	-3	-1	-1	3	-1	1
" YYy	1	-3	-1	-1	1	1	-3
" Yyy	1	-3	-1	-1	-1	1	3
" yyy	1	-3	-1	-1	-3	-1	-1

Calculated Parameters

ly Y	5.94	-1.72	-2.61	-0.38	1.42	0.79	0.04

	μ	Du_α	Du_β	Du_δ	Wx_α	Wx_β	Wx_δ
Du Wx	21.05	-0.98	-0.98	-0.22	4.34	6.28	1.09

	μ	M^{st}_α	M^{st}_β	M^{st}_δ	R^{st}_α	R^{st}_β	R^{st}_δ
R^{st} M^{st}	39.08	6.20	-4.27	0.11	11.90	-4.02	0.61

These figures, when multiplied by the appropriate orthogonal coefficient (i.e., in the same column and the row corresponding to the required genotype), are summed to give the expected value for that genotype.

Table 1 (Continued)

Parameters								
$I_{\alpha}^{Y}{}_{\alpha}$	$I_{\beta}^{Y}{}_{\alpha}$	$I_{\alpha}^{Y}{}_{\beta}$	$I_{\beta}^{Y}{}_{\beta}$	$I_{\alpha}^{Y}{}_{\delta}$	$I_{\beta}^{Y}{}_{\delta}$	$I_{\delta}^{Y}{}_{\delta}$	$I_{\delta}^{Y}{}_{\alpha}$	$I_{\delta}^{Y}{}_{\beta}$
9	-3	-3	1	3	-1	1	3	-1
3	-1	3	-1	-9	3	-3	1	1
-3	1	3	-1	9	-3	3	-1	1
-9	3	-3	1	-3	1	-1	-3	-1
3	3	-1	-1	1	1	-3	-9	3
1	1	1	1	-3	-3	9	-3	-3
-1	-1	1	1	3	3	-9	3	-3
-3	-3	-1	-1	-1	-1	3	9	3
-3	3	1	-1	-1	1	3	9	-3
-1	1	-1	1	3	-3	-9	3	3
1	-1	-1	1	-3	3	9	-3	3
3	-3	1	-1	1	-1	-3	09	-3
-9	-3	3	1	-3	-1	-1	-3	1
-3	-1	-3	-1	9	3	3	-1	-1
3	1	-3	-1	-9	-3	-3	1	-1
9	3	3	1	3	1	1	3	1
-0.54	-0.76	-0.14	-0.23	0.02	0.00	-0.03	-0.09	-0.08

du_{α}	Wx_{α}	Du_{β}	Wx_{α}	Du_{α}	Wx_{β}	Du_{β}	Wx_{β}	Du_{α}	Wx_{δ}	Du_{β}	Wx_{δ}	Du_{δ}	Wx_{δ}	Du_{δ}	Wx_{α}	Du_{δ}	Wx_{β}
-0.18		-0.20		-0.40		-0.40		-0.10		-0.13		-0.02		-0.04		-0.15	

M_{α}^{st}	R_{α}^{st}	M_{β}^{st}	R_{α}^{st}	M_{α}^{st}	R_{β}^{st}	M_{β}^{st}	R_{β}^{st}	M_{α}^{st}	R_{δ}^{st}	M_{β}^{st}	R_{δ}^{st}	M_{δ}^{st}	R_{δ}^{st}	M_{δ}^{st}	R_{α}^{st}	M_{δ}^{st}	R_{β}^{st}
1.26		0.69		0.70		-2.20		-1.30		-0.25		0.49		0.21		0.44	

Table 2

Genetic analysis of genotypes derived from ears segregating yellow, lemon and white kernels

Proposed Genotype	# ears	Mating	Segregation	$X^2_{d}ev$	Pr	X^2het.	Pr
(1) From Yellow Kernels				-	-	-	-
iyiyiy YYY	8	x	All Yellow				
iyiyiy YYy }	9	x	3Y:1L	0.18	0.7-0.5	6.78	0.7-0.5
or iyiyiy Yyy }							
(2) From Lemon Kernels				-	-	-	-
lylyly YYY	10	x	All Lemon	1.84	0.2-0.1	12.07	0.3-0.2
lylyly YYy or Yyy	10	x	3L:1W	0.006	0.95-0.9	1.83	0.9-0.8
lylyiy or lyiyiy YYY	6	x	1Y:3L	0.45	0.8	37.24	0.2
lylyiy YYy etc.	18	x	3Y:9L:4W				
(3) From White Kernels				-	-	-	-
lylyly yyy	2	x	All pure white	2.7	1.0	5.3	0.02
lyiyiy or lylyiy yyy	2	x	3W:1C				
iyiyiy yyy	-	none found					
lyiyiy yyy }	7	x iyiy YY	1Y:1L	3.8	0.5	2.33	0.9-0.8
or lylyiy yyy }							

Table 3

Yellow pigmentation of maize kernels, expressed as ppm of carotenoid in a hexane extract measured at 540 mμ and absorbancy = 250

	YYY	YYy	Yyy	yyy
lylyly	3.98(3.97)	3.79(3.79)	3.28(3.27)	1.00(1.01)
lylyiy	3.43(3.41)	3.40(3.35)	3.42(3.47)	0.76(0.77)
lyiyiy	6.12(6.14)	5.46(5.51)	3.28(3.23)	0.75(0.73)
iyiyiy	24.20(24.25)	19.50(19.47)	11.73(11.75)	0.94(0.89)

The $\underline{1y}_{\beta}$ effect, one of the dominance components has an increasing effect on yellow colour which counteracts the effect of $\underline{1y}_{\delta}$ & $\underline{y}_{\beta}$.

Interaction effects are mainly $\alpha\alpha$ or additive x additive at -4.86, but $\alpha\beta$ & $\beta\alpha$ or additive x dominance effects of 2.28 & 0.42 help to counteract the $\alpha\alpha$ effect.

Using the data on amylase content, the obviously greater effect of Wx over Du is highlighted.

Using WxWxWx DuDuDu as an example.

Expected Value = $1x\mu+3xDu_{\alpha}-1xDu_{\beta}+1xDu_{\delta}$ ..... $-1xDu_{\delta}$ Wx_{β}

= 1x21.05+3x-0.975-1x-0.975+1x-0.225+3x4.340-1x6.275+1x1.09+
9x-0.175-3x-0.200-3x-0.04+1x-0.400+3x-0.103-1x-0.125+1x-0.024+
3x-0.035-1x-0.150

= 26.372

These figures show that the positive $\underline{Wx}_{\alpha}$ effect = +13.02 has an effect about 4½ times greater than the negative $\underline{Du}_{\alpha}$ effect = -2.93.

Similarly the Wx dominance effect is about 6 times greater than the Du dominance effect. The use of Cockerham's model allows a numerical comparison to be made, rather than a subjective one.

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1. Centromeric meiotic abnormalities in experimental maize plants.

For about six years maize plants have been grown in growth chambers in this laboratory for sporocyte collection in connection with recombination and other studies. Until last May cytological abnormalities in the collected sporocytes were restricted to occasional asynchronies (with probable retardation of some cells) and occasional cellular disintegration, both apparently attributable to damage of parts roughly handled during the collection of other parts. Since last May meiotic abnormalities have been sporadically, and to date unpredictably, observed in growth chamber microsporocyte material. These have included synaptic failures, irregularities of chromosome contraction, and loss of chiasmate association to produce univalents recombinant for a heterozygous knob