

A GENETIC STUDY ON THE EFFECTS OF *OPAQUE-2* AND POLYGENES ON KERNEL QUALITY TRAITS IN MAIZE

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A genetic analysis is performed based on the genetic model suggested by Lou (1997) for lysine content, protein content, and oil content in maize. The results show that the *o2* gene has a strong influence on lysine content and protein content, but a weak influence on oil content. There is a large variability due to polygenes for all the three traits. Genotype by environment effects are large for protein content and oil content, but relatively small for lysine content.

1 Introduction

The discovery concerning the biochemical effects of *opaque-2* (*o2*)³ aroused considerable interest among maize (*Zea mays* L.) breeders. As a result breeding programs were initiated to upgrade the protein quality of maize endosperm by enhancing the levels of lysine and tryptophan. The *o2* mutation have been used extensively in different countries to obtain quality protein maize, but some drawbacks resulted from pleiotropic effects associated with mutation have limited the development of *o2* for commercial use. However, the discovery of modifier genes that cause the formation of a hard, vitreous endosperm⁴ allows the development of modified *o2* genotypes. The development of hard endosperm *o2* maize is the primary strategy to overcome the deleterious effects of *o2* gene. In addition to kernel appearance, effects of modifiers on protein content, etc., were also reported⁵. Furthermore, there were background effects resulted from other polygenes on lysine content, protein content and so on. In this situation the inheritances of kernel traits are controlled by a major gene as well as by polygenes, and the genetic model for quantitative seed traits with major gene effects must be employed to analyze the genetic effects.

The objectives of this study are to (1) estimate the *o2* gene effects on maize kernel traits; and (2) estimate the genetic parameters of polygenes.

2 Materials and Methods

15 maize inbred lines, which were randomly sampled from the populations of the normal maize inbred lines and the high lysine maize (*o2*) lines of Zhejiang Province, including 4 normal maize lines, 4 semihard endosperm *o2* maize lines and 7 soft endosperm *o2* maize lines, were used as parents to produce the hybrid F_1 's and reciprocal cross RF_1 's following a 7×8 incomplete diallel design in 1994. In 1995, the seeds of parents, F_1 's, RF_1 's, F_2 's, RF_2 's, BC_1 's, and BC_2 's were obtained at mature by hand-pollination at two locations, Zhejiang Agricultural University Experimental Farmer (Hangzhou) and Zhejiang Dongyang Maize Research Institute (Dongyang).

Data were taken based on the average of 200 kernels from each genetic entry for protein content, lysine content, and oil content. Contents were expressed as percent. Protein content was determined by the Lowry procedure. The dye binding lysine (DBL) method was used for lysine content determination. Oil content was evaluated by the Soxhlet extraction procedure.

Since *o2* mainly expresses in endosperm of seed, the genetic model suggested by Lou² was employed for analysis.

3 Results

3.1 *o2* Gene Effect and Its Interaction Effect

The estimation results of four endosperm *o2* genotype effects and their interaction effects are summarized in Table 1. The nulliplex (*o2o2o2*) considerably increased the lysine level and the estimate was significantly higher than the population mean, while the triplex (*O2O2O2*) decreased it. The estimate of the nulliplex was near 0.1 percent lysine higher than that of the triplex. The heterozygous genotypes were little different from that of the triplex. Their lysine contents were between those of the nulliplex and the triplex, but closer to the triplex. These suggest that the variation due to major gene genotypes is relatively large and the inheritance of lysine content is not entirely single recessive gene pattern. The triplex interaction effect is detected, but the magnitude was relatively smaller. The other genotype interaction effects are not significant except for the triplex.

Unlike lysine, of four genotypes, the nulliplex was the lowest, while the triplex was the highest for protein content. The heterozygous genotypes were between two homozygotes, but closer to the nulliplex. These showed that protein content displays incomplete dominance inheritance, and nearly no *o2* dosage effect. The interaction effects were large, and the variation due to interactions was nearly as large as due to genetic main effects. The duplex

Table 1: Estimates of population means and *o2* gene genotype effects

Effect	Percent lysine	Percent Protein	Percent oil
μ	0.311**	11.18**	4.15**
<i>O2O2O2</i>	-0.035**	0.93**	0.08
<i>O2O2o2</i>	0.006+	-0.13	-0.14
<i>O2o2o2</i>	-0.031**	-0.18*	-0.09
<i>O2o2o2</i>	0.060**	-0.62**	0.16*
<i>O2O2O2E1</i>	0.000	-0.02	-0.05
<i>O2O2o2E1</i>	-0.015**	0.73**	0.27
<i>O2o2o2E1</i>	0.010*	-0.46**	-0.18
<i>o2o2o2E1</i>	0.004**	-0.25**	-0.04

μ is the population mean

Estimates of *o2* genotype by environment 2 interaction effects are the opposite numbers of ones of environment 1

+, * and ** are significant at 0.1, 0.05 and 0.01 levels, respectively

interaction effect was the largest, and it implied that the duplex effect largely changed in different environments.

The *o2* gene influence on oil content was weak. Only the estimate of the nulliplex was significant, it was positive but small relative to the population mean. This indicated that the nulliplex could increase a little the oil level. All the estimates of interaction effects were not significant.

3.2 Variance Components of Polygenes Effects and Their Interactions

Estimation results showed that the variation of lysine content due to polygenes was mainly controlled by genetic main effects, including embryo additive, endosperm dominance and maternal additive (Table 2). The interaction effects were minor. These implied that the effects of polygenes were relatively stable across different environments. Of genetic main effects, additive effects (including embryo and maternal additive), were large. Since the portions of phenotypic variation could be stably transmitted from parents to their offspring, there would be a high degree of resemblance between relative individuals. Early generation selection and sib indirect selection would be effective for lysine content. Cytoplasmic interaction variance occupied a little share of the total phenotypic variance.

Protein content, however, was mainly controlled by interaction effects. Of

Table 2: Estimates of variance components of genetic effects and genotype by environment interaction effects of polygenes

Variance component	Percent lysine(10^{-2})	Percent protein	Percent oil
V_{Ao}	0.64**	0.70*	0.00
V_{Do}	0.00	0.00	0.00
V_{Ae}	0.00	0.00	0.66+
V_{De}	0.45**	0.77+	0.20+
V_{Am}	0.15**	1.04*	0.00
V_{Dm}	0.02+	0.00	0.00
V_C	0.00	0.00	0.00
V_{AoE}	0.00	4.91**	1.78**
V_{AeE}	0.08*	0.06	0.00
V_{DeE}	0.00	0.00	0.00
V_{AmE}	0.00	1.93*	1.10*
V_{DmE}	0.09*	1.61**	1.03**
V_{CE}	0.05**	2.13**	0.16+
V_{e}	0.20**	1.36**	0.38*
V_p	0.08**	0.88*	0.28+
V_P	1.76**	15.39**	5.59**

+, * and ** are significant at 0.1, 0.05 and 0.01 levels, respectively

interaction variance components, embryo additive was the largest, and occupied near one third of the phenotypic variance. Estimates of embryo additive and maternal additive variance were significant, but their proportions of the total variance were small.

All genetic main effect variances were not significant for oil content. Embryo additive interaction, endosperm dominance interaction and maternal additive interaction were important and the other effects were relatively minor.

4 Discussion

The results of this study showed that *o2* gene had a strong influence on lysine content and protein content, but its influence on oil content was relatively weak. Therefore *o2* is important to improve lysine and protein content. Utilization of *o2* would have a little or no effect on oil content. Expressions of *o2* gene

depend on environment, and the magnitude of dependence varied for different traits. The degree of dependence was relatively small for lysine content but large for protein content and oil content. The pattern of *o2* gene action was different with traits. *o2* displayed the nearly recessive single gene inheritance for lysine content and incomplete dominance for protein content.

There was large variability due to polygenes for all three traits studied. Utilization of polygenes could improve these traits and overcome some deleterious effects of *o2* gene. In general, the oil content was taken as endosperm trait, and/or influenced by maternal plant¹. It was controlled by endosperm and maternal plant as well as by embryo effects.

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