

Combining ability analysis of quality protein maize (QPM) and non-PM inbred lines for kernel quality and some agronomic characteristics

Mutimaamba, C.¹, Lungu, D.¹ & MacRobert, J.²

¹University of Zambia, P. O. Box 32379, Lusaka, Zambia

²CIMMYT, P.O. Box MP163, Harare, Zimbabwe

Corresponding author: cmtimamba@yahoo.com

Abstract

The biggest population in Zimbabwe depend on maize as a source of carbohydrates, yet it is deficient in protein and therefore makes the population prone to protein malnutrition. Quality Protein Maize (QPM) has double the amount of lysine and tryptophan and therefore desirable suitable to combat possible protein malnutrition. The Zimbabwe maize research programme is currently using QPM inbred lines whose combining ability for grain quality and agronomic traits has not been previously tested and validated. In this study, combining ability analysis was conducted to identify appropriate QPM donor inbred lines for use in the development of new QPM inbred lines and the conversion of non-QPM open pollinated varieties (OPVs) and inbred lines to QPM. From the study, the inbred lines CZL082 and CML511 are recommended for use as donors in the development of new QPM inbred lines and the conversion of non-QPM inbred lines and OPVs to QPM by the national maize research programme in Zimbabwe.

Keywords: Lysine, *opaque-2*, OPVs, tryptophan, protein malnutrition

Résumé

La plus grande population du Zimbabwe dépend de maïs comme source de glucides, toutefois déficient en protéines et de ce fait rendant la population sujette à la malnutrition protéique. Le maïs de qualité en protéines (QPM) a une concentration double de lysine et tryptophane et est ainsi souhaitable et convenable pour lutter contre la malnutrition protéique possible. Au Zimbabwe, le programme de recherche sur le maïs utilise actuellement les souches pures de QPM dont la capacité de combiner la qualité du grain et les caractères agronomiques n'a pas été préalablement testée et validée. Dans cette étude, l'analyse de l'aptitude à la combinaison a été menée pour identifier les souches pures de donneur QPM appropriées pour une utilisation dans le développement de nouvelles lignées pures de QPM et la conversion des variétés de non-QPM à pollinisation libre (OPVs) et des lignées pures en QPM. Dans

cette étude, les lignées pures CZL082 et CML511 sont recommandées pour les utiliser comme donneurs dans le développement de nouvelles lignées de QPM et la conversion des lignées pures de non-QPM et OPVs en QPM par le programme national de recherche sur le maïs au Zimbabwe.

Mots clés: Lysine, *opaque-2*, OPVs, tryptophane, la malnutrition protéique

Background

Conventional maize is deficient in lysine and tryptophan and thus predisposes mothers and children who depend on maize to the risk of malnutrition. Quality protein maize (QPM), has twice the lysine and tryptophan levels, and if consumed can potentially avert this nutritional risk. The Zimbabwe maize research programme is currently using QPM inbred lines whose combining ability for grain quality and agronomic traits has not been previously tested and validated. Therefore combining ability analysis was conducted in this study with the aim of identifying appropriate QPM donor inbred lines for use in the development of new QPM inbred lines and the conversion of non-QPM open pollinated varieties (OPVs) and inbred lines to QPM.

Literature Summary

In Zimbabwe, maize has been traditionally grown by 99 % of the population as a source of carbohydrates, despite being deficient in protein (Mashingaidze, 2004). Efforts are currently under way to minimise malnutrition through the promotion, production and consumption of QPM whose lysine and tryptophan levels are twice that of common maize (Krivanek *et al.*, 2006). QPM are genotypes where the *opaque-2* gene has been incorporated along with associated endosperm and amino acid modifiers and contains twice the amount of lysine and tryptophan compared to normal maize. Of the natural maize mutants conferring higher lysine and tryptophan, *opaque-2* was found to be the most suitable for genetic manipulation in QPM breeding programs (Vivek *et al.*, 2008).

Study Description

Five QPM and 12 non-QPM inbred lines were mated following a modified North Carolina Design II (Comstock and Robinson, 1952) in which each line was not used strictly as male or female. The 35 crosses successfully generated at CIMMYT Harare in 2008/09 were evaluated in winter 2009 following a lattice design with three replications under four environments at Chiredzi and Muzarabani in Zimbabwe. The number of days to flowering and grain yield were recorded and the anthesis-silking interval

determined for each plot. Twenty class 2 kernels from each plot were randomly drawn under the light table from F₂ grain and analysed for protein and tryptophan content following a procedure described by Villegas (1975) and Villegas *et al.* (1984).

Percent values for endosperm modification, protein, lysine and tryptophan content were transformed using arcsine transformation as illustrated by Zar (1974) before subjecting them to analysis of variance. PROC GLM (SAS Institute, 2007) was used to perform the analysis of variance per environment and across environments. The general combining ability (GCA) effects of parents and the specific combining ability (SCA) effects of crosses were estimated by line x tester analysis (Kempthorne, 1957), where females were designated as lines and males or donors as testers. A fixed effects model was assumed for the genotypes (donors, lines and crosses) and environments in the current study.

Assessments were made for the inbred lines for the relative importance of general (GCA) and specific combining ability (SCA) effects, and mid-parent heterosis in the phenotypic expression of endosperm modification (MOD), percent tryptophan (TRP), lysine (LYS) and protein (PROT), grain yield (GY), anthesis date (AD) and anthesis-silking interval (ASI).

Research Application

On the basis of GCA effects, line CML511 was the best donor for MOD, LYS and PROT, and gave good GCA effects for the highest number of agronomic traits and environments. Line CZL082 was the second best donor for MOD, TRP and LYS. In terms of SCA effects, line CZL082 was the best donor because it was involved in more cross combinations with desirable SCA effects for quality and agronomic traits under more environments. Line CML511 was the second best donor, given that it was involved in cross combinations that had the best SCA effects for MOD and LYS. Line CML511 was a constituent parent in separate cross combinations with the highest means for MOD and PROT. On the basis of mid-parent heterosis, line CML511 was the best donor for featuring in crosses with the highest positive mid-parent heterosis for MOD. The mid-parent heterosis of two of the five least modified crosses was higher for TRP, LYS and PROT than that for the best modified hybrids, with line CML511 featuring in one of these crosses. Additive genetic effects were preponderant in the control of all kernel quality traits.

Recommendation

The inbred lines CZL082 and CML511 are recommended for use as donors in the development of new QPM inbred lines and the conversion of non-QPM inbred lines and OPVs to QPM by the national maize research programme in Zimbabwe. Further work is necessary to validate the suitability of the lines CZL082 and CML511 as suitable donors through crossing them to more inbred lines.

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