

# Genetic diversity of maize inbred lines using ISSR markers and its implication on quantitative traits inheritance

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## ABSTRACT

Genetic distance (GD) among six maize inbred lines was determined based on the ISSR markers. A total of 96 amplification bands were produced by ten ISSR primers; 35 out of them were polymorphic (36.46 % polymorphism). Highest similarity level (94.3%) was between  $P_2$  and  $P_3$  that are closely related. Highest genetic diversity was between  $P_1$  and  $P_4$ . Inheritance of earliness, grain yield and its components in *three specific crosses* ( $P_2 \times P_3$  low diversity,  $P_5 \times P_6$  moderate diversity and  $P_1 \times P_4$  high diversity) were studied in a trial *consisting of 6 populations* ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $Bc_1$  and  $Bc_2$ ) during 2013 and 2014 years. Inbred line differences occurred regarding genetic background, genetic variance within  $F_2$  population, desirable heterosis and inbreeding depression were detected for all studied traits in the three crosses. Potence ratios were higher than unity indicating over-dominance towards the desirable parent. Additive gene effects (a) and dominance gene effects (d) were significant for most studied traits. High heritability in broad-sense was detected, except for grain yield plant<sup>-1</sup> in cross No.1. Heritability in narrow-sense was low. Variance in  $F_2$ , mean performance in  $F_1$  and GCV% increased with increasing GD in *the cross*  $P_1 \times P_4$  followed by cross  $P_5 \times P_6$  and then by cross  $P_2 \times P_3$ . Values of  $r$  were 0.98\*\* between GD and variance of  $F_2$ , 0.97\*\* between GD and mean performance of  $F_1$  and 0.79\*\* between GD and GCV% for grain yield plant<sup>-1</sup>. Hence, ISSR markers *method* proved powerful, reliable, fast and inexpensive for screening genetic diversity between maize inbred lines.

**Key words:** Maize, ISSR markers, Genetic diversity, and Heritability.

## INTRODUCTION

Maize (*Zea mays* L.) is one of vital cereal crops in Egypt and the world. It is widely used in bread making in rural Egypt and in industries such as glucose, oil starch and is a main component in animal feeds. It is a general policy in Egypt to mix wheat flour with maize flour (1:4) for bread making in order to decrease wheat consumption and import. Discriminating various genotypes using morphologic markers is difficult and

time-consuming. Isoenzymes and proteins that are the product of gene expression cannot demonstrate polymorphism among genotypes, and cannot identify hybrids that have close relationships. However, modern molecular markers like Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSR) and Inter-Simple Sequence Repeats (ISSR) have been used to identify different genotypes with reliable results.