

Molecular genetic diversity and its relationship with heterosis for grain yield and related traits in Sorghum [*Sorghum bicolor* (L.) Moench]

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ABSTRACT

The parental diversity has been proposed as a possible predictor of heterotic potential in many crops. Advances in molecular markers have generated considerable interest in assessing genetic diversity and predicting hybrid performance. The present study was aimed to assess the genetic diversity among parents at molecular level and investigate the extent of correlation between marker heterozygosity and hybrid heterosis using Random amplified polymorphic DNA (RAPDs) markers. Twenty four hybrids along with their parents (six lines x 4 testers) were evaluated for ten agronomic important traits including in a replicated field trial. The RAPD analysis revealed 48.4 per cent of polymorphism among the 10 genotypes. The genetic dissimilarity index obtained from the simple matching coefficient had a range of 0.390 (IS 3504 and IS 3541) to 0.938 (CO 28 and CO 27). As a whole, 10 genotypes were grouped into five clusters. The two fodder genotypes IS 3504 and IS 3541 originated from Sudan were grouped in the same cluster indicating the molecular similarity within them. Correlation coefficients computed between the genetic distances among parents and relative heterosis of their hybrids revealed a positive and significant association for leaf breadth ($r=0.467$), panicle length ($r=0.438$), panicle weight ($r=0.405$) and grain yield per plant ($r=0.383$) and positive and non significant relationship with leaf length. Results indicated that molecular markers like RAPDs may be useful for predicting heterotic potential of the hybrids based on the parental diversity.

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Key words : Random amplified polymorphic, DNA analysis, *Sorghum bicolor*, Heterosis, Genetic distance

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench], a traditional crop in much of Asia and Africa has an ability to tolerate drought and temperature extremes more effectively than the cereals. It has wide range of adaptation from sea level to an altitude of 3000 meters and from 40°S to 45°N latitude (Chopra, 2001). It plays a very important role in providing nutrition to human race along with wheat, rice and maize (Mohanraj *et al.*, 2006). Sorghum is fourth in worldwide economic importance among cereal crops and is grown throughout the arid and semi-arid tropics (Smith and Frederiksen, 2000). In India, sorghum ranks third in area and production after rice and wheat. Certainly sorghum, with average yield far below its potential has the opportunity with input from genetics and management comparable to rice, wheat and maize to become the global grain of the future.

Most of the national sorghum breeding programs in India focus on development of high yielding varieties and hybrids suitable for both grain and fodder production. Heterosis is an important component of hybrid yield performance and it has been shown to exist in a wide variety of crops for various yield and agronomic traits. In

sorghum, heterosis for yield has been reported to range from 39 to 80% (Quinby, 1962). The level of genetic diversity between the parents has been proposed as a possible predictor of hybrid performance and heterotic potential in many crops. Development of heterotic hybrids involves extensive field crossing and evaluation and is time consuming. If a simple, reliable and efficient method to assess heterotic potential of F_1 hybrids prior to field testing is developed, much of the field work associated with field crossing and multi environment testing would be eliminated (Xiao *et al.*, 1996).

In recent years, use of DNA-based markers for the genetic analysis and manipulation of important agronomic traits has become an increasingly useful tool in plant breeding. DNA markers have the potential to enhance the operation of a plant breeding program through a number of ways, ranging from finger printing of elite genetic stocks, assessment of genetic diversity, increasing the efficiency of selection for difficult traits, to making environment-neutral selection possible (Weising *et al.*, 2005). However, advances in molecular markers have generated considerable interest in assessing genetic diversity and predicting hybrid performance in crop breeding programmes (Krystkowiak *et al.*, 2009).

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