

RAPD markers for genetic diversity estimation and its correlation with hybrid performance in pearl millet

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The investigation was conducted to assess the association of genetic diversity of parental lines with mean performance of hybrids, mid parent heterosis, better parent heterosis and sca effects. The material for this study consisted of five male-sterile lines, eight pollinator lines, 40 F1 crosses, which were generated through Line x Tester matings. Whole of the material was grown in a Randomized Complete Block Design with three replications. All the parental lines were screened to detect polymorphism in the form of RAPD markers. Genetic diversity among the parental lines was determined by RAPD markers and morphological characters. The genetic distances so obtained were correlated with F1 mean performance and heterosis. Positive correlation was obtained between molecular marker diversity and F1 mean performance, heterosis over better parent but the value of correlation coefficient was found to be non-significant. In contrary, negative correlation was obtained between taxonomic distance and F1 mean performance; better parent heterosis. Our results have indicated that genetic-distance measures based on RAPDs may be useful for the grouping of parents, but not for predicting heterotic combinations in pearl millet.

Keywords: Genetic diversity, RAPD, Hybrids, fodder pearl millet.

Biography

G. Nagaraju has submitted his Ph.D. to Jawaharlal Nehru University, New Delhi, and published three papers of International repute and attended several national and international conferences and also presented posters.

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Genetic dermatological disease database

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Despite the high frequency of certain skin diseases in developing countries, they have so far not been regarded as a significant health problem in the development of public health strategies. This is due to the assumption that skin diseases are not life-threatening. On the contrary, dermatologic disorders generally have a major impact on patients' daily activities, psychologic and emotional state, and social relationships. Despite this, the study of genetic basis and susceptibility of individuals to different forms of dermatological disorders is still at its nascent stage. Due to the large role played by genetic factors on the development of many dermatological diseases, it becomes important to identify the genes and variants associated with a particular disease. A database specific to these variants would help to predict individuals with high susceptibility of developing the disease. With this preview, in the present study, we have developed a database of genetic variations associated with dermatological disorders. We presume that the analysis of mutations reported in the database may help researchers understand the nature and etiology of these diseases.

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