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Research Application Summary

Characterisation of genetic diversity among Sudanese sorghum accessions using molecular markers and phenotypic characteristics

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Abstract

Sorghum is an important staple food grain crop for the millions of people living in the semi-arid tropics in Asia, Africa and Latin America. The present study examined phenotypic and genotypic characteristics of 95 Sudanese sorghum accessions. Morphological and molecular markers were employed to study the genetic variability among the accessions. A total of 10 morphological markers and 15 simple sequence repeats (SSRs) primers were used. Cluster analysis based on morphological traits revealed thirteen distinct clusters basis on their morphological characters with two accessions forming independent cluster. Based on molecular markers, twelve distinct clusters were observed.

Key words: Sorghum accessions, SSR markers, phenotypic characterization, Sudan

Résumé

Le sorgho est une céréale importante utilisée comme aliment de base pour des millions de personnes vivant dans les tropiques semi-arides d'Asie, d'Afrique et d'Amérique latine. La présente étude a examiné les caractéristiques phénotypiques et génotypiques de 95 accessions de sorgho soudanais. Les marqueurs morphologiques et moléculaires ont été utilisés pour étudier la variabilité génétique parmi les accessions. Un total de 10 marqueurs morphologiques et de 15 premiers éléments des répétitions de séquences simples (SSRs) a été utilisé. Une analyse de groupement basée sur les caractères morphologiques a révélé treize groupes distincts sur la base de leurs caractères morphologiques avec deux accessions formant un groupe indépendant. Sur la base de marqueurs moléculaires, douze groupes distincts ont été observés.

Mots clés: Accessions de sorgho, marqueurs microsatellites, caractérisation phénotypique, au Soudan

Background

Sorghum (*Sorghum vulgaris* L.) is a major food crop in Sudan, and the majority of the people consider it as national bread of

Sudan. Sorghum contributes about 65% of Sudan consumption of grain. Studying the genetic variation of sorghum genotypes collection from Sudan attracts special interest for several reasons. Beyond the economic importance of the crop, Sudan is within the geographical range where sorghum is believed to have been domesticated for the first time, and where the largest genetic variation for both cultivated and wild sorghum is found. The objective of this study was to classify phenotypic and genotypic variation among a set of 95 Sudanese sorghum accessions.

Literature Summary

Conservation of genetic resources entails several activities, many of which may greatly benefit from knowledge generated through applying molecular marker technologies. Measurement of phenotypic and genotypic variance in field trials is a traditional approach to examine the genetic differences among genotypes. Analysis of phenotypic performance in the field in combination with molecular marker analysis provides useful information to increase the efficiency in plant breeding programmes. However, there are few reports about the relationship between molecular data and the phenotypic performance in sorghum (Anas and Yoshida, 2004).

Microsatellites have been developed in different crop plants (Philips and Vasil, 2001; Varshney *et al*., 2004). Among different classes of molecular markers, SSR markers are useful for a variety of applications in plant genetics and breeding because of their reproducibility, multiallelic nature, co-dominant inheritance, relative abundance and good genome coverage (Powell *et al*., 1996). SSR markers have been useful for integrating the genetic, physical and sequence-based physical maps in plant species, and simultaneously have provided breeders and geneticists with an efficient tool to link phenotypic and genotypic variation (Gupta and Varshney, 2000).

Study Description

In this study the three strategies were used to determine the diversity of the Sudanese sorghum accessions. Firstly, a phenotypic characterization of sorghum accessions was conducted in regular field experiment, using IBPGR Descriptor list for sorghum (IBPGR, 1984) and Distinctiveness, Uniformity and Stability (DUS)-test guidelines for sorghum (ICRISAT). Secondly, the phenotypic performance of the accession was evaluated in regular field experiment with two replications. Thirdly, representative samples of the accessions based on phenotypic evaluation were used to characterize the pattern of

genotypic variation using Simple Sequence Repeats (SSR) markers. These SSRs markers study are presently being done at the Biotechnology Laboratory of the ARC-Sudan in Wad Medani.

Research Application

The cluster analysis was used to obtain a dendrogram of the 95 sorghum accessions. The dendrogram clearly indicated the close relationship between sorghum accessions from almost all regions.

The 95 accessions were grouped in thirteen clusters basis on their morphological characters (Fig. 1). The number of accessions per cluster ranged from two in cluster 6 and 13 to fourteen in cluster 7.

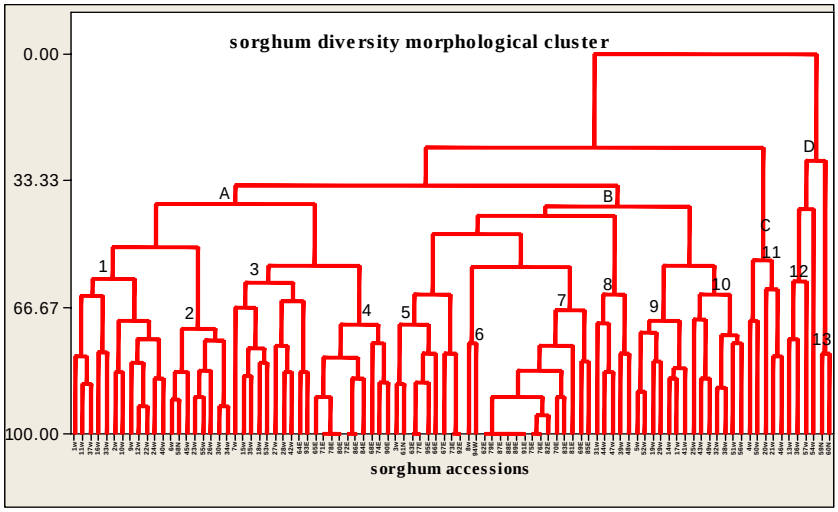

Figure 1. Dendrogram showing the morphological clustering patterns of the 95 sorghum accessions in northern, eastern and western Sudan.

Of the 15 SSR markers used in this study, 13 showed high reproducibility, with high consistency in the amplified product. Therefore, only 13 markers were included in the analysis (Fig. 2).

Recommendation

The study shows that considerable genetic diversity exists among the sorghum accessions collected from the three deferent regions in Sudan. The results of this study makes an important contribution to knowledge about sorghum diversity in these regions, even though further work is needed to assess the genetic diversity in all sorghum growing regions of the country.

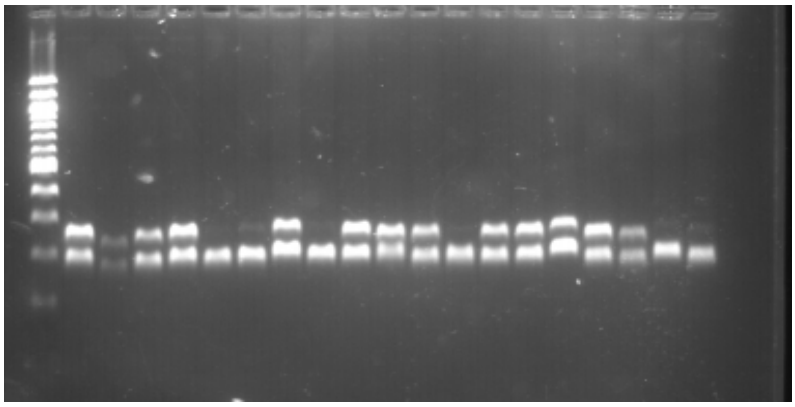

Figure 2. Photograph of Sybr-green -stained Agarose gel of polymorphic PCR products from sorghum genotypes amplified with two SSR-specific sorghum primers (duplex xcup26 + xcup11).

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References

Anas and Yoshida, T. 2004. Sorghum diversity evaluated by Simple Sequence Repeat (SSR) Markers and Phenotypic Performance. *Plant Prod. Sci.*7 (3):301-308.

Gupta, P.K. and Varshney, R.K. 2000. The development and use of microsatellite markers for genetic analysis and plant breeding with emphasis on bread wheat. *Euphytica* 113:163-185.

Philips, R.L. and Vasil, I.K. (Eds.). 2001. DNA-Based Markers in Plants. Kluwer Academic Publishers.

Powell, W. *et al*. 1996. Polymorphism revealed by simple sequence repeats. *Trends Plant Science* 1:215-222.

Varshney, R.K. *et al*. 2004. Molecular maps in cereals: methodology and progress. In: Cereal genomics. Gupta, P.K. and Varshney, R.K. (Eds.). Kluwer Academic Publishers. pp. 35-82.