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Breeding Strategies for Yield Improvement in Forage Sorghum

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Sorghum is one of the world's major cereal crops and a dietary staple for more than 500 million people in sub-saharan Africa and Asia. It ranks fifth after maize, rice, wheat, and barley. Sorghum can be used for human consumption, livestock feed and fodder, ethanol production and other industrial purposes. To enhance use of sorghum as a fodder and biofuel crop, it is important to improve biomass quality in terms of digestibility and saccharification of the stalk. Lignin content of cell walls determines, among other factors, sugar release and thus the efficiency of the fermentation process. The main goal of forage sorghum breeders is to develop cultivars with high fodder yield as well as high digestibility.

Some breeding strategies for yield improvement in forage sorghum

1. **Diallel analysis-** it provide information on general and specific combining abilities (GCA and SCA), determine genetic variances and estimate heritability. Combining ability describes the breeding value of parental lines to produce hybrids. Combining ability analysis helps in the identification of parents with high GCA and parental combinations with high SCA. Diallel Cross refers to mating of selected parents in all possible combinations and analysis of a set of diallel crosses is called diallel analysis.
2. **Line x tester-** line x tester analysis is a modified form of a top cross used for measuring general and specific combining ability variances and effects in large number of germplasm lines at a time. The concept of line x tester analysis was developed by Kempthorne in 1957. In case of top cross only one tester is used, while in case of line x tester cross several testers are used. The common parent crossed to several inbred lines is called tester and the hybrids produced are called test crosses or top crosses. It provide information about GCA and SCA variance and effects.

Characteristic of a tester

The most desirable tester is one in forage sorghum which provides maximum information about performance of a line in cross combinations under different environmental conditions. The important characteristics of a tester are given as follows:

- **Broad genetic base:** the tester with a broad genetic base include heterogeneous cultivars, populations or crosses. Such testers were considered more desirable to determine general combining ability in the early years of hybrid development programs.
- **Wider adaptability:** The tester should have wider adaptability so that it can be used for evaluation of inbred lines for combining ability under changing environmental conditions.
- **Low forage yield performance:** The best inbred line has a masking effect due to its desirable dominant alleles, therefore, it should not be used as a tester. Thus, to assess the real performance of a line, low forage yield performing tester should be used. An inferior synthetic developed by crossing together poor lines may be used as a tester.
- **Low Performance for other Traits:** A tester should be poor in the trait for which lines are to be evaluated. For example, a synthetic susceptible to lodging should be used to test

the capacity of lines to withstand lodging. It is difficult to have all these characteristics in one tester. Hence, several testers have to be used to meet various evaluation requirements.

Major advantage of this mating type we can evaluate upto 50 cross combination easily.

3. **Bi-parental analysis-** in bi-parental crossing of randomly selected plants in the F_2 or subsequent generation in a definite fashion. The concept of biparental cross analysis was originally developed by Comstock and Robinson (1948, 1952). In this technique, plants are randomly selected in F_2 or subsequent generation of a cross between two pure lines having contrasting characters and the selected plants are crossed in a definite fashion.

There are three mating type of bi-parental-

- **North carolina design 1-** NCD 1 is a design of biparental cross in which in F_2 each selected male is mated to a different group of female resulting in f crosses, where f is the number of female plants used for crossing in a set. This design is also known as nested design. In this design each male plant is crossed with equal number of female plants. Generally one male is crossed with 4 females, but it may vary from crop to crop. Each male is crossed with different group of females.
- **North carolina design 2-** NCD 2 is a design of biparental cross in which F_2 each selected male is mated to the same set of female resulting in mf crosses, where m and f denote the number of male and female plants in a set. This design is also known as factorial design and is similar to line x tester analysis.
- **North carolina design 3-** NCD 3 is a design of biparental cross in which in F_2 each randomly selected male is mated to P_1 and P_2 parents of original cross resulting in 2m crosses, where m is the number of male plants used for crossing in a set. This design involves backcrossing in F_2 or later generation.

Estimation of breeding value

There are two broad methods of estimating breeding value of an individual *viz.*, (i) biometrical techniques, and (ii) molecular techniques.

1. Biometrical techniques: Various biometrical techniques are used for estimating breeding value of an individual. Some biometrical techniques are used for calculation of additive and non additive gene effects in an individual. The most commonly used technique for estimating additive genetic effects include diallel cross, partial cross, line x tester cross, triallel cross, quadrallel cross, biparental cross, triple test cross and generation mean analysis. All these techniques are useful to evaluate the genetic materials in terms of their breeding value. These techniques provide information about the gene action involved in the expression of various traits. Mean deviation, regression analyses, heritability and combining ability analysis also provide information about the gene action and genetic worth of the individual.

2. Molecular Techniques: Now various DNA worker techniques are available which can be used to find out the genetic worth of an individual. Such techniques include RFLP, AFLP, RAPD, CAPS, SSR, SNP, etc.

Conclusion

Forage sorghum is an important fodder crop due to its high biomass production, adaptability to diverse environments and nutritional value. Breeding strategies such as diallel analysis, line × tester analysis, biparental mating designs and modern molecular techniques play a crucial role in understanding gene action, identifying superior parents and developing high-yielding cultivars. The integration of conventional and molecular breeding approaches will accelerate the development of forage sorghum varieties with improved yield, quality and climate resilience, thereby contributing to sustainable livestock production and fodder security.

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