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# GENETIC IMPROVEMENT OF FODDER TREES

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## ABSTRACT

India is the second largest producer of milk in the world with 15% of the world's livestock population thriving on 2% of global area. The pressure on arable land for food grains, pulses and oilseeds is increasing day by day leaving no scope for future expansion of area under fodder crops. This has resulted in huge gap in the demand and supply of the fodder. In this context, fodder trees are of great importance as a major feed resource especially during lean period in all parts of India. Research effort for the genetic improvement of fodder trees is, however, lacking as compared to massive effort for forage grasses and legumes. In this article, an attempt has been made to review the constraints, different approaches, present status of research and future strategies needed for genetic improvement of fodder trees.

**Key Words :** Fodder tree, plus tree selection, provenance test, selection criteria, conservation

Supporting about 15% of world's livestock population in India on her 2% of world's geographical area indicates the tremendous pressure of animal on the limited land resources. Furthermore, for meeting the projected requirement of green fodder by 2000 AD (1136 million tonnes) additional 5% of total cultivated land need to be diverted for production of fodder crops [1]. But the scope for increasing area under fodder crop is very less due to pressure on cultivated land for production of food and cash crops to meet the demand of the escalating population. However, a number of trees found in different agroclimatic regions with varying distribution (2) have enormous potential for producing nutritious green fodder. The important ones are *Acacia nilotca, A. senegal, A. tortilis, Albizia lebbeck, A. amara, Bauhinia variegata, Dalbergia sissoo, Ficus glomerata, Hardwickia binata, Leucaena leucocephala, Prosopis cineraria, Populus ciliata, Sesbania grandiflora* and *Ziziphus nummularia.* In arid as well as hilly region livestock are mainly maintained on tree lopping [3, 4]. Fodder trees can produce as much, if not more, green fodder per unit area as agricultural fodder crops [5] and are usually rich in protein, calcium and vitamins [6]. They can be grown in combination with any agricultural crop (as agroforestry system), pasture grasses and legumes (as silvipastoral system) or on wasteland without interfering the production of food grain or other agricultural crops, rather being a component of sustainable land use system.

In spite of paramount importance of fodder trees, efforts for their genetic improvement are lacking as compared to the massive efforts on forage grasses and legumes. The article attempts to review the constraints, breeding approaches, current status of research and future strategies for genetic improvement of fodder trees.

### *Constraints*

Though the genetic basis for breeding trees and agricultural crops is more or less same, the breeding approach for trees is quite different from that for agricultural crops. The tree breeder faces many constraints and limitations in the execution of breeding programmes [7].

Fodder tree improvement is a long-term policy and the wide generation time is the most obvious difference between trees and field crops. The great achievements in field crops including forage grasses and legumes could be because of their short life cycle in contrast to which, the long generation time of fodder trees makes the breeding programme slow and discourages the breeder to take initiative for their genetic improvement [8].

The basic information on floral biology, breeding system, heritability, nature of genetic effects of important traits relating to fodder yield and quality which are prime factors to determine breeding strategy is scanty for most of the fodder trees and this hinders the initiation of their genetic improvement programme. The long generation time and flowering time prolong the period for study of genetic parameter. The size of tree also creates problem in taking measurement, controlled pollination and collection of seed. The methods of plus tree selection, clonal multiplication, genetic testing and establishment of base -, breeding - and production population have not also been fully standardized so far.

### *Breeding approaches*

Like field crops, for fodder trees too, the efforts of survey and collection or creation of variability, evaluation (testing) and selection are basics to the breeding approaches for their genetic improvement. The breeding programme for fodder trees in India is quite young and most of the work is in progress.

*Plus tree selection.* Plus tree selection is the most commonly used breeding method for fodder trees [9]. Plus trees as defined as outstanding individuals exhibiting one or more desirable traits [10] are selected from the base population of natural stand containing trees of about same age (even-aged stand) or of different ages (uneven-aged stand) either by comparing phenotypic value of a candidate tree with that of base population (comparison method) or evaluating a candidate tree on the basis of its score (individual tree method) [11]. The comparison method is more efficient because this minimizes the confounding of environmental effect with genetic effect. The method includes comparison tree, base value and regression methods. In comparison tree method the superiority per cent of each candidate tree over the average value of all other trees in base population is the basis for selection of a plus tree.

Base value method is used for the traits which are less influenced by the difference in age among the trees of a stand i.e. traits having high narrow sense heritability. A base value for such trait is estimated as mean of a small sample (5-10%) of base population. Superiority per cent of a candidate for each trait is worked out over the base value. This approach has been successfully used by Sidhu [12].

Regression method is effective for the traits affected by age-difference in uneven-aged stand. The regression line is prepared for base population by plotting the observation of different trees against their ages. The value of candidate tree is plotted against age on respective regression line. The position of value for the candidate tree with reference to the regression line would help in determining the superiority per cent of candidate tree over the expected value based on regression line.

Under individual tree method, the candidate tree is evaluated for its own value without making any comparison with base population. The method is comparatively less effective as it does not take care of environmental effect. There are three kinds of individual tree method viz., total score, individual culling and selection index methods. In total score method, the scores assigned to the different traits of each candidate tree are added and a sum total of score is used to select or reject a candidate tree. Under independent culling method, the candidate is selected if it meets the minimum standard fixed for each trait. If the score of any trait of a candidate tree falls below the fixed level, then the tree is rejected regardless of its superiority in other traits. A selection index is estimated on the basis of genotypic and phenotypic variance and covariance and economic value of the trait in selection index method. This method is the most effective among the three individual tree methods.

After selection of plus trees the seedling seed orchard or clonal seed orchard is established through seed or vegetative propagation, respectively to produce genetically improved seed in bulk from the selected plus tree [13].

Though simple selection of plus trees based on phenotype has been successful in bringing genetic improvement in different fodder trees such as *Acacia tortilis, Prosopis cineraria* [14, 15], *Dalbergia sissoo* [12], and *A. catechu* [16], it is important to distinguish genetic variation from environmental one through well-designed progeny test [17]. This is because plus trees selected purely based on their phenotypic superiority need not to be genetically superior. Wrong choice of parent of planting material may result in serious loss or complete failure of the programme. Therefore, genetically improved and site- specific elite genotypes which should also ensure a sustained supply of planting material (seed or vegetative propagule) of high genetic quality need to be identified through progeny test. However, evaluation of plus trees through progeny test takes time and thus, plus trees are directly used to establish seed orchard to meet the immediate seed requirement of the growers. Later, based on the progeny test seedlings of only superior plus trees are retained in the seed orchard to supply the improved seeds. Selection based on progeny test has been successfully practised in important fodder trees [18-21].

Seed orchard also takes some years to produce seeds in large quantity. Therefore, to meet the interim needs for reasonably good quality seeds, it is a general practice to create seed production area by suitable conversion of some superior stands of base population to seed orchard by retention of only plus trees.

*Provenance test* It is another easy, well-established and widely accepted breeding approach for fodder trees in which seeds are collected from a number of widely scattered stands (usually natural) and trials are conducted in a particular region. The objective of conducting provenance test is to eventually arrive at a conclusion as to which provenance is best for planting and breeding programme in that particular region.

For collection of seeds of a provenance (types of trees having common genetic base), different areas where trees grow naturally should be identified. There should be a large number of trees, at least 20, for collection of seeds from one provenance. Selection of best provenance and then best individual plus trees through provenance test forms the foundation for seed orchard. However, the work starting from collection of provenance to establishment of seed orchard is at various stages [15,18,19,21,22].

Sidhu [23] proposed a very simple and effective breeding approach particularly for open-pollinated as well as vegetatively propagated agroforestry trees which may easily be applicable to fodder trees also. In this approach, progeny-cum-orchard is established in different breeding zones to provide multiplication trial and the cycle of selection, controlled crossing and testing continues to broaden the genetic base of breeding material and evolve superior line simultaneously.

### *Selection criteria*

An ideotype in fodder tree must take into consideration both forage yield and quality aspects. The latter is of specific importance as it relates to animal performance. In general, selection of fodder tree requires consideration of forage yield, quality, nutritive value in terms of intake, digestibility and utilization, high palatability with minimum or no toxic elements like tannin, mimosine, oxalate, cyanogenetic glycoside, saponin etc., seedling vigour and resistance to pests and diseases (24). In addition to these general characters, fodder trees should have different selection criteria for different systems under which they can be grown.

### *Selection criteria for Agroforestry System*

Ideal fodder tree for agroforestry should require following characters:

1. Phyllotaxis should permit penetration of light to reach ground for crop growth
2. A low ratio of crown diameter to bole diameter with straight and tall bole.
3. Leafing during dry period and less leaves during crop growth period.
4. Light and sparse branching, preferably at an angle.
5. Leaf litter of little allelopathic effect on companion crop with quick mineralising nature.
6. Strong tap root with less lateral roots.
7. Self-pruning property; otherwise, ability to tolerate high incidence of pruning.
8. Amenable to early wide spacement.

### *Selection criteria for Silvipastoral System*

1. Fodder tree should be compatible and have complementary association with forage grasses and legumes.
2. Little or no allelopathic effect of leaf litter or root on pasture.
3. Light canopy during monsoon.
4. Long tap root with less lateral roots.

### *Selection criteria for growing on wasteland*

1. Ability to thrive well under moisture-stress, harsh climatic condition (excessive heat, cold or frost condition) and inhospitable soil (saline, alkaline, acidic, calcareous or infertile).
2. Ability to increase soil productivity and to protect soil from erosion.

Sufficient scope exists for selection for different systems as good amount of genetic variability for these desirable characters exist in different fodder trees (22, 25-29).

### *Biotechnological approach*

Unlike in herbaceous annuals, conventional breeding methods have many limitations to achieve genetic gain in fodder trees. Most fodder trees take more than five years to mature and thus, crossing and progeny evaluation are inordinately delayed, particularly in the absence of positive correlation between juvenile and maturity trait. A high incidence of sexual incompatibility and limited success in vegetative propagation through root or stem cutting (30) further add to the restricted application of conventional breeding method. The significance of biotechnology as an additional tool is being increasingly realised, especially for rapid clonal multiplication of elite genotype of different fodder trees through *in vitro* micropropagation (31-36). It has also high potential for shortening the breeding cycle of fodder trees through *in vitro* flowering, hybridization through *in vitro* pollination and embryo rescue, gene identification through RFLP and RAPD techniques and gene transfer (37).

### *Conservation*

Most of fodder trees have very wide genetic base as a consequence of natural outcrossing and large population in a variety of habitats (38). Again, many fodder trees such as *Acacia nilotica, Albizia lebbeck, Azadirachta indica, Dalbergia sissoo, Prosopis cineraria* are native to the Indian sub-continent and have broad spectrum of genetic variation which should be conserved to act as a reserve for the present and future need through either *in situ* (on site) conservation of original habitat by establishing national park, biosphere reserve etc. or *ex situ* (off site) conservation involving preservation away from the site of original habitat under field condition by establishing seedling or clonal seed orchard or through storage of seed under controlled conditions in seed bank. Though seed storage is the most effective and economic approach but it is suited for the orthodox and long- lived seeds. An alternative approach of storage for recalcitrant and short-lived seed is *in vitro* conservation.

Two approaches are usually followed for *in vitro* conservation; (i) slow growth strategy through manipulation of culture media and/or environment and (ii) a state of suspended growth by cryopreservation of suspension culture, callus culture, shoot tip and bud culture, embryo, pollen and recalcitrant seeds. The research on standardization of the protocol of *in vitro* conservation is scanty, although some reports are there, for example in *Prosopis juliflora* and *P. cineraria* (39).

### *Future research needs/strategies*

The future research needs should concentrate on the following aspects:

1. Identification of most suited speceies for fodder purpose for different agroclimatic zones.

2. Basic information on floral morphology, reproductive biology, breeding system, presence of male sterility and/or self incompatibility, rate of seed setting, potentiality of vegetative propagation through stem/root cutting or grafting, efficiency for controlled pollination i.e. selfing and/or crossing (intra- or inter-specific), gene centre of different species identified for different zones.

3. Collection and evaluation of germplasm of selected species for different traits relating to forage yield and quality in different fodder trees.

4. Creation of variation through physical and chemical mutation, intra- and inter-specific hybridization, tissue culture (somaclonal variation) necessary (if any) for specific traits which are not available in collected germplasms.

5. Evaluation through progeny test (selfing, half sib, full sib etc.), selection of superior genotype from both base and advanced generation population and establishment of seed orchard.

6. Conservation of genetic variability

7. Genetic studies through RFLP, isozyme and RAPD technique to identify different genes for qualitative traits and biometrical studies (breeding value, heritability, nature of genetic effect, genetic correlation and diversity) of quantitative traits.

8. Attention also should be diverted towards development of hybrid for combination of specific traits.

9. Application of *in vitro* method for rapid clonal multiplication of elite genotype, conservation and also for supplementing the conventional breeding method.

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