Development of composite collection and genotyping of foxtail millet [Setaria italica (L.) Beauv.] composite collection

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Introduction

- Foxtail millet belongs to family Poaceae and subfamily Panicoideae
- A self-pollinating crop with chromosome number 2n=18
- Domesticated in highlands of central China, possibly about 4000 BC
- Cultivated in 26 countries, and ranks second in total world production of millets
- Produces six million tons of food mainly in southern Europe and in tropical Asia (Marathe 1993)
- An important crop in China, India, CIS countries, and Syria
- Possesses high nutrient quality.

Nutritional value of foxtail millet grain (100 g)
- Protein content: 10% to 12%
- Lysine content: 2.29% to 2.7%
- Fat content: 4% to 5%
- Energy: 351 kcal
- Thiamin: 0.59 (mg)

Classification of foxtail millet germplasm

Two Setaria species are known:
1. S. glauca and S. italica (Sub sp: viridis and italica)
2. S. italica consists of three races: Moharia, Maxima and Indica; and ten subraces: Aristata, Fusiformis, Glabra, Compacta, Spongiosa, Assamense, Erecta, Nana, Glabra and Profusa.

Status of foxtail millet germplasm at ICRISAT

- The entire foxtail millet germplasm (1535 accessions) constituted based on geographic origin and diversity for morpho-agronomic traits
- Following descriptors for important morpho-agronomic characters

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<tr>
<th>Trait</th>
<th>Number of accessions</th>
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<td>Leaf sample of 20-day old seedling of single representative plant from each of 500 accessions taken and DNA extracted by high-throughput procedure.</td>
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Genotyping

Leaf sample of 20-day old seedling of single representative plant from each of 500 accessions taken and DNA extracted by high-throughput procedure.

Primer optimization

- No SSR markers are available in foxtail millet
- SSR markers from closely related species identified
- Thirty-one unlabelled pearl millet SSR markers selected to genotype 8 diverse foxtail millet accessions (representing five countries)
- Primer optimization with Taguchi method (Taguchi et al. 1986) as described in Cobb and Clarkson (1994)
- Twelve markers showed polymorphism
- Additional SSR markers will be selected from other closely related species such as maize and sorghum.

Future plan

- Genotyping 500 accessions of composite collection using 20 SSR markers
- Identifying a reference collection consisting of most diverse accessions for use in crop improvement program.

References