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 temperate, subtropical, and 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, Assamens, Erecta, Nana, Glabra and Profusa.

Status of foxtail millet germplasm at ICRISAT

- The entire foxtail millet germplasm (1535 accessions) characterized for important morpho-agronomic characters following descriptions for S. italica and S. pumila (IBPGR 1985)
- Collection consists of 1470 landraces, 11 improved cultivars and 54 wild accessions
- A core collection (155 accessions), representing entire diversity, was developed based on geographic origin and quantitative traits.

Composite collection

- A composite collection of foxtail millet germplasm (500 accessions) (Table 2) constituted based on geographic origin and diversity for morpho-agronomic traits
- Composite collection consists of accessions representing all three races and ten subraces.

Diversity in foxtail millet germplasm.

Regeneration of foxtail millet germplasm.

Table 2. Accessions in foxtail millet composite collection.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Number of accessions</th>
</tr>
</thead>
<tbody>
<tr>
<td>1000 grain weight &gt; 3.7 g</td>
<td>9</td>
</tr>
<tr>
<td>Grain weight per plant &gt; 19 g</td>
<td>5</td>
</tr>
<tr>
<td>Basal tillers &gt; 29</td>
<td>25</td>
</tr>
<tr>
<td>Core collection</td>
<td>155</td>
</tr>
<tr>
<td>Dwarf (= 50 cm)</td>
<td>21</td>
</tr>
<tr>
<td>Early flowering accessions (= 40 days)</td>
<td>77</td>
</tr>
<tr>
<td>Improved cultivars</td>
<td>10</td>
</tr>
<tr>
<td>Short inflorescence length (=&lt;50 mm)</td>
<td>40</td>
</tr>
<tr>
<td>Long inflorescence length (=&gt;299 mm)</td>
<td>18</td>
</tr>
<tr>
<td>Short inflorescence width accessions (=5 mm)</td>
<td>23</td>
</tr>
<tr>
<td>Widest inflorescence accessions (&gt;39 mm)</td>
<td>25</td>
</tr>
<tr>
<td>Mono culm types (single tiller per plant)</td>
<td>59</td>
</tr>
<tr>
<td>Agronomically elite accessions</td>
<td>33</td>
</tr>
<tr>
<td>Total</td>
<td>500</td>
</tr>
</tbody>
</table>

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


