



Genotyping composite collection of finger millet [*Eleusine coracana* (L.) Gaertn.]

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Introduction

- Finger millet belongs to family *Poaceae* and subfamily *Panicoideae*
- A self-pollinating tetraploid species with $2n = 36$
- Cultivated in 23 countries (mainly in Africa and Asia) on 3.38 m ha producing 3.76 m t grain
- Very important crop in Uganda, Kenya, Ethiopia, Eritrea, Nepal and India
- A nutritionally rich crop for protein, minerals (Calcium and Iron), and amino acid methionine.

Origin and genepool

- Finger millet was first domesticated in eastern Africa, possibly in Ethiopia, about 5000 BC
- Two subspecies are known
 - i). *E. coracana* subsp. *coracana* (cultivated form) with four races: Elongata, Plana, Compacta, Vulgaris; and ten subraces: Confundere, Digitata, Grandigluma, Incurvata, Laxa, Liliacea, Reclusa, Seriata, Sparsa, Stellata (race compacta has no subrace)
 - ii). *E. coracana* subsp. *africana* (wild form) with two races: *Africana*, *Spontanea*.

Table 1: Major holdings of finger millet germplasm in the world

Genebank / Country	Number of Accessions
ICRISAT, India	5949
AICSMIP, UAS, Bangalore, India	6000
Uganda	1231
Ethiopia	1989
Kenya	1500
Malawi	1000
Nepal	869

Status of finger millet germplasm at ICRISAT Genebank

- The entire ICRISAT collection (5949 accessions) has been characterized for 8 qualitative and 14 quantitative characters
- The entire collection represents 5658 landraces, 136 advanced cultivars, 50 breeding lines, and 105 wild accessions
- A core collection (622 accessions) based on geographical origin and data on 14 quantitative traits has been developed (Upadhyaya et al. 2006).
- A mini core collection (65 accessions) has also been developed.

Genotyping composite collection

- Composite collection consisting of 1000 accessions (Table: 2) (Upadhyaya et al. 2005) planted in field in third week of July 2006.

Table: 2 Composite collection of finger millet

Trait	Number of Accessions
ICRISAT core collection	622
Agronomic traits	222
Indian NARS core	50
Resistance to stresses	85
Grain nutrition traits	12
Genetic diversity	9
Total	1000



Diversity in finger millet inflorescence and grain

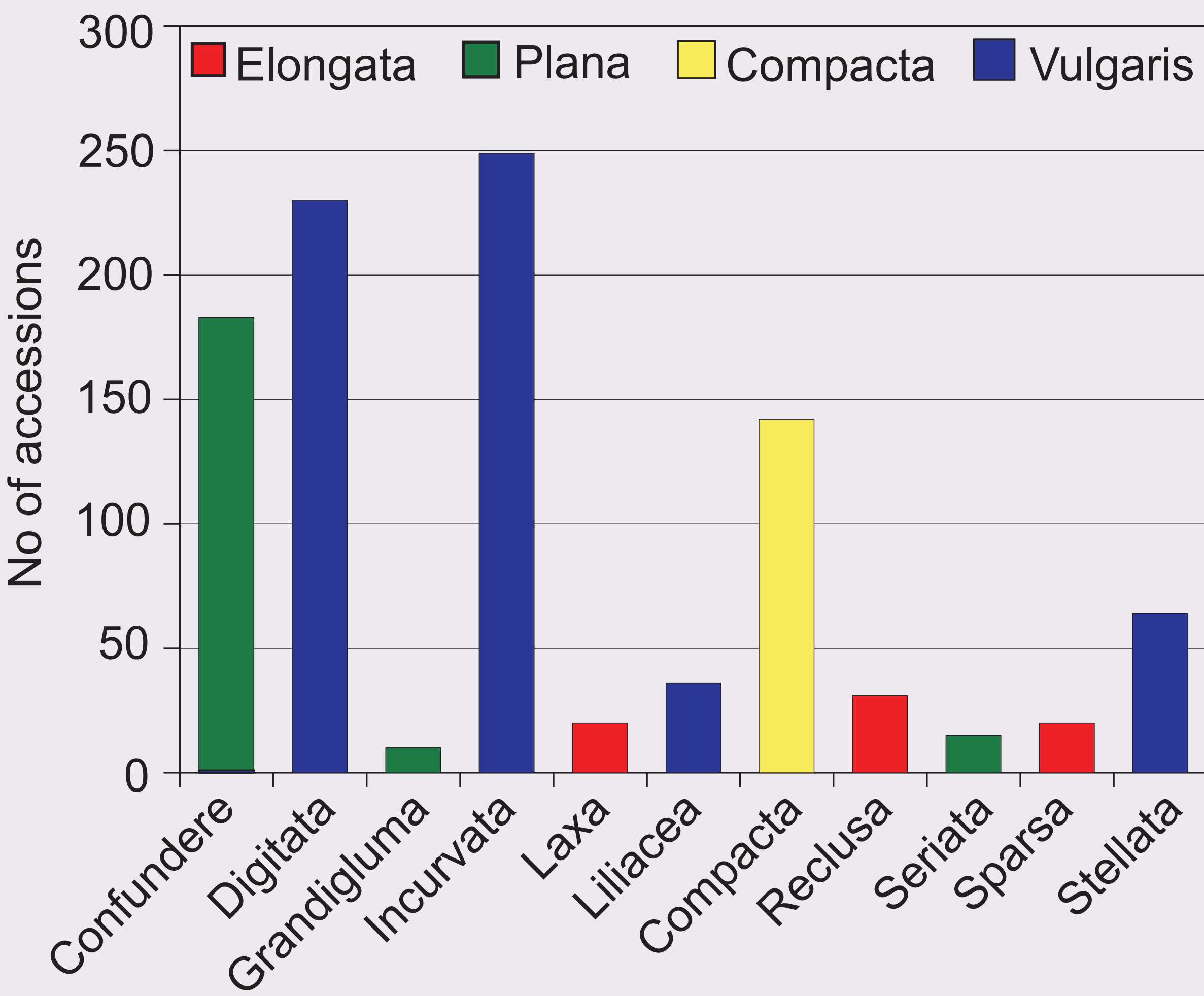
Genotyping

Leaf sample of 20-day old seedling of single representative plant for each of the 1000 accessions taken and DNA extracted by high-throughput procedure.

Primer optimization

- Thirty-one SSR markers optimized by Taguchi method (Taguchi et al. 1986) as described in Cobb Clarkson (1994) using 8 diverse accessions consisting of five landraces, and three wild types from eight countries
- Twenty-eight SSR markers showed polymorphism.

Representation of races and subraces in finger millet germplasm



Future plan

- Genotyping the composite collection using 20 SSR markers
- Identifying a reference collection of 300 most diverse accessions for use in crop improvement programs.

Reference

Cobb BD and Clarkson JM. 1994. A simple procedure for optimizing polymerase chain reaction (PCR) using modified Taghuchi methods. *Nucleic Acid Research* 22: 3801-3805.

Taguchi G. 1986. Introduction to quality engineering. Asian productivity organization. American supplies Institute Inc., Dearborn, MI.

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Upadhyaya HD, Gowda CLL, Pundir RPS, Reddy Gopal V and Sube Singh, 2006. Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genetic Resources and Crop Evolution* 53: 679-685.