



Development of composite collection and genotyping of pearl millet [*Pennisetum glaucum* (L.) R. Br.]



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About pearl millet

- Staple food for millions of people in the arid and semi-arid regions of Africa and Asia; forms an important source of feed and forage in the Americas
- Cultivated over an estimated area of about 26 million ha (FAO, 2005)
- Hardest crop; thrives even on poor soils of dry regions in hot climates.

Origin and domestication

- Originated in a diffuse belt stretching from Senegal to western Sudan
- Domesticated 4000 years ago at its place of origin
- Reached eastern Africa and India about 3000 years ago
- Spread to southern Africa about 2000 years ago (Fig. 1).

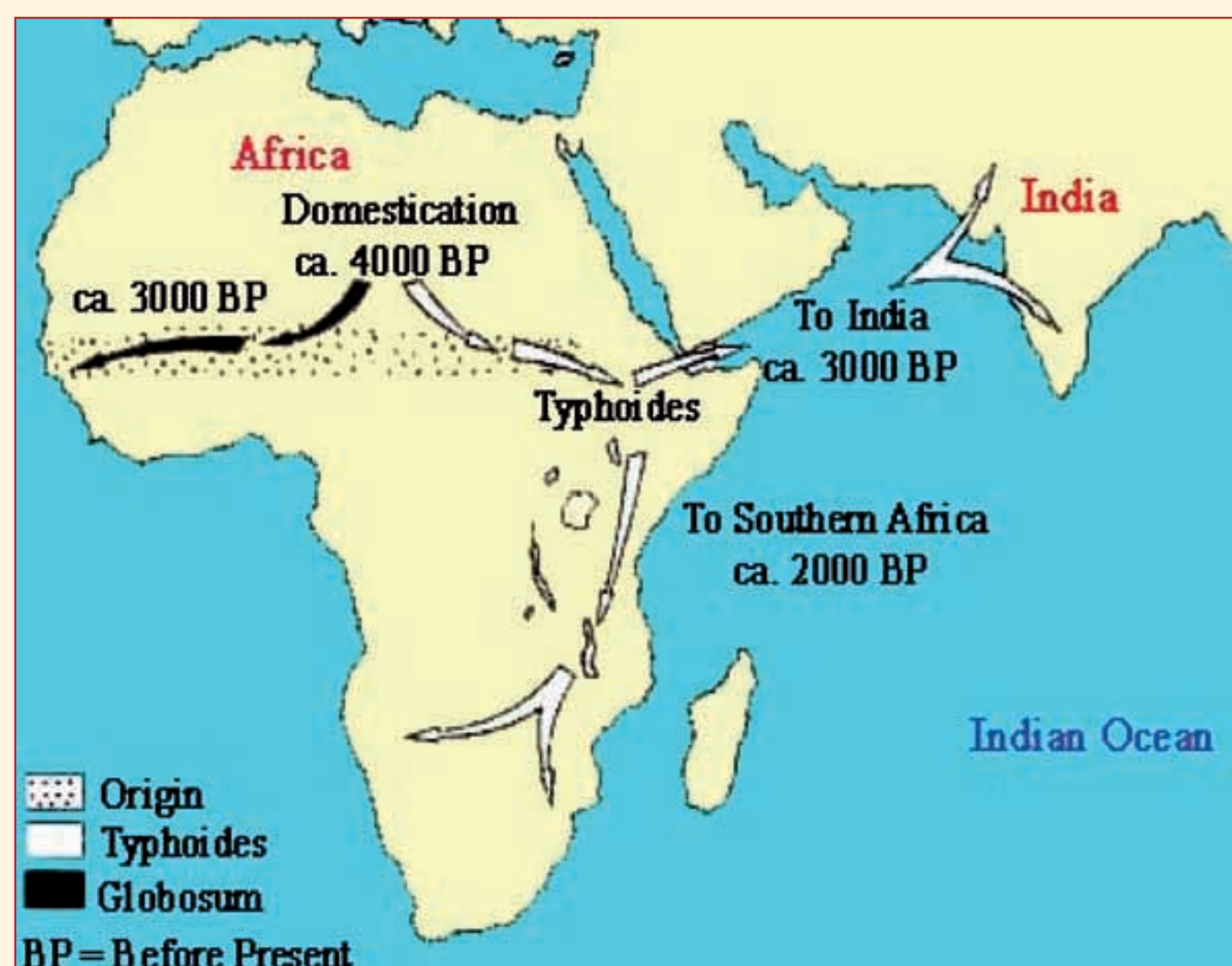


Fig 1. Origin and domestication of pearl millet.

Major centers holding pearl millet germplasm

- At ICRISAT, Patancheru, the RS Paroda Genebank holds the largest collection of 21 594 pearl millet germplasm accessions including 750 accessions of wild relatives, from 50 countries.
- The other centers holding pearl millet germplasm include:
 - National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India (6610 accessions)
 - *Institut de Recherché pour le Développement* (formerly ORSTOM), France (3607 accessions)
 - Ministry of Agriculture, Malawi (291 accessions)
 - United States Department of Agriculture (USDA), USA (5228 accessions).

Development of composite collection

- Composite collection of pearl millet developed using available data on phenotypic characterization, agronomic evaluation, geographic origin and taxonomy.
- Composite collection includes accessions of core collection at ICRISAT (504); tolerant to drought (6), heat (3) and salinity (20); resistant to downy mildew (42), ergot (20), rust (23), smut



Diversity in panicle size, shape and color in the world collection of pearl millet.

(15) and multiple diseases (8); high seed iron and zinc content (4), protein content (20); yellow endosperm (2), high stalk sugar content (12), forage type (8), trait specific selections (197), genepools (4), released cultivars (5), elite breeding lines (47) and other *Pennisetum* species (60).

- Accessions in composite collection represent 30 countries across all continents except Oceania.
- Biologically, landraces dominated with 694 accessions followed by breeding lines/released cultivars (246), and wild species (60).

Selection of SSR markers

- About 100 SSR markers derived from genomic DNA, BAC and EST-libraries are available at ICRISAT.
- Markers will be used to initially screen a set of eight diverse genotypes (included in the composite collection), one each from Botswana, Burkina Faso, India, and five from ICRISAT, to select highly polymorphic markers representing all the seven linkage groups.
- Pearl millet being a cross-pollinated species with large intra-accession variation, the selected set of markers will also be used to screen the artificial pools comprising different proportions of genomic DNA of two genotypes, which are polymorphic for a given marker.
- The selected SSR markers will be screened on DNA extracted from the pooled tissues of 15 plants from each of 1000 accessions of the composite collection.

Present status of research

- The composite collection was planted during the last week of August 2006, and leaf samples from 15-day old seedlings will be collected from 15 representative plants for DNA extraction.

Future plan of work

- DNA extraction from 15 plants per accession following high-throughput procedure
- DNA quantification and optimization of PCR conditions
- Screening of SSR markers on 8 diverse genotypes
- Screening artificial pools with polymorphic markers
- Identification of 20 suitable SSR markers capable of detecting heterogeneity



- Fingerprinting the composite collection with 20 markers
- Data analysis to determine population structure and genetic diversity
- Identification of a reference collection of 300 diverse accessions.

References

FAOSTAT 2005. <http://apps.fao.org/>