Development of a Bambara Groundnut Core Collection from IITA Germplasm Based on Characterization and Evaluation Data.

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Bambara Groundnut (Vigna subterranea)
Used by small scale subsistence (women)farmers

Bambara Groundnut in northern Namibia

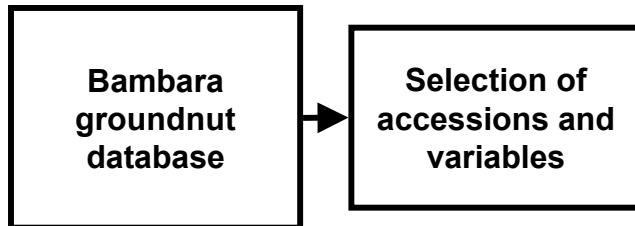**Bambara Groundnut pods at harvesting**

Genetic Diversity in the IITA Germplasm

Requirements for a core collection

- Representation of the main collection
- Maximum diversity within core collection
- Minimum size

- Linkage between core collection and main collection
- Linkage between core collection and phenotypic data
- Adjustable size

Data flow towards cluster analysis

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│  Bambara        │─────▶│  Selection of   │
│  groundnut      │      │  accessions and │
│  database       │      │  variables      │
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ΠΙΠ

Selection of Descriptors and Accessions

Selected Descriptors		
metric N=22		**nominal / ordinal N=11**
Emergence	Internode length	Growth habit
First flower	Node number	Pod shape
50%flower	Branch number	Pod texture
Pod lenght	Stem number	Testa pattern
Pod width	Pods number	Testa ground colour
Shelling percentage	Seeds per pod	Eye pattern
Leaflet length	100 seed weight	Petiole colour
Leaflet width	Seed length	Leaf shape
Leaf number	Seed width	Vigour
Spread	Yield	Cercospora
Height	Petiole length	Virus

- 23 variables were excluded from analysis due to incomplete data
- Out of 2030 accessions 1013 with full data sets for selected descriptors were used for hierarchical cluster analysis
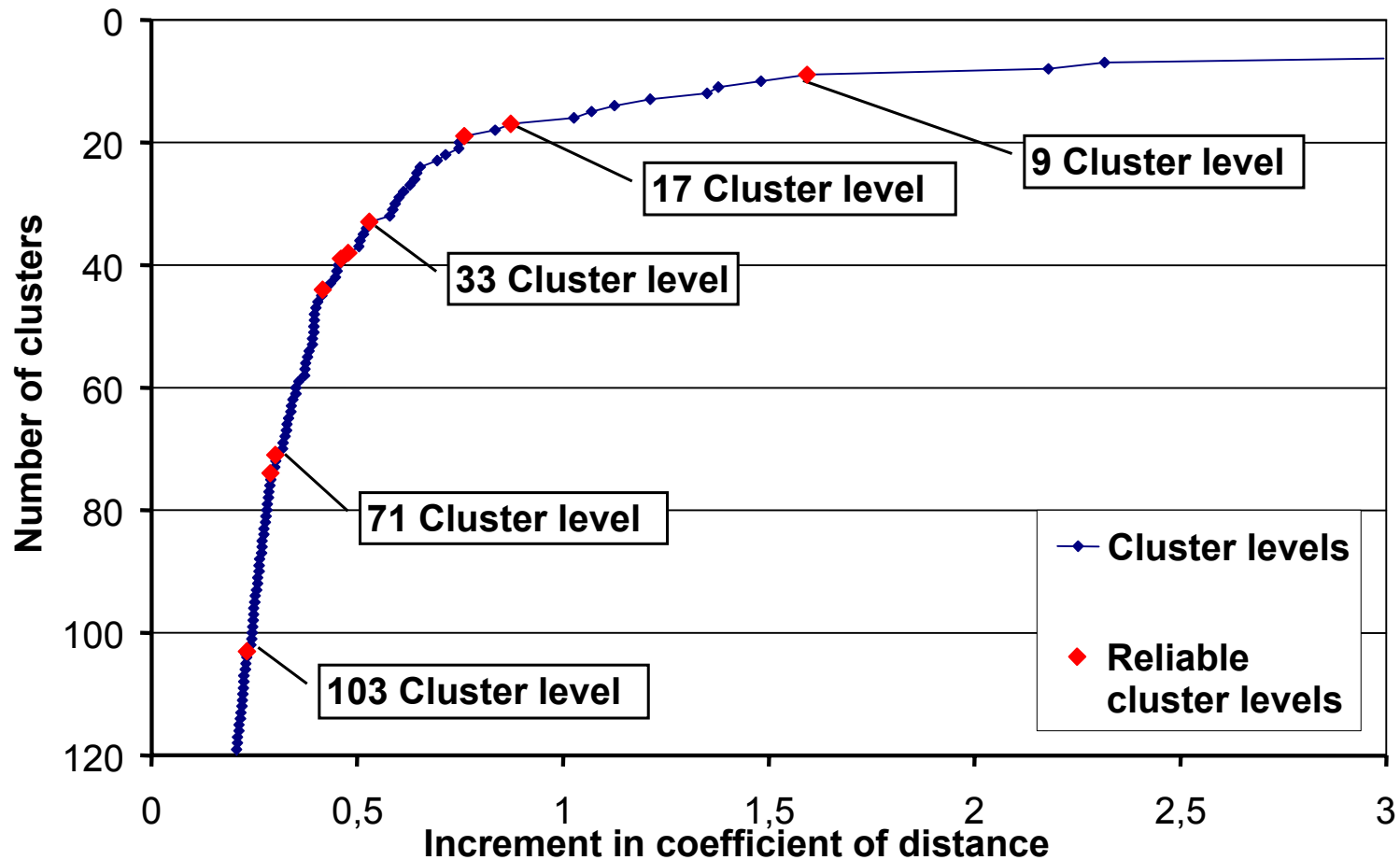
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Data flow towards cluster analysis
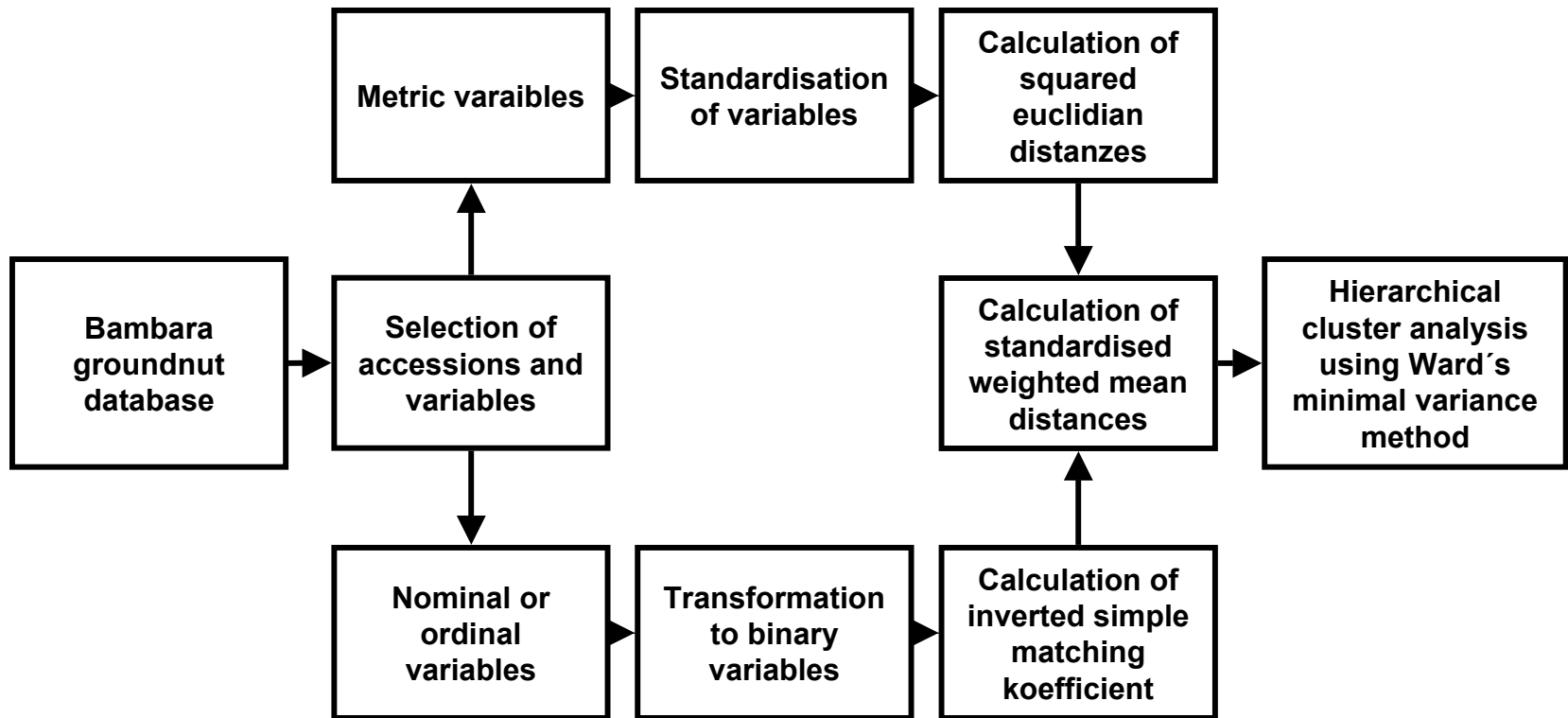
# Definition of core collections based on cluster analysis

| Identification of reliable cluster levels | → | Selection of cluster levels for core collections | → | Identification of cluster representatives | → | Definition of core collections |

At the highest level the cluster representatives define the core collection

At each lower level representatives of new clusters are added

Nested core collection
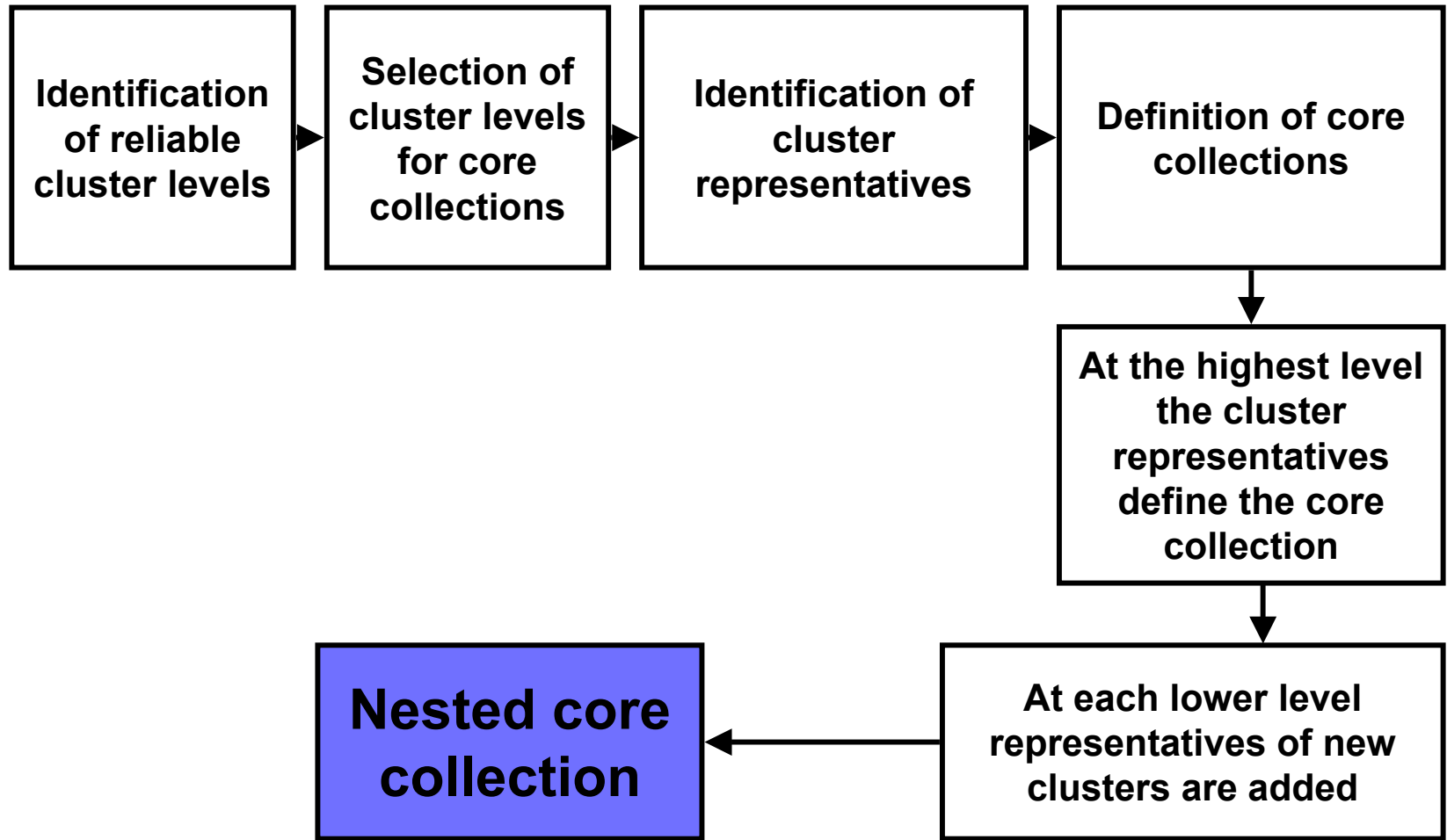
Selection of reliable cluster levels

Core collections at different clusterlevels

9 Cluster Level   **17 Cluster Level**   **33 Cluster Level**   **103 Cluster Level**
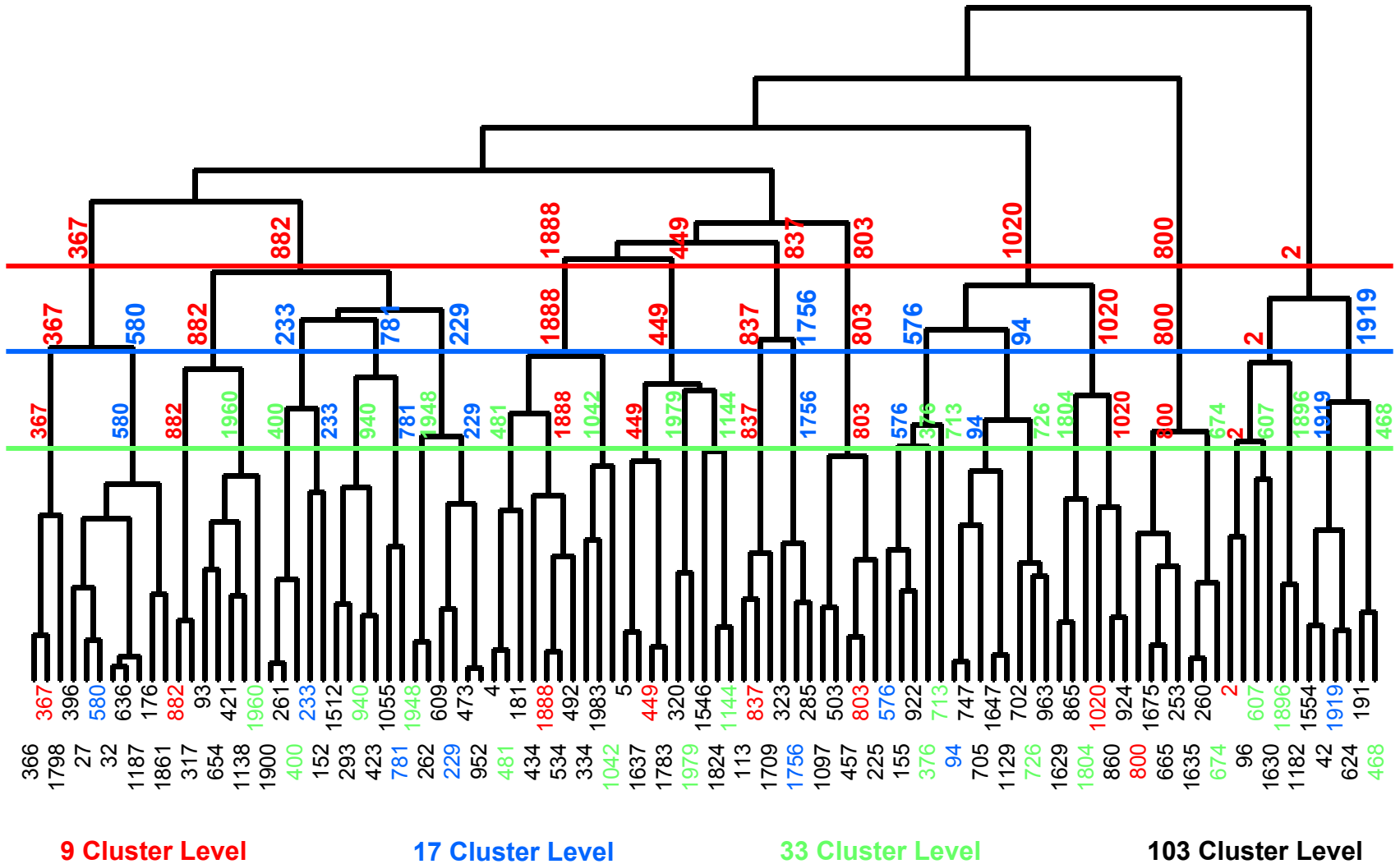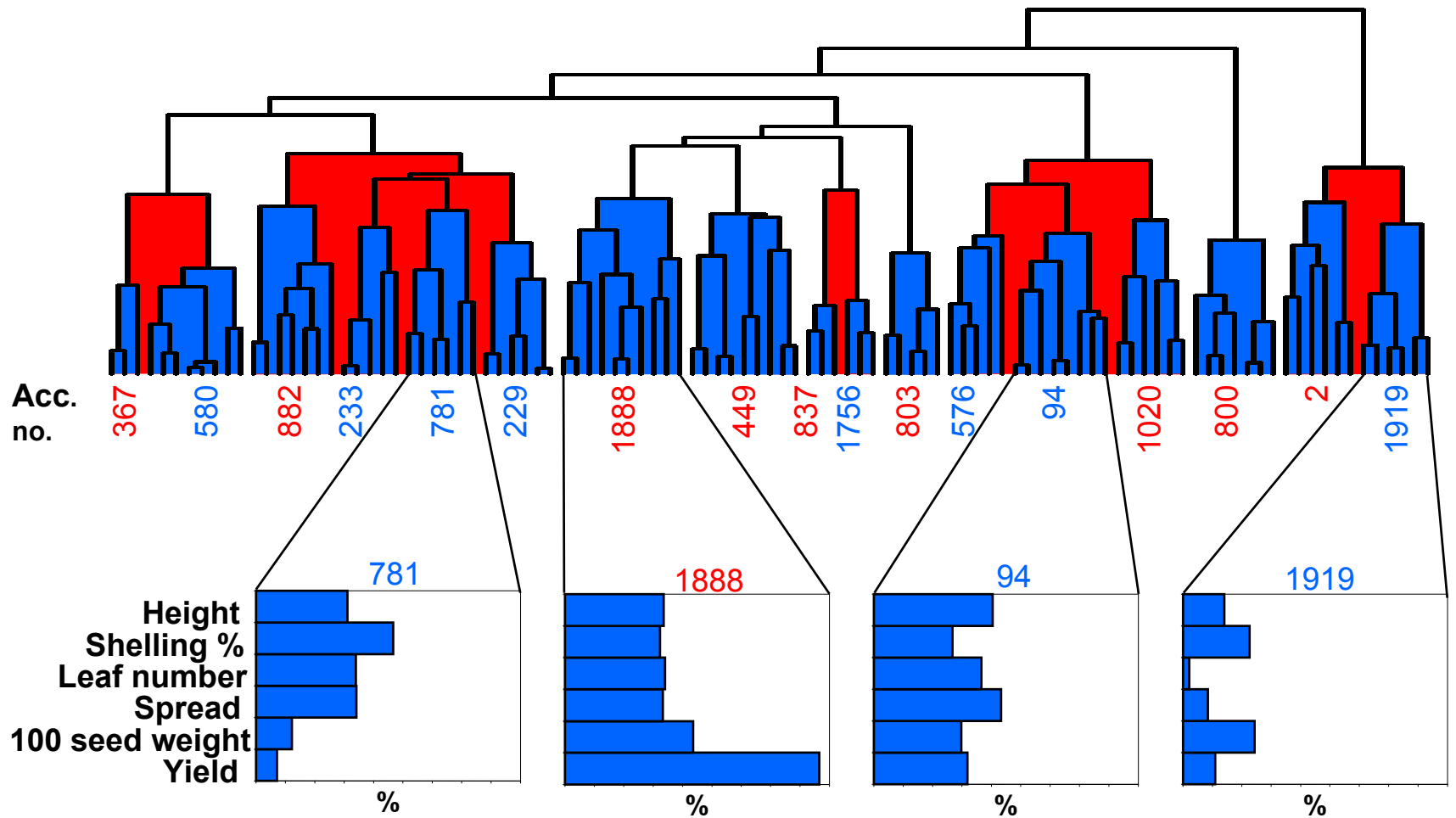
Potential use of a nested core collection in a breeding program
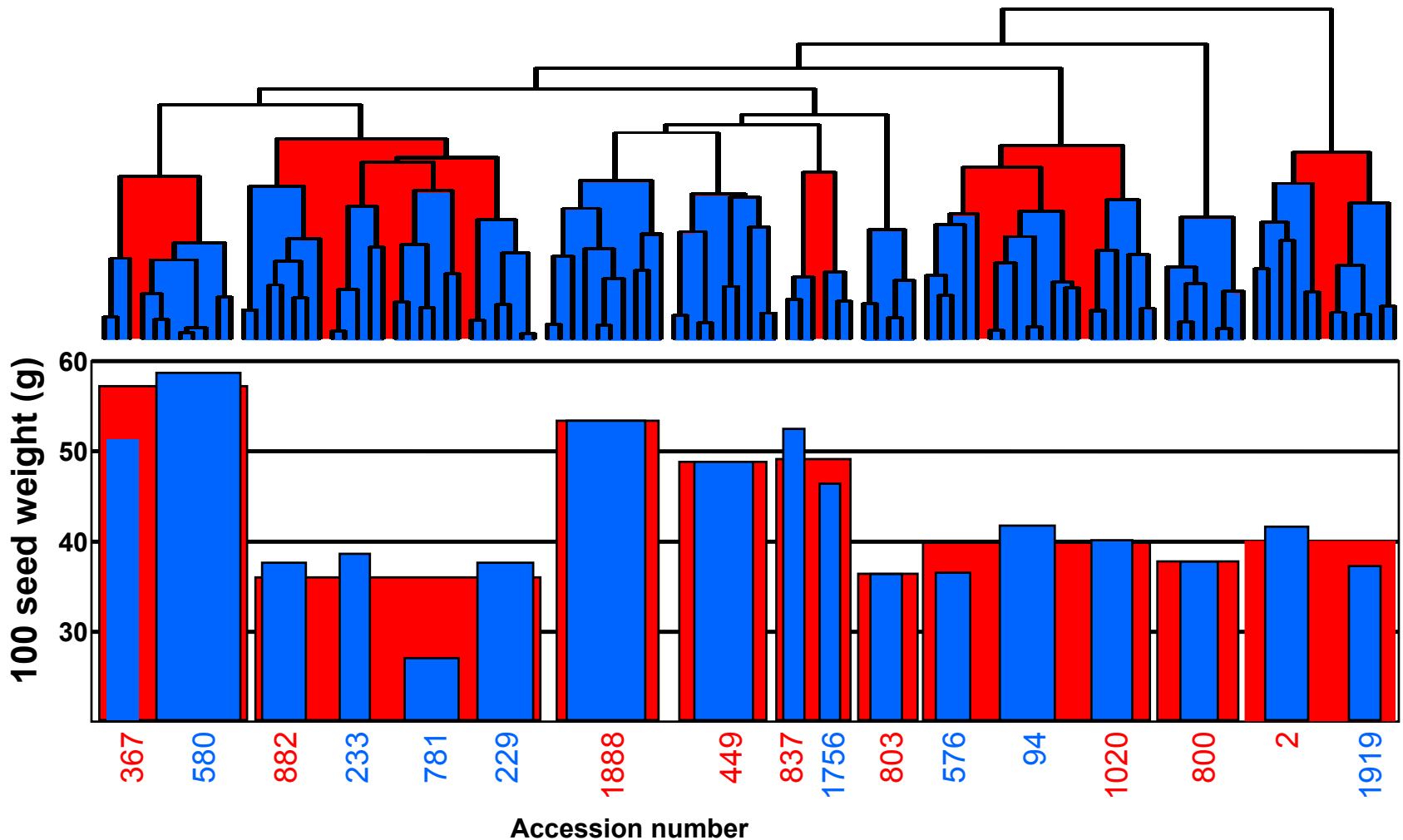
Linking clusters and core collections to representative phenotypes

Advantages of
Nested Core Collections

- Size of core collection can be choosen according to given inquiry
- Size of each core collection is defined by structure of data
- Core collections at any level represent the variability of main collection
- Linkage of core collection to main collection improves use of all accessions
- The nested core collection is an open structure; Additional levels can be included
- Hierarchical structure of core collection enables detailed analysis of specific branches if desired
- Information on cluster membership can be directly used in a breeding program
- Clusters corresponding to ideotypes can be identified
- Landraces can be linked to clusters and recommendations for introduction of promising germplasm can be given

Outlook

- Information on genetic similarity of accessions can be improved by use of molecular markers

- Decisions based on molecular markers will be more reliable, since they are not biased by environmental interaction

- Genetic fingerprints of any genotype can be used to link it to certain clusters, related genotypes and corresponding phenotypes

- Information on core collection and cluster membership could be included in Bambara groundnut database to maximise use