

Unintended selection might have occurred at PGRP

Disappearance of bands observed in 12 accessions of PGRP

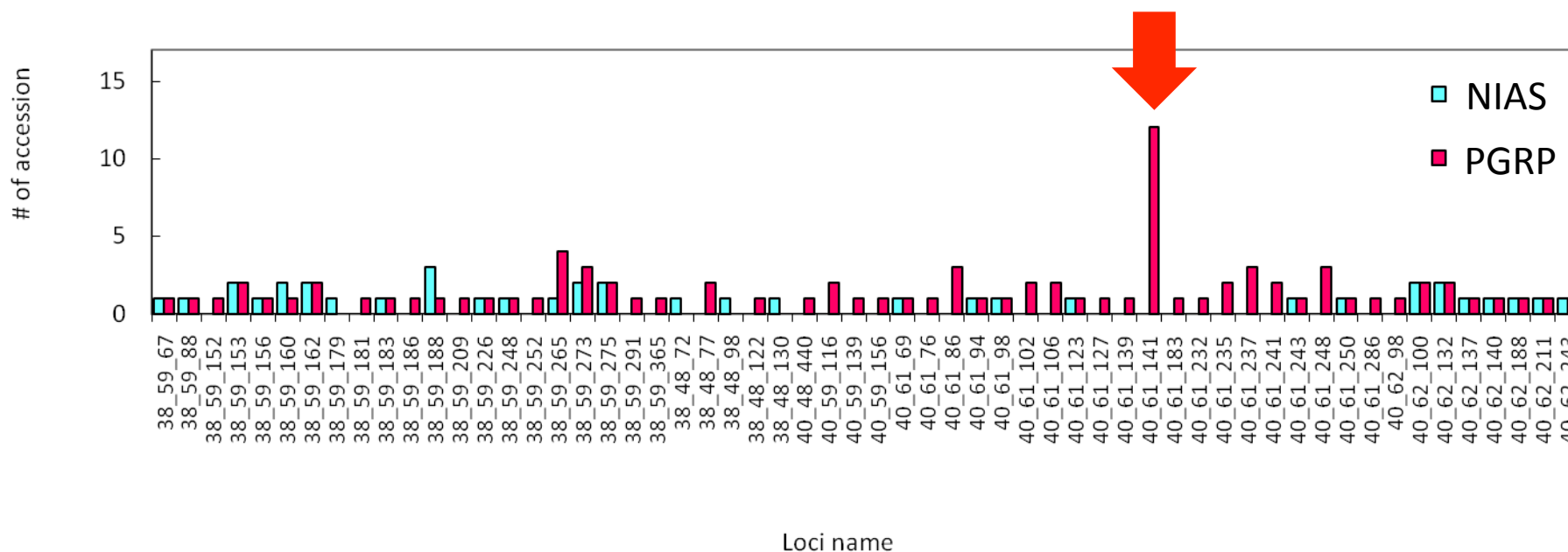


Fig. Disappearance of bands in wheat landraces at different loci

Conclusions

- No significant genetic between genebanks with different management
- Practical number of seed for regeneration
 - Small genetic variation by AMOVA
 - n/s by Chi-sq. test

NIAS

- about 15 individuals
- No selection except one accession

PGRP

- Few individuals
- Possible selection

Better to use about 15 individuals for regeneration with splitting into sub-accessions

Genetic diversity demonstrated by transposon display in foxtail millet

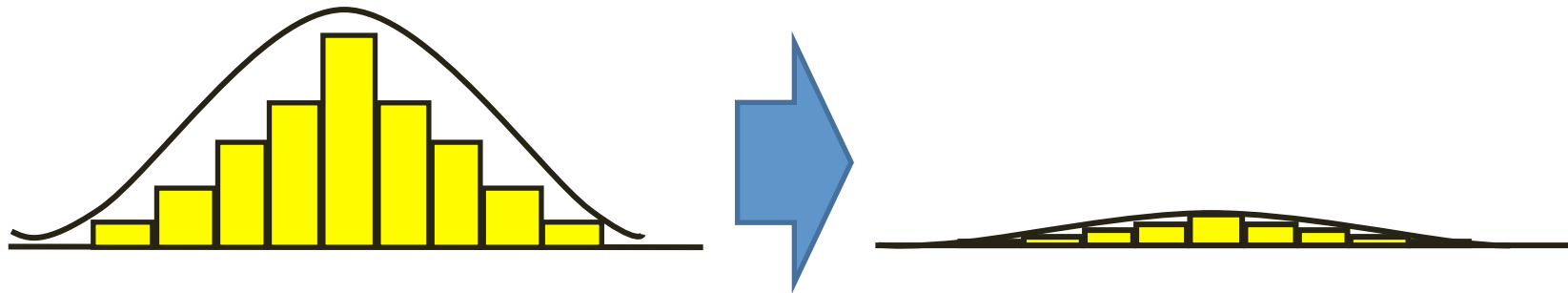
Objective:

How to enhance utilization of minor crop species conserved in genebank?



Genetic Diversity Study and Selection of Core Collection of Foxtail millet

What's Core Collection ?



- Represent total variance with small number of individuals
- Several core collections are available in different genebanks

Materials and Methods

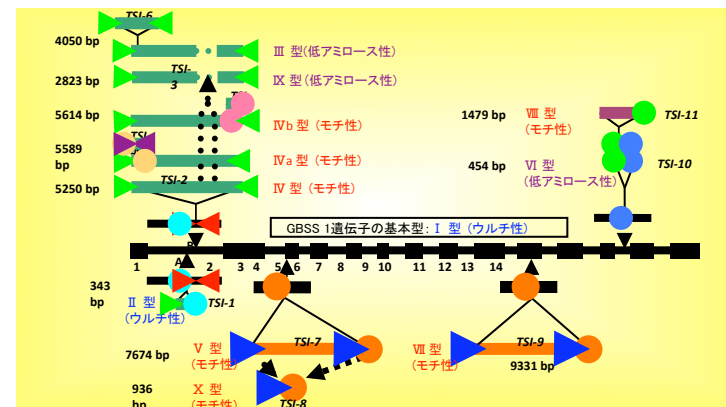
Foxtail millet: *Setaria italica* (L.) P. Beauv.



- Long history of cultivation in Eurasia
- Higher morphological diversity
- Lack of systematic breeding
- One of the best materials for domestication study
- Absence of genome wide marker

Transposon display (Casa et al., 2000)

- Detect diversity of insertion site of transposable element
- Spread genome wide
- Transposable element as is a preference for insertion in or near transcriptionally active genomic regions
=>Supposed as a functional marker
- Transposable elements in *GBSS1* gene of foxtail millet have identified (Kawase et al. 2005)



Europe & Central Asia
Belgium, Bulgaria, Czech, France,
Georgia, Germany, Hungary, Kirghizia,
Poland, Russia (Primorskii,
Novosibirskaya), Spain, Swiss, Turkey,
Ukraine, Uzbekistan: 28 accessions

East Asia
China and its vicinity, Japan
Korea, Taiwan : 211
accessions

Africa
Ethiopia, Kenya, Morocco,
South Africa: 6 accessions

South & Southeast Asia
Afghanistan, Bangladesh, Bhutan,
India, Indonesia, Iran, Laos, Lebanon,
Myanmar, Nepal, Pakistan,
Philippines, Sri Lanka, Thailand: 180
accessions

S. Italica spp. *viridis*
(out group)
12 accessions

Foxtail millet landraces: 425 strains from NIAS genebank

Results and Discussions

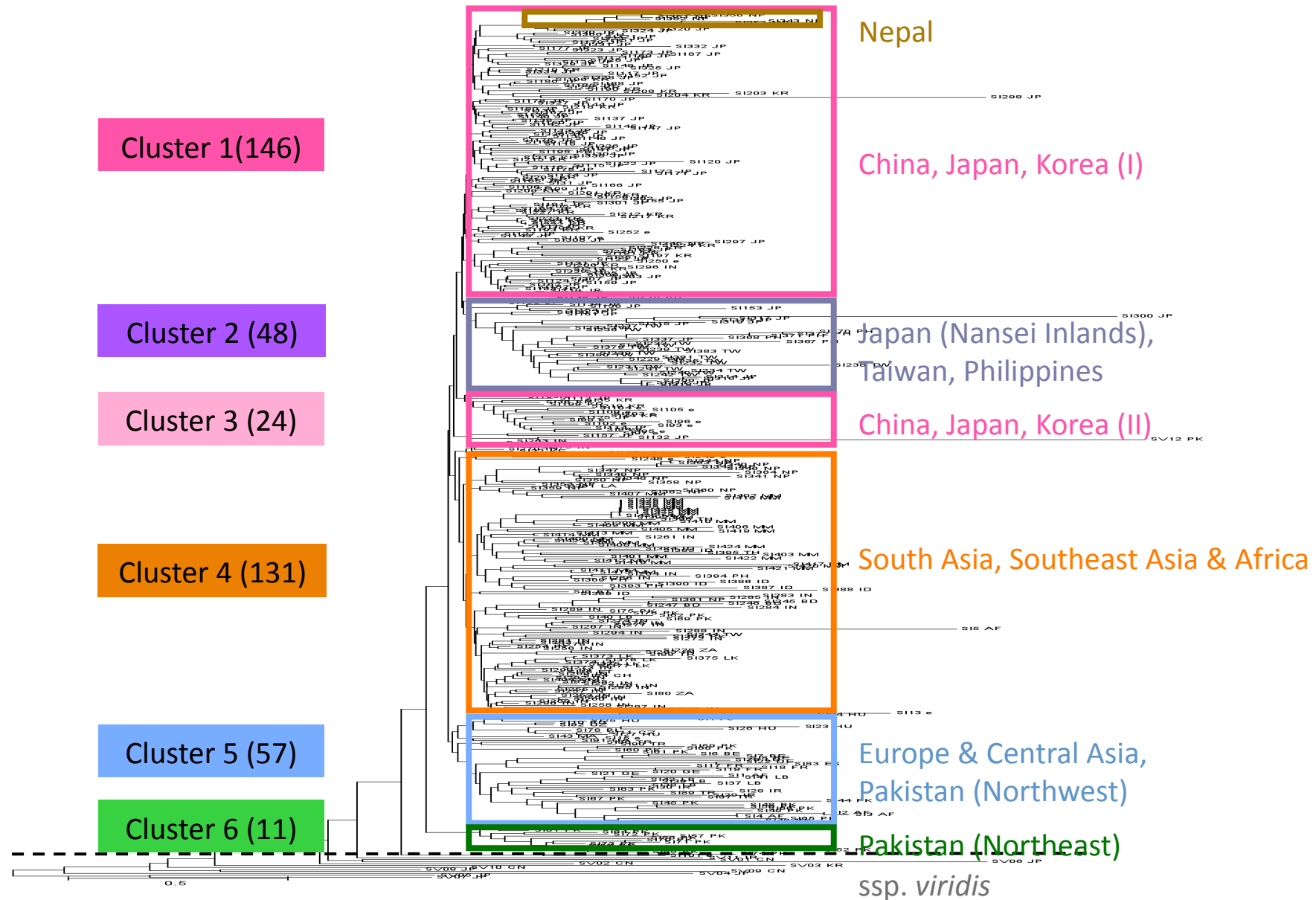


Fig. NJ tree based on the Nei's genetic distance

Selection of Diversity Research Subset

- **Recommended size of diversity subset**
 - **10 %** of total collection can retain **70 % of variation**
(neutral allele and infinite population size assumed)
(Brown, 1989)
 - **20-30 %** range is recommended in case of genetic structure of total collection assumed (Yonezawa et al., 1995)
 - In case of huge collection, classification based on passport data needed (ICRISAT sorghum collection)

Table Diversity calculated for different number of research subset

Selected % for subset	N	Prop. loci polym.	Hj	Mean # of Frag. / indiv	Total # of polym. Frag.	(%)
0.2	8	34.3	0.118	69.1	122	34.3
5	21	32.0	0.117	67.7	171	48.0
10	43	36.8	0.121	68.2	235	66.0
20	83	36.0	0.119	67.2	255	71.6
50	211	35.1	0.116	66.3	302	84.8
100	425	36.2	0.120	66.5	356	100

Detected gene diversity do not change significantly

20% is optimal to retain more than 70% of total polymorphic fragment

Conclusions

- Genetic diversity and the characteristics of foxtail millet collection of NIAS genebank
- Optimal size of research subset is 10-20 % of total collection size for this collection
- Diversity research set of foxtail millet was selected to enhance utilization of genebank materials