

# Genetic diversity and breeding of teak in Myanmar

Yazar Minn Ph.D.

Forest Botany and Tree Improvement Section

Forest Research Institute

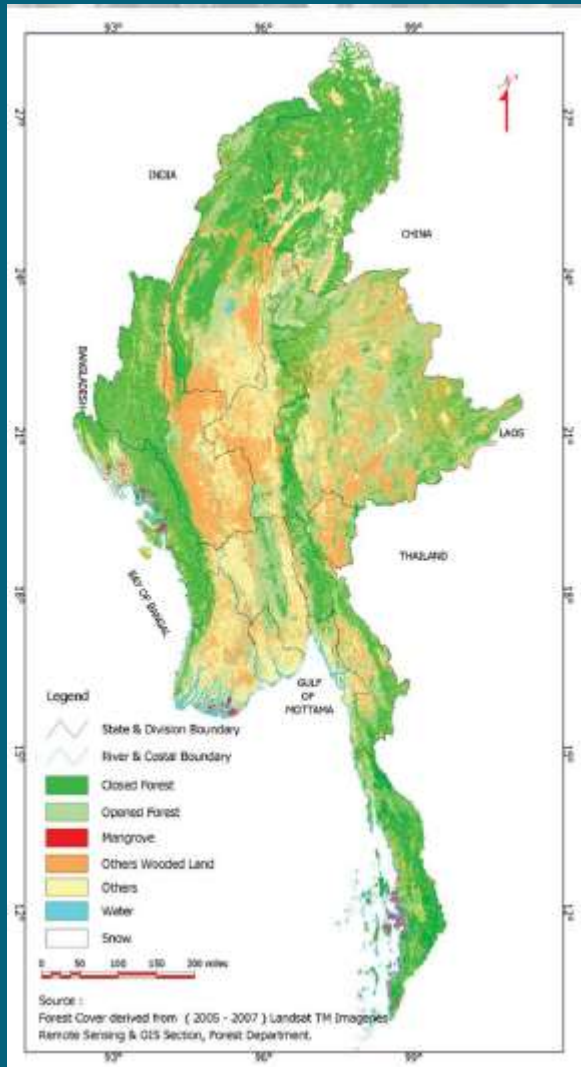
Yezin, Nay Pyi Taw, Myanmar

Email: [yazarminn@gmail.com](mailto:yazarminn@gmail.com)

# Outlines

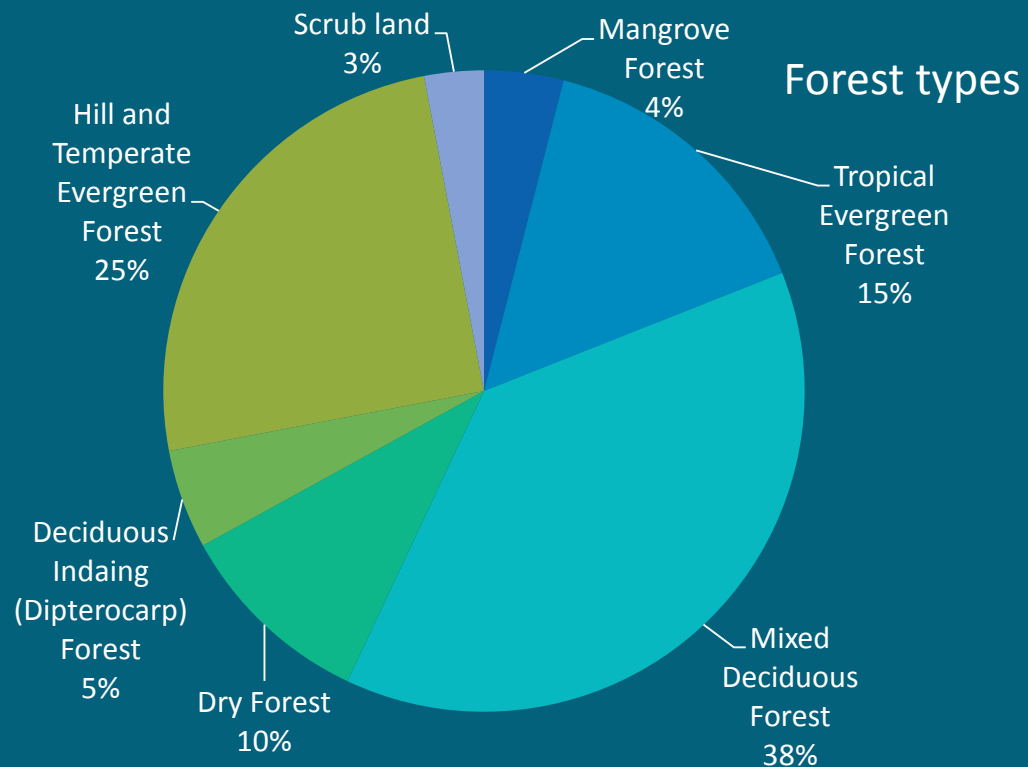
- ▶ Status of forests and teak resources in Myanmar
- ▶ Genetic diversity of teak in Myanmar
- ▶ Current status on breeding of teak in Myanmar
- ▶ Conclusion

# Forest status in Myanmar



Forest cover status of Myanmar 2010

Forest Category	Area (,000 ha)	% of land area
Forest cover	31,773	46.96



Source: FRA 2010

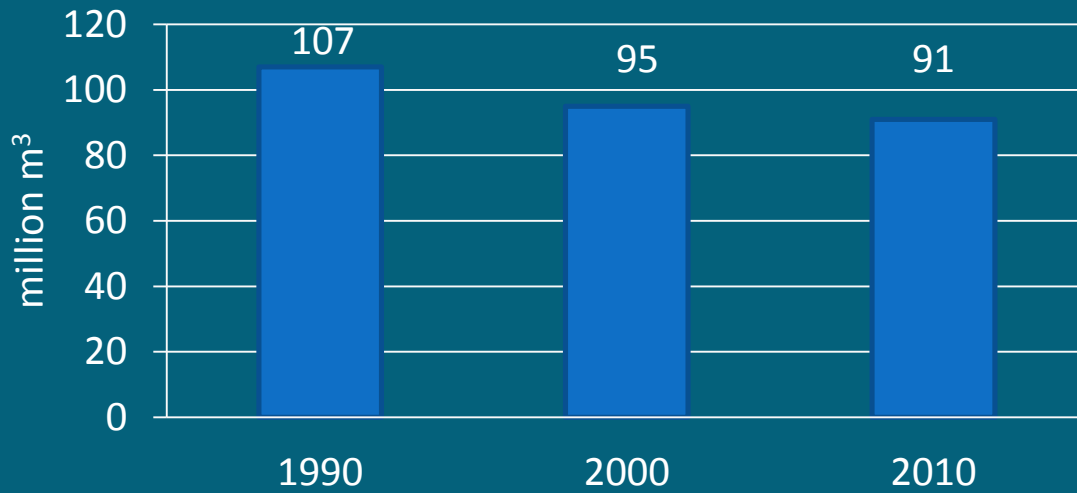
# Teak resources in Myanmar

## Area of teak forests<sup>1</sup>

	2010 (Area) (,000 ha)	% of total
India	6,810	23.45
Lao PDR	1.5	0.01
Myanmar	13,479	46.42
Thailand	8,744	30.12
Total	29,035	100.00

16,517,700 ha of teak forests in 1998<sup>2</sup>

14,600,000 ha of teak forests in 1976/1979<sup>1</sup>



## Growing stock of teak<sup>3</sup>

Deforestation rate<sup>4</sup>:

- 435,000 ha/ year (1990-2000)
- 310,000 ha/year (2000-2010)

<sup>4</sup> 1. Kollert and Cherubini 2010 teak resources and market assessment 2010, 2. Gyi and Tint 1998. FAO.; 3. FRA Country Report 2010; 4. FAO (2011) State of World Forests;

# Management of teak forests in Myanmar

- Myanmar Selection System
- Selective removal of target diameter trees
- Exploitable diameter limit: 63cm dbh

## Impacts of selective logging?

- Selection against desirable phenotype (dysgenic selection)
- Reduced genetic diversity
- Increased inbreeding

No impact<sup>1,2</sup>

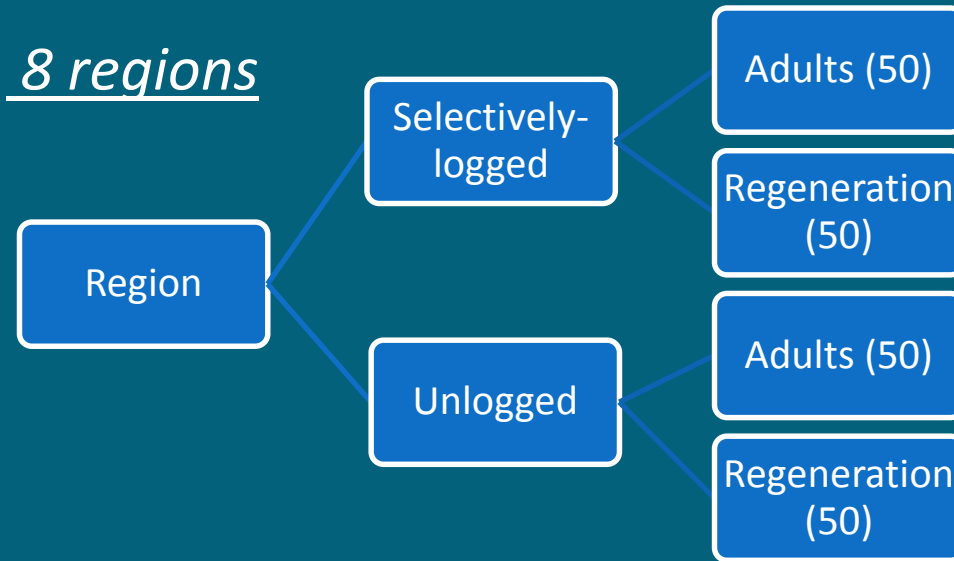


Negative impacts<sup>3,4</sup>

# Genetic diversity of teak in Myanmar



8 regions



- ❖ 71 Amplified Fragment Length Polymorphism marker
- ❖ 10 microsatellite markers

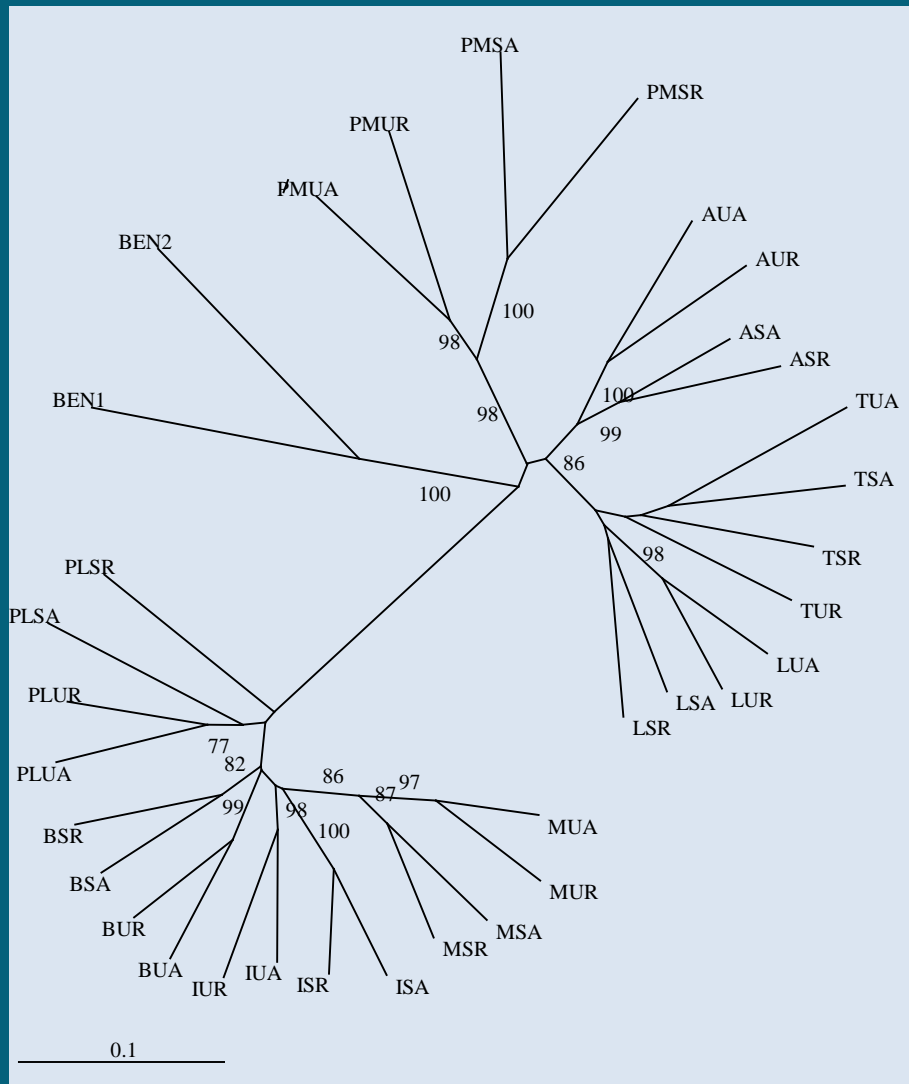
$AFLPs_n$	$PPL$	$H_j$	$SSRs_n$	$A_R$	$H_E$	$H_O$	$F_{IS}$
45	72.2	0.215	49.2	6.5	0.586	0.564	0.037

# Genetic diversity at SSRs

	$N$	$A_R$	$H_O$	$H_S$	$F_{IS}$	$F_{ST}$
Sample types (adults vs. regeneration)						
Adult	16	6.4	0.568	0.582	0.025	0.120
Regen.	16	6.5	0.552	0.583	0.053	0.116
Management types (UL vs. SL)						
UL	16	6.5	0.564	0.585	0.037	0.114
SL	16	6.5	0.555	0.580	0.042	0.123
Regions (northern vs. southern)						
Northern	16	6.1 <sup>a</sup>	0.561	0.579	0.031	0.027
Southern	16	7.0 <sup>b</sup>	0.559	0.587	0.048	0.034

- No difference in genetic diversity of adults and regeneration
- No impact of logging on genetic diversity of teak
- Singificantly higher allelic richness in Southern Populations

# Genetic clusters at SSRs



Southern Populations

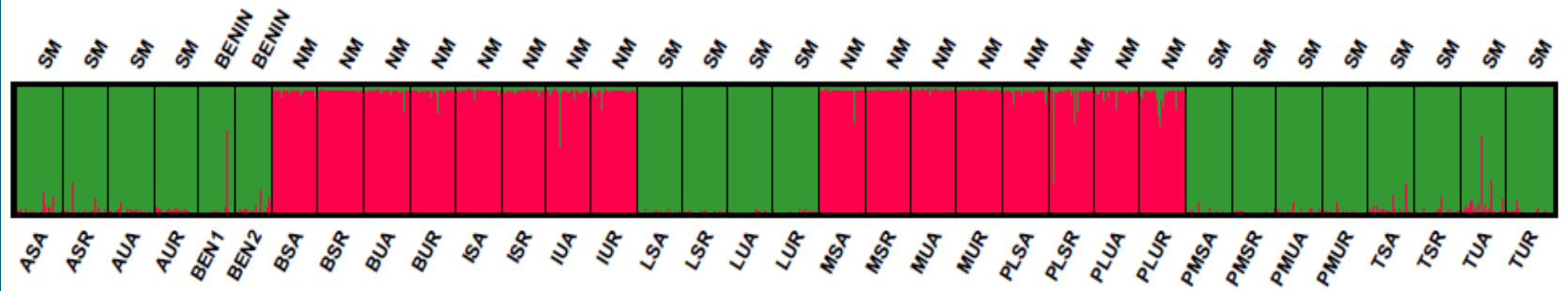
Northern Populations

- ▶ Strong genetic differentiation between two regions

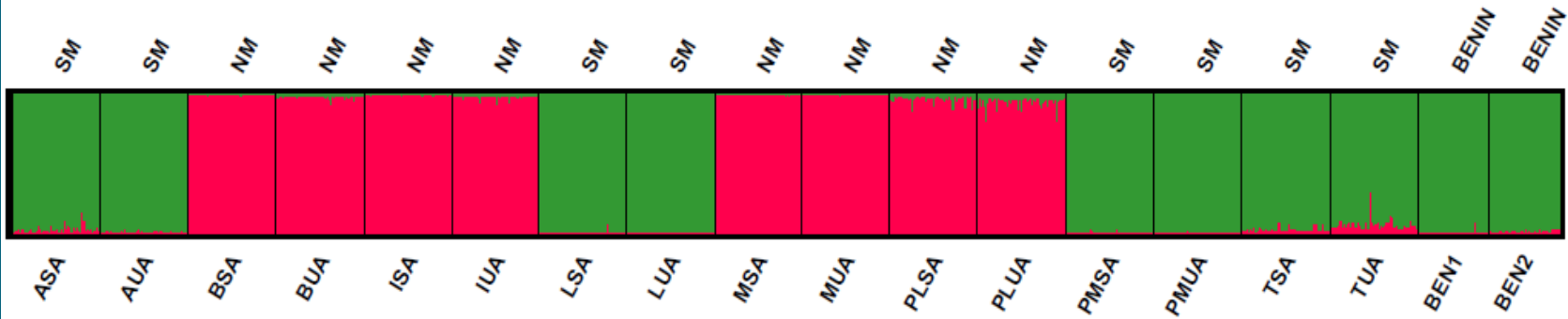


# Genetic structure of teak at SSRs

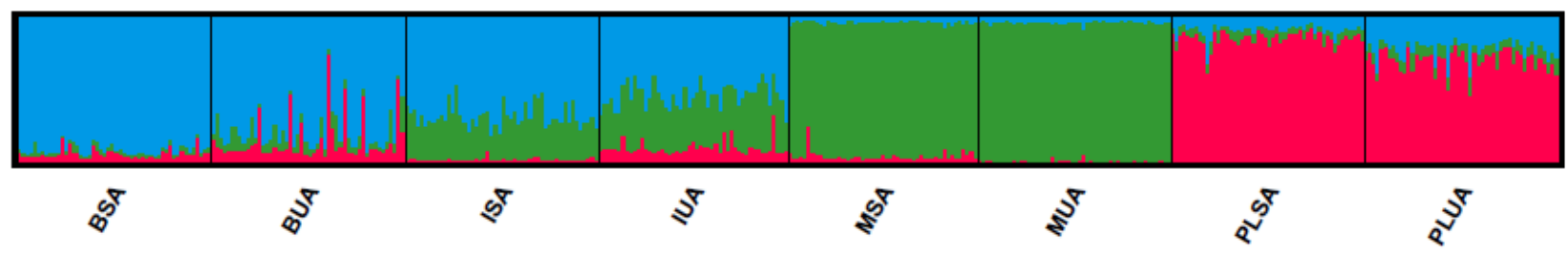
All



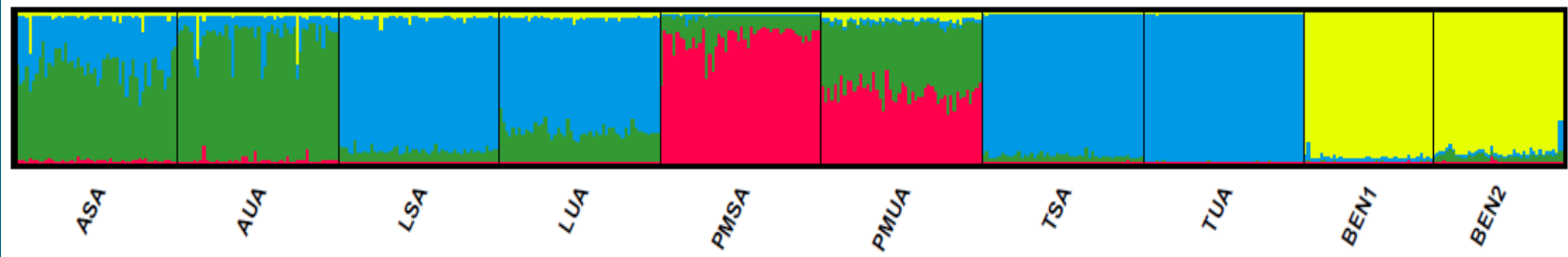
All adults



Northern Adults

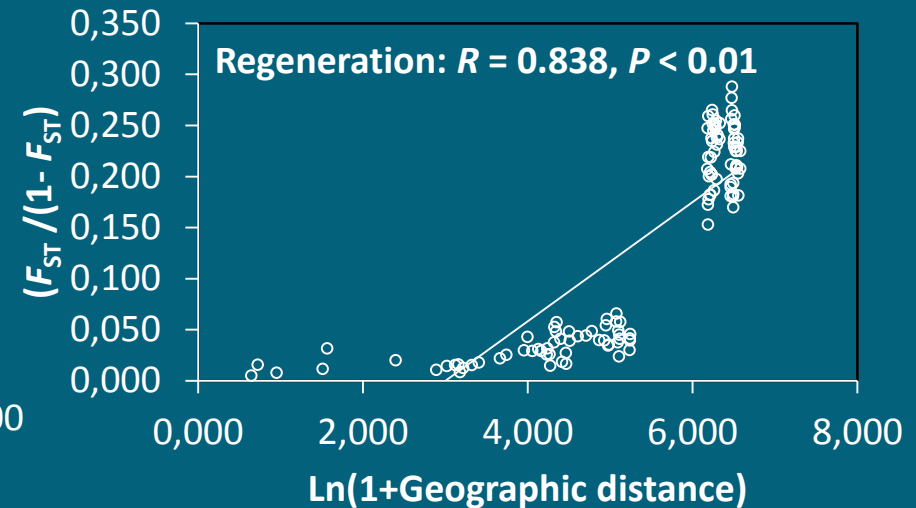
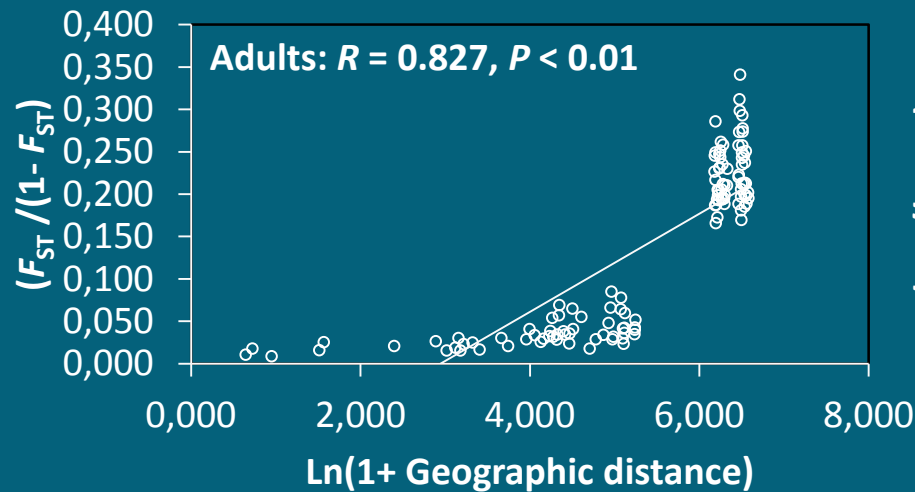


Southern Adults+ Benin



# Mantel tests at SSRs

All Myanmar populations



Populations within regions

Regions	Adults ( $R$ )	Regeneration ( $R$ )
Northern	0.557**	0.688**
Southern	0.611**	0.716**

\*\*  $P < 0.01$

- Isolation by Distance (IBD)
- Inclusion of many widely-separated forests for conservation

# Analysis of Molecular Variances at SSRs

Source of variation	d.f.	V %	$\Phi$ statistics	<i>P</i> value
<b>All Myanmar populations</b>				
Among populations	31	11.58	$\Phi_{ST} = 0.116$	< 0.001
Within populations	3142	88.42		
<b>Adults and regeneration</b>				
Among groups	1	-0.71	$\Phi_{CT} = -0.007$	> 0.05
Among populations within groups	30	11.99	$\Phi_{SC} = 0.119$	< 0.001
Within population	3142	88.72	$\Phi_{ST} = 0.113$	< 0.001
<b>Unlogged and selectively-logged populations</b>				
Among groups	1	-0.59	$\Phi_{CT} = -0.006$	> 0.05
Among populations within groups	30	11.92	$\Phi_{SC} = 0.119$	< 0.001
Within population	3142	88.67	$\Phi_{ST} = 0.113$	< 0.001
<b>Northern and southern populations</b>				
Among groups	1	15.65	$\Phi_{CT} = 0.157$	< 0.001
Among populations within groups	30	2.63	$\Phi_{SC} = 0.031$	< 0.001
Within population	3142	81.72	$\Phi_{ST} = 0.183$	< 0.001

# Breeding of teak in Myanmar

- ▶ Due to the high genetic diversity of teak, Myanmar still possesses strong genetic basis for breeding programs.
- ▶ Existing breeding activities
  - ▶ Selection of plus trees
  - ▶ Vegetative propagation (Hegde gardens/ Tissue culture)
  - ▶ Clonal Seed Orchards/ Seedling Seed Orchards
  - ▶ Seed Production Areas
- ▶ Some provenance trials but no progeny test/ no clonal tests yet
- ▶ Thus, much efforts are still needed for breeding of teak in Myanmar.

# Plus tree selection



- ▶ 155 plus trees have been identified so far.
- ▶ Operational guidelines for selection of plus trees already available
- ▶ Still need to intensify the selection of plus trees

# Status on improvement of teak resources



## Hedge gardens established with plus trees

- Research on shoot cutting in 1995-1996
- Field planting of rooted cutting in some forest district in 2002



## Two Mini-tissue culture Labs under FD

- First batch of plants field planted (2002)
- Growing with good health and performance
- still at experimental stage, not for operational uses

# Status on improvement of teak resources (contd.)



CSO in Oktwin, Myanmar

- ▶ Clonal Seed Orchard (CSO)
- ▶ Seedling Seed Orchards (SSO)
- ▶ Inconsistent seed production at orchards

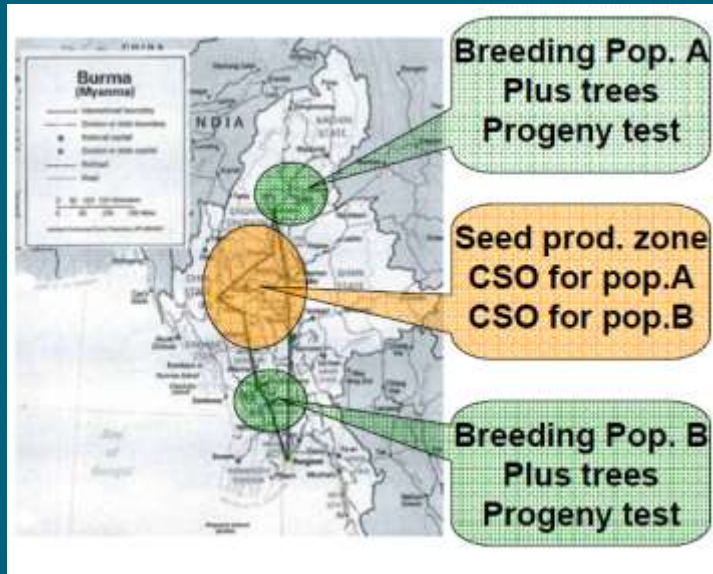
## Seed Production Areas (SPA)

- ▶ Operational guidelines for establishment of SPA already available
- ▶ Numbers of SPA= 191
- ▶ Area of SPA= 3206 ha

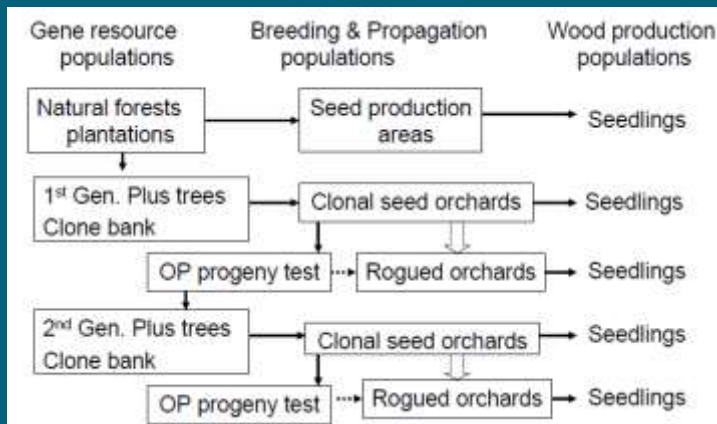


SPA in Yedashe, Myanmar

# Proposed long-term breeding strategy



- ▶ Two breeding zones and one seed production zone
- ▶ Selection of plus trees and progeny tests in each breeding zone
- ▶ CSO in drier region for better production of seeds
- ▶ Recurrent selection with CSOs



Ref: *Ex situ* and *In situ* conservation of teak to support SFM (ITTO Project PD 27/04 Rev. 2 (F))



# Conclusion

- Teak still has high genetic diversity
  - Importance for *in situ* and *ex situ* conservation
- Different conservation and breeding regions in Northern and Southern Myanmar
- Inclusion of widely-separated teak forests for conservation
- No impact of logging but further investigation by adaptive markers recommendable

## Conclusion (contd.)

- Provenance delineation for transfer of seeds and seedlings
- Inclusion of many trees for breeding
- Strong genetic basis for breeding programs due to high genetic diversity
- More efforts are needed to realize genetic gains from breeding of teak while strengthening existing breeding strategies .

**Thank you for your attention!**