



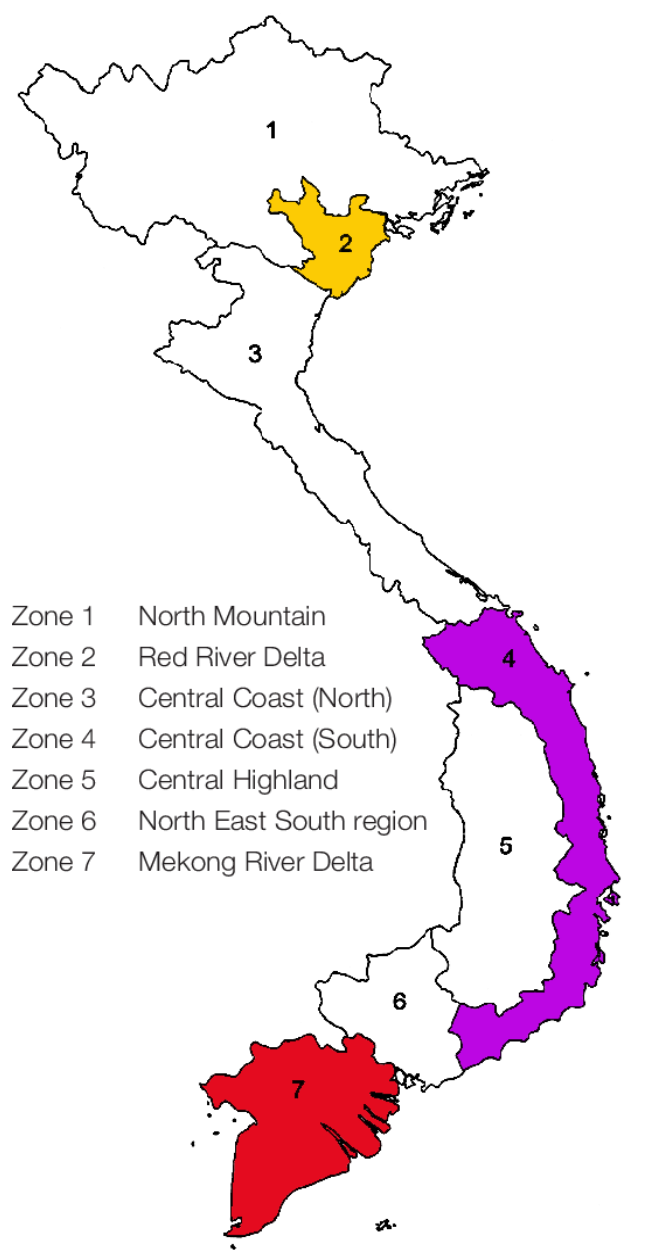
# Large scale screening for potential stresses tolerant rice germplasms in Vietnam

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## INTRODUCTION

- The irrigated and intensively managed rice production in Vietnam recently has been severely affected by climate change. To cope with increasing severe unfavored conditions, breeding for new rice varieties which effectively tolerant to abiotic stresses such as submergence, salinity and drought is a priority in the restructuring strategy of Vietnam agriculture sector.
- Possessing one of the most diverse genetic resources of rice, evaluation and exploitation of rice germplasm for rice breeding/improvement programs have been addressed as important task in Vietnam.
- In this study, a panel of 150 Vietnam rice genotypes that included landraces, elite and popular cultivars/breeding lines for the Northern, South Central Coast and Mekong Delta regions were evaluated both phenotypically and genetically for abiotic/biotic stresses tolerances.



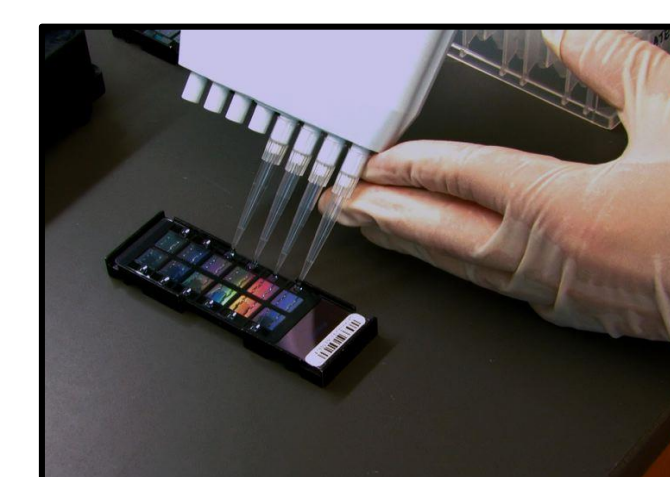
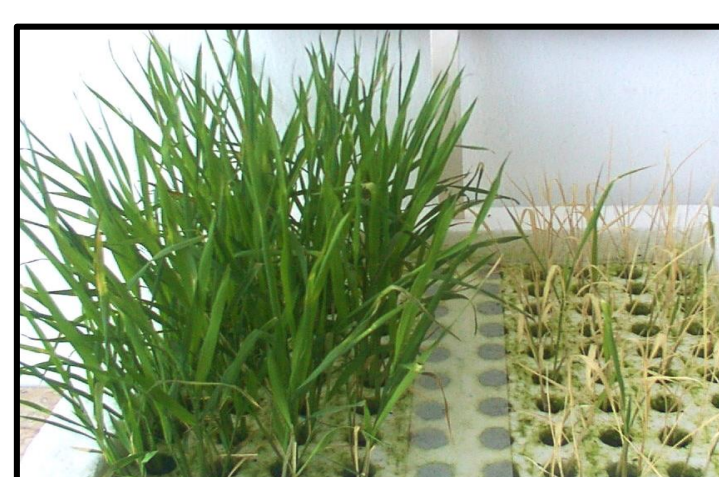
## MATERIALS AND METHODS



**Sample Collection:**  
150 rice genotypes across Vietnam



**Phenotyping:**  
- Abiotic-stresses tolerance (Salinity, submergence and drought)  
- Biotic-stresses resistance (Blast, Plant Brown Hopper and Blight Leaf Bacteria)



**Genotyping:**  
7K SNP Chip

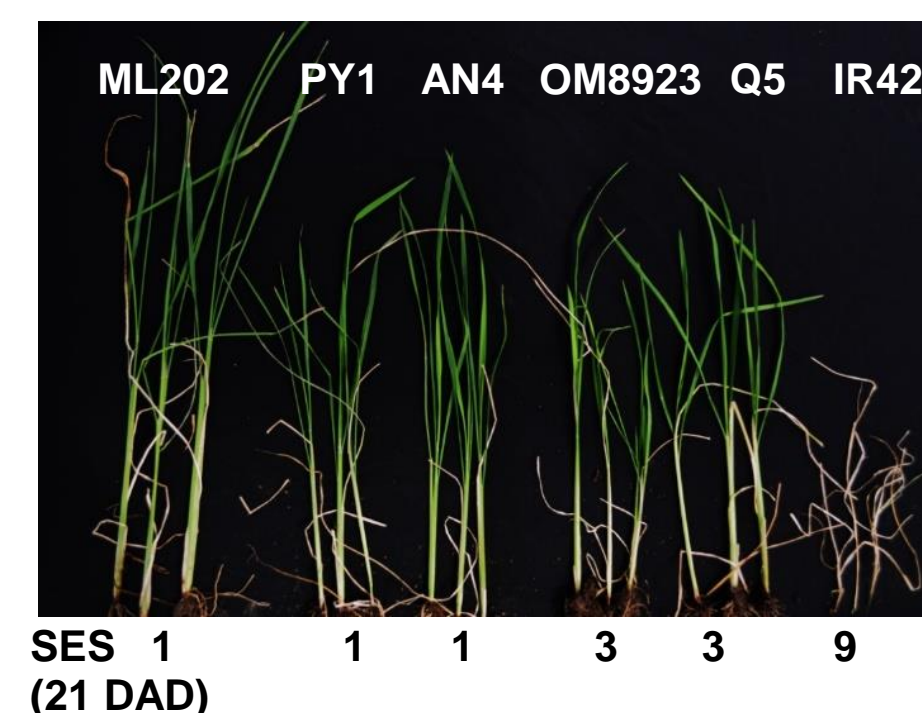
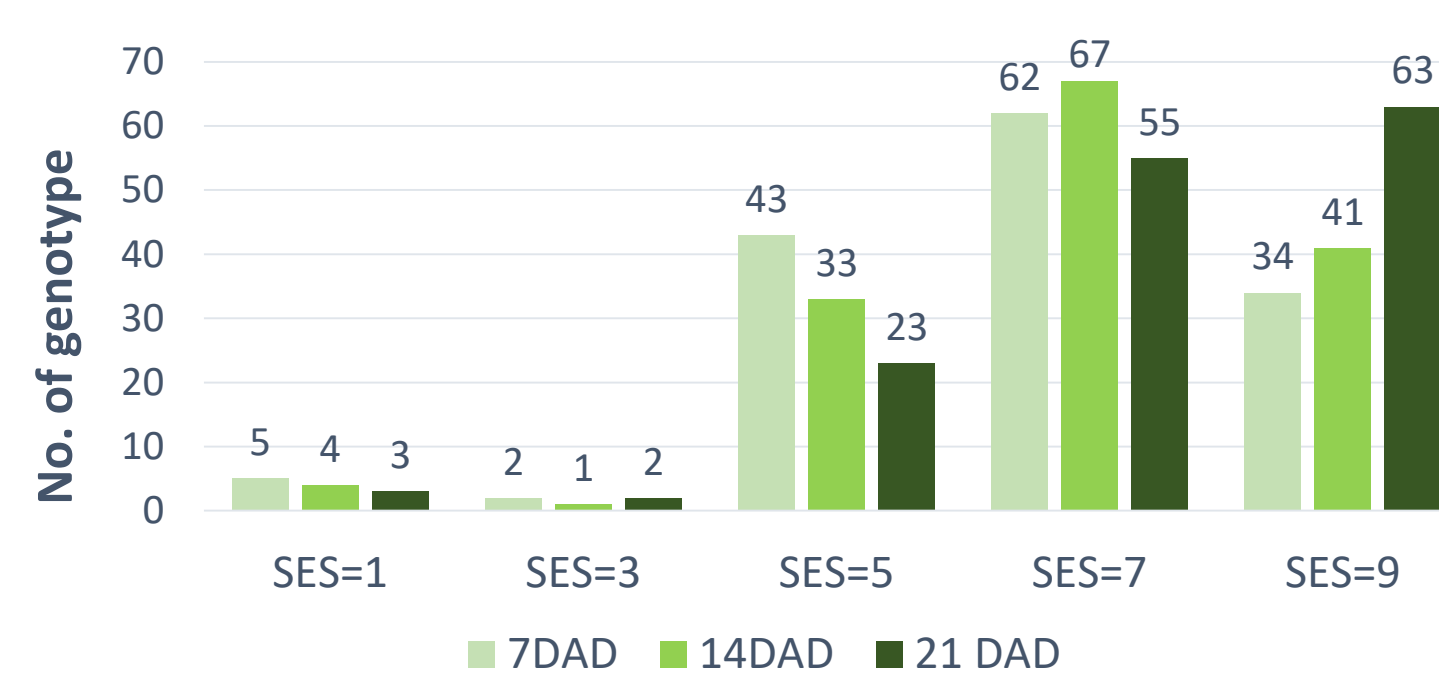


**Data analysis:**  
Tassel 5; STRUCTURE 2.3.4;  
GenAlEx 6.5

## RESULTS

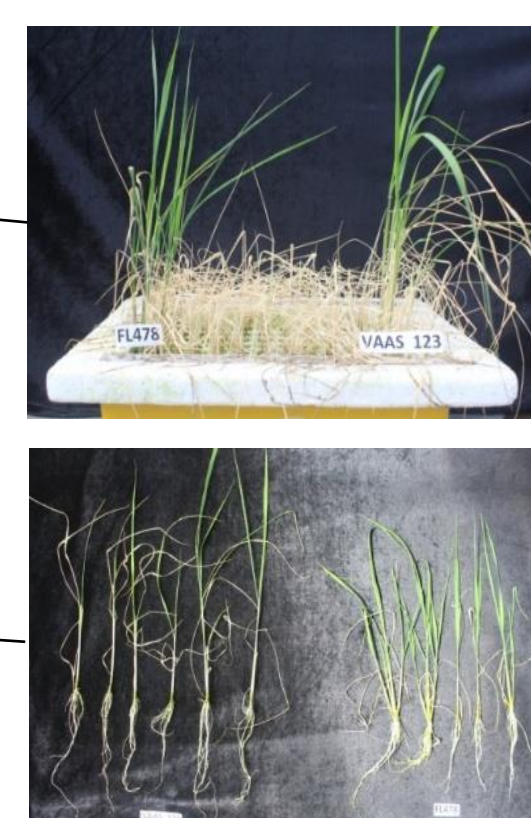
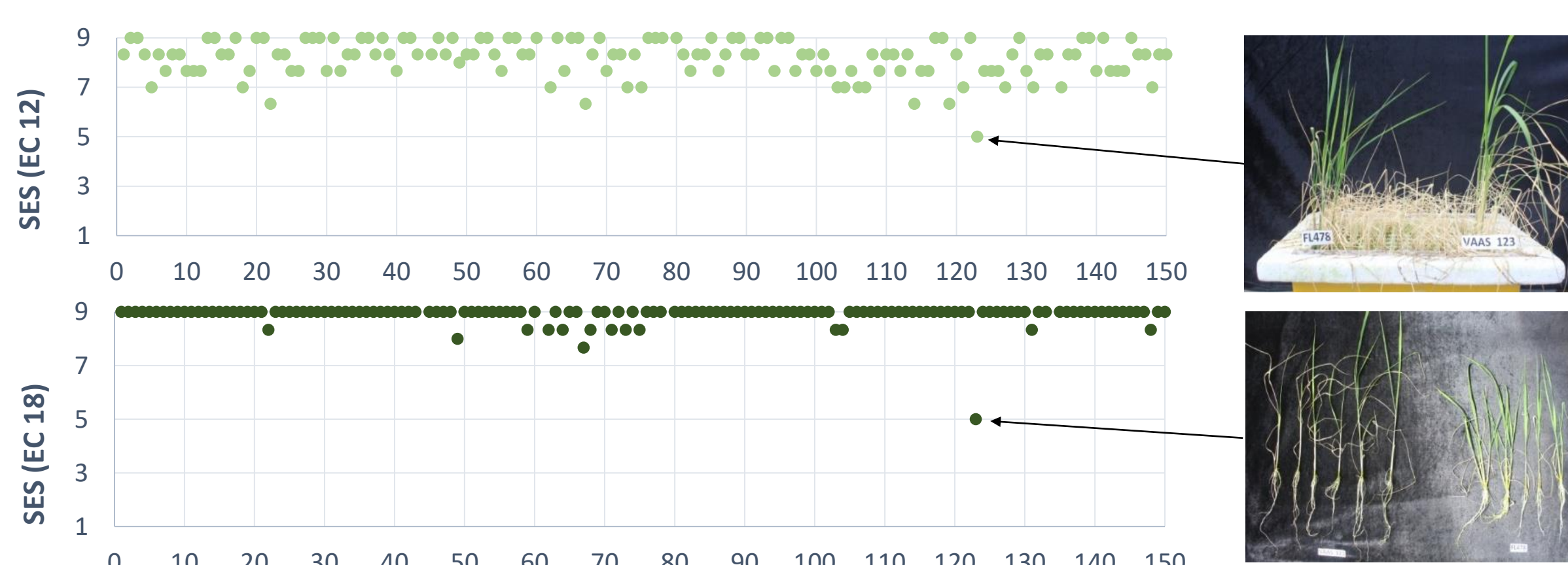
### 1. Submergence tolerance screening:

- Most of rice genotypes were susceptible to submergence stress in seedling stage.
- In treatment of 21 days after de-submergence, only three (ML202, PY1, AN4) and two (OM8923, Q5) genotypes showed very high and high tolerance.



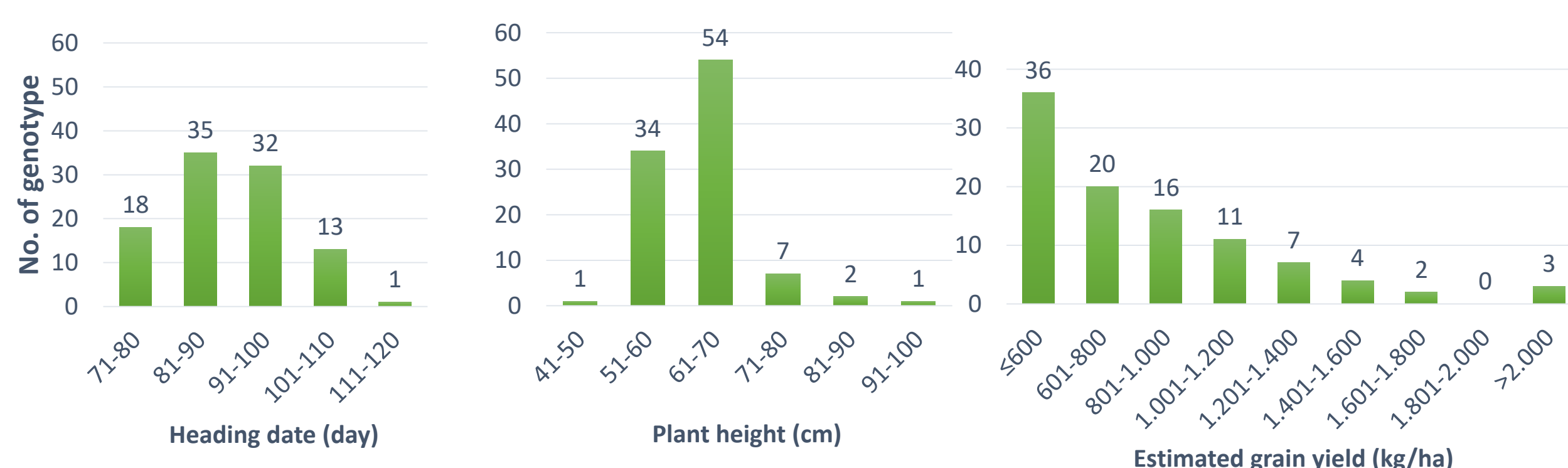
### 2. Salinity tolerance screening:

- Only Doc Trang was identified as moderate tolerant to salinity (EC 12 and EC 18) at vegetative stage with visual symptoms similar to those of control variety (FL478).



### 3. Drought tolerance screening:

- 99/150 genotypes flowered after drought treatment at reproductive stage.
- 16 genotypes showed strong recovery from stress (grain yield > 1,200 kg.ha<sup>-1</sup>). Particularly, DDH120, ML202 and KroHomThngonh had very high yield (> 2,000 kg.ha<sup>-1</sup>)

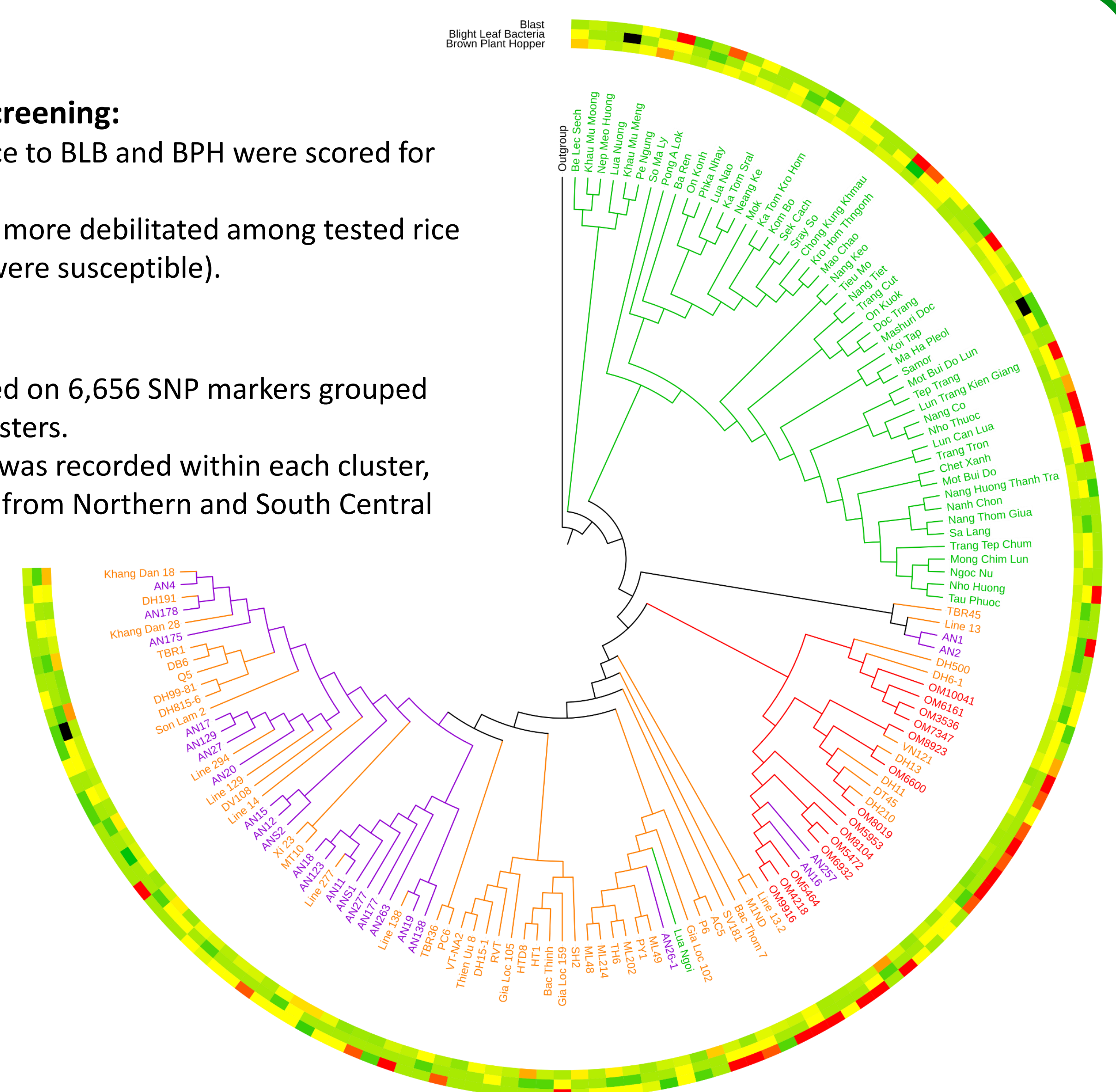


### 4. Biotic stress resistance screening:

- Moderate to high resistance to BLB and BPH were scored for most of genotypes.
- Blast resistance was found more debilitated among tested rice panel (63/144 genotypes were susceptible).

### 5. Genetic analysis:

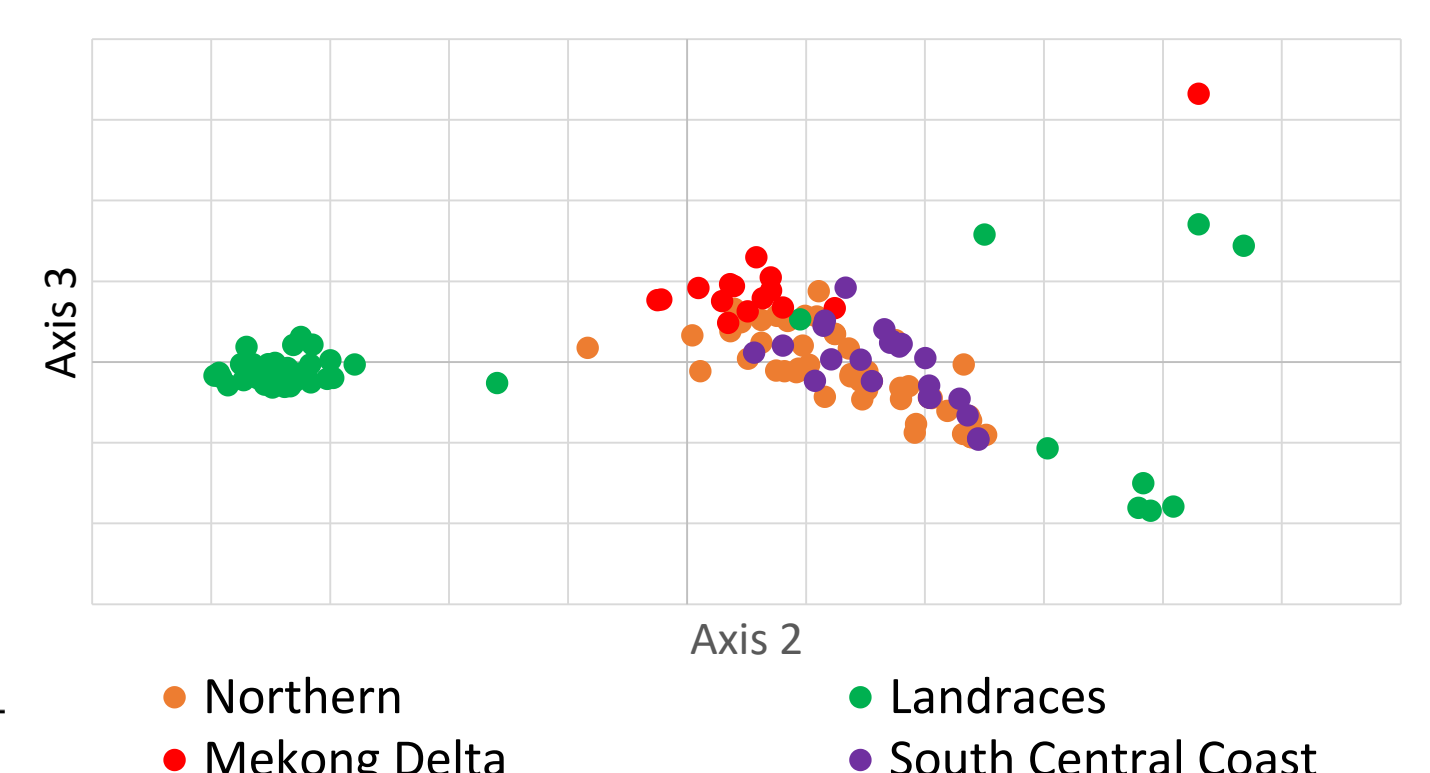
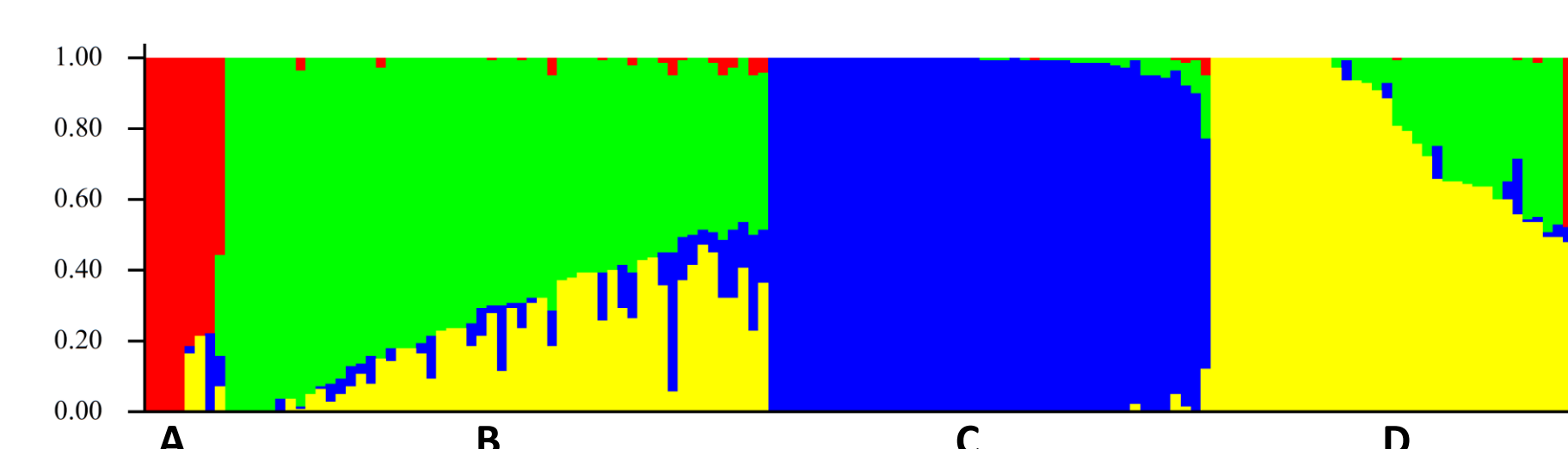
- Neighbor-Joining tree based on 6,656 SNP markers grouped 144 rice genotypes in 4 clusters.
- Strong genetic correlation was recorded within each cluster, except those of genotypes from Northern and South Central Coast regions.



### 6. Population structure inference :

- Model-based population structure analysis inferred four cluster A, B, C and D.
- Except landraces which was divided into two “pure” groups A and C, other breeding lines representing Northern, South Central Coast and Mekong Delta regions were clustered into other two groups B and D having vigorous “admixture” genetic backgrounds.
- PC analysis harmonized with inferred population structure.

Genotype groups	Inferred cluster				n
	A	B	C	D	
Landraces	0.130	0.024	0.820	0.025	53
Northern region	0.006	0.432	0.058	0.504	52
South Central Coast	0.003	0.401	0.020	0.576	24
Mekong Delta	0.039	0.878	0.022	0.060	15
n	8	54	44	38	
Fst	0.661	0.654	0.709	0.807	



## CONCLUSIONS

- Trials identified five genotypes highly tolerant to submergence, one genotype moderately tolerant to salinity at EC 18 and 16 genotypes exhibiting potential yield performance under drought stress.
- SNP which associate with characterized genes/QTs conferring targeted abiotic stresses tolerance were observed for most of potential rice genotypes except that showing tolerance to salinity. It implies that, there are other genetic elements may involving in salinity tolerance machinery.
- The panel of 150 Vietnamese rice genotypes possess high genetic diversity between landrace and breeding/cultivar groups but quite narrow genetics background within breeding genotypes.