

MAIZE BREEDING FOR DROUGHT TOLERANCE VIA MARKER-ASSISTED SELECTION

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Genetic divergence analysis due to UPGMA clustering (included 62 maize accessions in the IAS gene bank) was carried out through SSRs. Eighty crosses exhibited their significant heterosis due to exploiting genetic distance values among genetic clusters. Some hybrids obtained desired agronomical traits and significantly overyielded as compared to the leading hybrid in Southern Vietnam as **C919**.

QTL analysis was conducted through the phenotypic variation of ASI (anther silking interval) and grain yield under drought stress in the field. Single marker analysis and interval mapping analysis reported that in F₂ population of D12 (high yielding) x CML 161 (donor), putative QTLs were located on chromosomes 1, 3 and 9. Especially, the target QTL on chromosome 1 closely linked to SSR markers **bnlg 1811** and **bnlg 1429**. These were applied to improve the drought tolerance in maize breeding of the IAS to identify the hybrid from VE8 x BC₃F₃-28, which exhibited the most promising high-yielding genotype adapted to drought prone in Southern Vietnam.

Table 1. Phenotyping under two main plots concerning normal irrigation and drought stress at flowering

	Donor parent		Recurrent parent		Mean of F ₂		Boundary	
	Irrigated	Non-irrigated	Irrigated	Non-irrigated	Irrigated	Non-irrigated	Irrigated	Non-irrigated
ASI (day)	1.67	8.67	3.33	5.33	2.89	7.64	1.3-5.0	4.3-10.3
Yield (g/plot)	656.7	413.3	543.3	398.3	761.5	581.5	420-1170	393-860

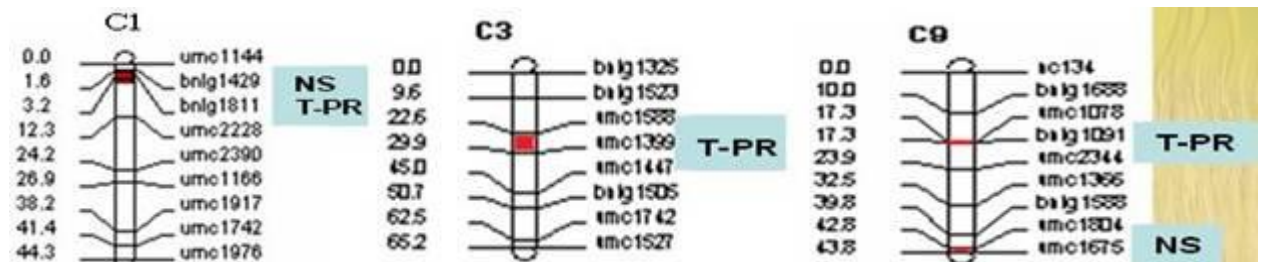


Figure 1. QTL mapping of grain yield and ASI in F₂ population of D12 x CML 161
NS: grain yield; T-PR: anther silking interval

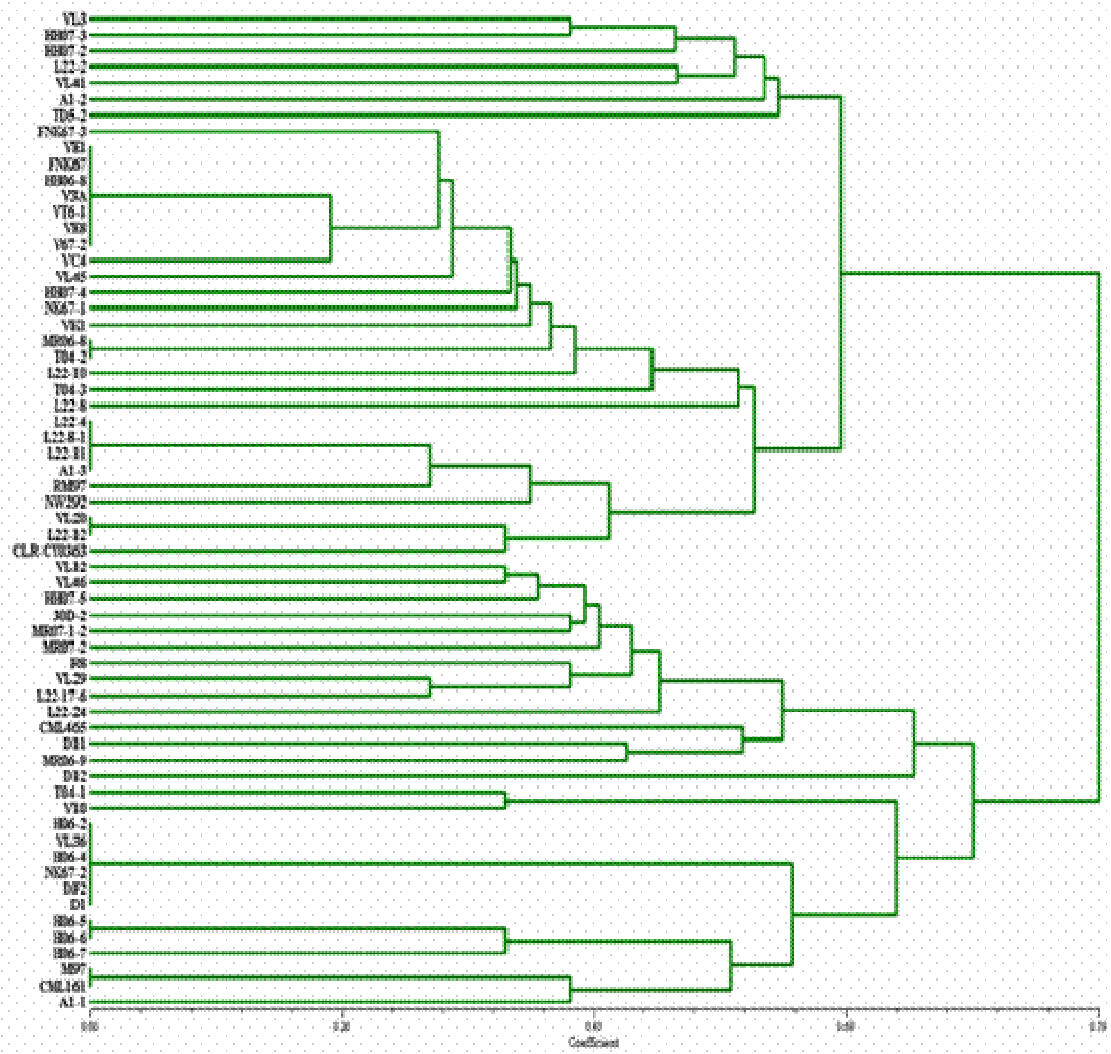


Figure 2. Genetic clustering due to UPGMA analysis