

Supplementary file 1. List of the main experimental trials studying the genetics of adaptation to water deficit in maritime pine

Trial ID	Trial description	Environment (region, country)	Phenotype	Genetic material	Parameters estimated	Reference
1	Provenance-progeny tests	Wet, Cestas (FR), 800 mm	CR, WUE, growth	6 pop*8fam*5HS (half-sibs) =240 samples	Q_{ST} , h^2 , PP (σ_E , σ_{GxE}), cor_G	Lamy <i>et al.</i> (2011)
2		Dry, Calcena (ES), 400 mm	CR, growth	6 pop*8fam*5HS =240 samples		Lamy <i>et al.</i> (2014)
3	<i>In situ</i>	Highly variable (several countries)	CR, growth	7 pop*11indiv =77 samples	σ_P	
4	Progeny test	3 sites: dry, semi-humid, humid (Aquitaine, FR)	WUE, growth	50 fam*12 HS/site =1,800 samples	h^2 , PP (σ_E , σ_{GxE}), cor_G	Marguerit <i>et al.</i> (2014)
5	Progeny test	1 site: wet (Aquitaine, FR)	WUE, growth	12*12 half-diallel = 564 samples	h^2 , cor_G	Brendel <i>et al.</i> (2002)
6	Pot exp. in greenhouse	dry vs. well-watered	WUE, g, A, root/shoot	3 populations	σ_P	Guehl <i>et al.</i> (1996)
7	Pot exp. in greenhouse	dry vs. well-watered	WUE, water potential, biomass allocation	4 populations	h^2 , cor_G	Aranda <i>et al.</i> (2010)
8	Provenance-progeny test	2 sites: dry/humid (ES)	Growth, WUE	3 populations	h^2	Corcuera <i>et al.</i> (2010)
9	Provenance-progeny test	2 sites: dry/humid (ES)	CR, wood density	6 populations	Q_{ST}	Corcuera <i>et al.</i> (2011)
10	Pot exp. in greenhouse	dry vs. well-watered	WUE, hydraulic conductance, growth, biomass allocation, root morphology, xylem anatomy	5 populations	cor	Corcuera <i>et al.</i> (2012)
11	Provenance test	1 site: sub-humid (ES), 578 mm	Growth, WUE, survival	7 populations	Q_{ST} , cor	Correia <i>et al.</i> (2008)
12	Mapping population	1 site: humid, (Aquitaine, FR)	WUE, growth	1 family = 470 samples	QTL (number, position, effect)	Marguerit <i>et al.</i> (2014)
13	Mapping population	1 site: humid, (Aquitaine, FR)	WUE, growth	1 family = 200 samples	QTL (number, position, effect)	Brendel <i>et al.</i> (2002)
14	Mapping population	dry vs. well-watered	WUE, g, A, fluorescence Chl.a	1 family = 103 samples	QTL (number, position, effect)	de Miguel <i>et al.</i> (2014)
15	Mapping population	dry vs. Well-watered	WUE, g, A, fluorescence Chl.a	1 family = 103 samples	h^2 , cor_G	de Miguel <i>et al.</i> (2012)

Abbreviations – WUE: water use efficiency, CR: cavitation resistance, g: stomatal conductance, A: Photosynthetic rate, h^2 : heritability, Q_{ST} : quantitative trait differentiation index, cor: phenotypic correlations, cor_G : genetic correlations, QTL: quantitative trait loci, PP : phenotypic plasticity, σ_E : environmental variance, σ_{GxE} : genotype-by-environment variance