- 1 Title
- 2 Tissue culture as a source of replicates in non-model plants: variation in cold
- 3 tolerance in *Arabidopsis lyrata* ssp. *petraea*
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Abstract

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Whilst genotype–environment interaction is increasingly receiving attention by ecologists and evolutionary biologists, such studies need genetically homogeneous replicates—a challenging hurdle in outcrossing plants. This could potentially be overcome by using tissue culture techniques. However, plants regenerated from tissue culture may show aberrant phenotypes and "somaclonal" variation. Here we examined the somaclonal variation due to tissue culturing using the response of the photosynthetic efficiency (chlorophyll fluorescence measurements for F_v/F_m , F_v'/F_m' and Φ_{PSII} , representing maximum efficiency of photosynthesis for dark- and lightadapted leaves, and the actual electron transport operating efficiency, respectively) to cold treatment, compared to variation among half-sibling seedlings from three different families of Arabidopsis lyrata ssp. petraea. Somaclonal variation was limited and we could successfully detect within-family variation in change in chlorophyll fluorescence by cold shock with the help of tissue-culture derived replicates. Icelandic and Norwegian families exhibited higher chlorophyll fluorescence, suggesting higher cold tolerance, than a Swedish family. Although the main effect of tissue culture on F_v/F_m , F_v'/F_m' and Φ_{PSII} was small, there were significant interactions between tissue culture and family, suggesting that the effect of tissue culture is genotype-specific. Tissue-cultured plantlets were less affected by cold treatment than seedlings, but to a different extent in each family. These interactive effects, however, were comparable to, or much smaller than the single effect of family. These results suggest that tissue culture is a useful method for obtaining genetically homogenous replicates for studying genotype–environment interaction related to adaptively relevant phenotypes, such as cold tolerance, in non-model outcrossing plants.

Introduction

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Genotype-environment interaction on a phenotype or reaction norm may modulate natural selection (Wright 1931; Sultan 1987). The genetic basis of genotypeenvironment interaction is increasingly receiving attention (El-Soda et al. 2014; Yap et al. 2011); however, such advances have been concentrated in inbreeding organisms such as Arabidopsis thaliana (e.g. Bloomer et al. 2014; El-Soda et al. 2014; Sasaki et al. 2015; Stratton 1998) and Caenorhabditis elegans (Gutteling et al. 2007), because genetically isogenic individuals permit a given genotype to be exactly repeated in multiple environments. Recently, the wild relatives of model organisms are increasingly being exploited by evolutionary biologists to understand adaptation and speciation (Clauss & Koch 2006; Mitchell-Olds 2001). However, one disadvantage of non-model plants with outcrossing mating systems is that they cannot usually be exploited to produce the genetically homogeneous or inbred recombinant lines that enable researchers to study the reaction norms of a single genotype in multiple environments (Dorn et al. 2000) or to map novel QTLs in previously-genotyped lines (Alonso-Blanco et al. 2005). This disadvantage could be compensated for by using cutting techniques to produce multiple clones from single genotypes (Sultan & Bazzaz 1993; Waitt & Levin 1993; Wu 1998). This method is only applicable to plants capable of vegetative propagation, and it also needs relatively large plant bodies to produce many replicate clones. Another technique applicable to a wider range of plants with relatively small starting plant material is tissue culture (George & Sherrington 1984). However, tissue culture has been exploited rarely for studies on the genetic basis of genotype-environment interaction, and the few existing studies (Glock 1989; Glock & Gregorius 1986) focused only on callus characteristics as target phenotypes. One potential issue that should be carefully considered is that

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tissue-culture derived microshoots can express phenotypic, "somaclonal" variation (Larkin & Scowcroft 1981) or may sometimes show aberrant morphology and physiology in vitro (Joyce et al. 2003). This somaclonal variation resembles that induced by physical mutagens, with elevated levels of chromosome breakage and rearrangement, polyploidy, aneuploidy, transposon activation and point mutation (D' Amato & Bayliss 1985). Therefore, with a view to exploiting the techniques of tissue culturing more widely in studies of genotype-environment interaction in outcrossing plants, it is necessary to extend our knowledge on how propagation by tissue culture generates variation in phenotypes that are relevant to adaptation in natural environments, compared to other sources of genetically-related replicates such as outbred siblings. Key plant properties that have attracted marked attention in the field of adaptation to various environments are stress tolerances (e.g. Hong & Vierling 2000; Kwon et al. 2007; Lexer et al. 2003; Quesada et al. 2002; Steponkus et al. 1998; Zhang et al. 2004; Zhen & Ungerer 2008). One trait that can be used to indicate tolerance against various physical stressors in plants is photosynthetic performance. Photosystem II (PSII) activity is sensitive to both biotic and physical environmental factors (Murchie & Lawson 2013). Chlorophyll fluorescence can be used to determine the maximum efficiency with which light absorbed by pigments of photosystem II (PSII) is used to drive photochemistry in dark- (F_v/F_m) or light- (F_v/F_m) adapted material and the operating efficiency of PSII (Φ_{PSII}). It is a reliable indicator of photoinhibition and damage to the photosynthetic electron transport system (Maxwell & Johnson 2000; Quick & Stitt 1989). Changes in chlorophyll fluorescence have been successfully used in Arabidopsis thaliana to quantify tolerance to cold and freezing temperatures

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(Ehlert & Hincha 2008; Heo et al. 2014; Mishra et al. 2014), drought (Bresson et al. 2015; McAusland et al. 2013; Woo et al. 2008), and salt and heavy-metal stress (Yuan et al. 2013), as well as in various other plants for tolerance to cold and freezing temperatures (Baldi et al. 2011; Khanal et al. 2015; Medeiros et al. 2012; Xie et al. 2015), drought (Jansen et al. 2009) and salt (Yuan et al. 2013). If variation in chlorophyll fluorescence can be properly estimated using tissue-culture derived clones, therefore, it would enhance studies in genotype–environment interaction for stress tolerance in outcrossing plants. To this end, we have studied change in chlorophyll fluorescence following cold shock in a wild relative of a model plant species. Arabidopsis lyrata ssp. petraea is a close relative of the model species A. thaliana, but with a different ecology, life history and population genetics (Charlesworth et al. 2003; Davey et al. 2008; Davey et al. 2009; Kuittinen et al. 2008; Kunin et al. 2009). Whilst A. thaliana is mainly selfing, with a low level of genetic diversity within a population, A. lyrata ssp. petraea is outcrossing, with a high level of genetic diversity even within a population (Clauss & Mitchell-Olds 2006; Heidel et al. 2006; Kunin et al. 2009; Schierup et al. 2008). Further studies on genetic and phenotypic variation in spatially distinct individuals and in closely-related plants will clarify whether or not locally advantageous alleles are fixed and if local populations are in evolutionary equilibrium, and are thus important in our understanding of the evolutionary responses to environmental change. Distinguishing phenotypic variation among closely related individuals from measurement errors is difficult; however, this becomes possible if we can quantify the error within the same genotype using tissue-cultured clones.

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In this study, we measured the chlorophyll fluorescence parameters F_v/F_m , F_v'/F_m' and Φ_{PSII} before and after cold shock, as an index of cold tolerance, for seedlings from three families from geographically isolated populations of A. lyrata ssp. petraea, and tissue cultured plantlets derived from several genotypes (seeds) in each of those families (Table 1). In order to evaluate the usefulness of tissue culture for obtaining genetically homogenous replicates and to assess how much adaptively-relevant variation exists within the species, we tested whether (i) among-genotype phenotypic variation could be detected with the help of replication of tissue cultured plantlets, (ii) somaclonal variation would remain in the range of other components of variation such as within-family variation of seedlings, (iii) phenotypic variation in adaptively relevant traits would exist between families and (iv) tissue-culturing affected these measurements of chlorophyll fluorescence. Material and Methods **Plants** Seeds of Arabidopsis l. petraea were collected from geographically separated populations in Ardal (Norway) (61°19′25″N, 7°50′00″E, alt. 63 m), Notsand (Sweden) (62°36′31″N, 18°03′37″E, alt. 3 m) and Sandfell (Iceland) (64°04′14″N, 21°41′06″E, alt. 123 m). No specific permits were required for the seed collection for this study because these locations were not privately owned or protected in any way and because the species was not protected in these countries. The species is a perennial herb and keeps leaves throughout the year. We used a family of seeds that were at least half-siblings, from one mother plant in each population. We grew 28–40

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seedlings per family and in each case derived 44–69 tissue-cultured plantlets from 2–3 seeds (1 genotype = cloned plantlets from one seed) of each family. Tissue culture Seeds were sterilised in 10% commercial bleach for 20 min, washed in sterile water and stored at 4°C overnight. The seeds were then placed onto 50% strength Murashige and Skoog (MS) medium (Melford Laboratories Ltd, Ipswich, UK), pH 5.7, supplemented with 1 % sucrose, 5 mg/L silver thiosulphate and solidified with 1 % plant agar (Melford Labs. Ltd). The agar plates were held vertically, allowing for maximum recovery of root tissue. After 4 weeks the root systems were excised and placed intact onto Callus Induction Medium (CIM) (Clarke et al., 1992) solidified with 0.55% plant agar. Plates were incubated at 23 °C for 3 days then the roots were cut into 5 mm lengths and placed in bundles on fresh CIM plates that were further incubated at 20°C for 2–3 days. The root sections from each plant were resuspended in 10 ml molten Shoot Overlay Medium (SOM) (Clarke et al., 1992) solidified with 0.8 % low gelling-temperature agarose and poured over a single 90 mm plate of Shoot Induction Medium (SIM) (Clarke et al., 1992) solidified with 0.55 % plant agar and lacking antibiotics. The plates were incubated at 20 °C under a 16-hour day length. Once shoots started to form from the calli they were transferred to 50 % strength MS medium, pH5.7, supplemented with 1 % sucrose and solidified with 0.55% plant agar, such that each plate contained 9 clones of the same genotype. A total of 4–9 plantlets survived per plate. Each plate was treated as a block in the following experiment. Seedling growth

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Seeds were sown in Levington M3 compost within individual plug trays. Families were randomised within each tray and trays were randomly repositioned every other day. Plants were watered from the base of the pot as required with reverse-osmosis (RO) purified water. No additional nutrients were added to the soil or water. Plants were established to 6–8 leaf stage in controlled-environment growth cabinets (Conviron Controlled Environments Limited, Canada) set to a 12/12 hour day/night cycle, 20/15 °C day/night, 70 % humidity; atmospheric CO₂ concentration was 400 ppm and photosynthetically-active radiation 250 µmol m⁻² s⁻¹. Chlorophyll fluorescence measurements were taken just prior to and after a 24 hour cold treatment in which plants were exposed to the same conditions as above, apart from the temperature being decreased to 3 °C. 5–8 seedlings from the same family were treated as a block in the following experiment. Chlorophyll fluorescence Pre-cold and post-cold treatment measurements of chlorophyll fluorescence were obtained using a chlorophyll fluorescence imager using Fluorimager software (Technologica Ltd., Colchester, UK). Each block of plants was dark adapted for at least 15 minutes before the maximum efficiency of photosystem II (F_v/F_m) was measured to a blue light pulse at 3000 µmol m⁻² s⁻¹ for 200 ms. Following this pulse, the plants were exposed to an actinic light of 150 µmol m⁻² s⁻¹ for six minutes, followed by pulses of 3000 µmol m⁻² s⁻¹ for 200 ms to obtain measures of maximum efficiency of photosystem II (F_v'/F_m') of light-adapted plant material and the operating efficiency of photosystem II (Φ_{PSII}) in light-adapted plant material. Mean

205 values of F_{ν}/F_m , F_{ν}'/F_m' and Φ_{PSII} for each plant were taken from the image of each 206 whole plant. 207 All these phenotypic data are available in Dryad Digital Repository: 208 http://dx.doi.org/10.5061/dryad.xxxxx. 209 210 Statistical analyses 211 212 To examine the relative importance of among-family and among-genotype variation 213 in cold tolerance, we used nested ANOVA to partition the total variance in the 214 difference in each chlorophyll fluorescence measurement (F_v/F_m , F_v'/Fm' or Φ_{PSII}) 215 induced by cold shock: 216 217 $VD \sim VF / VG / VB$ 218 219 where VD was the total variance in difference in each type of chlorophyll 220 fluorescence for a plant individual between two measurements (i.e. value after cold 221 shock minus that before cold shock), VF was the component of among-family 222 variance, VG was the component of among-genotype variance nested in VF and VB 223 was the component of among-block variance nested in VG. We did this analysis 224 separately for the tissue-cultured plants and seedlings, in order to evaluate variation in 225 each natural and tissue-cultured condition. The VG term was not applied to the 226 analysis for seedlings. We also conducted variance component analysis using the 227 varcomp function in the ape library and the lme function using R = 2.8.0(R)228 Development Core Team 2008). 229

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We tested whether variance in the change of F_v/F_m , Fv'/Fm' or Φ_{PSII} due to cold shock among tissue-culture derived plantlets within each genotype was different from that in seedlings of half-siblings of the same family using Bartlett tests. Because the number of blocks differed between seedlings and tissue-cultured plantlets (Table 1), we checked first whether the difference in the number of blocks affected the variance, by re-sampling all possible combinations of 4 blocks from the 10 blocks of halfsiblings in Ardal and Notsand. Reducing block number changed the original variance for 10 blocks only $< \pm 3$ % without systematic bias. Finally, we evaluated the effect of several factors on each type of chlorophyll fluorescence measurement before and after cold treatment. We constructed the following linear mixed-effect model, in which plant individual was treated as a random effect: $CF = I|B/P + C + T + F + C \times T + T \times F + C \times F + C \times T \times F$ where CF was a single measurement of either F_v/F_m , Fv'/Fm' or Φ_{PSII} and I|B/P was the intercept with random effects of block, and individual plant nested in each block, C was a binary variable of cold shock (1 for shocked and 0 for not), T was a binary variable of tissue culture (1 for tissue cultured and 0 for not) and F was a categorical variable of family (3 families), followed by the interaction terms among those variables. The effect of each term was estimated by the lme function using the statistical software R 2.8.0 (R Development Core Team 2008). Akaike's Information Criterion (AIC) was compared between the full model and a model lacking each term

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in a stepwise manner and the best model with the lowest AIC was selected, followed by testing the significance of each selected parameter using the Wald test. Results *Variance components in cold-response of Fv/Fm Fv'/Fm' and* Φ_{PSII} In the seedlings, the changes in F_v/F_m , F_v'/F_m' or Φ_{PSII} by cold treatment varied significantly among families, explaining 4.9–9.1 % of the total variance (Table 2). For the tissue-cultured plantlets, the change in those indices by cold treatment did not vary significantly among families, but did vary significantly among genotypes within family, this component explaining 8.5–31.5 % of the total variance. The within-block variance component for tissue-cultured plantlets was 61.7–81.8 % and tended to be smaller than this component for seedlings (89.1–92.2 %). Evaluation of somaclonal variation in comparison to within-family variation Variances in the change of F_{ν}/F_m , F_{ν}'/F_m' or Φ_{PSII} among clones within genotype were clearly smaller than those among half-siblings of the same family in the Sandfell family. Most genotypes had significantly smaller variances in F_v/F_m , F_v'/F_m' and Φ_{PSII} than half-sibs as shown by the Bartlett test (Fig. 1). Similar patterns were observed in Notsand and Ardal. No studied genotype had larger variance among clones than the variance among half-siblings in any family. Effects of cold shock, tissue culturing and family on Fv/Fm Fv'/Fm' and Φ_{PSII}

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All single effects of cold shock, tissue culture and family and all possible interaction combinations among them affected F_{ν}/F_{m} and F_{ν}'/F_{m}' , and all such effects except the 3-way interaction between cold shock, tissue culture and family affected Φ_{PSII} , according to the best model (Table 3) based on Akaike's Information Criterion (AIC). Cold shock and family were the strongest single effects. The interaction between these two factors was also found to change all three measurements of chlorophyll fluorescence, indicating that the effect of cold shock depended on family. The effect of tissue culture was relatively small and not significant for any of the chlorophyll fluorescence measures. We found substantial interactions between tissue culture and family and interactions among cold shock, tissue culture and family, indicating that the effect of tissue culture depended on family. Discussion Among-genotype variance We were able to test for among-genotype variance using replicates generated by tissue culture within genotypes and we detected such variance in F_v/F_m , F_v'/F_m' and Φ_{PSII} measurements (Table 2). On the other hand, we showed significant but low somaclonal variation. The within-block variance component for tissue-cultured plantlets was relatively small (Table 2). The Bartlett tests showed that somaclonal variation was smaller than, or at least remained within the range of, the within-family variance, which is the smallest naturally observed component of variation in the hierarchy of genetic structure (Fig. 1). In A. thaliana, studies of natural variation have focused mainly on between-population variation (e.g. (Shindo et al. 2007). In contrast,

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A. lyrata has substantial within-population variation, for example in the composition of glucosinolates (Clauss et al. 2006) or self-incompatibility genes (Schierup et al. 2008). In this paper, we showed that there is within-family as well as among-family, and thus among-population, genetic variation in A. lyrata ssp. petraea. Within-family genetic variance was relatively large in Sandfell (Iceland). The observed withinfamily genetic variances in adaptively relevant traits highlight the wide potential for evolutionary adaptation of the species and further validates the usefulness of relatives of model organisms in evolutionary biology (Clauss & Koch 2006; Mitchell-Olds 2001). Among-family variance There was significant or marginally significant among-family variance in the change of F_v/F_m , F_v'/F_m' and Φ_{PSII} values by cold treatment for seedlings (Table 2). In A. thaliana, the change in chlorophyll fluorescence from before to after cold shock correlates with tolerance to sub-zero temperatures measured by electrolyte leakage or survival and, therefore, this is regarded as an indicator of cold tolerance (Ehlert & Hincha 2008; Heo et al. 2014; Khanal et al. 2015). Therefore, our result also represents evidence for among-family (thus possibly among-population) variance in cold tolerance. Linear mixed models (Table 3) showed that F_v'/F_m' after cold-shock was higher in family Ardal and Sandfell, and F_{ν}/F_m and Φ_{PSII} after cold-shock was higher in family Sandfell, compared to Notsand (Sweden). These results are consistent with families Aradal (Norway) and Sundfell (Iceland) being derived from relatively high latitude and high altitude and so having high cold tolerance. This among-family effect was weaker for tissue-cultured plantlets (Table 3). This may be due to the small

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number of genotypes for each family in our nested experimental design, or, could be explained by the main part of the among-family variance detected for seedlings being due to among-genotype variance within families. Effects of tissue culturing We detected genotype-specific effects of tissue culture on F_v/F_m , F_v'/F_m' and Φ_{PSII} (Table 3). This is consistent with a previous report of a genotype-specific effect on callus characteristics (Glock 1989; Glock & Gregorius 1986). The three measured parameters of chlorophyll fluorescence $(F_{\nu}/F_m, F_{\nu}'/F_m')$ and Φ_{PSII}) all decreased after the cold treatment (Table 3), indicating a decrease in photosystem II activity, as reported in previous studies (Finazzi et al. 2006). A positive effect of interaction between tissue culture and cold shock for Φ_{PSII} suggests that tissue-cultured plants were less affected by cold shock than seedlings, and an interaction between tissue culture, cold shock and family suggests that the extent to which tissue-cultured plants were less affected by cold shock differed among families. Any differences among families in traits related to responses to the tissue-culture environment, including rootcutting, callus formation and growth on medium, might explain these observed interactions between tissue culture and family. This finding is consistent with the report that somaclonal variation is genotype-dependent and influenced by both the explant source and the tissue-culture protocol (George & Sherrington 1984), and a recent study that found that the effect of tissue culture on somatic mutations depended on genotype (Zhang et al. 2010). The effects of tissue culture–genotype interaction, however, were comparable to, or much smaller than the single effect of family (Table 3), indicating that such interactions would not mask the single effect of genotype. The

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interaction between tissue culture and family was much smaller in Φ_{PSII} (the range between maximum and minimum estimates was 0.043 - (-0.005) = 0.048, Table 2) than in F_v/F_m (0.082 – 0 = 0.082) and F_v/F_m (0.181 – 0 = 0.181). The interaction between cold shock, tissue culture and family was detected only in F_v/F_m and F_v'/F_m' . Also, the relative impact of among-genotype variance was smaller for Φ_{PSII} (8.5% of the total variance, Table 2) than F_{ν}/F_{m} (31.5 %) and F_{ν}'/F_{m}' (10.9 %). These results imply that, although the maximum efficiencies of photosynthesis for dark- (F_{ν}/F_{m}) and light-adapted leaves (F_v'/F_m') were affected by tissue culturing in genotypespecific ways, the actual electron transport operating efficiency (Φ_{PSII}) was less affected by tissue culture. Conclusion Overall, we successfully detected among-genotype variance, with low somaclonal variation, indicating that the advantage of tissue culturing in generating genetically isogenic replicates exceeded its disadvantage in amplifying somaclonal variation in our study system. We detected interaction effects of tissue culture with genotype for an adaptively relevant trait, cold tolerance; however, such variation would not mask the single effect of genotype. Therefore, although one should carefully consider effects of tissue culturing when interpreting any results relying on the technique, tissue culturing is a useful method for obtaining genetically homogenous replicates in this, and probably other non-model organisms. It can provide critical additional power when studying phenotypes such as cold tolerance related to adaptation in natural environments, the variation in the phenotypes among families or populations, the reaction norms of a genotype or the QTLs accounting for phenotypes.

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545 Figure

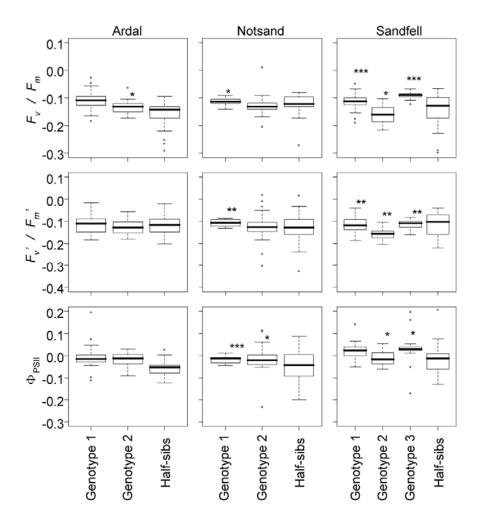


Figure. 1. Change in chlorophyll fluorescence (F_v/F_m , F_v'/F_m' and Φ_{PSII}) in seedlings or plantlets originating from Norway (Ardel), Sweden (Notsand) and Iceland (Sandfell) after cold-treatment (*values after shock* – *those before shock*). *, ** and *** = P<0.05, P<0.01 and P<0.001, respectively, (Bartlett test) indicate a significantly lower variance of the genotype than among half-siblings in the same family. Three F_v/F_m values (0.340, 0.375, 0.592) and an F_v'/F_m' value (0.354) in

- Sandfell half-siblings were out of the vertical ranges shown but were included in the
- statistical tests.

Tables

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- Table 1. Numbers of plants and blocks in each family (Ardal, Notsand and Sandfell).
- Plants were either seedlings in a half-sibling family or tissue-cultured clonal plantlets
- from genotypes derived from a seed from each family.

Genotype 1 Genotype 2 Genotype 3 Half sib								
Ardal								
Number of plants	33	36	-	40				
Number of blocks	4	4	-	10				
Plants / block (min - max)	6 - 9	9 - 9	-	4 - 4				
Notsand								
Number of plants	13	31	-	40				
Number of blocks	2	4	-	10				
Plants / block (min - max)	5 - 8	4 - 9	-	4 - 4				
Sandfell								
Number of plants	45	28	23	28				
Number of blocks	5	4	3	4				
Plants / block (min - max)	9 - 9	5 - 9	5 - 9	5 - 8				

Table 2. Analysis of variance for change in F_v/F_m , F_v'/F_m' and Φ_{PSII} by cold treatment for non-tissue cultured seedlings and tissue-cultured plantlets. Family and Block refer to variation among families and among blocks within families, respectively

	See	dling	S			Tissue cultures						
	Df	Sum Sq	Mean Sq	F	Р	Variance component (%)	Df	Sum Sq	Mean Sq	F	Р	Variance component (%)
Fv/Fm												
Family	2	0.027	0.013	2.84	0.081	4.9	2	0.002	0.001	0.06	0.946	0.0
Genotype							4	0.080	0.020	11.52	0.000	31.5
Block Within	21	0.098	0.005	1.11	0.351	6.1	19	0.033	0.002	1.91	0.016	6.8
Block	84	0.353	0.004			89.1	183	0.167	0.001			61.7
F_{v}'/F_{m}'												
				10.0								
Family	2	0.081	0.041	1	0.001	7.8		0.005	0.002	0.24	0.798	0.0
Genotype							4	0.041	0.010	3.27	0.034	10.9
Block Within	21	0.085	0.004	0.33	0.997	0.0	19	0.059	0.003	2.54	0.001	14.1
Block	84	1.048	0.012			92.2	183	0.225	0.001			74.9
Φ_{PSII}												
Family	2	0.026	0.013	8.44	0.002	9.1	2	0.044	0.022	2.81	0.173	7.7
Genotype							4	0.031	0.008	3.37	0.030	8.5
Block Within		0.032	0.002	0.45	0.978	0.0	19	0.044	0.002	1.23	0.241	2.0
Block	84	0.282	0.003			90.9	183	0.349	0.002			81.8

Table 3. The best linear mixed models for F_v/F_m , F_v'/F_m' and Φ_{PSII} , based on AIC. Intercepts represent the mixture of background conditions, i.e. not cold shocked, not tissue cultured, and family Notsand. Fam A and Fam S refer to families Ardal and Sandfell, respectively.

	Estimates	SE	DF	t	Р
Fv/Fm					
Intercept	0.787	0.011	311	71.3	<0.001
Cold shock	-0.122	0.008	311	-15.9	<0.001
Tissue culture	-0.017	0.015	302	-1.1	0.252
Fam A	-0.026	0.015	302	-1.7	0.093
Fam S	-0.091	0.017	302	-5.4	<0.001
Cold shock x Tissue culture	-0.007	0.011	311	-0.7	0.506
Cold shock x Fam A	-0.035	0.011	311	-3.2	0.002
Cold shock x Fam S	-0.007	0.012	311	-0.5	0.584
Tissue culture x Fam A	0.029	0.020	302	1.5	0.147
Tissue culture x Fam S	0.082	0.021	302	3.9	<0.001
Cold shock x Tissue culture x Fam A	0.043	0.014	311	3.0	0.003
Cold shock x Tissue culture x Fam S Fv'/Fm'	0.015	0.015	311	1.0	0.327
Intercept	0.695	0.014	311	50.9	<0.001
Cold shock	-0.131	0.011	311	-12.1	<0.001
Tissue culture	-0.019	0.019	302	-1.0	0.304
Fam A	-0.050	0.019	302	-2.6	0.009
Fam S	-0.167	0.021	302	-7.9	<0.001
Cold shock x Tissue culture	0.011	0.015	311	8.0	0.446
Cold shock x Fam A	0.015	0.015	311	0.9	0.345
Cold shock x Fam S	0.068	0.017	311	4.0	<0.001
Tissue culture x Fam A	0.070	0.025	302	2.8	0.006
Tissue culture x Fam S	0.181	0.026	302	6.9	<0.001
Cold shock x Tissue culture x Fam A	-0.013	0.020	311	-0.7	0.514
Cold shock x Tissue culture x Fam S Φ _{PSII}	-0.077	0.021	311	-3.7	<0.001
Intercept	0.403	0.012	313	34.2	< 0.001
Cold shock	-0.047	0.006	313	-7.7	<0.001
Tissue culture	-0.027	0.016	302	-1.7	0.090
Fam A	-0.029	0.016	302	-1.8	0.081
Fam S	-0.086	0.018	302	-4.7	<0.001
Cold shock x Tissue culture	0.034	0.006	313	5.8	< 0.001
Cold shock x Fam A	-0.004	0.007	313	-0.5	0.610
Cold shock x Fam S	0.028	0.007	313	3.9	< 0.001
Tissue culture x Fam A	-0.005	0.021	302	-0.2	0.822
Tissue culture x Fam S	0.043	0.022	302	2.0	0.051