Mihai G, Mirancea I, Birsan M, Dumitrescu A (2018).
Patterns of genetic variation in bud flushing of *Abies alba* populations
iForest – Biogeosciences and Forestry – doi: 10.3832/ifor2314-011

Supplementary Material

Tab. S1 - Analysis of variance of the half-diallel and expected mean squares (Griffing 1956a). σ^2_p = variance among plots, σ^2_w = variance among full-sib within-plots, $\sigma^2_p = \sigma^2_e - \sigma^2_w / n$, $\sigma^2_{GCA} = (MS_{GCA} - MS_{SCA}) / (p - 2)$, $\sigma^2_{SCA} = MS_{SCA} - MS_E$, p = number of parents, n = number of seedlings per plot, r = number of replications.

Source	df	MS	E(MS)	F test
Replication	$r - 1$	MS_{Rep}	$\sigma^2_w + n[p(p - 1) / 2]\sigma^2_R$	MS_{Rep}/MS_E
GCA	$p - 1$	MS_{GCA}	$\sigma^2_w + nr\sigma^2_{SCA} + nr(p - 2)\sigma^2_{GCA}$	MS_{GCA}/MS_{SCA}
SCA	$p(p - 3) / 2$	MS_{SCA}	$\sigma^2_w + nr\sigma^2_{SCA}$	MS_{SCA}/MS_E
Error	$(r - 1)\{[(p^2 - p) / 2] - 1\}$	MS_E	$\sigma^2_e = \sigma^2_p + \sigma^2_w / n$	
Within-plot error	$r[p(p - 1) / 2](n - 1)$	MS_W	σ^2_w	

Tab. S2 - Variance components and their standard errors for bud flushing in full-sib and open-pollinated progenies. The percentage of additive genetic variance from phenotypic variance is in brackets. σ^2_{GCA} = the variance of general combining ability, σ^2_{SCA} = the variance of specific combining ability, σ^2_{Ph} = the phenotypic variance, σ^2_A = the additive genetic variance, σ^2_A = the family variance, σ^2_E = the error variance , σ^2_w = the variance within-plots, SE = the standard error.

Genetic parameters	**Evaluations**				
	I-2012	**II-2012**	**III-2012**	**IV-2012**	**I-2013**
Full-sib progeny					
σ^2_{GCA} ± SE	0.089 ± 0.050	0.336 ± 0.185	0.115 ± 0.169	0.251 ± 0.288	0.328 ± 0.254
σ^2_{SCA} ± SE	0.261 ± 0.059	0.985 ± 0.216	2.311 ± 0.519	3.697 ± 0.789	2.383 ± 0.521
σ^2_A ± SE	0.358 ± 0.050 (25)	1.342 ± 0.185 (25)	0.459 ± 0.169 (7)	1.006 ± 0.288 (6)	1.314 ± 0.254 (12)
σ^2_E ± SE	0.021 ± 0.009	0.049 ± 0.022	0.175 ± 0.024	0.087 ± 0.012	0.115 ± 0.016
σ^2_w ± SE	0.129 ± 0.009	0.416 ± 0.031	0.603 ± 0.014	0.523 ± 0.012	1.542 ± 0.036
σ^2_{Ph}	0.372	1.370	2.601	4.036	2.826
$\sigma^2_{SCA}/\sigma^2_{GCA}$	2.9	2.9	20.1	14.7	7.2
Open-pollinated progeny					
σ^2_A ± SE	0.021 ± 0.040 (87)	0.231 ± 0.126 (93)	0.563 ± 0.283 (95)	0.354 ± 0.179 (62)	0.871 ± 0.179 (50)
σ^2_F	0.005 ± 0.010	0.058 ± 0.032	0.141 ± 0.071	0.089 ± 0.045	0.218 ± 0.045
σ^2_E	0.004 ± 0.002	0.194 ± 0.086	0.448 ± 0.140	0.457 ± 0.087	1.428 ± 0.155
σ^2_{Ph}	0.024	0.247	0.592	0.573	1.730

Tab. S3 - Regression equations and associated R^2 values for bud flushing with geographic and climatic parameters of the parental location of origin. CC-II-2012 = the bud flushing score in the full-sib progeny of the second evaluation in the year 2012, OP-II-2012 = the bud flushing score in the open-pollinated progeny of the second evaluation in the year 2012, LAT = latitude, LONG = longitude, ALT = elevation, TMA = mean annual temperature, PMA = mean annual precipitation.

Dependent variable	**R^2**	**$p < 0.05$**	**Equations**
CC-II-2012	0.84	*	-112.21 + 1.21LAT + 1.28LONG - 0.01ALT + 1.58TMA + 0.26PMA
OP-II-2012	0.97	*	10.84 - 0.12LAT - 0.13LONG + 0.01ALT