Appendices from *In situ* estimation of genetic variation of functional and ecological traits in *Quercus petraea* and *Q.robur*

Hermine Alexandre[1], Laura Truffaut[1], Alexis Ducousso[1], Jean-Marc Louvet[1], Gérard Nepveu[2],
José Torres-Ruiz[1,3], Frédéric Lagane[1], Cyril Firmat[1,4], Brigitte Musch[5]
Sylvain Delzon[1], Antoine Kremer[1]

[1]BIOGECO, INRA, Univ. Bordeaux, 33610 Cestas, France

[2]UMR SILVA, INRA, 54280 Champenoux, France

[3]PIAF, Univ. Clermont-Auvergne, INRA, 63000 Clermont-Ferrand, France

[4]UFP3F, INRA, 86600 Lusignan, France

[5]BIOFORA, INRA, ONF, CS 40001 Ardon, 45075 Orléans Cedex 2, France

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Appendix 1

Study populations and pedigree relationship between G2 and G1 in the in situ setting

The study population consists in a mixed oak stand (*Q. petraea* and *Q. robur*) of natural origin located the Petite Charnie State Forest (Latitude: 48.086 N; Longitude: 0.168 W) located in the North West of France. This stands is part of a long term experiment aiming at monitoring ecological and evolutionary processes in oak forests. Our study entails now two successive generations. To sum up the history of the investigations, the long term study started when a seed cut was practiced in 1989 leaving on ground 422 trees (196 *Q. petraea* and 226 *Q. robur*), about 90 to 100 years old.

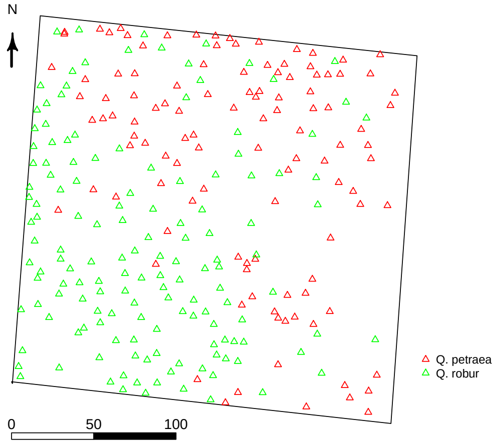


Figure 1.1: Geographic position over the forest stand of G1 trees. *Q. petraea* individuals are in red and *Q. robur* in green, scale represents distance in meters.

The seed cut was followed by two additional thinnings and a final cut was practiced in 1998-2001. The adult trees composing the stand from 1989 to 2001 correspond to our generation G1 (identified as cohort 1 in Truffaut et al. (2017)). The final clear cut of the 298 remaining trees was done over three years (1999, 2000 and 2001) to ease the harvest and manipulation of log samples for later wood and anatomical assessments. In between 1989 and 2001, as the canopy was opened by successive thinnings, seeds originating from open pollination among the remaining adult trees germinated and developed into saplings. Recruitment was quite successful resulting into a total number of about 11 000 saplings in *Q. robur* and 30 000 in *Q. petraea* (Truffaut et al. (2017), table 3) as assessed in 2014 when a demographic inventory was achieved. This sapling population constitutes generation G2 (cohort 2 in Truffaut et al. (2017)), which was 14 to 26 years old when our investigation started in summer 2014. At that time, a sampling of 2510 saplings was made in G2 corresponding to the systematic collection of one sapling every 3 to 6 m.

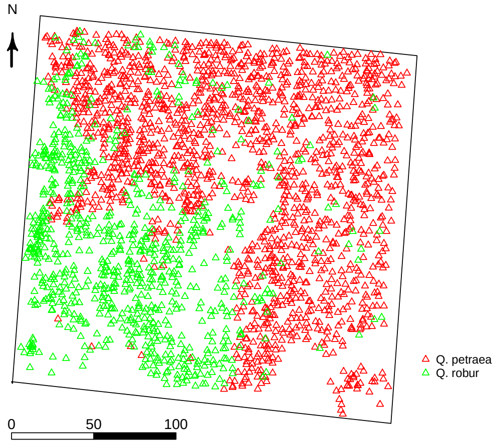


Figure 1.2: Geographic position over the forest stand of each genotyped G2 tree. *Q. petraea* individuals are in red and *Q. robur* in green, scale represents distance in meters.

A parentage analysis was conducted to assign parent offspring relationships between G1 and G2 (Truffaut et al., 2017) based on 80 SNP loci, and using CERVUS v.3.0.7 (Marshall et al., 1998) with stringent parameters, assuming no errors in genotyping (a strict exclusion analysis: 0.0 error rate) and a high confidence level (95%). The parentage analysis showed that a very few number of adult trees did not contribute to the next generation (10 *Q. robur* and 3 *Q. petraea*). For 122 of *Q. petraea* and 193 saplings of *Q. robur* the two parents could be assigned and one parent only for 636 *Q. petraea* saplings and 443 *Q. robur* saplings (Table 1.1). However oaks being monoecious it was not possible to separately assign the male or female parentage.

Based on the parentage analysis we identified a set of saplings for phenotypic assessments in G2 as a sample for estimating heritability *in situ* in G2 (M3 design, Figure 2). This set comprised offspring belonging to all full sib (FS) families detected in G2, e.g. saplings for which the two parents were found within G1, and all half sib families for which the identified parent was also parent of at least one full sib family (Table 1.2).

Table 1.1: Results of the parentage analysis conducted in G2, according to (Truffaut et al., 2017)

	Q. petraea	***Q. robur***
Generation G1		
Total number of G1 parental trees	110	135
Number of G1 trees which generated at least one offspring	107 (97.3%)	125 (92.6%)
Generation G2		
Total number of G2 saplings sampled	1570	820
Number of offspring assigned to two parents	122 (7.8%)	193 (23.5%)
Number of offspring assigned to only one parent	636 (40.5%)	443 (54.0%)
Number of offspring assigned to no parent	811 (51.7%)	183 (22.3%)
Mean number of offspring per parental tree *	8.1	6.2

Table 1.2: Breakdown of sample sizes of full and half sib families used for heritability estimation in G2 (M3 design)

	Q. petraea	***Q. robur***
Number of full sib families	89	148
Mean number of offspring/ full sib family	1.24	1.18
Number of half sib families	80	85
Mean number of offspring/ full sib family	3.24	2.54
Number of parents	[illegible]	df
Total sample size	370	390

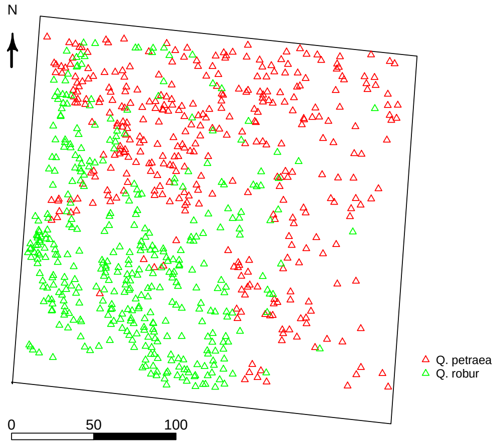


Figure 1.3: Geographic position over the forest stand of each G2 tree phenotyped at least once. *Q. petraea* individuals are in red and *Q. robur* in green, scale represents distance in meters.

Appendix 2

Open pollinated progeny test and pedigree relationships of *Quercus petraea* and *Quercus robur* used for *ex situ* estimation of heritability (M6 and M7 method)

In the fall 1995, acorns were collected on 23 *Q. petraea* and 28 *Q. robur* randomly sampled trees of the parental generation (G1) in parcel 26 of the Petite Charnie State Forest. Acorns were sown in the spring 1996 at the State Nursery of Guéméné Penfao (~~tude: 47.6288 N; Longitude: 1.8492 W)~~ located in the North West of France about 150 km West of the Petite Charnie Forest. Two years later in march 1998, seedlings of *Q. petraea* and *Q. robur* were transplanted back in Petite Charnie forest in parcel 37. Parcel 37 is located about 600 meters South of parcel 26 (Figure 2.1).

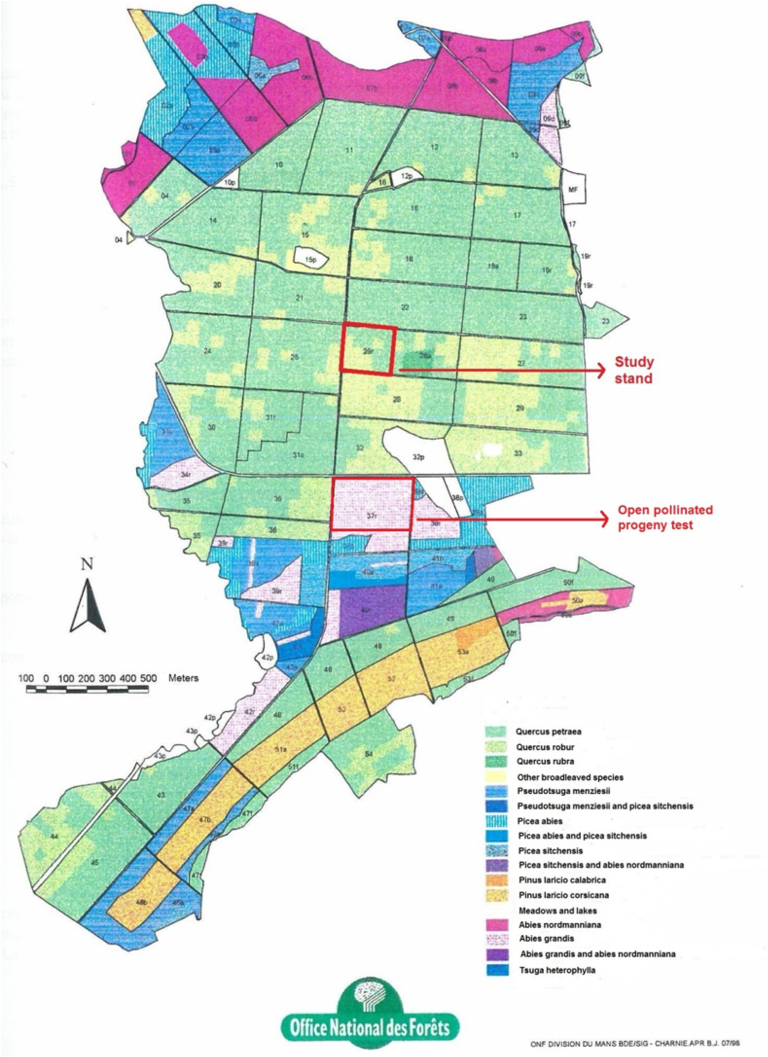


Figure 2.1: Geographic location of the study stand and the open pollinated progeny test

Two separate contiguous progeny trials were installed for *Q. petraea* and *Q. robur* according to a randomized incomplete block design. Each incomplete block comprised 7 open pollinated (OP) progeny plots, and plots comprised 6 OP trees (Table 2.1). When the plantation was made, offsprings of a given progeny were assumed to be half sibs (known female parents, unknown male parents).

In 2009, buds and leaves were harvested on all living trees of the plantation (3512 still living trees, 93% survival) for DNA extraction and genotyping with 12 microsatellites (Lagache et al., 2013, 2014). A parentage analysis, assuming no errors in genotyping (a strict exclusion analysis: 0.0 error rate) and a high confidence level (95%), was implemented to assign parents to the offspring, using CERVUS v.3.0.7 (Marshall et al. (1998), Table 2.2). Male parents were identified for 42% and 43% of the offspring of *Q. petraea* and *Q. robur*, while all female parents were confirmed by parentage analysis (Lagache et al., 2013, 2014).

Additive variances of the different phenotypic traits were estimated on the subset of 641 and 982 *Q. petraea* and *Q. robur* offspring for which male parents of G1 were identified by parentage analysis.

Table 2.1: Description of the experimental design of the two progeny tests

	Q. petraea	***Q. robur***
Number of OP families	23	28
Number of blocks	36	54
Number of OP families/block	7	7
Number of trees/plot	6	6
Total number of trees/OP family	18 to 108	18 to 44
Total number of trees	1512	2262

Table 2.2: Statistics of the parentage analysis condcuted in the open pollianted progeny tests

	Q. petraea	***Q. robur***
Number of offspring with recovered male parent (%)	641 (42%)	982 (43%)
Number of male parents contributing to the offspring	78	129
Average number of offspring/male parent	8.23	7.61
Number of female parents contributing to the offspring	23	28
Average number of offspring/ female parent	66	81

Appendix 3

Assessment of resilience components based on ring width analysis ~~Data~~

Resilience components are based on the response of tree ring width during and after so called ”negative pointer years”, where growth was substantially lower to previous years (Lloret et al., 2011). Ring widths of the 298 trees were measured [illegible] the felling of the trees at the final cut. Assessments were made over the whole age of the trees (about 100 years old). 112 trees were felled and measured in 1999, 126 in 2000 and 60 in 2001. Ring width measurements were performed on a stem section cut on the main stem at 1.30 meter from the ground level. Ring width assessments were made later in the lab on 4 [illegible]~~us~~ along the cardinal points. In what follows, we used mean values over the 4 [illegible]~~us.~~

Identification of negative pointer years

To identify negative pointer years we used the method based on relative growth change, initially proposed by Schweingruber et al. (1998). This method compares tree growth in a particular year to the average growth during a given number of preceding years. A calendar year was considered as a negative pointer year when at least 75% of the trees exhibited growth width 20% lower (for negative pointer year or higher for positive pointer year) than the mean of the three previous years. Computations were done within each species, given that the two species *Q.petraea* and *Q.robur* are known to respond differently to the climate (Arend et al., 2013). Admixed trees were not taken into account due to the very low number of individuals. Finally, the computations were done on 121 *Q.petraea* and 164 *Q.robur* for a total number of 285 individuals. Species assignment was based on SNP data and morphological traits (Truffaut et al., 2017). We found 7 negative pointer years in *Q. petraea* and 10 in *Q. robur* (Table 3.1).

Estimation of resilience components

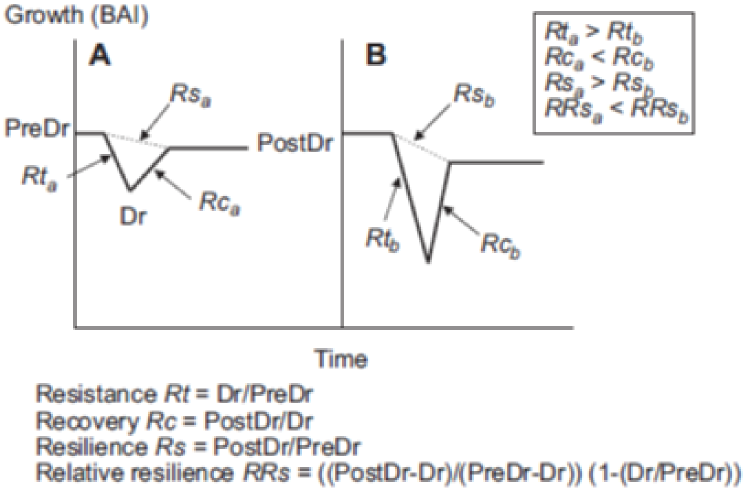
Four resilience components were estimated (Lloret et al. (2011); see figure below)

- The component ’resistance’ (inverse of growth reduction during the episode), is conceptually identical to ’abrupt growth changes’ as described in Schweingruber et al. (1998).
- ’Recovery’ (increased growth relative to the minimum growth during the episode) is the ability of tree growth to recover after disturbance.

Table 3.1: Pointer years

height	***Q. petraea***	***Q. robur***
Negative pointer years	1921	1921
	1932	1922
	1941	1932
	1952	1952
	1954	1953
	1976	1954
	1996	1974
		1976
		1990
		1996

- 'Resilience' reflects the ability of trees to reach pre-disturbance growth levels (Scheffer et al., 2001; Folke et al., 2004).
- 'Relative resilience' is resilience weighted by the damage incurred during the episode.



Resistance Rt = Dr/PreDr
Recovery Rc = PostDr/Dr
Resilience Rs = PostDr/PreDr
Relative resilience RRs = ((PostDr-Dr)/(PreDr-Dr)) (1-(Dr/PreDr))

Figure 3.1: Illustration of resilience components according to Lloret et al. (2011)

To estimate components of resilience we used the package pointRes (Van der Maaten-Theunissen et al., 2015) in the R statistical suite (R Core Team, 2016). For the calculation of resilience components, we consider pre-disturbance (PreDr) and post-disturbance (PostDr) period as the average of the ring width 3 years before and after the disturbance. In order to define the lag of the pre or post disturbance period, we calculated the different resilience components by varying the lag from 2 to 5 years. We then considered the correlation matrix between the values obtained for the components in successive years and then decided on the lag period when the matrix exhibited mostly positive values. The final lag of 3 years was also used in other applications of the method (Merlin et al., 2015).

To avoid overlap between the pre- or post-disturbance period and adjacent drought events we decided to use the pre- and post-disturbance period before and after the adjacent events. For instance, the post-disturbance period for 1952 and the pre-disturbance period for 1954 overlap, so we use the 1954 post-disturbance period to calculate the 1952 indices and the 1952 pre-disturbance period for the 1954 indices.

We calculate resilience components on 3 periods corresponding to 3 different stages of tree development:

- Juvenile stage (20-30 years)
- Middle age stage (30-60 years)
- Mature stage (older than 60 years)

For *Q.petraea* (121 trees):

- Resilience components for juvenile stage corresponding to the average of years 1921 and 1932 (except for 3 trees without data on 1921)
- Resilience components for middle age stage corresponding to the average of years 1952 and 1954
- Resilience components for mature stage corresponding to the average of years 1976 and 1996 (except for 33 trees without data in 1996)

For *Q.robur* (164 trees):

- Resilience components for juvenile stage corresponding to the average of years 1921 and 1922 (except for 4 trees without data in 1921)
- Resilience components for middle age stage corresponding to the average of years 1952, 1953 and 1954.
- Resilience components for mature stage corresponding to the average of years 1976 and 1996 (except for 46 trees without data in 1996). We did not take the average between 1990 and 1996 because resistance and resilience indices were not correlated between these two years, whereas for 1976 and 1996 all the indices were positively correlated.

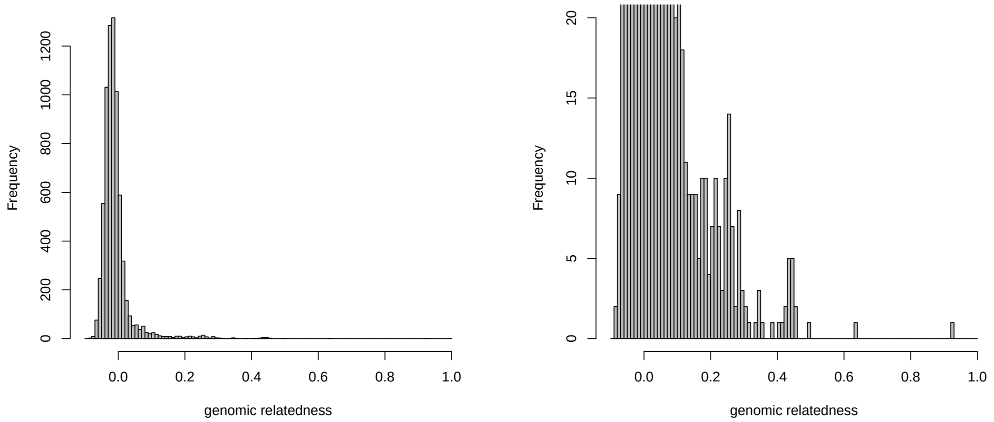
Appendix 4

Distribution and variance of genomic relatedness among individuals in both species

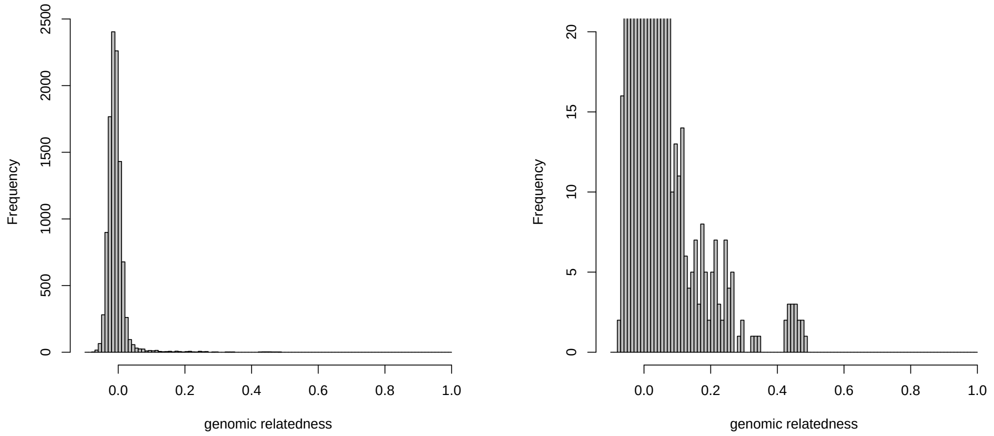
In a companion paper, relatedness among all pairs of individuals in the G1 population were calculated for a subset of markers corresponding to different MAF thresholds (Lesur et al., 2018). We report here the variances of relatedness corresponding to the different thresholds together with the resulting number of markers (Table 4.1). We also illustrate the distribution of pairwise relatedness with a close up on the tails with the larger values (Figure 4.1)

Table 4.1: Variance of genomic relatedness within each species depending on the MAF threshold used to select markers. var(G) is the variance of relatedness and n is the number of markers corresponding to each MAF threshold.

MAF threshold	***Q. petraea***		***Q. robur***	
	var(G)	n	var(G)	n
1%	0.002247	32047	0.000978	33131
5%	0.002455	15274	0.001067	16408
10%	0.002532	9502	0.001143	10225
15%	0.002613	6753	0.001211	7143
30%	0.002870	2849	0.001447	3058
40%	0.003286	1454	0.001825	1561



(a) *Q. petraea* (b) *Q. petraea* zoom in



(c) *Q. robur* (d) *Q. robur* zoom in

Figure 4.1: Distribution of genomic relatedness computed with SNPs selected at MAF>5% for *Q. petraea* and *Q. robur*. Figures (a) and (c) are the distribution of relatedness of all individuals whereas Figures (b) and (d) are the right tails of the distribution (zoomed for classes with less that 20 occurences).

Appendix 5

Summary of Variance decomposition in both species

Table 5.1: Variance estimates for *Q. petraea*. mth : the method as described in main text Figure 2 with which the trait was analysed; μ: mean of the model fitted values; V_p : observed inter-individual phenotypic variance; V_a: additive genetic variance; V_{sp}: variance of the spatial effects, when included in the model; h^2_{obs}: Heritability computed with the observed phenotypic variance; h^2_{calc}: Heritability computed with the phenotypic variance estimated from the model; I_a: Evolvability; spt : ΔAIC between full model and model without spatial effect (a positive value represent a better fit of the model with a spatial effect); add: ΔAIC between full model and model without additive effect (a positive value represent a better fit of the model with an additive effect). (exp) stands for traits with an exponential distribution. Numbers in brackets represent the 95% CI obtained from 1000 simulation bootstraps.

trait	mth	μ	V_p	V_a	V_{sp}	h^2_{obs}	h^2_{calc}	I_a	spt	add
Growth										
CIRC	**M1**	**190.8261**	**948.387**	**734.5 [5.1396 - 1011.15]**	**60.77 [0.6089 - 275.905]**	**0.7745 [0.006 - 0.9371]**	**0.8455 [0.0059 - 0.9831]**	**0.0202 [1e-04 - 0.0279]**	**-1.5874**	**2.3397**
CIRC	M3	33.5739	164.7723	21.09 [0.2647 - 71.5678]	10.19 [0.0906 - 29.1438]	0.128 [0.0017 - 0.4289]	0.1306 [0.0017 - 0.4229]	0.0187 [2e-04 - 0.0625]	2.2369	-1.3922
CIRC	M4	33.5739	164.7723	19.45 [0.3496 - 73.7567]	10.6 [0.1078 - 30.7925]	0.118 [0.0024 - 0.4548]	0.1202 [0.0024 - 0.4481]	0.0173 [3e-04 - 0.0649]	2.6211	-1.4067
CIRC	M5	70.8102	4817.4703	4.489 [0.7363 - 63.754]	20.11 [0.1493 - 57.955]	9e-04 [0.0022 - 0.1788]	0.0121 [0.0021 - 0.1736]	9e-04 [1e-04 - 0.0132]	2.9095	-1.9661
CIRC	**M6**	**147.8302**	**5340.1252**	**686 [157.4975 - 1472.225]**	**1353 [696.155 - 2130.8]**	**0.1285 [0.0305 - 0.2624]**	**0.1264 [0.0303 - 0.256]**	**0.0314 [0.0072 - 0.0698]**	**-**	**10.994**
CIRC	**M7**	**147.8302**	**5340.1252**	**713.5 [153.8975 - 1423.075]**	**1342 [716.8925 - 2176.125]**	**0.1336 [0.0285 - 0.2574]**	**0.1314 [0.0279 - 0.2529]**	**0.0326 [0.0069 - 0.0656]**	**-**	**9.9973**
HGHT	**M1**	**2655.2174**	**24960.9412**	**20950 [149.0975 - 27211]**	**1097 [16.5505 - 5900.75]**	**0.8393 [0.0075 - 0.9426]**	**0.9089 [0.0075 - 0.9845]**	**0.003 [0 - 0.0039]**	**-1.7727**	**0.7856**
HGHT	**M3**	**1120.307**	**59533.7031**	**14110 [1769.125 - 27491]**	**25090 [9484.975 - 48154.25]**	**0.237 [0.0288 - 0.4772]**	**0.2201 [0.0284 - 0.4411]**	**0.0112 [0.0013 - 0.0241]**	**48.0909**	**3.2197**
HGHT	**M4**	**1120.307**	**59533.7031**	**17280 [4138.775 - 31803.25]**	**24720 [9035.8 - 45640.25]**	**0.2903 [0.0658 - 0.5666]**	**0.2697 [0.0618 - 0.5162]**	**0.0138 [0.0031 - 0.0271]**	**44.5944**	**5.1395**
HGHT	M5	1453.5584	452521.6554	317.3 [141.6525 - 7095.975]	9744 [2627.625 - 19271.75]	7e-04 [0.0032 - 0.1515]	0.0064 [0.0031 - 0.1466]	2e-04 [1e-04 - 0.0035]	35.1047	-2.094
HGHT	**M6**	**620.7132**	**36857.5347**	**7321 [2886.7 - 12680]**	**14270 [7944.75 - 23640.25]**	**0.1986 [0.0796 - 0.3303]**	**0.1942 [0.0783 - 0.3255]**	**0.019 [0.0075 - 0.0335]**	**-**	**48.4126**
HGHT	**M7**	**620.7132**	**36857.5347**	**7748 [2994.225 - 13670.25]**	**14220 [8364.625 - 21672]**	**0.2102 [0.081 - 0.3611]**	**0.205 [0.0809 - 0.3509]**	**0.0201 [0.0074 - 0.0367]**	**-**	**47.3424**
RSURF	**M1**	**2631.6727**	**748389.0774**	**477600 [12766.75 - 576905]**	**9251 [431.015 - 96566.5]**	**0.6382 [0.0171 - 0.7709]**	**0.3804 [0.0117 - 0.5217]**	**0.069 [0.0019 - 0.0879]**	**-2.0347**	**1.7635**
RSURF	M3	448.7549	92647.5562	4882 [1349.225 - 5938.125]	7260 [2447.5 - 13130.5]	0.0527 [0.0146 - 0.0641]	0.0228 [0.01 - 0.0646]	0.0242 [0.0063 - 0.0457]	1.6351	-1.9839
RSURF	M4	448.7549	92647.5562	2724 [530.56 - 3450.125]	7468 [2676.65 - 12962.25]	0.0294 [0.0057 - 0.0372]	0.0127 [0.004 - 0.0352]	0.0135 [0.0025 - 0.0247]	2.0346	-2.087
RSURF	M5	1846.6697	1600417.138	9663 [3700.875 - 10791.75]	6548 [1619 - 13712.25]	0.006 [0.0023 - 0.0067]	0.0021 [8e-04 - 0.0027]	0.0028 [0.001 - 0.0039]	-0.2673	-2.1721
RWDTH	**M1**	**2.8833**	**0.1973**	**0.1551 [0.0058 - 0.1874]**	**0.0014 [2e-04 - 0.0316]**	**0.786 [0.0295 - 0.9497]**	**0.1914 [0.008 - 0.2462]**	**0.0187 [7e-04 - 0.0234]**	**-2.0624**	**2.6609**
RWDTH	M3	2.7274	0.833	0.0196 [0.0021 - 0.0286]	0.0542 [0.0175 - 0.1046]	0.0236 [0.0025 - 0.0344]	0.0167 [0.0046 - 0.0722]	0.0026 [3e-04 - 0.0041]	2.8253	-2.0643
RWDTH	M4	2.7274	0.833	0.0178 [0.0019 - 0.0285]	0.0544 [0.0171 - 0.1013]	0.0214 [0.0023 - 0.0342]	0.0151 [0.0044 - 0.0702]	0.0024 [3e-04 - 0.0039]	2.8154	-2.0566
RWDTH	M5	2.8256	0.4297	0.018 [0.0073 - 0.0227]	0.0289 [0.0105 - 0.0525]	0.0418 [0.017 - 0.0528]	0.013 [0.0092 - 0.0313]	0.0022 [9e-04 - 0.0029]	1.4616	-2.0645
R success										
NOFF	**M1**	**8.7191**	**81.1361**	**66.83 [0.9449 - 90.22]**	**14.77 [0.1413 - 42.2218]**	**0.8237 [0.011 - 0.9238]**	**0.7829 [0.0107 - 0.977]**	**0.8791 [0.0151 - 2.2972]**	**1.0722**	**0.6427**
Phenology										
LUs	**M2**	**2.4219**	**1.3245**	**1.12 [0.0585 - 1.3872]**	**0.1934 [6e-04 - 0.6535]**	**0.8456 [0.0442 - 1.0474]**	**0.8465 [0.0481 - 0.9825]**	**0.1909 [0.0093 - 0.2966]**	**-**	**16.0096**
LUs	**M3**	**4.0449**	**1.9337**	**1.038 [0.3551 - 1.7991]**	**0.2248 [0.0194 - 0.5622]**	**0.5368 [0.1836 - 0.9304]**	**0.5392 [0.2011 - 0.8699]**	**0.0634 [0.0216 - 0.116]**	**2.158**	**8.0346**
LUs	**M4**	**4.0449**	**1.9337**	**0.9667 [0.2603 - 1.72]**	**0.2078 [0.0073 - 0.527]**	**0.4999 [0.1346 - 0.8895]**	**0.5073 [0.1453 - 0.8495]**	**0.0591 [0.0157 - 0.11]**	**2.2363**	**8.1052**
LUs	**M6**	**2.2461**	**1.142**	**0.3584 [0.2747 - 0.4504]**	**0.2008 [0.103 - 0.3108]**	**0.3138 [0.2405 - 0.3944]**	**0.302 [0.2385 - 0.3695]**	**0.071 [0.0505 - 0.0988]**	**-**	**188.7006**
LUs	**M7**	**2.2461**	**1.142**	**0.3547 [0.2685 - 0.4477]**	**0.2014 [0.1082 - 0.3244]**	**0.3106 [0.2351 - 0.392]**	**0.2997 [0.2336 - 0.3658]**	**0.0703 [0.0496 - 0.0992]**	**-**	**190.5778**
Lud	**M2**	**105.5218**	**22.7381**	**19.55 [0.5471 - 24.4108]**	**1.6567 [0.004 - 7.7655]**	**0.8598 [0.026 - 0.9508]**	**0.9138 [0.0241 - 0.9881]**	**-**	**-**	**20.5593**
LS	**M2**	**305.7786**	**15.3089**	**12.66 [0.3094 - 16.05]**	**1.7025 [0.0063 - 5.8742]**	**0.827 [0.019 - 0.8977]**	**0.8714 [0.0197 - 0.9793]**	**-**	**-**	**3.4352**
GSL	**M2**	**200.2139**	**34.7263**	**28.38 [0.4559 - 35.8205]**	**4.545 [0.01 - 17.9061]**	**0.8172 [0.0139 - 0.9388]**	**0.8537 [0.0145 - 0.9856]**		**-**	**10.9387**
FFLW	M1	123.214	47.5872	14.03 [0.1188 - 27.056]	0.2001 [0.0115 - 8.4535]	0.2948 [0.0025 - 0.5686]	0.9547 [0.0189 - 0.9786]	-	-2.0127	-0.7387
MFLW	**M1**	**120.1784**	**35.043**	**16.25 [0.2459 - 23.177]**	**0.1015 [0.0123 - 5.5061]**	**0.4637 [0.007 - 0.6614]**	**0.9826 [0.0173 - 0.9841]**	**-**	**-2.0344**	**5.2571**
MAR	M1	0.7917	2.293	0.2048 [1e-04 - 0.9147]	0.0011 [0 - 0.1593]	0.0893 [1e-04 - 0.9216]	0.2191 [1e-04 - 0.9634]	0.3268 [2e-04 - 1.6089]	-2.0465	-1.8562
Physiology										
C	M2	455.3283	785.3835	183.8 [0.0992 - 752.3275]	-	0.234 [1e-04 - 0.9187]	0.2357 [1e-04 - 0.9582]	9e-04 [0 - 0.0036]	-	-1.9429
C	M3	459.0698	593.9026	4.096 [0.2437 - 180.8725]	35.42 [0.0127 - 101.5075]	0.0069 [5e-04 - 0.2948]	0.0067 [5e-04 - 0.2969]	0 [0 - 9e-04]	0.5036	-2.0228
C	M4	459.0698	593.9026	5.062 [0.2049 - 171.8225]	35.09 [0.0117 - 111.1825]	0.0085 [4e-04 - 0.2838]	0.0083 [4e-04 - 0.2785]	0 [0 - 8e-04]	0.2749	-2.0167
C.N	M2	24.3475	12.5891	1.311 [0.0014 - 11.3413]	-	0.1041 [1e-04 - 0.9062]	0.1046 [1e-04 - 0.9447]	0.0022 [0 - 0.0192]	-	-1.9591
C.N	M3	19.3065	4.5348	0.4714 [0.0171 - 1.9514]	0.7118 [0.0798 - 1.6911]	0.104 [0.004 - 0.4212]	0.0992 [0.0039 - 0.4137]	0.0013 [0 - 0.0053]	14.7864	-1.7479
C.N	M4	19.3065	4.5348	0.5976 [0.0193 - 1.9458]	0.7137 [0.0866 - 1.717]	0.1318 [0.0045 - 0.4177]	0.1256 [0.0044 - 0.4087]	0.0016 [1e-04 - 0.0052]	14.29	-1.6342
d13C	M2	-29.6116	1.304	0.0763 [1e-04 - 1.0911]	-	0.0585 [1e-04 - 0.8374]	0.0587 [1e-04 - 0.8725]	1e-04 [0 - 0.0012]	-	-1.9814
d13C	**M3**	**-29.5366**	**1.069**	**0.3796 [0.0523 - 0.796]**	**0.1343 [0.0061 - 0.3119]**	**0.3551 [0.0509 - 0.7148]**	**0.3523 [0.0485 - 0.6779]**	**4e-04 [1e-04 - 9e-04]**	**2.7839**	**3.0466**
d13C	**M4**	**-29.5366**	**1.069**	**0.4632 [0.1123 - 0.8959]**	**0.116 [0.0053 - 0.2967]**	**0.4333 [0.1111 - 0.8432]**	**0.433 [0.1074 - 0.8202]**	**5e-04 [1e-04 - 0.001]**	**1.3399**	**5.2009**
d15N	**M2**	**-3.3505**	**1.8222**	**1.574 [0.0056 - 2.109]**	**-**	**0.8638 [0.0035 - 0.9487]**	**0.8808 [0.0035 - 0.9886]**	**0.1402 [5e-04 - 0.1922]**	**-**	**0.8272**
d15N	**M3**	**-6.4981**	**0.8863**	**0.1647 [0.0124 - 0.3822]**	**0.6586 [0.2337 - 1.1541]**	**0.1858 [0.0124 - 0.4227]**	**0.1402 [0.0112 - 0.3761]**	**0.0039 [3e-04 - 0.0096]**	**60.2578**	**0.4112**
d15N	M4	-6.4981	0.8863	0.1056 [0.0077 - 0.3097]	0.6522 [0.2844 - 1.1511]	0.1191 [0.0079 - 0.3077]	0.0906 [0.0072 - 0.2692]	0.0025 [2e-04 - 0.0076]	60.6673	-0.9627
N	M2	19.0384	6.3556	0.8565 [7e-04 - 5.8692]	-	0.1348 [1e-04 - 0.9018]	0.1355 [1e-04 - 0.9449]	0.0024 [0 - 0.0163]	-	-1.9491
N	M3	24.0214	6.9429	0.2496 [0.0021 - 2.2862]	0.379 [1e-04 - 1.1774]	0.036 [3e-04 - 0.3107]	0.0353 [3e-04 - 0.3079]	4e-04 [0 - 0.004]	2.4782	-1.9535

N	M4	24.0214	6.9429	0.6083 [0.009 - 2.7276]	0.3926 [0.0015 - 1.206]	0.0876 [0.0014 - 0.3909]	0.0857 [0.0014 - 0.3872]	0.0011 [0 - 0.0047]	2.5239	-1.7577
SLA	M2	11.719	5.2619	9e-04 [5e-04 - 4.2129]	-	2e-04 [1e-04 - 0.8532]	2e-04 [1e-04 - 0.8677]	0 [0 - 0.0309]	-	-2.001
SLA	**M3**	**13.3166**	**12.0123**	**4.154 [0.2895 - 8.9597]**	**1.107 [0.0411 - 2.9817]**	**0.3458 [0.0239 - 0.7163]**	**0.3365 [0.0229 - 0.6885]**	**0.0234 [0.0016 - 0.0499]**	**4.8645**	**1.4142**
SLA	**M4**	**13.3166**	**12.0123**	**3.673 [0.2566 - 8.625]**	**1.094 [0.0219 - 2.8908]**	**0.3058 [0.0224 - 0.671]**	**0.2983 [0.0208 - 0.6616]**	**0.0207 [0.0015 - 0.0482]**	**4.1966**	**1.0039**
MLA	M2	44.801	111.6555	53.39 [0.0182 - 117.325]	-	0.4782 [2e-04 - 0.9333]	0.4869 [2e-04 - 0.982]	0.0266 [0 - 0.0599]	-	-0.778
MLA	**M3**	**32.0433**	**77.5867**	**20.99 [0.1232 - 51.515]**	**0.0907 [0.0026 - 4.5686]**	**0.2705 [0.0018 - 0.627]**	**0.2696 [0.0018 - 0.6251]**	**0.0204 [1e-04 - 0.049]**	**-2.0696**	**2.081**
MLA	M4	32.0433	77.5867	13.56 [0.0248 - 39.502]	0.1071 [6e-04 - 4.3364]	0.1748 [3e-04 - 0.5126]	0.1739 [3e-04 - 0.5042]	0.0132 [0 - 0.0393]	-2.0616	-0.348
Resilience										
REC	M1	1.3393	0.0223	0 [0 - 0.0065]	4e-04 [0 - 0.0048]	0.0015 [1e-04 - 0.2922]	0.0788 [0.0167 - 0.9561]	0 [0 - 0.0037]	-1.9307	-2.0056
REL	M1	0.8509	0.0103	5e-04 [0 - 0.0031]	0.0014 [0 - 0.0042]	0.0464 [2e-04 - 0.2983]	0.2547 [0.0107 - 0.9488]	7e-04 [0 - 0.0042]	-0.3347	-1.8761
RET	M1	0.6647	0.0057	5e-04 [0 - 0.002]	0 [0 - 9e-04]	0.0854 [1e-04 - 0.354]	0.9533 [0.0187 - 0.968]	0.0011 [0 - 0.0047]	-2.0092	-1.6311
Structure										
WD	M1	576.7698	886.685	417.4 [2.9645 - 875.3225]	173.6 [1.667 - 477.715]	0.4707 [0.0038 - 0.8906]	0.448 [0.0038 - 0.9222]	0.0013 [0 - 0.0027]	-0.959	-0.6863
WD	**M3**	**507.0777**	**1121.0502**	**443.2 [112.745 - 807.985]**	**268.5 [80.4813 - 559.4675]**	**0.3953 [0.1102 - 0.7261]**	**0.3883 [0.1077 - 0.6926]**	**0.0017 [4e-04 - 0.0032]**	**32.9723**	**5.0942**
WD	**M4**	**507.0777**	**1121.0502**	**492.1 [143.2675 - 838.0275]**	**255.5 [82.5705 - 527.9175]**	**0.439 [0.1317 - 0.7554]**	**0.43 [0.1357 - 0.7185]**	**0.0019 [5e-04 - 0.0033]**	**30.4821**	**3.9837**
WD	**M5**	**523.6702**	**1935.5673**	**481.8 [228.4975 - 760.4025]**	**-**	**0.2489 [0.2394 - 0.6761]**	**0.4577 [0.2398 - 0.672]**	**0.0018 [8e-04 - 0.0028]**	**-**	**29.1774**
Leaf morphology										
BS	**M1**	**3.9635**	**0.6307**	**0.4317 [0.0072 - 0.572]**	**0.0418 [4e-04 - 0.1781]**	**0.6844 [0.0114 - 0.9068]**	**0.9031 [0.0161 - 0.9853]**	**0.0275 [4e-04 - 0.0369]**	**-1.5294**	**6.0746**
HR	M1	3.3708	0.7707	0.0685 [8e-04 - 0.1128]	0.0018 [1e-04 - 0.0368]	0.0889 [0.0011 - 0.1464]	0.117 [0.0181 - 0.9782]	0.006 [1e-04 - 0.01]	-2.0416	-1.8682
LDR	M1	26.2344	31.5929	2.39 [0.0539 - 5.2668]	5.585 [0.7704 - 12.4017]	0.0757 [0.0017 - 0.1667]	0.095 [0.0083 - 0.7282]	0.0035 [1e-04 - 0.0076]	-0.4375	-1.978
LL	M1	92.5365	310.0745	50.02 [0.868 - 72.99]	25.86 [0.3115 - 64.003]	0.1613 [0.0028 - 0.2354]	0.1995 [0.0128 - 0.9459]	0.0058 [1e-04 - 0.0087]	-1.107	-1.7996
LW	M1	28.4354	40.2459	2.989 [0.0603 - 5.0841]	3.027 [0.0595 - 7.4134]	0.0743 [0.0015 - 0.1263]	0.0841 [0.0107 - 0.8963]	0.0037 [1e-04 - 0.0063]	-1.2125	-1.9517
LWR	M1	30.5788	11.3129	5.039 [0.0837 - 6.6942]	0.0272 [0.0034 - 1.2253]	0.4454 [0.0074 - 0.5917]	0.5172 [0.0165 - 0.9874]	0.0054 [1e-04 - 0.0071]	-2.0678	-0.7868
NL	**M1**	**11.2051**	**2.3663**	**1.846 [0.0355 - 2.3403]**	**0.0162 [0.0011 - 0.4235]**	**0.7801 [0.015 - 0.989]**	**0.978 [0.0209 - 0.9879]**	**0.0147 [3e-04 - 0.019]**	**-2.0121**	**2.7978**
NV	**M1**	**0.323**	**0.2549**	**0.1939 [0.0029 - 0.2566]**	**9e-04 [1e-04 - 0.045]**	**0.7607 [0.0113 - 1.0068]**	**0.9647 [0.0166 - 0.987]**	**1.8582 [0.0284 - 3.2702]**	**-2.0185**	**0.2139**
OB	M1	54.2075	21.6011	2.206 [0.0542 - 6.5899]	7.361 [0.4659 - 17.3665]	0.1021 [0.0025 - 0.3051]	0.225 [0.0074 - 0.697]	8e-04 [0 - 0.0023]	2.5572	-1.7428
PL	M1	16.9551	25.8648	0.2235 [0.0107 - 0.9484]	2.43 [0.5555 - 4.919]	0.0086 [4e-04 - 0.0367]	0.0098 [0.0046 - 0.3983]	8e-04 [0 - 0.0033]	-0.316	-2.0532
PR	M1	15.2147	9.1948	0.1273 [1e-04 - 0.407]	0.074 [0 - 0.3599]	0.0138 [0 - 0.0443]	0.0149 [0.0138 - 0.9627]	5e-04 [0 - 0.0017]	-2.008	-2.0375
PV	**M1**	**3.0765**	**31.5445**	**27.92 [0.5413 - 35.924]**	**0.2392 [0.0172 - 5.6771]**	**0.8851 [0.0172 - 1.1388]**	**0.9762 [0.0198 - 0.9877]**	**2.95 [0.053 - 5.4005]**	**-2.0164**	**1.1456**
SW	M1	20.6742	20.674	0.3935 [0.0081 - 1.1194]	1.445 [0.0225 - 3.271]	0.019 [4e-04 - 0.0541]	0.0209 [0.0068 - 0.7697]	9e-04 [0 - 0.0026]	-1.2963	-2.0273
WP	M1	50.3258	120.6494	55.56 [1.0239 - 76.1213]	9.1 [0.0703 - 31.2218]	0.4605 [0.0085 - 0.6309]	0.6686 [0.0157 - 0.9824]	0.0219 [4e-04 - 0.0302]	-1.2919	-0.7932
Defence										
CNFL (exp)	M1	0.7782	3.8295	0.0048 [2e-04 - 0.2036]	0.0584 [0 - 0.1622]	0.0121 [7e-04 - 0.6977]	0.0157 [7e-04 - 0.7051]	0.0048 [2e-04 - 0.2036]	2.564	-2.01
CSTG (exp)	M1	3.5445	23.8251	1e-04 [0 - 0.0147]	0.0016 [0 - 0.0064]	0.0034 [2e-04 - 0.8427]	0.0036 [2e-04 - 0.8572]	1e-04 [0 - 0.0147]	-1.3323	-2.0219
CSTL (exp)	M1	0.275	1.1465	1e-04 [0 - 0.2349]	0 [0 - 0.0535]	3e-04 [1e-04 - 0.7069]	3e-04 [1e-04 - 0.7276]	1e-04 [0 - 0.2349]	-2.0006	-2.0009
CWSK (exp)	**M1**	**1.0311**	**54.4825**	**1.529 [0.001 - 2.7502]**	**0.0084 [1e-04 - 0.479]**	**0.1219 [1e-04 - 0.2756]**	**0.1493 [1e-04 - 0.3011]**	**1.529 [0.001 - 2.7502]**	**-2.0604**	**0.8847**
EGNL (exp)	M1	-1.2847	0.4896	0.0305 [1e-04 - 1.0222]	5e-04 [0 - 0.2006]	0.0084 [1e-04 - 0.4794]	0.0146 [1e-04 - 0.4979]	0.0305 [1e-04 - 1.0222]	-2.0068	-2.0111
ELAC (exp)	M1	0.6114	1.4765	0.1354 [1e-04 - 0.2986]	7e-04 [0 - 0.0433]	0.4049 [2e-04 - 0.8256]	0.4476 [2e-04 - 0.8673]	0.1354 [1e-04 - 0.2986]	-2.0622	-0.0089
ELTOT (exp)	M1	3.4654	261.8303	1e-04 [0 - 0.1629]	0 [0 - 0.034]	3e-04 [1e-04 - 0.7706]	3e-04 [1e-04 - 0.7799]	1e-04 [0 - 0.1629]	-2.0006	-2.0009
GRDN	M1	8.0904	9.1947	2.046 [0.0015 - 9.0711]	0.0203 [2e-04 - 1.6156]	0.2225 [2e-04 - 0.9266]	0.2222 [2e-04 - 0.9655]	0.0313 [0 - 0.1418]	-2.0442	-1.7102
MVL (exp)	M1	-0.1098	0.5417	1e-04 [0 - 0.3001]	1e-04 [0 - 0.0606]	1e-04 [1e-04 - 0.7283]	2e-04 [1e-04 - 0.7364]	1e-04 [0 - 0.3001]	-2.0006	-2.0009
PNTL (exp)	M1	-1.6259	0.018	0.0165 [0 - 0.238]	0.0141 [0 - 0.0788]	0.0404 [1e-04 - 0.7852]	0.056 [1e-04 - 0.804]	0.0165 [0 - 0.238]	-1.6178	-1.9896
ROBA (exp)	M1	1.5048	2.3083	0.0102 [4e-04 - 0.0678]	0.0412 [0.0047 - 0.0958]	0.0941 [0.0044 - 0.6617]	0.0914 [0.0043 - 0.6517]	0.0102 [4e-04 - 0.0678]	7.0827	-1.92
ROBB	M1	6.8903	5.7242	0.0498 [0.0023 - 4.3551]	0.9873 [4e-04 - 2.9472]	0.0087 [4e-04 - 0.7703]	0.0082 [4e-04 - 0.765]	0.001 [0 - 0.0951]	0.5364	-2.0164
ROBC (exp)	M1	1.7064	7.7695	0.006 [0 - 0.1215]	0.0199 [0 - 0.067]	0.032 [2e-04 - 0.7902]	0.0369 [2e-04 - 0.8021]	0.006 [0 - 0.1215]	-0.7547	-1.9922
ROBD	M1	8.6726	11.6933	1.44 [0.0016 - 11.3305]	0.0121 [2e-04 - 2.1233]	0.1231 [1e-04 - 0.9139]	0.1177 [1e-04 - 0.9456]	0.0191 [0 - 0.1537]	-2.0222	-1.9537
ROBE (exp)	M1	2.0943	5.447	9e-04 [1e-04 - 0.0527]	0.0193 [0 - 0.0526]	0.0105 [0.0018 - 0.7153]	0.0109 [0.0018 - 0.7139]	9e-04 [1e-04 - 0.0527]	3.8424	-2.0186
SYRG	M1	5.3094	6.4986	0.4608 [5e-04 - 3.9126]	0.0144 [1e-04 - 0.7443]	0.0709 [1e-04 - 0.9207]	0.1107 [1e-04 - 0.9626]	0.0163 [0 - 0.1421]	-2.0177	-1.9701
TWSK (exp)	M1	0.0692	38.728	1.405 [0.0085 - 2.853]	0.3487 [0.0015 - 1.205]	0.1016 [6e-04 - 0.2121]	0.0902 [6e-04 - 0.2317]	1.405 [0.0085 - 2.853]	-1.4833	-1.1858
VNL	M1	3.0451	2.5027	0.4337 [5e-04 - 1.8052]	0.2087 [1e-04 - 0.8111]	0.1733 [3e-04 - 0.8947]	0.2257 [3e-04 - 0.9307]	0.0468 [1e-04 - 0.2088]	-1.4977	-1.9173
VSCG	M1	18.1981	23.872	0.1925 [0.0024 - 20.232]	0.0012 [4e-04 - 4.877]	0.0081 [1e-04 - 0.8931]	0.0082 [1e-04 - 0.9064]	6e-04 [0 - 0.0638]	-1.9888	-2.0011
VSCL (exp)	M1	0.6366	4.2427	0.001 [0 - 0.2957]	0.0083 [0 - 0.0812]	0.0016 [1e-04 - 0.7322]	0.0025 [1e-04 - 0.7693]	0.001 [0 - 0.2957]	-1.8817	-2.0073
2PHL (exp)	M1	-2.1278	0.0072	0.0015 [0 - 0.2844]	0.015 [0 - 0.0877]	0.0029 [1e-04 - 0.7588]	0.0039 [1e-04 - 0.7791]	0.0015 [0 - 0.2844]	-1.858	-2.0087

Table 5.2: Variance estimates for *Q. robur*. mth : the method as described in main text Figure 2 with which the trait was analysed; μ: mean of the model fitted values; V_p : observed inter-individual phenotypic variance; V_a: additive genetic variance; V_{sp}: variance of the spatial effects, when included in the model; h^2_{obs}: Heritability computed with the observed phenotypic variance; h^2_{calc}: Heritability computed with the phenotypic variance estimated from the model; I_a: Evolvability; spt : ΔAIC between full model and model without spatial effect (a positive value represent a better fit of the model with a spatial effect); add: ΔAIC between full model and model without additive effect (a positive value represent a better fit of the model with an additive effect). (exp) stands for traits with an exponential distribution. Numbers in brackets represent the 95% CI obtained from 1000 simulation bootstraps.

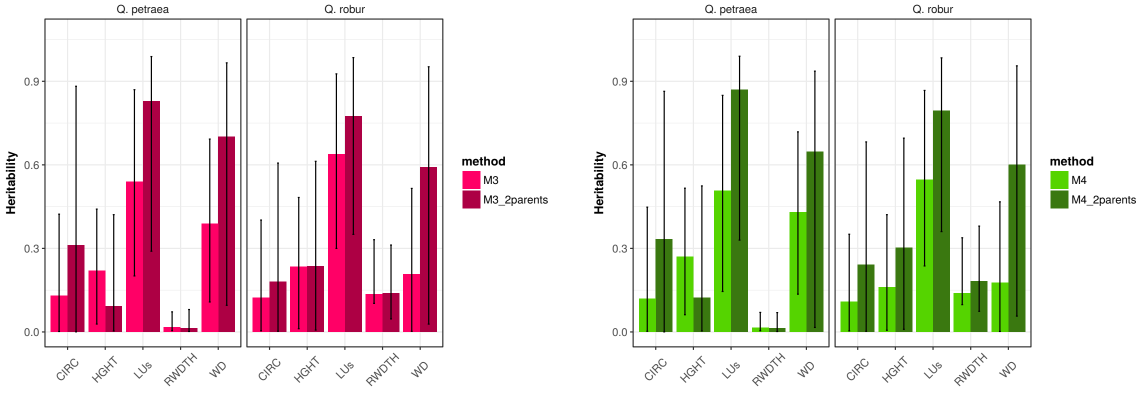
trait	mth	μ	V_p	V_a	V_{sp}	h^2_{obs}	h^2_{calc}	I_a	spt	add
Growth										
CIRC	M1	167.4394	554.8436	68.84 [0.881 - 425.6625]	77.27 [0.0893 - 223.4575]	0.1241 [0.0019 - 0.7982]	0.1308 [0.0019 - 0.8438]	0.0025 [0 - 0.0155]	0.1687	-1.9547
CIRC	M3	27.386	78.7278	9.051 [0.2835 - 30.491]	10.33 [1.2242 - 23.4105]	0.115 [0.0042 - 0.4097]	0.1233 [0.0042 - 0.4018]	0.0121 [4e-04 - 0.0416]	6.5267	-0.8949
CIRC	M4	27.386	78.7278	7.941 [0.2766 - 25.9303]	10.16 [1.5138 - 23.7812]	0.1009 [0.004 - 0.3657]	0.1084 [0.0039 - 0.3509]	0.0106 [3e-04 - 0.0352]	5.9601	-1.1618
CIRC	M5	69.727	4351.2221	19.43 [0.6732 - 63.071]	11.49 [0.1628 - 28.7048]	0.0045 [0.0032 - 0.2697]	0.0849 [0.0032 - 0.2693]	0.004 [1e-04 - 0.0131]	0.4691	-0.2909
CIRC	**M6**	**159.4237**	**5111.5907**	**827.4 [343.9225 - 1476.1]**	**470.6 [254.28 - 718.0225]**	**0.1619 [0.067 - 0.2757]**	**0.1606 [0.0668 - 0.2736]**	**0.0326 [0.013 - 0.0593]**	**-**	**34.895**
CIRC	**M7**	**159.4237**	**5111.5907**	**800.8 [280.975 - 1462.2]**	**474.5 [249.805 - 746.0275]**	**0.1567 [0.0568 - 0.2805]**	**0.1556 [0.0565 - 0.274]**	**0.0315 [0.0105 - 0.0567]**	**-**	**35.3801**
HGHT	M1	2518.4848	26338.5265	7525 [223.655 - 19331.75]	18000 [5160.775 - 35534.25]	0.2857 [0.0076 - 0.6516]	0.2081 [0.0071 - 0.6294]	0.0012 [0 - 0.0031]	13.6569	-1.2132
HGHT	**M3**	**943.4935**	**37848.1152**	**7360 [381.425 - 15770]**	**3603 [330.4475 - 8654.375]**	**0.1945 [0.0124 - 0.4939]**	**0.2347 [0.0116 - 0.4829]**	**0.0083 [4e-04 - 0.0176]**	**5.9275**	**2.1782**
HGHT	M4	943.4935	37848.1152	5088 [191.8975 - 12862.75]	4134 [856.8975 - 9055.1]	0.1344 [0.0063 - 0.4298]	0.1602 [0.006 - 0.4212]	0.0057 [2e-04 - 0.0144]	7.1963	-0.0542
HGHT	M5	1356.4464	514791.618	1643 [73.307 - 6167]	2635 [300.285 - 6117.075]	0.0032 [0.0024 - 0.1927]	0.0523 [0.0024 - 0.1894]	9e-04 [0 - 0.0033]	4.0747	-1.3056
HGHT	**M6**	**632.0172**	**30825.812**	**6896 [3179.3 - 11720.5]**	**7158 [4358.95 - 10561.25]**	**0.2237 [0.1043 - 0.372]**	**0.2205 [0.1021 - 0.3663]**	**0.0173 [0.0076 - 0.0299]**	**-**	**74.3619**
HGHT	**M7**	**632.0172**	**30825.812**	**6660 [2968.825 - 10711.75]**	**7179 [4458.575 - 10412.5]**	**0.2161 [0.1038 - 0.3415]**	**0.2135 [0.1034 - 0.3388]**	**0.0167 [0.0073 - 0.0275]**	**-**	**75.413**
RSURF	M1	1976.6407	351707.3123	6022 [756.8225 - 7854.625]	59300 [26017.5 - 100760]	0.0171 [0.0022 - 0.0223]	0.0087 [0.0018 - 0.0214]	0.0015 [2e-04 - 0.0021]	0.3481	-2.0624
RSURF	M3	357.1333	58445.0405	9712 [4384.6 - 11093]	20620 [9209.775 - 35045.25]	0.1662 [0.075 - 0.1898]	0.0463 [0.0231 - 0.0866]	0.0761 [0.0235 - 0.2209]	14.2753	-0.2808
RSURF	M4	357.1333	58445.0405	8800 [3872.05 - 10140.5]	20360 [10157.75 - 34850.75]	0.1506 [0.0663 - 0.1735]	0.042 [0.0192 - 0.077]	0.069 [0.0198 - 0.2466]	13.5281	-0.7364
RSURF	M5	1558.1192	782897.1412	6733 [2716.275 - 7865.325]	15120 [6236 - 26552]	0.0086 [0.0035 - 0.01]	0.0036 [0.0015 - 0.0049]	0.0028 [0.001 - 0.0036]	3.3323	-2.1245
RWDTH	M1	2.4974	0.1383	0.0039 [6e-04 - 0.005]	0.018 [0.0063 - 0.0345]	0.0283 [0.0044 - 0.0359]	0.0059 [0.0011 - 0.0095]	6e-04 [1e-04 - 8e-04]	-0.5393	-2.1188
RWDTH	**M3**	**2.6695**	**0.6782**	**0.1497 [0.0697 - 0.1749]**	**0.0059 [1e-04 - 0.0212]**	**0.2207 [0.1028 - 0.2579]**	**0.1356 [0.1026 - 0.3313]**	**0.021 [0.01 - 0.0266]**	**-1.8866**	**1.7777**
RWDTH	**M4**	**2.6695**	**0.6782**	**0.1539 [0.0665 - 0.1799]**	**0.0046 [1e-04 - 0.0196]**	**0.2269 [0.0981 - 0.2653]**	**0.1394 [0.098 - 0.3382]**	**0.0216 [0.0086 - 0.0274]**	**-1.9536**	**1.8914**
RWDTH	**M5**	**2.5443**	**0.2844**	**0.0741 [0.0518 - 0.0852]**	**0.0016 [1e-04 - 0.0057]**	**0.2606 [0.1822 - 0.2995]**	**0.0677 [0.0694 - 0.138]**	**0.0114 [0.0078 - 0.0137]**	**-2.194**	**2.532**
R success										
NOFF	M1	6.093	26.9444	2.947 [0.0481 - 21.9028]	4.198 [0.0148 - 12.0928]	0.1094 [0.0019 - 0.8008]	0.1061 [0.0019 - 0.8353]	0.0794 [0.001 - 0.7408]	0.7685	-1.8921
Phenology										
LUs	**M2**	**3.3609**	**1.5921**	**1.288 [0.0435 - 1.5541]**	**0.1008 [3e-04 - 0.3423]**	**0.809 [0.0273 - 0.9762]**	**0.9154 [0.0319 - 0.9826]**	**0.114 [0.0039 - 0.1399]**	**-**	**5.9259**
LUs	**M3**	**3.7171**	**1.5781**	**0.9981 [0.4315 - 1.5749]**	**0.0353 [9e-04 - 0.14]**	**0.6325 [0.2734 - 0.998]**	**0.6385 [0.2999 - 0.9267]**	**0.0722 [0.0316 - 0.1184]**	**-1.6954**	**22.6171**
LUs	**M4**	**3.7171**	**1.5781**	**0.8643 [0.3354 - 1.4832]**	**0.0389 [0.0011 - 0.1531]**	**0.5477 [0.2126 - 0.9399]**	**0.5475 [0.237 - 0.8672]**	**0.0626 [0.0243 - 0.1113]**	**-1.6381**	**15.3716**
LUs	**M6**	**1.9972**	**1.2233**	**0.4913 [0.4267 - 0.5642]**	**0.1485 [0.0952 - 0.2207]**	**0.4016 [0.3488 - 0.4612]**	**0.4136 [0.367 - 0.4588]**	**0.1232 [0.0945 - 0.1598]**	**-**	**621.9963**
LUs	**M7**	**1.9972**	**1.2233**	**0.4912 [0.4184 - 0.5621]**	**0.1491 [0.0923 - 0.2207]**	**0.4015 [0.342 - 0.4595]**	**0.4133 [0.3619 - 0.4608]**	**0.1231 [0.0966 - 0.1619]**	**-**	**620.7063**
Lud	**M2**	**101.9689**	**39.1092**	**32.06 [1.033 - 38.3775]**	**1.6463 [0.0064 - 7.3301]**	**0.8198 [0.0294 - 0.9099]**	**0.9005 [0.0315 - 0.9853]**	**-**	**-**	**2.1757**
LS	M2	306.3261	14.4259	1.051 [0.0404 - 1.6353]	4.2619 [1.6723 - 8.0648]	0.0729 [0.0069 - 0.2854]	0.0663 [0.0088 - 0.3961]	-	-	-1.9854
GSL	**M2**	**204.0522**	**43.1537**	**32.79 [0.7395 - 40.053]**	**5.3522 [0.0219 - 13.9751]**	**0.7598 [0.0179 - 0.8593]**	**0.7823 [0.0193 - 0.9767]**	**8e-04 [0 - 0.001]**	**-**	**0.6816**
FFLW	**M1**	**120.7989**	**27.054**	**13.48 [0.2953 - 17.7203]**	**0.0319 [0.0067 - 2.9453]**	**0.4983 [0.0109 - 0.655]**	**0.9713 [0.0223 - 0.9823]**	**-**	**-2.0204**	**2.5067**
MFLW	**M1**	**117.9556**	**32.2575**	**16.89 [0.3639 - 22.2225]**	**0.2 [0.0085 - 4.3279]**	**0.5236 [0.0113 - 0.6889]**	**0.9717 [0.0199 - 0.9827]**	**-**	**-1.9784**	**4.3772**
MAR	M1	1.0294	2.9028	0.6461 [0.0013 - 1.018]	0.0017 [0 - 0.0967]	0.2226 [0.0014 - 0.8969]	0.7126 [0.0014 - 0.9811]	0.6097 [0.0012 - 1.0633]	-2.0766	-0.4242
Physiology										
C	M2	461.5233	66.8823	49.59 [0.0621 - 73.6105]	-	0.7415 [9e-04 - 0.9049]	0.7757 [9e-04 - 0.9865]	2e-04 [0 - 3e-04]	-	-0.4399
C	M3	465.0559	255.5694	27.4 [0.0605 - 102.8125]	4.069 [0.002 - 20.8815]	0.1072 [2e-04 - 0.4023]	0.1063 [2e-04 - 0.3963]	1e-04 [0 - 5e-04]	-1.3914	-1.6093
C	M4	465.0559	255.5694	30.02 [0.1115 - 101.955]	4.043 [0.004 - 23.6722]	0.1175 [4e-04 - 0.3935]	0.1164 [4e-04 - 0.39]	1e-04 [0 - 5e-04]	-1.3964	-1.5194
C.N	M2	23.6579	12.7377	0.0068 [0.0016 - 11.3212]	-	5e-04 [1e-04 - 0.9293]	5e-04 [1e-04 - 0.9782]	0 [0 - 0.0205]	-	-2.0013
C.N	**M3**	**20.0517**	**5.7817**	**1.447 [0.0206 - 3.3416]**	**0.1601 [0.0031 - 0.5774]**	**0.2503 [0.0038 - 0.5779]**	**0.2606 [0.0038 - 0.5746]**	**0.0036 [1e-04 - 0.0083]**	**-1.1782**	**2.3859**
C.N	**M4**	**20.0517**	**5.7817**	**1.448 [0.0283 - 3.1997]**	**0.1597 [0.002 - 0.6604]**	**0.2504 [0.0056 - 0.5558]**	**0.2607 [0.0056 - 0.5464]**	**0.0036 [1e-04 - 0.008]**	**-1.1816**	**2.4033**
d13C	**M2**	**-30.0694**	**1.1119**	**0.971 [0.0092 - 1.162]**	**-**	**0.8733 [0.0088 - 0.9029]**	**0.9784 [0.0088 - 0.9882]**	**0.0011 [0 - 0.0013]**	**-**	**8.3192**
d13C	**M3**	**-29.7046**	**0.8841**	**0.2998 [0.058 - 0.5783]**	**0.3881 [0.1438 - 0.7227]**	**0.3391 [0.0559 - 0.5607]**	**0.274 [0.0551 - 0.5318]**	**3e-04 [1e-04 - 6e-04]**	**26.1661**	**6.3232**
d13C	**M4**	**-29.7046**	**0.8841**	**0.2989 [0.0724 - 0.5788]**	**0.4088 [0.1439 - 0.7801]**	**0.3381 [0.0745 - 0.5583]**	**0.2679 [0.0716 - 0.5309]**	**3e-04 [1e-04 - 7e-04]**	**25.7712**	**5.6912**
d15N	**M2**	**-2.276**	**1.5707**	**1.404 [0.0039 - 1.672]**	**-**	**0.8938 [0.0024 - 0.9052]**	**0.9743 [0.0024 - 0.9877]**	**0.271 [7e-04 - 0.331]**	**-**	**4.7475**
d15N	**M3**	**-4.1561**	**2.6515**	**0.2026 [0.0165 - 0.5285]**	**1.123 [0.4823 - 1.9801]**	**0.0764 [0.0089 - 0.2954]**	**0.0946 [0.0077 - 0.268]**	**0.0117 [9e-04 - 0.0344]**	**58.8223**	**0.35**
d15N	M4	-4.1561	2.6515	0.1691 [0.0136 - 0.4852]	1.14 [0.4696 - 2.0155]	0.0638 [0.0074 - 0.2671]	0.0784 [0.0066 - 0.234]	0.0098 [8e-04 - 0.0315]	59.5558	-0.199
N	M2	19.8252	6.0234	0.0343 [9e-04 - 4.9336]	-	0.0057 [1e-04 - 0.8576]	0.0057 [1e-04 - 0.902]	1e-04 [0 - 0.0126]	-	-2.001

N	**M3**	**23.505**	**7.7211**	**2.924 [0.5577 - 5.5019]**	**0.1466 [0.005 - 0.6786]**	**0.3787 [0.082 - 0.707]**	**0.3944 [0.0817 - 0.695]**	**0.0053 [0.001 - 0.01]**	**-1.4443**	**6.4934**
N	**M4**	**23.505**	**7.7211**	**2.911 [0.6071 - 5.6224]**	**0.1237 [0.0033 - 0.6132]**	**0.377 [0.0866 - 0.7294]**	**0.3931 [0.0861 - 0.7051]**	**0.0053 [0.0011 - 0.0103]**	**-1.6372**	**6.5752**
SLA	**M2**	**13.7571**	**9.381**	**8.225 [0.2446 - 10.2308]**	**-**	**0.8768 [0.0293 - 0.9048]**	**0.9415 [0.0293 - 0.9875]**	**0.0435 [0.0013 - 0.0546]**	**-**	**2.5715**
SLA	M3	13.7343	11.9319	2.168 [0.1142 - 5.305]	4.953 [1.6634 - 9.5934]	0.1817 [0.0095 - 0.4322]	0.1569 [0.0087 - 0.3973]	0.0115 [6e-04 - 0.0294]	35.4158	-0.788
SLA	M4	13.7343	11.9319	2.464 [0.1919 - 5.7007]	5.015 [1.8376 - 9.4703]	0.2065 [0.0149 - 0.436]	0.1772 [0.0137 - 0.4194]	0.0131 [0.0011 - 0.0314]	32.2456	-0.6621
MLA	**M2**	**35.7683**	**104.5311**	**68.57 [0.0394 - 112.3025]**	**-**	**0.656 [4e-04 - 0.9018]**	**0.6905 [4e-04 - 0.9836]**	**0.0536 [0 - 0.0877]**	**-**	**0.385**
MLA	M3	23.2063	46.1773	0.2818 [0.1432 - 12.8742]	8.248 [1.7688 - 18.1232]	0.0061 [0.0031 - 0.2819]	0.0058 [0.0031 - 0.2668]	5e-04 [3e-04 - 0.0239]	9.3583	-2.0832
MLA	M4	23.2063	46.1773	0.2888 [0.136 - 11.4905]	8.236 [1.3268 - 17.8665]	0.0063 [0.0031 - 0.2392]	0.0059 [0.0031 - 0.2321]	5e-04 [3e-04 - 0.0208]	8.6468	-2.0827
Resilience										
REC	M1	1.6164	0.1241	0.0163 [0 - 0.0416]	0.0046 [0 - 0.0248]	0.1315 [2e-04 - 0.3353]	0.7537 [0.0191 - 0.9609]	0.0062 [0 - 0.0161]	-1.872	-1.308
REL	M1	0.8583	0.0515	2e-04 [1e-04 - 0.0107]	0.0137 [4e-04 - 0.031]	0.0035 [0.0016 - 0.208]	0.0128 [0.008 - 0.607]	2e-04 [1e-04 - 0.0157]	12.9654	-2.0389
RET	M1	0.5792	0.0141	0 [0 - 0.0027]	0.002 [0 - 0.0058]	0.0029 [4e-04 - 0.1906]	0.0194 [0.0107 - 0.9043]	1e-04 [0 - 0.0082]	6.2005	-2.0336
Structure										
WD	**M1**	**549.5415**	**756.3841**	**600 [7.7446 - 745.0125]**	**15.18 [0.2725 - 105.0075]**	**0.7932 [0.0114 - 0.8962]**	**0.9393 [0.0113 - 0.9828]**	**0.002 [0 - 0.0025]**	**-1.995**	**3.3434**
WD	**M3**	**498.8194**	**5043.3787**	**1062 [10.777 - 2639.15]**	**98.55 [0.5989 - 480.21]**	**0.2106 [0.0023 - 0.5159]**	**0.2083 [0.0023 - 0.5154]**	**0.0043 [0 - 0.0107]**	**-1.6473**	**0.0846**
WD	M4	498.8194	5043.3787	902.8 [9.3607 - 2512.825]	137.7 [0.6702 - 529.9375]	0.179 [0.0019 - 0.4709]	0.1762 [0.0019 - 0.4672]	0.0036 [0 - 0.0101]	-1.4534	-0.5424
WD	**M5**	**514.0477**	**4295.2229**	**753.7 [31.3128 - 1537.1]**	**-**	**0.1755 [0.0085 - 0.3961]**	**0.1996 [0.0085 - 0.3944]**	**0.0029 [1e-04 - 0.0058]**	**-**	**3.0998**
Leaf morphology										
BS	**M1**	**6.5928**	**1.5555**	**0.7368 [0.0197 - 0.9625]**	**0.8134 [0.1613 - 1.605]**	**0.4737 [0.0126 - 0.6188]**	**0.47 [0.0133 - 0.756]**	**0.017 [5e-04 - 0.0233]**	**12.2287**	**2.8342**
HR	M1	1.3284	0.4631	0.0322 [7e-04 - 0.0436]	2e-04 [0 - 0.0073]	0.0695 [0.0015 - 0.0942]	0.0817 [0.023 - 0.981]	0.0182 [4e-04 - 0.0251]	-2.0191	-1.8387
LDR	**M1**	**42.949**	**79.3401**	**50.91 [1.0907 - 62.3365]**	**0.0364 [0.0214 - 8.1577]**	**0.6417 [0.0137 - 0.7857]**	**0.9607 [0.0213 - 0.9855]**	**0.0276 [6e-04 - 0.0339]**	**-2.0179**	**2.0453**
LL	M1	78.4243	199.7889	76.48 [1.705 - 95.4317]	0.5553 [0.0315 - 13.663]	0.3828 [0.0085 - 0.4777]	0.4482 [0.0232 - 0.9859]	0.0124 [3e-04 - 0.0155]	-2.0589	-0.0828
LW	**M1**	**24.7889**	**26.5269**	**13.31 [0.3694 - 16.661]**	**0.078 [0.0056 - 2.2466]**	**0.5018 [0.0139 - 0.6281]**	**0.6213 [0.0289 - 0.9859]**	**0.0217 [6e-04 - 0.027]**	**-2.0501**	**1.3548**
LWR	**M1**	**31.3872**	**8.436**	**5.263 [0.1264 - 6.6193]**	**0.1679 [0.0025 - 1.2042]**	**0.6239 [0.015 - 0.7846]**	**0.9285 [0.0234 - 0.9832]**	**0.0053 [1e-04 - 0.0067]**	**-1.927**	**0.4713**
NL	M1	8.7356	1.7074	0.4353 [0.0097 - 0.6261]	0.1062 [8e-04 - 0.3138]	0.2549 [0.0057 - 0.3667]	0.3231 [0.0192 - 0.9655]	0.0057 [1e-04 - 0.0083]	-1.3837	-1.5014
NV	M1	2.9019	2.1461	1.032 [0.0256 - 1.32]	0.2621 [0.0023 - 0.7418]	0.4809 [0.0119 - 0.6151]	0.659 [0.0211 - 0.9623]	0.1225 [0.003 - 0.1835]	2.8135	-0.3589
OB	**M1**	**57.0648**	**26.9943**	**10.45 [0.2126 - 15.4515]**	**0.023 [0.0055 - 3.1632]**	**0.3871 [0.0079 - 0.5724]**	**0.9737 [0.0231 - 0.9776]**	**0.0032 [1e-04 - 0.0047]**	**-2.0258**	**0.9377**
PL	M1	4.6418	4.5531	0.4451 [0.0095 - 0.6128]	0.0047 [3e-04 - 0.1191]	0.0978 [0.0021 - 0.1346]	0.1075 [0.022 - 0.9793]	0.0207 [4e-04 - 0.0288]	-2.02	-1.9069
PR	M1	5.3415	5.0951	2.057 [0.0599 - 2.5661]	0.0196 [9e-04 - 0.3659]	0.4037 [0.0118 - 0.5036]	0.481 [0.0268 - 0.9852]	0.0721 [0.002 - 0.0902]	-2.0326	-1.2302
PV	M1	33.8468	274.5848	144.9 [3.6387 - 187.6225]	47.05 [0.4336 - 111.4025]	0.5277 [0.0133 - 0.6833]	0.6929 [0.017 - 0.9604]	0.1265 [0.0033 - 0.1969]	6.132	-0.4726
SW	M1	13.7697	8.478	2.14 [0.0437 - 2.843]	0.0165 [0.0011 - 0.5144]	0.2524 [0.0052 - 0.3353]	0.3142 [0.0204 - 0.9833]	0.0113 [2e-04 - 0.0151]	-2.0632	-1.1659
WP	**M1**	**44.6226**	**81.5738**	**54 [1.2526 - 69.0618]**	**0.0586 [0.021 - 7.5011]**	**0.662 [0.0154 - 0.8466]**	**0.9353 [0.0242 - 0.9855]**	**0.0271 [6e-04 - 0.0351]**	**-2.0166**	**3.2263**
Defence										
CNFL (exp)	M1	0.9685	6.9258	0.0011 [1e-04 - 0.2613]	0.0052 [0 - 0.0577]	0.0016 [1e-04 - 0.6908]	0.0029 [1e-04 - 0.7173]	0.0011 [1e-04 - 0.2613]	-1.9374	-2.0061
CSTG (exp)	M1	3.496	19.9558	2e-04 [0 - 0.0122]	0 [0 - 0.0018]	0.012 [2e-04 - 0.8275]	0.0145 [2e-04 - 0.8701]	2e-04 [0 - 0.0122]	-1.9972	-2.0012
CSTL (exp)	**M1**	**0.2009**	**1.308**	**0.2337 [0.0032 - 0.2793]**	**0.0105 [1e-04 - 0.0555]**	**0.6977 [0.0135 - 0.7892]**	**0.8293 [0.0134 - 0.8738]**	**0.2337 [0.0032 - 0.2793]**	**-1.3352**	**5.5538**
CWSK (exp)	M1	-1.9029	0.0807	0.0577 [2e-04 - 0.936]	0.0013 [0 - 0.1585]	0.0283 [1e-04 - 0.4838]	0.03 [1e-04 - 0.5346]	0.0577 [2e-04 - 0.936]	-2.0114	-1.9961
EGNL (exp)	M1	-1.6995	0.1494	0.102 [3e-04 - 0.7043]	0.0822 [0 - 0.2724]	0.0326 [2e-04 - 0.5273]	0.0787 [2e-04 - 0.5714]	0.102 [3e-04 - 0.7043]	0.0327	-1.9502
ELAC (exp)	M1	0.5203	0.7528	0.0209 [1e-04 - 0.1533]	0.0119 [0 - 0.0534]	0.0956 [4e-04 - 0.7563]	0.1048 [4e-04 - 0.7964]	0.0209 [1e-04 - 0.1533]	-0.858	-1.9036
ELTOT (exp)	M1	3.8073	393.525	0.001 [0 - 0.1225]	0.0102 [0 - 0.0402]	0.005 [2e-04 - 0.7187]	0.0058 [2e-04 - 0.7285]	0.001 [0 - 0.1225]	-0.3366	-2.0132
GRDN	M1	6.5559	8.3491	4.519 [0.0037 - 8.8821]	0.0244 [2e-04 - 1.0253]	0.5413 [5e-04 - 0.894]	0.5555 [5e-04 - 0.9798]	0.1051 [1e-04 - 0.208]	-2.0671	-0.8921
MVL (exp)	M1	-0.3239	0.2823	0.0624 [0.0011 - 0.401]	0.0929 [5e-04 - 0.2548]	0.0985 [0.0021 - 0.6133]	0.0937 [0.0021 - 0.6516]	0.0624 [0.0011 - 0.401]	2.2135	-1.9168
PNTL (exp)	M1	-1.5888	0.0262	0.0233 [3e-04 - 0.2924]	0.0535 [0 - 0.1595]	0.0361 [6e-04 - 0.6607]	0.0518 [6e-04 - 0.6917]	0.0233 [3e-04 - 0.2924]	3.2031	-1.9722
ROBA (exp)	M1	1.8007	6.348	4e-04 [0 - 0.0851]	0.0079 [0 - 0.0289]	0.0027 [2e-04 - 0.7385]	0.0034 [2e-04 - 0.7804]	4e-04 [0 - 0.0851]	0.1862	-2.0272
ROBB	M1	6.3067	4.3557	1.248 [0.0012 - 4.3232]	0.0528 [1e-04 - 0.5983]	0.2865 [3e-04 - 0.881]	0.292 [3e-04 - 0.9548]	0.0314 [0 - 0.1084]	-2.0077	-1.6943
ROBC (exp)	M1	1.5316	6.2893	0.0444 [0 - 0.1954]	7e-04 [0 - 0.0265]	0.1827 [2e-04 - 0.7875]	0.1978 [2e-04 - 0.8566]	0.0444 [0 - 0.1954]	-2.0222	-1.7505
ROBD	M1	8.4567	12.5036	0.0498 [0.002 - 9.1923]	2e-04 [1e-04 - 1.277]	0.004 [2e-04 - 0.7879]	0.0042 [2e-04 - 0.8345]	7e-04 [0 - 0.1294]	-1.9665	-2.0014
ROBE (exp)	M1	1.894	3.3626	0.0603 [2e-04 - 0.0897]	1e-04 [0 - 0.0094]	0.5705 [0.0024 - 0.8595]	0.7185 [0.0024 - 0.945]	0.0603 [2e-04 - 0.0897]	-2.0445	-0.5345
SYRG	M1	6.6793	12.5141	0.0633 [0.0018 - 7.2206]	0.3356 [1e-04 - 1.961]	0.0051 [2e-04 - 0.8473]	0.0071 [2e-04 - 0.8994]	0.0014 [0 - 0.169]	-1.553	-2.0067
TWSK (exp)	**M1**	**-2.2078**	**0.3077**	**0.9215 [0.0027 - 1.2623]**	**0.0202 [1e-04 - 0.1954]**	**0.4144 [0.0014 - 0.5226]**	**0.4587 [0.0014 - 0.6016]**	**0.9215 [0.0027 - 1.2623]**	**-1.9625**	**0.9468**
VNL	M1	3.7411	3.8353	8e-04 [5e-04 - 2.2532]	0 [0 - 0.2876]	2e-04 [2e-04 - 0.8456]	3e-04 [2e-04 - 0.8922]	1e-04 [0 - 0.1648]	-2.0006	-2.0013
VSCG	M1	22.9715	25.0507	13.16 [0.0254 - 23.8702]	0.3441 [8e-04 - 3.8481]	0.5253 [0.001 - 0.89]	0.5782 [0.001 - 0.977]	0.0249 [0 - 0.0455]	-1.954	-0.4071
VSCL (exp)	**M1**	**0.6863**	**3.3081**	**0.2731 [0.0038 - 0.3283]**	**0.0113 [1e-04 - 0.0573]**	**0.6084 [0.0138 - 0.7703]**	**0.7989 [0.0131 - 0.8591]**	**0.2731 [0.0038 - 0.3283]**	**-1.3436**	**2.3264**
2PHL (exp)	M1	-2.0999	0.0179	1e-04 [1e-04 - 0.3599]	0 [0 - 0.0546]	1e-04 [1e-04 - 0.6675]	2e-04 [1e-04 - 0.7121]	1e-04 [1e-04 - 0.3599]	-2.0006	-2.0013

Appendix 6

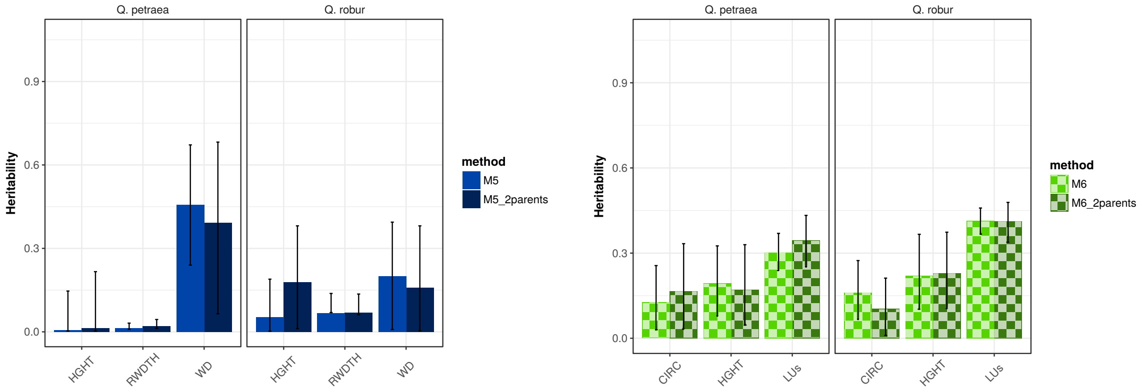
Comparison of heritability estimation when one parent vs. two parents are used to ~~built~~ the pedigree relationships

The parentage analysis performed on the second generation individuals enabled to retrieve both parents for 122 individuals in *Q. petraea* and 193 in *Q. robur*, and at least one parent for 758 individuals in *Q. petraea* and 636 in *Q. robur* (Truffaut et al., 2017). To make the most complete usage of phenotypic data available on the second generation, we presented the analyses performed on all individuals with at least one parent known. However, when using only individuals with both parents known, the number of individuals decreases but the pedigree becomes more complete. We present here the comparison of heritability estimation (h^2_{calc}) with two different sets of individuals: (1) all phenotyped individuals with at least one parent known, and (2) all phenotyped individuals with two parents known.



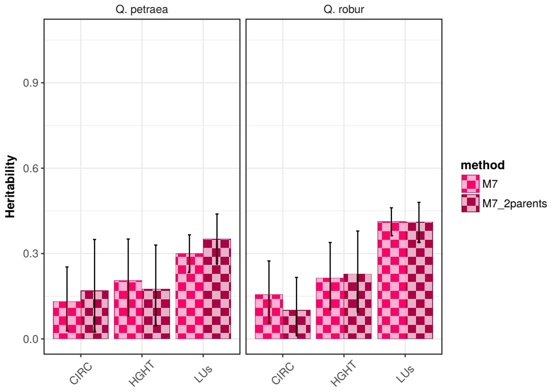
(a) method M3

(b) method M4



(c) method M5

(d) method M6

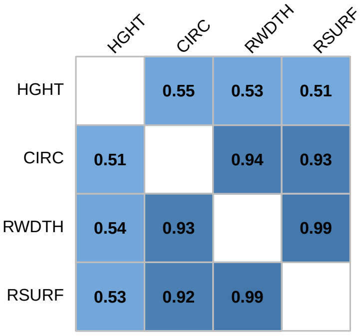


(e) method M7

Figure 6.1: Comparison of heritability estimates (h^2_{calc}) when one or two parents are used to build the pedigree. Methods M3 to M7 correspond to the methods described in the main text (Figure 2).

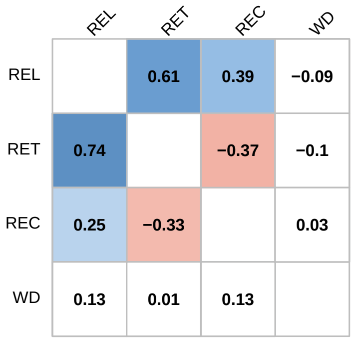
Appendix 7

Genetic correlation among traits



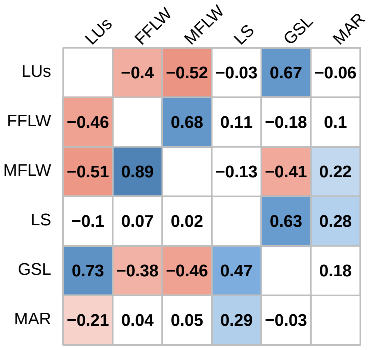
	HGHT	CIRC	RWDTH	RSURF
HGHT		0.55	0.53	0.51
CIRC	0.51		0.94	0.93
RWDTH	0.54	0.93		0.99
RSURF	0.53	0.92	0.99	

(a) growth



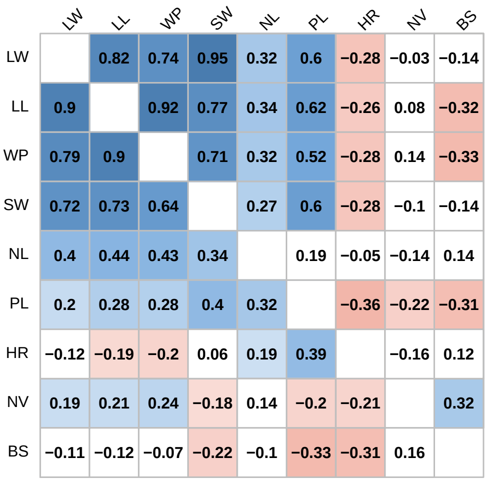
	REL	RET	REC	WD
REL		0.61	0.39	−0.09
RET	0.74		−0.37	−0.1
REC	0.25	−0.33		0.03
WD	0.13	0.01	0.13	

(b) resilience



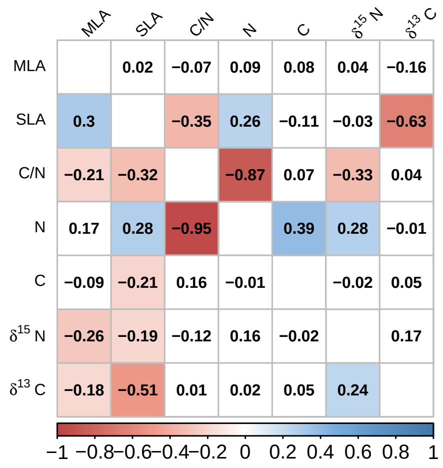
	LUs	FFLW	MFLW	LS	GSL	MAR
LUs		−0.4	−0.52	−0.03	0.67	−0.06
FFLW	−0.46		0.68	0.11	−0.18	0.1
MFLW	−0.51	0.89		−0.13	−0.41	0.22
LS	−0.1	0.07	0.02		0.63	0.28
GSL	0.73	−0.38	−0.46	0.47		0.18
MAR	−0.21	0.04	0.05	0.29	−0.03	

(c) phenology



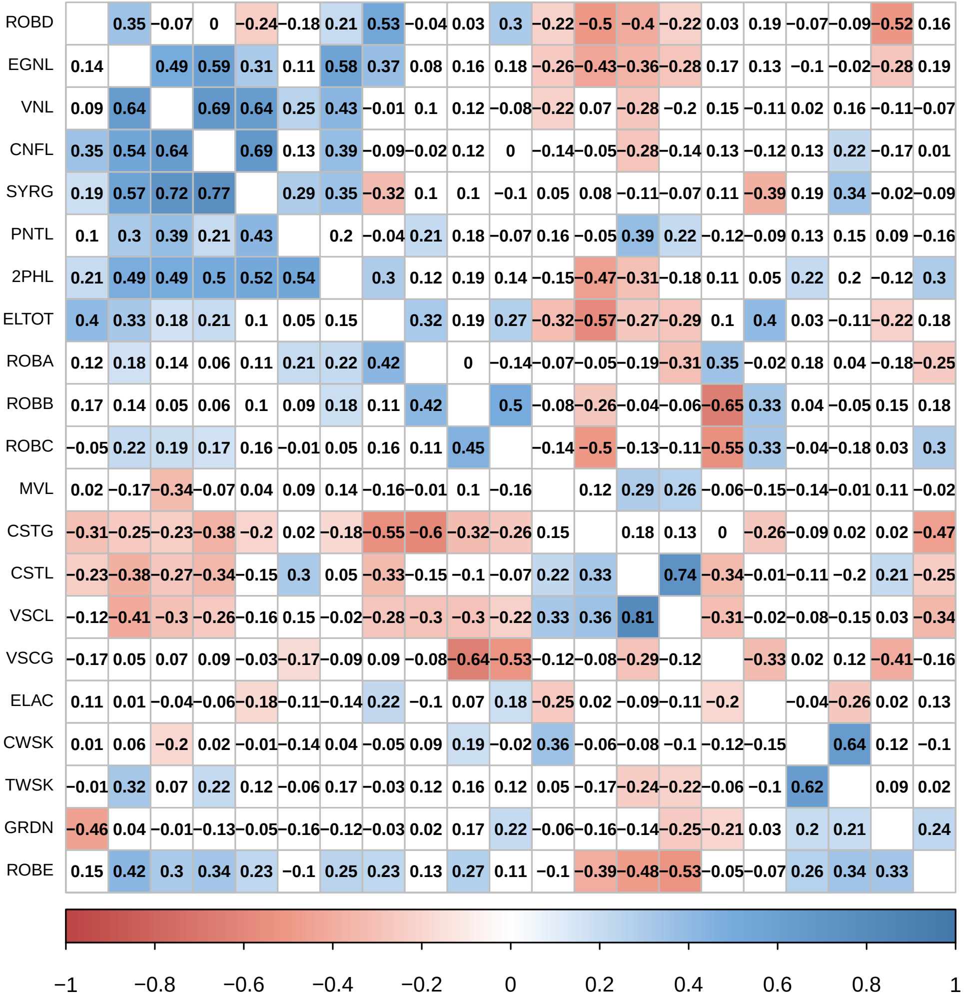
	LW	LL	WP	SW	NL	PL	HR	NV	BS
LW		0.82	0.74	0.95	0.32	0.6	−0.28	−0.03	−0.14
LL	0.9		0.92	0.77	0.34	0.62	−0.26	0.08	−0.32
WP	0.79	0.9		0.71	0.32	0.52	−0.28	0.14	−0.33
SW	0.72	0.73	0.64		0.27	0.6	−0.28	−0.1	−0.14
NL	0.4	0.44	0.43	0.34		0.19	−0.05	−0.14	0.14
PL	0.2	0.28	0.28	0.4	0.32		−0.36	−0.22	−0.31
HR	−0.12	−0.19	−0.2	0.06	0.19	0.39		−0.16	0.12
NV	0.19	0.21	0.24	−0.18	0.14	−0.2	−0.21		0.32
BS	−0.11	−0.12	−0.07	−0.22	−0.1	−0.33	−0.31	0.16	

(d) foliar morphology



	MLA	SLA	C/N	N	C	δ^{15}N	δ^{13}C
MLA		0.02	−0.07	0.09	0.08	0.04	−0.16
SLA	0.3		−0.35	0.26	−0.11	−0.03	−0.63
C/N	−0.21	−0.32		−0.87	0.07	−0.33	0.04
N	0.17	0.28	−0.95		0.39	0.28	−0.01
C	−0.09	−0.21	0.16	−0.01		−0.02	0.05
δ^{15}N	−0.26	−0.19	−0.12	0.16	−0.02		0.17
δ^{13}C	−0.18	−0.51	0.01	0.02	0.05	0.24	

(e) physiology



	ROBD	EGNL	VNL	CNFL	SYRG	PNTL	2PHL	ELTOT	ROBA	ROBB	ROBC	MVL	CSTG	CSTL	VSCL	VSCG	ELAC	CWSK	TWSK	GRDN	ROBE
ROBD		0.35	−0.07	0	−0.24	−0.18	0.21	0.53	−0.04	0.03	0.3	−0.22	−0.5	−0.4	−0.22	0.03	0.19	−0.07	−0.09	−0.52	0.16
EGNL	0.14		0.49	0.59	0.31	0.11	0.58	0.37	0.08	0.16	0.18	−0.26	−0.43	−0.36	−0.28	0.17	0.13	−0.1	−0.02	−0.28	0.19
VNL	0.09	0.64		0.69	0.64	0.25	0.43	−0.01	0.1	0.12	−0.08	−0.22	0.07	−0.28	−0.2	0.15	−0.11	0.02	0.16	−0.11	−0.07
CNFL	0.35	0.54	0.64		0.69	0.13	0.39	−0.09	−0.02	0.12	0	−0.14	−0.05	−0.28	−0.14	0.13	−0.12	0.13	0.22	−0.17	0.01
SYRG	0.19	0.57	0.72	0.77		0.29	0.35	−0.32	0.1	0.1	−0.1	0.05	0.08	−0.11	−0.07	0.11	−0.39	0.19	0.34	−0.02	−0.09
PNTL	0.1	0.3	0.39	0.21	0.43		0.2	−0.04	0.21	0.18	−0.07	0.16	−0.05	0.39	0.22	−0.12	−0.09	0.13	0.15	0.09	−0.16
2PHL	0.21	0.49	0.49	0.5	0.52	0.54		0.3	0.12	0.19	0.14	−0.15	−0.47	−0.31	−0.18	0.11	0.05	0.22	0.2	−0.12	0.3
ELTOT	0.4	0.33	0.18	0.21	0.1	0.05	0.15		0.32	0.19	0.27	−0.32	−0.57	−0.27	−0.29	0.1	0.4	0.03	−0.11	−0.22	0.18
ROBA	0.12	0.18	0.14	0.06	0.11	0.21	0.22	0.42		0	−0.14	−0.07	−0.05	−0.19	−0.31	0.35	−0.02	0.18	0.04	−0.18	−0.25
ROBB	0.17	0.14	0.05	0.06	0.1	0.09	0.18	0.11	0.42		0.5	−0.08	−0.26	−0.04	−0.06	−0.65	0.33	0.04	−0.05	0.15	0.18
ROBC	−0.05	0.22	0.19	0.17	0.16	−0.01	0.05	0.16	0.11	0.45		−0.14	−0.5	−0.13	−0.11	−0.55	0.33	−0.04	−0.18	0.03	0.3
MVL	0.02	−0.17	−0.34	−0.07	0.04	0.09	0.14	−0.16	−0.01	0.1	−0.16		0.12	0.29	0.26	−0.06	−0.15	−0.14	−0.01	0.11	−0.02
CSTG	−0.31	−0.25	−0.23	−0.38	−0.2	0.02	−0.18	−0.55	−0.6	−0.32	−0.26	0.15		0.18	0.13	0	−0.26	−0.09	0.02	0.02	−0.47
CSTL	−0.23	−0.38	−0.27	−0.34	−0.15	0.3	0.05	−0.33	−0.15	−0.1	−0.07	0.22	0.33		0.74	−0.34	−0.01	−0.11	−0.2	0.21	−0.25
VSCL	−0.12	−0.41	−0.3	−0.26	−0.16	0.15	−0.02	−0.28	−0.3	−0.3	−0.22	0.33	0.36	0.81		−0.31	−0.02	−0.08	−0.15	0.03	−0.34
VSCG	−0.17	0.05	0.07	0.09	−0.03	−0.17	−0.09	0.09	−0.08	−0.64	−0.53	−0.12	−0.08	−0.29	−0.12		−0.33	0.02	0.12	−0.41	−0.16
ELAC	0.11	0.01	−0.04	−0.06	−0.18	−0.11	−0.14	0.22	−0.1	0.07	0.18	−0.25	0.02	−0.09	−0.11	−0.2		−0.04	−0.26	0.02	0.13
CWSK	0.01	0.06	−0.2	0.02	−0.01	−0.14	0.04	−0.05	0.09	0.19	−0.02	0.36	−0.06	−0.08	−0.1	−0.12	−0.15		0.64	0.12	−0.1
TWSK	−0.01	0.32	0.07	0.22	0.12	−0.06	0.17	−0.03	0.12	0.16	0.12	0.05	−0.17	−0.24	−0.22	−0.06	−0.1	0.62		0.09	0.02
GRDN	−0.46	0.04	−0.01	−0.13	−0.05	−0.16	−0.12	−0.03	0.02	0.17	0.22	−0.06	−0.16	−0.14	−0.25	−0.21	0.03	0.2	0.21		0.24
ROBE	0.15	0.42	0.3	0.34	0.23	−0.1	0.25	0.23	0.13	0.27	0.11	−0.1	−0.39	−0.48	−0.53	−0.05	−0.07	0.26	0.34	0.33	

(f) defence

Figure 7.1: Genetic correlations computed from Pearson correlation, for each trait category (a: growth, b: resilience, c: phenology, d: physiology, e: foliar morphology, f: defence). Correlation coefficients for *Q. petraea* are above the matrix diagonals and *Q. robur* are below the [illegible]onal. Colors correspond to the correlation sign (gradient from blue for positive to red for negative correlations). Only correlations significant at a 5% threshold are colored.

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