

Genotypic variability enhances the reproducibility of an ecological study

Alexandru Milcu^{1,2*}, Ruben Puga-Freitas³, Aaron M. Ellison^{4,5}, Manuel Blouin^{3,6}, Stefan Scheu⁷, Grégoire T. Freschet², Laura Rose⁸, Sébastien Barot⁹, Simone Cesarz^{10,11}, Nico Eisenhauer^{10,11}, Thomas Girin¹², Davide Assandri¹³, Michael Bonkowski¹⁴, Nina Buchmann¹⁵, Olaf Butenschoen^{7,16}, Sébastien Devidal¹, Gerd Gleixner¹⁷, Arthur Gessler^{18,19}, Agnès Gigon³, Anna Greiner⁸, Carlo Grignani¹³, Amandine Hansart²⁰, Zachary Kayler^{19,21}, Markus Lange^{10,17}, Jean-Christophe Lata²², Jean-François Le Galliard^{20,22}, Martin Lukac^{23,24}, Neringa Mannerheim¹⁵, Marina E. H. Müller¹⁸, Anne Pando⁶, Paula Rotter⁸, Michael Scherer-Lorenzen^{10,18}, Rahme Seyhun²², Katherine Urban-Mead², Alexandra Weigelt^{10,11}, Laura Zavattaro¹³ and Jacques Roy¹

Many scientific disciplines are currently experiencing a 'reproducibility crisis' because numerous scientific findings cannot be repeated consistently. A novel but controversial hypothesis postulates that stringent levels of environmental and biotic standardization in experimental studies reduce reproducibility by amplifying the impacts of laboratory-specific environmental factors not accounted for in study designs. A corollary to this hypothesis is that a deliberate introduction of controlled systematic variability (CSV) in experimental designs may lead to increased reproducibility. To test this hypothesis, we had 14 European laboratories run a simple microcosm experiment using grass (*Brachypodium distachyon* L.) monocultures and grass and legume (*Medicago truncatula* Gaertn.) mixtures. Each laboratory introduced environmental and genotypic CSV within and among replicated microcosms established in either growth chambers (with stringent control of environmental conditions) or glasshouses (with more variable environmental conditions). The introduction of genotypic CSV led to 18% lower among-laboratory variability in growth chambers, indicating increased reproducibility, but had no significant effect in glasshouses where reproducibility was generally lower. Environmental CSV had little effect on reproducibility. Although there are multiple causes for the 'reproducibility crisis', deliberately including genetic variability may be a simple solution for increasing the reproducibility of ecological studies performed under stringently controlled environmental conditions.

Reproducibility—the ability to duplicate a study and its findings—is a defining feature of scientific research. In ecology, it is often argued that it is virtually impossible to accurately duplicate any single ecological experiment or observational study. The rationale is that the complex ecological interactions between the ever-changing environment and the extraordinary diversity of biological systems exhibiting a wide range of plastic responses at

different levels of biological organization make exact duplication unfeasible^{1,2}. Although this may be true for observational and field studies, numerous ecological (and agronomic) studies are carried out with artificially assembled simplified ecosystems and controlled environmental conditions in experimental microcosms or mesocosms (henceforth, 'microcosms')^{3–5}. Since biotic and environmental parameters can be tightly controlled in microcosms, the results

¹Ecotron (Unité Propre de Service 3248), Centre National de la Recherche Scientifique, Campus Baillarguet, Montferrier-sur-Lez, France. ²Centre d'Ecologie Fonctionnelle et Evolutive, Centre National de la Recherche Scientifique, Unité Mixte de Recherche 5175, Université de Montpellier/Université Paul Valéry – École Pratique des Hautes Études, Montpellier, France. ³Institut de l'Ecologie et des Sciences de l'Environnement de Paris, Université Paris-Est Créteil, Créteil, France. ⁴Harvard Forest, Harvard University, Petersham, MA, USA. ⁵Tropical Forests and People Research Centre, University of the Sunshine Coast, Maroochydore DC, Queensland, Australia. ⁶Agroécologie, AgroSup Dijon, Institut National de la Recherche Agronomique, Université Bourgogne Franche-Comté, Dijon, France. ⁷Johann-Friedrich-Blumenbach Institute for Zoology and Anthropology, Georg August University Göttingen, Göttingen, Germany. ⁸Department of Geobotany, Faculty of Biology, University of Freiburg, Freiburg, Germany. ⁹Institut de Recherche pour le Développement, Institut de l'Ecologie et des Sciences de l'Environnement de Paris, Université Pierre et Marie Curie, Paris, France. ¹⁰German Centre for Integrative Biodiversity Research, Halle-Jena-Leipzig, Leipzig, Germany. ¹¹Institute of Biology, Leipzig University, Leipzig, Germany. ¹²Institut Jean-Pierre Bourgin, INRA, AgroParisTech, Centre National de la Recherche Scientifique, Université Paris-Saclay, Versailles, France. ¹³Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco, Italy. ¹⁴Cluster of Excellence on Plant Sciences, Terrestrial Ecology Group, Institute for Zoology, University of Cologne, Cologne, Germany. ¹⁵Institute of Agricultural Sciences, ETH Zurich, Zurich, Switzerland. ¹⁶Senckenberg Biodiversität und Klima Forschungszentrum, Frankfurt, Germany. ¹⁷Max Planck Institute for Biogeochemistry, Postfach 100164, Jena, Germany. ¹⁸Leibniz Centre for Agricultural Landscape Research, Institute of Landscape Biogeochemistry, Müncheberg, Germany. ¹⁹Swiss Federal Research Institute, Zürcherstrasse 111, Birmensdorf, Switzerland. ²⁰Département de Biologie, Ecole Normale Supérieure, Université de recherche Paris Sciences & Lettres Research University, Centre National de la Recherche Scientifique, Unité Mixte de Service 3194 (Centre de Recherche en Écologie Expérimentale et Prédictive-Ecotron IleDeFrance), Saint-Pierre-lès-Nemours, France. ²¹Department of Soil and Water Systems, University of Idaho, Moscow, ID, USA. ²²Institut de l'Ecologie et des Sciences de l'Environnement de Paris, Sorbonne Universités, Paris, France. ²³School of Agriculture, Policy and Development, University of Reading, Reading, UK. ²⁴Faculty of Forestry and Wood Sciences, Czech University of Life Sciences, Prague, Czech Republic. *e-mail: alex.milcu@cnrs.fr

from such studies should be easier to reproduce. Even though microcosms have frequently been used to address fundamental ecological questions^{4,6,7}, there has been no quantitative assessment of the reproducibility of any microcosm experiment.

Experimental standardization—the implementation of strictly defined and controlled properties of organisms and their environment—is widely thought to increase both the reproducibility and sensitivity of statistical tests^{8,9} because it reduces within-treatment variability. This paradigm has recently been challenged by several studies on animal behaviour, suggesting that stringent standardization may, counterintuitively, be responsible for generating non-reproducible results^{9–11} and contribute to the actual reproducibility crisis^{12–15}; the results may be valid under given conditions (that is, they are local ‘truths’), but are not generalizable^{8,16}. Despite rigorous adherence to experimental protocols, laboratories inherently vary in many conditions that are not measured and are thus unaccounted for, such as experimenter, micro-scale environmental heterogeneity, physico-chemical properties of reagents and laboratory-ware, pre-experimental conditioning of organisms, and their genetic and epigenetic background. It has even been suggested that attempts to stringently control all sources of biological and environmental variability might inadvertently lead to amplification of the effects of these unmeasured variations among laboratories, thus reducing reproducibility^{9–11}.

Some studies have gone even further, hypothesizing that the introduction of controlled systematic variability (CSV) among the replicates of a treatment (for example, using different genotypes or varying the organisms’ pre-experimental conditions among the experimental replicates) should lead to less variable mean response values between the laboratories that duplicate the experiments^{9,11}. In short, it has been argued that reproducibility may be improved by shifting the variance from among experiments to within them⁹. If true, introducing CSV will increase researchers’ ability to draw generalizable conclusions about the directions and effect sizes of experimental treatments and reduce the probability of false positives. The trade-off inherent to this approach is that increasing within-experiment variability will reduce the sensitivity (that is, the probability of detecting true positives) of statistical tests. However, it currently remains unclear whether introducing CSV increases the reproducibility of ecological microcosm experiments and, if so, at what cost for the sensitivity of statistical tests.

To test the hypothesis that introducing CSV enhances reproducibility in an ecological context, we had 14 European laboratories simultaneously run a simple microcosm experiment using grass (*Brachypodium distachyon* L.) monocultures and grass and legume (*Medicago truncatula* Gaertn.) mixtures. As part of the reproducibility experiment, the 14 laboratories independently tested the hypothesis that the presence of the legume species *M. truncatula* in mixtures would lead to higher total plant productivity in the microcosms and enhanced growth of the non-legume *B. distachyon* via rhizobia-mediated nitrogen fertilization and/or nitrogen-sparing effects^{17–19}.

All laboratories were provided with the same experimental protocol, seed stock from the same batch and identical containers in which to establish microcosms with grass only and grass-legume mixtures. Alongside a control with no CSV and containing a homogenized soil substrate (a mixture of soil and sand) and a single genotype of each plant species, we explored the effects of five different types of within- and among-microcosm CSV on experimental reproducibility of the legume effect (Fig. 1): (1) within-microcosm environmental CSV (ENV_W) achieved by spatially varying soil resource distribution through the introduction of six sand patches into the soil; (2) among-microcosm environmental CSV (ENV_A), which varied the number of sand patches (none, three or six) among replicate microcosms; (3) within-microcosm genotypic CSV (GEN_W), which used three distinct genotypes per species planted in

homogenized soil in each microcosm; (4) among-microcosm genotypic CSV (GEN_A), which varied the number of genotypes (one, two or three) planted in homogenized soil among replicate microcosms; and (5) both genotypic and environmental CSV (GEN_W+ENV_W) within microcosms, which used six sand patches and three plant genotypes per species in each microcosm. In addition, we tested whether CSV effects are modified by the level of standardization within laboratories by using two common experimental approaches ('setups' hereafter): growth chambers with tightly controlled environmental conditions and identical soil (eight laboratories) or glasshouses with more loosely controlled environmental conditions and different soils (six laboratories; see Supplementary Table 1 for the physico-chemical properties of the soils).

We measured 12 parameters representing a typical ensemble of response variables reported for plant-soil microcosm experiments. Six of these were measured at the microcosm level (shoot biomass, root biomass, total biomass, shoot-to-root ratio, evapotranspiration and decomposition of a common substrate using a simplified version of the ‘tea bag litter decomposition method’²⁰). The other six were measured on *B. distachyon* alone (seed biomass, height and four shoot-tissue chemical variables: N%, C%, δ¹⁵N and δ¹³C). All 12 variables were used to calculate the effect of the presence of a nitrogen-fixing legume on ecosystem functions in grass-legume mixtures ('net legume effect' hereafter) (Supplementary Table 2), calculated as the difference between the values measured in the microcosms with and without legumes—an approach often used in grass-legume binary cropping systems^{19,21} and biodiversity-ecosystem function experiments^{17,22}.

Statistically significant differences among the 14 laboratories were considered an indication of irreproducibility. In the first instance, we assessed how our experimental treatments (CSV and setup) affected the number of laboratories that produced results that could be considered to have reproduced the same finding. We then determined how experimental treatments affected the s.d. of the legume effect for each of the 12 variables both within and among laboratories (lower among-laboratory s.d. implies that the results were more similar, suggesting increased reproducibility). Finally, we explored the relationship between within- and among-laboratory s.d. and how the experimental treatments affected the statistical power of detecting the net legume effect.

Results

Although each laboratory followed the same experimental protocol, we found a remarkably high level of among-laboratory variation for most response variables (Supplementary Fig. 1) and the net legume effect on those variables (Fig. 2). For example, the net legume effect on mean total plant biomass varied among laboratories from 1.31 to 6.72 g dry weight per microcosm in growth chambers, suggesting that unmeasured laboratory-specific conditions outweighed the effects of experimental standardization. Among glasshouses, the differences were even larger: the net legume effect on mean plant biomass varied by two orders of magnitude from 0.14 to 14.57 g dry weight per microcosm (Fig. 2). Furthermore, for half of the variables (root biomass, litter decomposition, grass height, foliar C%, δ¹³C and δ¹⁵N), the direction of the net legume effect varied with the laboratory.

Mixed-effects models were used to test the effect of legume species presence, laboratory, CSV and their interactions (with experimental block—within-laboratory growth chamber or glasshouse bench—as a random factor) on the 12 response variables. The impact of the presence of legumes varied significantly with laboratory and CSV for half of the variables, as indicated by the legume × laboratory × CSV three-way interaction (Table 1 and Supplementary Figs. 2 and 3). For the other half, significant two-way interactions between legume × laboratory and CSV × laboratory were found. The same significant interactions were found when analysing the first (PC1) and second (PC2)

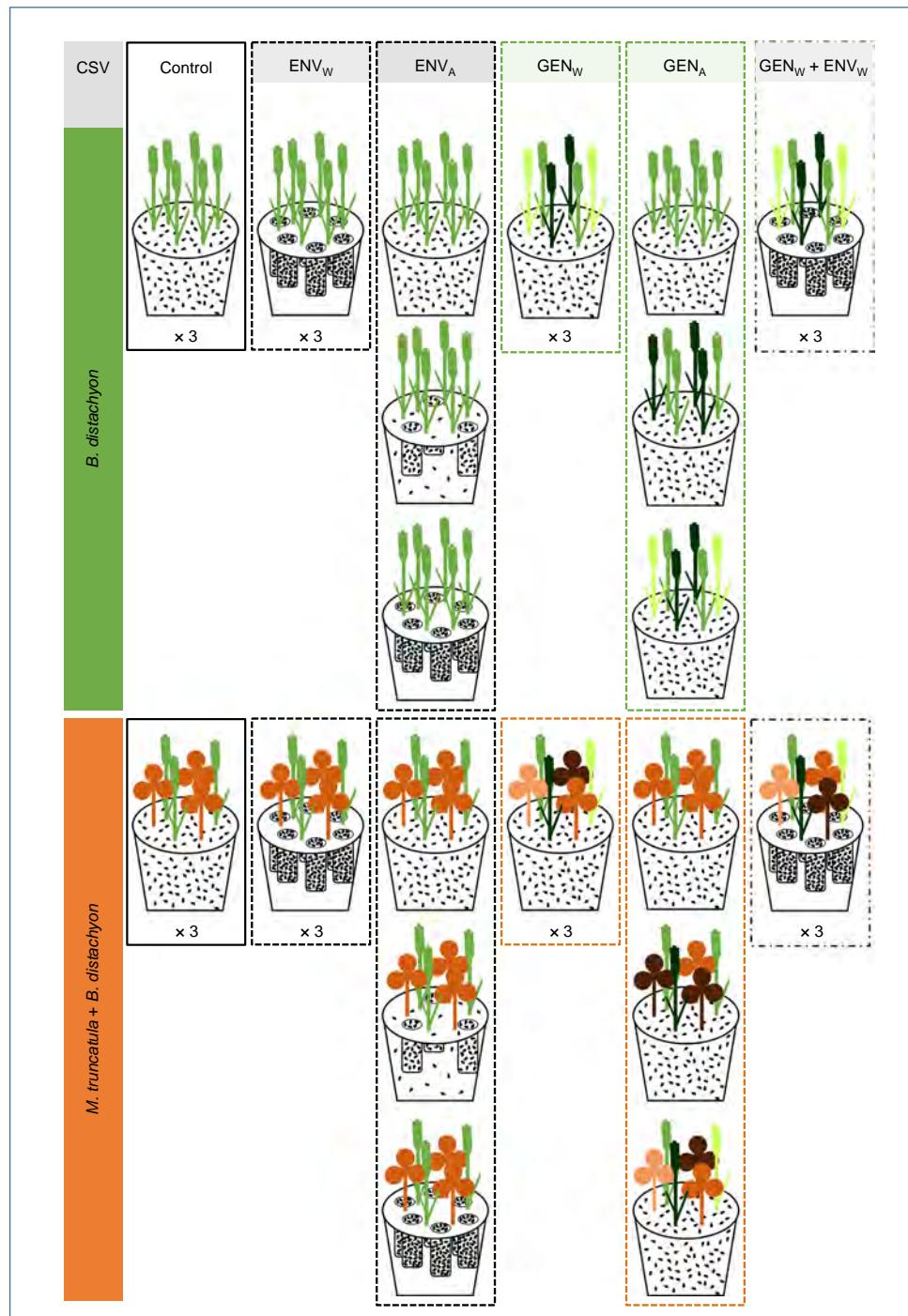


Fig. 1 | Experimental design of one block. Grass monocultures of *Brachypodium distachyon* (genotypes Bd21, Bd21-3 and Bd3-1 represented by green shades) and grass-legume mixtures with the legume *M. truncatula* (genotypes L000738, L000530 and L000174 represented by orange-brown shades) were established in 14 laboratories. Combinations of these distinct genotypes were used to establish genotypic CSV. Plants were established in a substrate with equal proportions of sand (black spots) and soil (white), with the sand being either mixed with the soil or concentrated in sand patches to induce environmental controlled systematic variability (CSV). As indicated, for some treatments, the same genotypic and sand composition was repeated in three microcosms per block. The spatial arrangement of the microcosms in each block was re-randomized every two weeks. For the growth chamber setups, the blocks represent two distinct chambers, whereas for glasshouse setups they represent two distinct growth benches in the same glasshouse.

principal components from a principal component analysis that included all 12 response variables. PC1 and PC2 together explained 45% of the variation (Table 1 and Supplementary Fig. 4a,b). Taken together, these results suggest that the effect size or direction of the net legume effect was significantly different (that is, not reproducible) in some laboratories and that the introduced CSV treatment affected

reproducibility. In a complementary analysis including the setup in the model (and accounting for the laboratory effect as a random factor), we found that the impact of the CSV treatment varied significantly with the setup (CSV × setup or legume × CSV × setup interactions; Supplementary Table 3), suggesting that the reproducibility of the results differed between glasshouses and growth chambers.

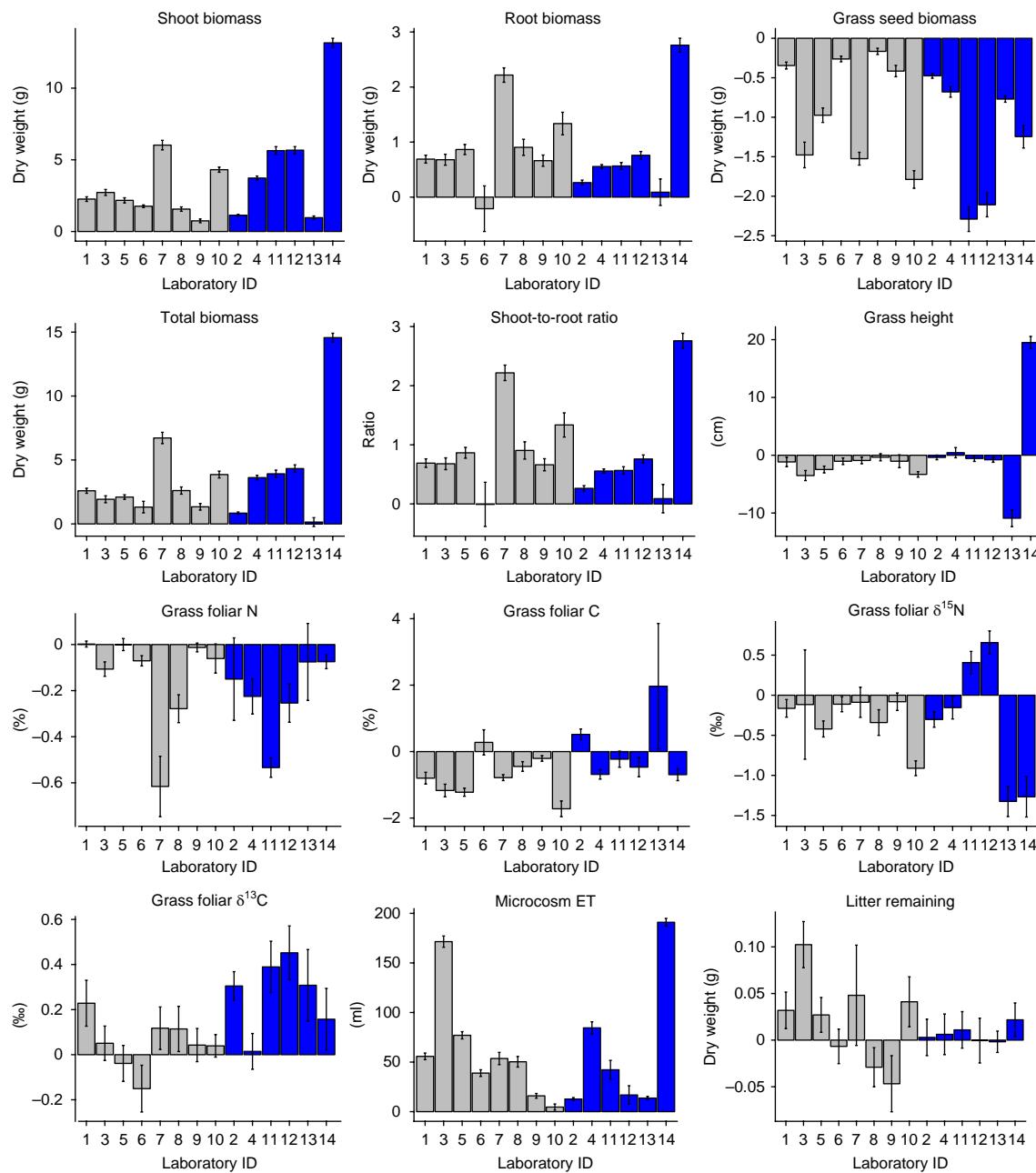


Fig. 2 | Net legume effect for the 12 response variables in 14 laboratories as affected by laboratory and setup (growth chamber versus glasshouse) treatments. The grey and blue bars represent laboratories that used growth chamber and glasshouse setups, respectively. ET, evapotranspiration. Bars show means by laboratory obtained by averaging over all CSV treatments, with error bars indicating ± 1 s.e.m. ($n=72$ microcosms per laboratory).

To answer the question of how many laboratories produced results that were statistically indistinguishable from one another (that is, reproduced the same finding), we used Tukey's post-hoc honest significant difference test for the laboratory effect on PC1 and PC2 describing the net legume effect, which together explained 49% of the variation (Supplementary Fig. 4c,d). Of the 14 laboratories, 7 (PC1) and 11 (PC2) were statistically indistinguishable in controls. This value increased in the treatments with environmental or genotypic CSV for PC1 but not PC2 (Table 2). When we analysed the responses in growth chambers alone, five of eight laboratories were statistically indistinguishable in controls, but this increased to six laboratories when we considered treatments with only environmental CSV and seven in treatments with genotypic CSV (GEN_w , GEN_A and GEN_w+ENV_w). In glasshouses, introducing CSV did not affect the number of statistically indistinguishable laboratories

with respect to PC1, but decreased the number of statistically indistinguishable laboratories with respect to PC2 (Table 2).

We also assessed the impact of the experimental treatments on the among- and within-laboratory s.d. Analysis of the among-laboratory s.d. of the net legume effect revealed a significant CSV \times setup interaction ($F_{5,121}=7.38$, $P<0.001$; Fig. 3a,b). This interaction included significantly lower fitted coefficients (that is, lower among-laboratory s.d.) in growth chambers for GEN_w ($t_{5,121}=-3.37$, $P=0.001$), GEN_A ($t_{5,121}=-2.95$, $P=0.004$) and ENV_w+GEN_w treatments ($t_{5,121}=-3.73$, $P<0.001$) relative to the control (see full model output for among-laboratory s.d. in the Supplementary Note). For these three treatments, the among-laboratory s.d. of the net legume effect was 18% lower with genotypic CSV than without it, indicating increased reproducibility (Fig. 3a). The same analysis performed on within-laboratory s.d. of the net legume effect only

Table 1 | Impact of experimental treatments on response variables

	DF	Shoot biomass (n=1,005)	Root biomass (n=989)	Seed biomass ^a (n=997)	Total biomass (n=976)	Shoot/root (n=987)	Grass height ^a (n=1,008)	Shoot N% ^a (n=1,008)
Legume	1	4602.95****	1131.65****	2186.64****	690.73****	1137.01****	3.33*	449.87****
CSV	5	15.57****	23.93****	58.01****	1.78 (NS)	23.98****	23.36****	0.78 (NS)
Laboratory	13	1088.67****	182.53****	364.57****	1251.96****	183.42****	317.33****	335.18****
Legume × CSV	5	23.64****	4.48****	33.62****	3.49***	4.51****	2.62**	1.34 (NS)
Legume × laboratory	13	235.99****	40.58****	78.17****	116.63****	40.38****	49.89****	14.12****
CSV × laboratory	65	6.55****	3.15****	6.93****	7.33****	3.17****	10.16****	1.98***
Legume × laboratory × CSV	65	2.22****	1.12 (NS)	2.70****	1.18 (NS)	1.12 (NS)	1.45**	1.71****
	DF	Shoot C% ^a (n=1,008)	Shoot δ ¹⁵ N ^a (n=963)	Shoot δ ¹³ C ^a (n=973)	Evapotranspiration (n=1,002)	Litter (n=974)	PC1 (n=1,008)	PC2 (n=1,008)
Legume	1	110.67****	14.43****	26.62****	1269.93****	1.81 (NS)	1242.53****	988.88****
CSV	5	0.16 (NS)	8.85****	75.73****	9.37****	1.05 (NS)	12.87****	22.56****
Laboratory	13	174.50****	258.30****	888.42****	748.66****	117.34****	920.65****	513.83****
Legume × CSV	5	2.55**	6.48****	5.15****	1.24 (NS)	1.77 (NS)	7.08****	11.79****
Legume × laboratory	13	11.90****	16.78****	2.52**	172.74****	2.05**	118.12****	28.22****
CSV × laboratory	65	1.67***	4.39****	4.97****	21.69****	2.97****	7.22****	2.76****
Legume × laboratory × CSV	65	1.33**	1.84****	1.23 (NS)	1.53***	1.17 (NS)	0.93 (NS)	1.65**

Mixed-effects model outputs summarizing the *F* and *P* values (as asterisks) for the impacts of the presence of legumes, CSV and laboratory on the 12 response variables. We also present the impact of experimental treatments on PC1 and PC2 of all 12 response variables.^aResponse variables measured for the grass *B. distachyon* only. The rest of the variables were measured at the microcosm level; that is, including the contribution of both the legume and the grass species.*****P*<0.001; ****P*<0.01; ***P*<0.05; **P*<0.1; DF, degrees of freedom; NS, not significant (*P*>0.1).

Table 2 | Impact of experimental treatments on the number of laboratories that reproduced the same finding

Source	All laboratories (n=14)		Glasshouses (n=6)		Growth chambers (n=8)	
	PC1	PC2	PC1	PC2	PC1	PC2
Control	7	11	3	5	5	5
ENV _W	10	9	3	3	6	6
ENV _A	8	8	3	4	6	6
GEN _W	8	10	3	3	6	7
GEN _A	11	10	3	3	7	8
ENV _W + GEN _W	11	10	4	3	7	7

Numbers represent the total number of statistically indistinguishable laboratories based on a Tukey's post-hoc honest significant difference test of PC1 and PC2 of the net legume effect of the 12 response variables (see Supplementary Fig. 4c,d for the principal component analysis results). For a detailed description of experimental treatments and abbreviations, see Fig. 1.

found a slight but significant increase of within-laboratory s.d. in the GEN_A treatment ($t_{5,121}=3.52$, $P<0.001$) (see model output for within-laboratory s.d. in the Supplementary Note). We then tested whether there was a relationship between within- and among-laboratory s.d. with a statistical model for among-laboratory s.d. as a function of within-laboratory s.d., setup, CSV and their interactions. We found a significant within-laboratory s.d. × setup × CSV three-way interaction ($F_{5,109}=2.4$, $P<0.040$) affecting among-laboratory s.d. (Supplementary Note). This interaction was the result of a more negative relationship between within- and among-laboratory s.d. in glasshouses relative to growth chambers, but with different slopes for the different CSV treatments (Fig. 4).

Introducing CSV can increase within-laboratory variation, as indicated by the positive coefficients fitted in some of the CSV treatments (see model output for within-laboratory s.d. in the Supplementary Note). Thus, for the three CSV treatments

that produced the most consistent results (GEN_W, GEN_A and ENV_W+GEN_W), we analysed the statistical power of detecting the net legume effect within individual laboratories. In growth chambers, adding genotypic CSV led to a slight reduction in statistical power relative to the control (57% in the control versus 46% in the three treatments containing genotypic variability) that could have been compensated for by using 11 instead of 6 replicated microcosms per treatment. In glasshouses, owing to a higher effect size of legume presence on the response variables, the statistical power for detecting the legume effect in the control was slightly higher (68%) than in growth chambers, but was reduced to 51% on average for the three treatments containing genotypic CSV—a decrease that could have been compensated for by using 16 replicated microcosms instead of 6.

Discussion

Overall, our study shows that results produced by microcosm experiments can be strongly biased by laboratory-specific factors. Based on the PC explaining most of the variation in the 12 response variables (PC1), only 7 of the 14 laboratories produced results that can be considered reproducible (Table 2) with the current standardization procedures. This result is in line with ref. ¹², which reports that out of ten laboratories, only four generated similar leaf growth phenotypes of *Arabidopsis thaliana* (L.). In addition to highlighting that approximately one in two ecological studies performed in microcosms under controlled environments produce statistically different results, our study provides supporting evidence for the hypothesis that introducing genotypic CSV can increase the reproducibility of ecological studies^{9–11}. However, the effectiveness of genotypic CSV for enhancing reproducibility varied with the setup; that is, it led to lower (~18%) among-laboratory s.d. in growth chambers only, with no benefit observed in glasshouses. Lower among-laboratory s.d. in growth chambers implies that the microcosms containing genotypic CSV were less strongly affected by unaccounted-for laboratory-specific environmental or biotic variables. Analyses performed at the level of individual variables (Table 1) showed that introduc-

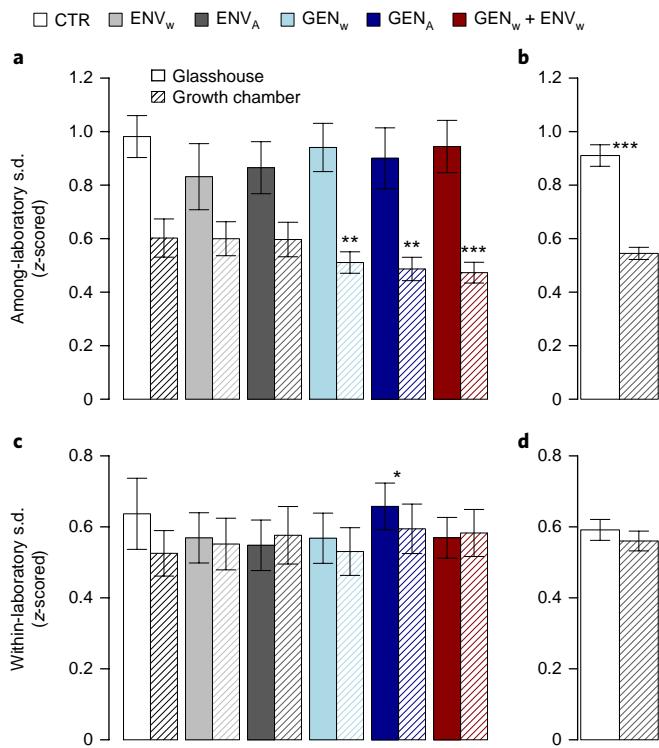


Fig. 3 | Among- and within-laboratory s.d. of the net legume effect as affected by experimental treatments. **a,b**, Among-laboratory s.d. as affected by CSV and setup (**a**) and setup only (**b**). **c,d**, Within-laboratory s.d. as affected by CSV and setup (**c**) and setup only (**d**). Lower among-laboratory s.d. indicates enhanced reproducibility. Solid and striped bars represent glasshouse ($n=6$) and growth chamber setups ($n=8$), respectively. P values ($***P < 0.001$, $**P < 0.01$ and $*P < 0.05$) indicate significantly different fitted coefficients according to the mixed-effects models (see Supplementary Note for full model outputs). The asterisk in **c** indicates the significant difference between GEN_A and the control, irrespective of the type of setup.

ing genotypic CSV affected the among-laboratory s.d. in most, but not all variables. This suggests that the relationship between genotypic CSV and reproducibility is probabilistic and results from the decreased likelihood that microcosms containing CSV will respond to unaccounted-for laboratory-specific environmental factors in the same direction and with the same magnitude. The mechanism is likely to be analogous to the stabilizing effect of biodiversity on ecosystem functions under changing environmental conditions^{23–26}, but additional empirical evidence is needed to confirm this conjecture.

Introducing genotypic CSV increased reproducibility in growth chambers (with stringent control of environmental conditions), but not in glasshouses (with more variable environmental conditions). Higher among-laboratory s.d. in glasshouses may indicate the existence therein of stronger laboratory-specific factors and our deliberate use of different soils in the glasshouses presumably contributed to this effect. However, the among-laboratory s.d. in glasshouses decreased with increasing within-laboratory s.d., irrespective of CSV—an effect that was less clear in growth chambers (Fig. 4). This observation appears to be in line with the hypothesis put forward in ref. ⁹, where it was proposed that increasing the variance within experiments can reduce the among-laboratory variability of the mean effect sizes observed in each laboratory. Yet, despite the negative correlation between within- and among-laboratory s.d. observed in glasshouses, the among-laboratory s.d. remained higher in glasshouses than growth chambers. Therefore, we consider that the hypothesized mechanistic link between

CSV-induced higher within-laboratory s.d. and increased reproducibility is poorly supported by our dataset. Nevertheless, one possible explanation for the lack of effect on reproducibility in glasshouses is that our CSV treatments did not introduce a sufficiently high level of within-laboratory variability to buffer against laboratory-specific factors for all response variables; across the 12 response variables, the average main effect (that is, without the interaction terms) of the CSV treatment contributed to a low percentage ($2.6\% \pm 1.6$ s.e.m.) of the total sum of squares relative to the main effects of laboratory ($43.4\% \pm 5.2$ s.e.m.) and legumes ($10.9\% \pm 3.1$ s.e.m.). A similar conjecture was put forward by the other two studies that explored the role of CSV for reproducibility in animal behaviour^{9,10}. At present, we are unable to conclude that the introduction of stronger sources of controlled within-laboratory variability can increase reproducibility in glasshouses with more loosely controlled environmental conditions and different soils.

Our results indicate that genotypic CSV is more effective at increasing reproducibility than environmental CSV, irrespective of whether the CSV is introduced within or among individual replicates (that is, microcosms). However, we cannot discount the possibility that we found this result because our treatments with environmental CSV were less successful in increasing within-microcosm variability. Additional experiments could test whether other types of environmental CSV, such as soil nutrients, texture or water availability, might be more effective at increasing reproducibility.

We expected higher overall productivity (that is, a net legume effect) in the grass-legume mixtures and enhanced growth of *B. distachyon* because of the presence of the nitrogen-fixing *M. truncatula*. However, these species were not selected because of their routine pairings in agronomic or ecological experiments (they are rarely used that way), but rather because they are frequently present in controlled environment experiments looking at functional genomics. In contrast with our expectation and despite the generally lower ¹⁵N signature of *B. distachyon* in the presence of nitrogen-fixing *M. truncatula* (suggesting that some of the nitrogen fixed by *M. truncatula* was taken up by the grass), the biomass of *B. distachyon* was lower in the microcosms containing *M. truncatula*. The seed mass and shoot N% data of *B. distachyon* were lower in mixtures (Supplementary Fig. 1), suggesting that the two species competed for nitrogen. The lack of a significant nitrogen fertilization effect of *M. truncatula* on *B. distachyon* could have resulted from the asynchronous phenologies of the two species: the eight- to ten-week life cycle of *B. distachyon* may have been too short to benefit from the nitrogen fixation by *M. truncatula*.

Because well-established meta-analytical approaches can account for variation caused by local factors and still detect the general trends across different types of experimental setup, environment and population, we should ask whether the additional effort required for introducing CSV in experiments is worthwhile. Considering the current reproducibility crisis in many fields of science²⁷, we suggest that it is, for at least three reasons. First, some studies become seminal without any attempts to reproduce them. Second, even if a seminal study that is flawed due to laboratory-specific biases is later proven wrong, it usually takes significant time and resources before its impact on the field abates. Third, the current rate of reproducibility is estimated to be as low as one-third^{12–14}, implying that most data entering any meta-analysis are biased by unknown laboratory-specific factors. The addition of genotypic CSV may enhance the reproducibility of individual experiments and eliminate potential biases in the data used in meta-analyses. Additionally, if each individual study was less affected by laboratory-specific unknown environmental and biotic factors, we would also need fewer studies to draw solid conclusions about the generality of phenomena. Therefore, we argue that investing more in making individual studies more reproducible and generalizable will be beneficial in both

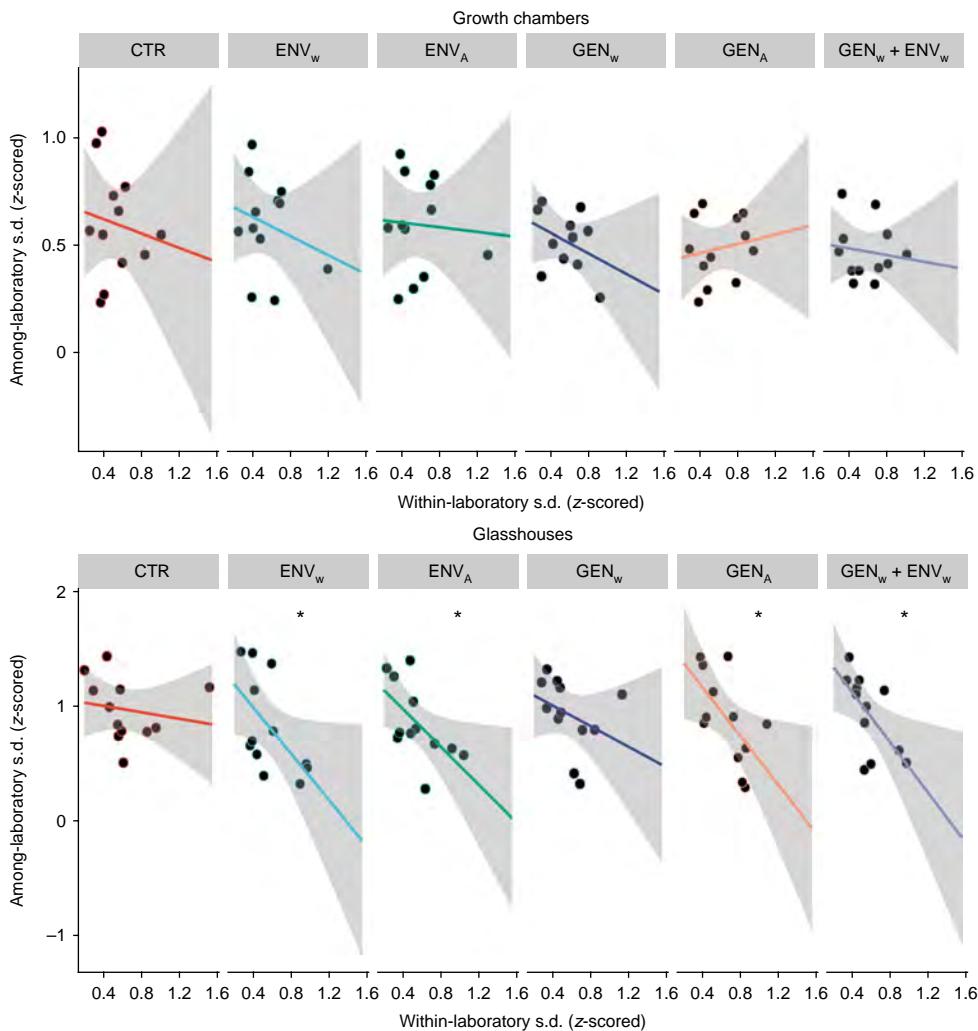


Fig. 4 | Relationship between within-laboratory s.d. and among-laboratory s.d. of the net legume effect as affected by experimental treatments.

Significant within-laboratory s.d. \times setup \times CSV three-way interaction ($F_{5,109} = 2.4$, $P < 0.040$) affecting among-laboratory s.d. (Supplementary Note). This interaction is the result of a more negative relationship between within- and among-laboratory s.d. in glasshouses relative to growth chambers, but with different slopes for the different CSV treatments. Points represent the 12 response variables. Asterisks represent P values < 0.05 for the individual linear regressions. Note the different scale for the y-axis between growth chambers and glasshouses.

the short and long term. At the same time, adding CSV can reduce the statistical power to detect experimental effects, so some additional experimental replicates would be needed when using it.

Arguably, our use of statistical significance tests of effect sizes to determine reproducibility might be viewed as overly restrictive and better suited to assessing the reproducibility of parameter estimates rather than the generality of the hypothesis under test²⁷. We used this approach because no generally accepted alternative framework is available to assess how close the multivariate results from multiple laboratories need to be to conclude that they reproduced the same finding. It is worth noting that although the direction of the legume effect was the same in the majority of laboratories, the differences among laboratories were very large (for example, up to two orders of magnitude for shoot biomass) and in 10% of the 168 laboratory \times variable combinations (14 laboratories \times 12 response variables) the direction of the legume effect differed from the among-laboratory consensus (Fig. 2).

Conclusion

Our study shows that the current standardization procedures used in ecological microcosm experiments are inadequate in accounting

for laboratory-specific environmental factors and suggests that introducing controlled variability in experiments may buffer some of the effects of laboratory-specific factors. Although there are multiple causes for the reproducibility crisis^{15,28,29}, deliberately including genetic variability in the studied organisms may turn out to be a simple solution for increasing the reproducibility of ecological studies performed in controlled environments. However, as the introduced genotypic variability only increased reproducibility in experimental setups with tightly controlled environmental conditions (that is, in growth chambers using identical soil), our study indicates that the reproducibility of ecological experiments may be enhanced by a combination of rigorous standardization of environmental variables at the laboratory level as well as controlled genotypic variability.

Methods

All laboratories tried, to the best of their abilities, to carry out identical experimental protocols. While not all laboratories managed to precisely recreate all of the details of the experimental protocol, we considered this to be a realistic scenario under which ecological experiments using microcosms are performed in glasshouses and growth chambers.

Germination. The seeds from three genotypes of *B. distachyon* (Bd21, Bd21-3 and Bd3-1) and *M. truncatula* (L000738, L000530 and L000174) were first sterilized by soaking 100 seeds in 100 ml of a sodium hypochlorite solution with 2.6% active chlorine, which was stirred for 15 min using a magnet. Thereafter, the seeds were rinsed three times in 250 ml of sterile water for 10–20 s under shaking. Sterilized seeds were germinated in trays (10 cm deep) filled with vermiculite. The trays were kept at 4 °C in the dark for 3 days before being moved to light conditions (300 $\mu\text{mol m}^{-2}\text{s}^{-1}$ photosynthetically active radiation) and 20 °C and 60% relative air humidity during the day and 16 °C and 70% relative air humidity at night. When the seedlings of both species reached 1 cm in height above the vermiculite, they were transplanted into the microcosms.

Preparation of microcosms. All laboratories used identical containers (21 volume, 14.8 cm diameter and 17.4 cm height). Sand patches were created using custom-made identical ‘patch makers’ consisting of six rigid polyvinyl chloride tubes (2.5 cm in diameter and 25 cm long) arranged in a circular pattern with an outer diameter of 10 cm. A textile mesh was placed at the bottom of the containers to prevent the spilling of soil through drainage holes. The filling of microcosms containing sand patches started with the insertion of the empty tubes into the containers. Thereafter, in growth chambers, 2,000 g dry weight of soil, subtracting the weight of the sand patches, was added to the containers and around the ‘patch maker’ tubes. Because different soils were used in the glasshouses, the dry weight of the soil differed depending on the soil density and was first estimated individually in each laboratory as the amount of soil needed to fill the pots up to 2 cm from the top. After the soil was added to the containers, the tubes were filled with a mixture of 10% soil and 90% sand. When the microcosms did not contain sand patches, the amount of sand otherwise contained in the six patches was homogenized with the soil. During the filling of the microcosms, a common substrate for measuring litter decomposition was inserted at the centre of the microcosm at 8 cm depth. For simplicity, as well as for its fast decomposition rate, we used a single batch of commercially available tetrahedron-shaped synthetic tea bags (mesh size of 0.25 mm) containing 2 g of green tea (Lipton; Unilever), as proposed by the ‘tea bag index’ method²⁰. Once filled, the microcosms were watered until water could be seen pouring out of the pot. The seedlings were then manually transplanted to pre-determined positions (Fig. 1), depending on the genotype and treatment. Each laboratory established two blocks of 36 microcosms, resulting in a total of 72 microcosms per laboratory, with blocks representing two distinct chambers in the growth chamber setups or two distinct growth benches in the same glasshouse.

Soils. All laboratories using growth chamber setups used the same soil, whereas the laboratories using glasshouses used different soils (see Supplementary Table 1 for the physico-chemical properties of the soils). The soil used in growth chambers was classified as a nutrient-poor cambisol and was collected from the top layer (0–20 cm) of a natural meadow at the Centre de Recherche en Ecologie Expérimentale et Prédictive (Saint-Pierre-lès-Nemours, France). Soils used in glasshouses originated from different locations. The soil used by laboratory 2 was a fluvisol collected from the top layer (0–40 cm) of a quarry site near Avignon in the Rhône valley, Southern France. The soil used by laboratory 4 was collected from near the La Cage field experimental system (Versailles, France) and was classified as a luvisol. The soil used by laboratories 11 and 12 was collected from the top layer (0–20 cm) within the haugh of the river Dreisam in the East of Freiburg, Germany. This soil was classified as an umbric gleysol with high organic carbon content. The soil used by laboratory 14 was classified as a eutric fluvisol and was collected on the field site of the Jena Experiment, Germany. Before the establishment of microcosms, all soils were air-dried at room temperature for several weeks and sieved using a 2 mm mesh sieve. A common inoculum was provided to all laboratories to ensure that rhizobia specific to *M. truncatula* were present in all soils.

Abiotic environmental conditions. The set points for environmental conditions were 16 h light (at 300 $\mu\text{mol m}^{-2}\text{s}^{-1}$ photosynthetically active radiation) and 8 h dark, at 20 °C and in 60% relative air humidity during the day and 16 °C and 70% relative air humidity at night. Different soils (for glasshouses) and treatments with sand patches likely affected water drainage and evapotranspiration. The watering protocol was thus based on dry weight relative to weight at full water-holding capacity (WHC). The WHC was estimated based on the weight difference between the dry weight of the containers and the wet weight of the containers 24 h after abundant watering (until water was flowing out of the drainage holes in the bottom of each container). Soil moisture was maintained between 60 and 80% of WHC (that is, the containers were watered when the soil water dropped below 60% of WHC and water was added to reach 80% of WHC) during the first 3 weeks after seedling transplantation and between 50 and 70% of WHC for the rest of the experiment. Microcosms were watered twice a week with estimated WHC values from two microcosms per treatment. To ensure that the patch/heterogeneity treatments did not become a water availability treatment, all containers were weighed and brought to 70 or 80% of WHC every 2 weeks. This operation was synchronized with within-block randomization. All 14 experiments were performed between October 2014 and March 2015.

Sampling and analytical procedures. After 80 days, all plants were harvested. Plant shoots were cut at the soil surface, separated by species and dried at 60 °C for 3 days. Roots and any remaining litter in the tea bags were washed out of the soil using a 1 mm mesh sieve and dried at 60 °C for 3 days. The microcosm evapotranspiration rate was measured before the harvesting as the difference in weight changes from 70% of WHC after 48 h. Shoot C%, N%, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ were measured on pooled shoot biomass (including seeds) of *B. distachyon* and analysed at the Göttingen Centre for Isotope Research and Analysis using a coupled system consisting of an Elemental Analyzer (NA 1500; Carlo-Erba) and a gas isotope mass spectrometer (Finnigan MAT 251; Thermo Electron Corporation).

Data analysis and statistics. All analyses were done using R version 3.2.4 (ref. ³⁰). Before data analyses, each laboratory was screened individually for outliers. Values that were lower or higher than $1.5 \times$ interquartile range³¹ within each laboratory, and representing less than 1.7% of the whole dataset, were considered to be outliers due to measurement errors or typos. These values were removed and subsequently treated as missing values. We then assessed whether the impact of the presence of legume varied with laboratory and the treatment of CSV. This was tested individually for each response variable (Table 1) with a mixed-effects model using the ‘nlme’ package³². Following the guidelines suggested by ref. ³³, we first identified the most appropriate random structure using a restricted maximum likelihood approach and then selected the random structure with the lowest Akaike information criterion. For this model, CSV and laboratory were included as fixed factors, as well as experimental block as a random factor and a ‘varIdent’ weighting function to correct for heteroscedasticity resulting from more heteroscedastic data at the laboratory and legume level (R syntax: ‘model = lme (response variable ~ legume*CSV*laboratory, random = ~1|block, weights = varIdent (form = ~1|laboratory*legume)’) (Table 2). As the laboratory and setup experimental factors were not fully crossed (that is, laboratories performed the experiment only in one type of setup), the two experimental variables could not be included simultaneously as fixed effects. Therefore, to test for the setup effect, we used an additional complementary model including CSV and setup as fixed effects and laboratory as a random factor (R syntax: ‘model = lme (response variable ~ legume*CSV*setup, random = ~1|laboratory/block, weights = varIdent (form = ~1|laboratory*legume)’) (Supplementary Table 3). To test whether the results were affected by the collinearity among the response variables, the two models were also run on PC1 and PC2 of the 12 response variables (Fig. 4a,b). PCs were estimated using the ‘FactoMineR’ package³⁴, with missing values replaced using a regularized iterative multiple correspondence analysis³⁵ in the ‘missMDA’ package³⁶. The same methodology was used to compute a second principal component analysis derived from the net legume effect on the 12 response variables (Supplementary Fig. 3c,d). To assess how many laboratories produced results that were statistically indistinguishable from one another, we applied Tukey’s post-hoc honest significant difference test in the ‘multcomp’ package to laboratory-specific estimates of PC1 and PC2 (Table 2).

To assess how the CSV treatments affected the among- and within-laboratory variability, we used the s.d. instead of the coefficient of variation, because the net legume effect contained both positive and negative values. To calculate among- and within-laboratory s.d., we centred and scaled the raw values using the z-score normalization (z-scored variable = (raw value – mean)/s.d.) individually for each of the 12 response variables. Among-laboratory s.d. was computed from the mean of the laboratory z-scores for each response variable, CSV and setup treatment ($n = 144$; 6 CSV levels \times 2 setup levels \times 12 response variables). Within-laboratory s.d. was computed from the values measured in the six replicated microcosms for each CSV and setup treatment combination, individually for each response variable, resulting in a dataset with the same structure as that for among-laboratory s.d. ($n = 144$; 6 CSV levels \times 2 setup levels \times 12 response variables). Some of the 12 response variables were intrinsically correlated, but most had correlation coefficients < 0.5 (Supplementary Fig. 5) and were therefore treated as independent variables. To analyse and visualize the relationships between the s.d. calculated from variables with different units, before the calculation of the among- and within-laboratory s.d., the raw values of the 12 response variables were centred and scaled.

The impact of experimental treatments on among- and within-laboratory s.d. was analysed using mixed-effects models following the same procedure described for the individual response variables. The model with the lowest Akaike information criterion included a random slope for the setup within each response variable, as well as a ‘varIdent’ weighting function to correct for heteroscedasticity at the variable level (R syntax: ‘model = lme (s.d. ~ CSV*setup, random = ~setup|variable, weights = varIdent (form = ~1|variable)’) (see also Supplementary Note). The relationship between within- and among-laboratory s.d. was also tested with a model with similar random structure but with among-laboratory s.d. as a dependent variable and within-laboratory s.d., CSV and setup as predictors.

Because the treatments containing genotypic CSV increased reproducibility in growth chambers but slightly increased within-laboratory s.d., we also examined the effect of adding CSV on the statistical power for detecting the net legume effect in each individual laboratory. This analysis was done with the ‘power.anova.test’ function in the ‘base’ package. We computed the statistical power of detecting a

significant net legume effect (if one had used a one-way analysis of variance for the legume treatment) for the control, GEN_w, GEN_A and ENV_w+GEN_w treatments for each laboratory and response variable. This allowed us to calculate the average statistical power for the aforementioned treatments and how many additional replicates would have been needed to achieve the same statistical power as we had in the control.

Life sciences reporting summary. Further information on experimental design is available in the Life Sciences Reporting Summary.

Data availability. The data that support the findings of this study are publicly available at <https://doi.pangaea.de/10.1594/PANGAEA.880980>.

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Author contributions

A.M. and J.R. designed the study with input from M. Blouin, S.B., M. Bonkowski and J.-C.L. Substantial methodological contributions were provided by S.S., T.G., L.R. and M.S.-L. Conceptual feedback on an early version was provided by G.T.F., N.E., J.R. and A.M.E. Data were analysed by A.M. with input from A.M.E. A.M. wrote the manuscript with input from all authors. All authors were involved in carrying out the experiments and/or analyses.

Competing interests

The authors declare no competing financial interests.

Additional information

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Corresponding author(s): Alexandru Milcu

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► Experimental design

1. Sample size

Describe how sample size was determined.

As the aim of our study was to test how reproducible are typical microcosm experiments, we used a typical sample size for this type of experiment, i.e. six replicated microcosms per treatment. We also report the statistical power for the different treatments.

2. Data exclusions

Describe any data exclusions.

Data from each laboratory was first screen individually for outliers. We found that there was an inaccuracy in the earlier description of the outlier removal procedure. We used the Tukey fences method and considered that values that are higher or lower than $1.5 \times$ interquartile range are outliers. This is now corrected in text and we added the relevant citation [Tukey, John W (1977). Exploratory Data Analysis]. These values are considered to be measurement errors and typos, etc. We applied the outlier removal after visually inspecting the data, but without knowing the impact on the results.

3. Replication

Describe whether the experimental findings were reliably reproduced.

The conclusions are based on the results from repeating the same experiment in eight growth chambers and six glasshouses.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

We used a randomized block design in each laboratory, with the blocks representing two distinct chambers in growth chamber setups, whereas in glasshouse setups the blocks represent two distinct growth benches in the same glasshouse. The spatial arrangement of the microcosms in each block was re-randomized every two weeks.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

The investigators were not blinded to group allocation during data collection and/or analysis.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- A statement indicating how many times each experiment was replicated
- The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
- A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

All analyses were performed using R version 3.2.4.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). [Nature Methods guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

Not applicable.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Not applicable.

10. Eukaryotic cell lines

- a. State the source of each eukaryotic cell line used.
- b. Describe the method of cell line authentication used.
- c. Report whether the cell lines were tested for mycoplasma contamination.
- d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

Not applicable.

Not applicable.

Not applicable.

Not applicable.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

Not applicable.

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

Not applicable.

In the format provided by the authors and unedited.

Genotypic variability enhances the reproducibility of an ecological study

Alexandru Milcu^{1,2*}, Ruben Puga-Freitas³, Aaron M. Ellison^{4,5}, Manuel Blouin^{3,6}, Stefan Scheu⁷, Grégoire T. Freschet², Laura Rose⁸, Sébastien Barot⁹, Simone Cesarz^{10,11}, Nico Eisenhauer^{10,11}, Thomas Girin¹², Davide Assandri¹³, Michael Bonkowski¹⁴, Nina Buchmann¹⁵, Olaf Butenschönen^{7,16}, Sébastien Devidal¹, Gerd Gleixner¹⁷, Arthur Gessler^{18,19}, Agnès Gigon³, Anna Greiner⁸, Carlo Grignani¹³, Amandine Hansart²⁰, Zachary Kayler^{19,21}, Markus Lange¹⁷, Jean-Christophe Lata²², Jean-François Le Galliard^{20,22}, Martin Lukac^{23,24}, Neringa Mannerheim¹⁵, Marina E. H. Müller¹⁸, Anne Pando⁶, Paula Rotter⁸, Michael Scherer-Lorenzen^{10,11}, Rahme Seyhun²², Katherine Urban-Mead², Alexandra Weigelt^{10,11}, Laura Zavattaro¹³ and Jacques Roy¹

¹Ecotron (Unité Propre de Service 3248), Centre National de la Recherche Scientifique, Campus Baillarguet, Montferrier-sur-Lez, France. ²Centre d'Ecologie Fonctionnelle et Evolutive, Centre National de la Recherche Scientifique, Unité Mixte de Recherche 5175, Université de Montpellier/Université Paul Valéry - École Pratique des Hautes Études, Montpellier, France. ³Institut de l'Ecologie et des Sciences de l'Environnement de Paris, Université Paris-Est Créteil, Créteil, France. ⁴Harvard Forest, Harvard University, Petersham, MA, USA. ⁵Tropical Forests and People Research Centre, University of the Sunshine Coast, Maroochydore DC, Queensland, Australia. ⁶Agroécologie, AgroSup Dijon, Institut National de la Recherche Agronomique, Université Bourgogne Franche-Comté, Dijon, France. ⁷Johann-Friedrich-Blumenbach Institute for Zoology and Anthropology, Georg August University Göttingen, Göttingen, Germany. ⁸Department of Geobotany, Faculty of Biology, University of Freiburg, Freiburg, Germany. ⁹Institut de Recherche pour le Développement, Institut de l'Ecologie et des Sciences de l'Environnement de Paris, Université Pierre et Marie Curie, Paris, France. ¹⁰German Centre for Integrative Biodiversity Research, Halle-Jena-Leipzig, Leipzig, Germany. ¹¹Institute of Biology, Leipzig University, Leipzig, Germany. ¹²Institut Jean-Pierre Bourgin, INRA, AgroParisTech, Centre National de la Recherche Scientifique, Université Paris-Saclay, Versailles, France. ¹³Department of Agricultural, Forest and Food Sciences, University of Turin, Grugliasco, Italy. ¹⁴Cluster of Excellence on Plant Sciences, Terrestrial Ecology Group, Institute for Zoology, University of Cologne, Cologne, Germany. ¹⁵Institute of Agricultural Sciences, ETH Zurich, Zurich, Switzerland. ¹⁶Senckenberg Biodiversität und Klima Forschungszentrum, Frankfurt, Germany. ¹⁷Max Planck Institute for Biogeochemistry, Postfach 100164, Jena, Germany. ¹⁸Leibniz Centre for Agricultural Landscape Research, Institute of Landscape Biogeochemistry, Müncheberg, Germany. ¹⁹Swiss Federal Research Institute, Zürcherstrasse 111, Birmensdorf, Switzerland. ²⁰Département de Biologie, Ecole Normale Supérieure, Université de recherche Paris Sciences & Lettres Research University, Centre National de la Recherche Scientifique, Unité Mixte de Service 3194 (Centre de Recherche en Ecologie Expérimentale et Prédictive-Ecotron IleDeFrance), Saint-Pierre-lès-Nemours, France. ²¹Department of Soil and Water Systems, University of Idaho, Moscow, ID, USA. ²²Institut de l'Ecologie et des Sciences de l'Environnement de Paris, Sorbonne Universités, Paris, France. ²³School of Agriculture, Policy and Development, University of Reading, Reading, UK. ²⁴Faculty of Forestry and Wood Sciences, Czech University of Life Sciences, Prague, Czech Republic. *e-mail: alex.milcu@cnrs.fr

23 **Supplementary Table 1 | Physico-chemical properties of the soils used in growth chamber and glasshouse setups.**

SETUP	Lab ID	C (g/kg)	N (g/kg)	C/N	Organic matter (g/kg)	P (g/kg)	Cation exchange (cmol+/kg)	Clay (g/100g)	Silt (g/100g)	Sand (g/100g)	pH
Growth chamber	L1, L3, L5, L6, L7, L8, L9, L10	7.26	0.57	12.67	12.57	0.09	3.46	10.53	19.23	70.23	5.88
Glasshouse	L2	7.41	0.45	15.23	12.83	<0.005	3.06	8.43	23.87	67.70	8.68
Glasshouse	L4	19.73	1.63	12.13	34.17	0.12	10.80	18.57	36.63	44.80	6.66
Glasshouse	L11, L12	50.03	4.58	10.90	86.53	0.05	16.73	22.83	25.00	52.17	5.35
Glasshouse	L13	16.83	1.94	8.67	29.10	0.19	8.02	18.00	10.00	72.00	5.78
Glasshouse	L14	20.13	1.83	11.00	34.77	0.06	10.70	22.60	45.97	31.23	8.23

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32 **Supplementary Table 2 | The net legume effect on measured response variables as affected by SETUP (glasshouse vs. growth**
 33 **chamber).** Selected variables are typical for plant-soil microcosm experiments measuring plant productivity, biomass allocation,
 34 shoot tissue chemistry, evapotranspiration and litter decomposability (BM = biomass). † symbol indicates response variables
 35 measured for the grass *B. distachyon* only, while the rest of the variables have been measured at the microcosm level, i.e. including the
 36 contribution of both the legume and the grass species.

Variable abbreviation	Description	Unit	Mean net legume effect (\pm SE)	
			Glasshouse	Growth chamber
Shoot BM	shoot biomass	g DW	5.05 \pm 0.29	2.72 \pm 0.11
Root BM	root biomass	g DW	0.80 \pm 0.08	0.96 \pm 0.08
Seed BM [†]	<i>B. distachyon</i> total seed biomass	g DW	-1.28 \pm 0.07	0.88 \pm 0.05
Total BM	total biomass (shoot + root + seeds)	g DW	4.57 \pm 0.34	2.80 \pm 0.15
Shoot.Root	shoot (+seed) to root biomass ratio	dimensionless	-2.51 \pm 0.28	-0.88 \pm 0.13
Grass height [†]	<i>B. distachyon</i> average size	cm	1.17 \pm 0.72	-1.87 \pm 0.28
Shoot N% [†]	<i>B. distachyon</i> shoot (+seed) nitrogen %	%	-0.26 \pm 0.04	-0.16 \pm 0.02
Shoot C% [†]	<i>B. distachyon</i> shoot (+seed) carbon %	%	0.32 \pm 0.0	0.73 \pm 0.07
Shoot $\delta^{15}\text{N}$ [†]	<i>B. distachyon</i> shoot (+seed) $\delta^{15}\text{N}$ signature	\textperthousand	-0.27 \pm 0.09	-0.29 \pm 0.1
Shoot $\delta^{13}\text{C}$ [†]	<i>B. distachyon</i> shoot (+seed) $\delta^{13}\text{C}$ signature	\textperthousand	0.26 \pm 0.04	0.05 \pm 0.03
ET	evapotranspiration prior to experimental harvest	$\text{ml}^{-24\text{h}}$	67.27 \pm 5.41	59.8 \pm 3.29
Litter	litter substrate remaining at the end of experiment	g DW	0.01 \pm 0.009	0.04 \pm 0.01

38 **Supplementary Table 3 | Complementary analysis for the results from Table 1 (article text) presenting the impact of**
 39 **experimental treatments on response variables using laboratory ID as a random factor.** Mixed-effects output summarizing the
 40 F- and P-values (as asterisks) for impact of the presence of legumes (LEG), controlled systematic variability (CSV) and laboratory
 41 setup (SETUP) on the 12 response variables. In addition to the results for the 12 response variables, we also present the effect of
 42 experimental treatments on the first second principal components (PC1 and PC2) summarizing all 12 response variables. The response
 43 variables shown represent a typical ensemble of variables measured in plant-soil microcosm experiments (BM = biomass). † symbol
 44 indicates response variables measured for the grass *B. distachyon* only, while the rest of the variables have been measured at the
 45 microcosm level, i.e. including the contribution of both the legume and the grass species. Asterisks indicate the significance levels
 46 (***) for $P < 0.001$; ** for $P < 0.01$; * for $P < 0.05$; + for $P < 0.1$; ns for $P > 0.1$). DF = numerator degrees of freedom.
 47

	DF	Shoot BM	Root BM	Seed BM [†]	Total BM	Shoot/Root	Grass height [†]	Shoot N% [†]
LEG	1	1843.37 (***)	705.35 (***)	729.57 (***)	637.80 (***)	706.29 (***)	30.90 (***)	54.14 (***)
CSV	5	9.10 (***)	20.91 (***)	39.52 (***)	3.87 (**)	21.00 (***)	20.16 (***)	0.75 (ns.)
SETUP	1	2.99 (ns.)	7.35 (*)	1.34 (ns.)	0.75 (ns.)	7.52 (*)	5.28 (*)	15.13 (**)
LEG×CSV	5	12.41 (***)	3.30 (**)	21.51 (***)	0.55 (ns.)	3.32 (**)	1.70 (ns.)	1.28 (ns.)
LEG×SETUP	1	209.81 (***)	30.33 (**)	87.11 (***)	132.91 (***)	30.37 (***)	10.92 (**)	35.93 (***)
CSV×SETUP	5	23.31 (***)	5.59 (***)	22.70 (***)	18.34 (***)	5.57 (***)	3.37 (**)	0.91(ns.)
LEG×CSV×SETUP	5	7.34 (***)	1.03 (ns.)	0.82 (ns)	1.13 (ns.)	1.00 (ns.)	2.58 (*)	3.77 (**)
	n = 1005	n = 989	n = 997	n = 976	n = 987	n = 1008	n = 1008	
	DF	Shoot C% [†]	Shoot δ ¹⁵ N [†]	Shoot δ ¹³ C [†]	ET	Litter	PC1	PC2
LEG	1	197.32 (***)	56.15 (***)	22.20 (***)	650.80 (***)	3.63 (+)	1002.71 (***)	588.49 (***)
CSV	5	0.02 (ns.)	8.07 (***)	77.50 (***)	1.20 (***)	0.79 (ns.)	9.43 (***)	28.11 (***)

SETUP	1	4.98 (*)	0.32 (ns.)	0.55 (ns.)	0.08 (ns.)	0.03 (ns.)	0.00 (ns.)	12.27 (**)
LEG×CSV	5	2.31 (*)	6.38 (***)	6.55 (***)	0.50 (ns.)	2.08 (+)	2.84 (*)	10.12 (***)
LEG×SETUP	1	11.56 (***)	4.61(*)	16.98 (***)	281.92 (***)	1.03 (ns.)	2.31 (ns.)	6.59 (*)
CSV×SETUP	5	2.05 (+)	6.76 (***)	9.89 (***)	12.44 (***)	1.38 (ns.)	15.65 (***)	1.42 (ns.)
LEG×CSV×SETUP	5	0.65 (ns.)	1.56 (ns.)	0.98 (ns.)	4.31 (***)	1.24 (ns.)	10.03 (***)	1.42 (ns.)
		n = 1008	n = 963	n = 973	n = 1002	n = 974	n = 1008	n = 1008

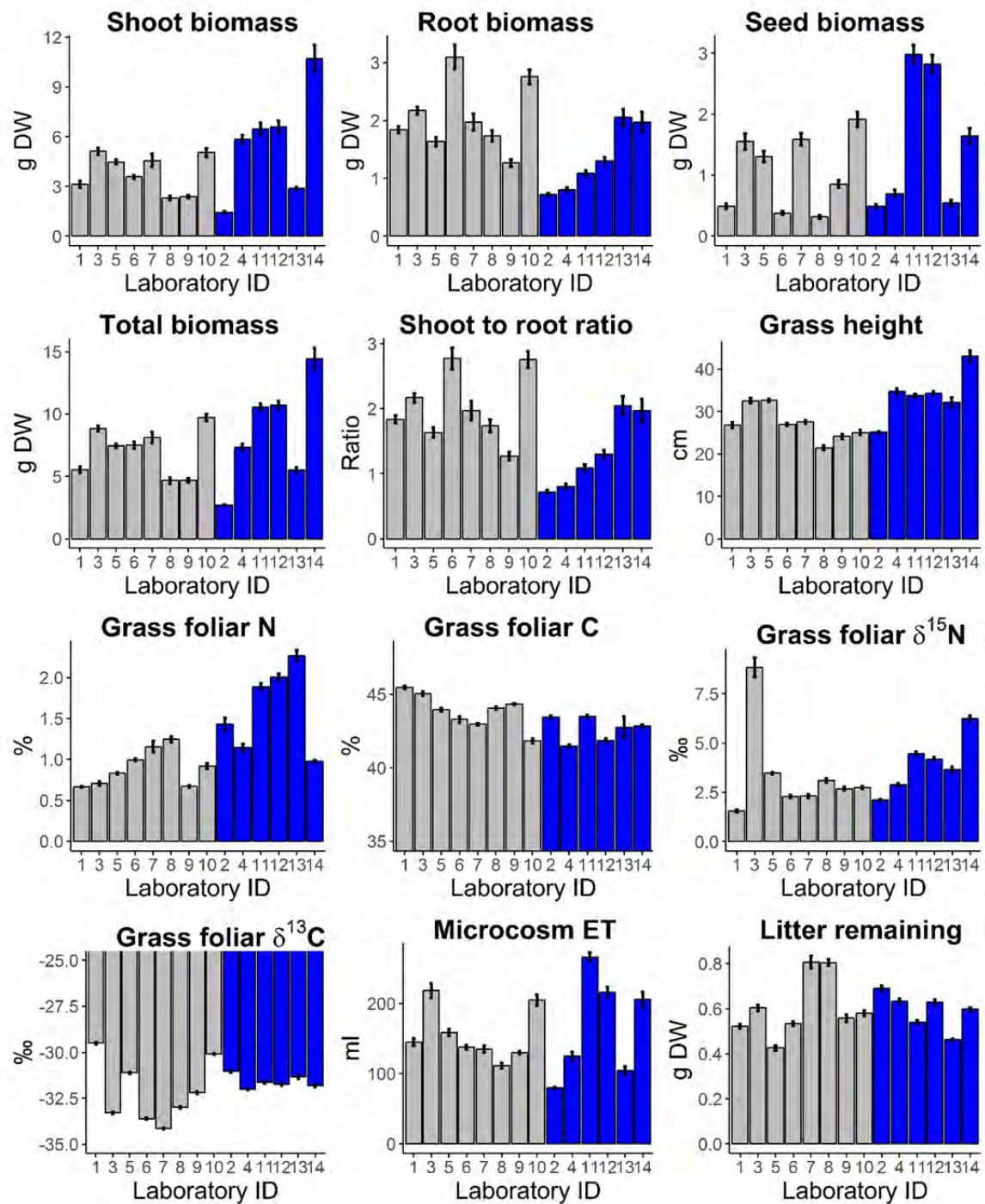
48

49

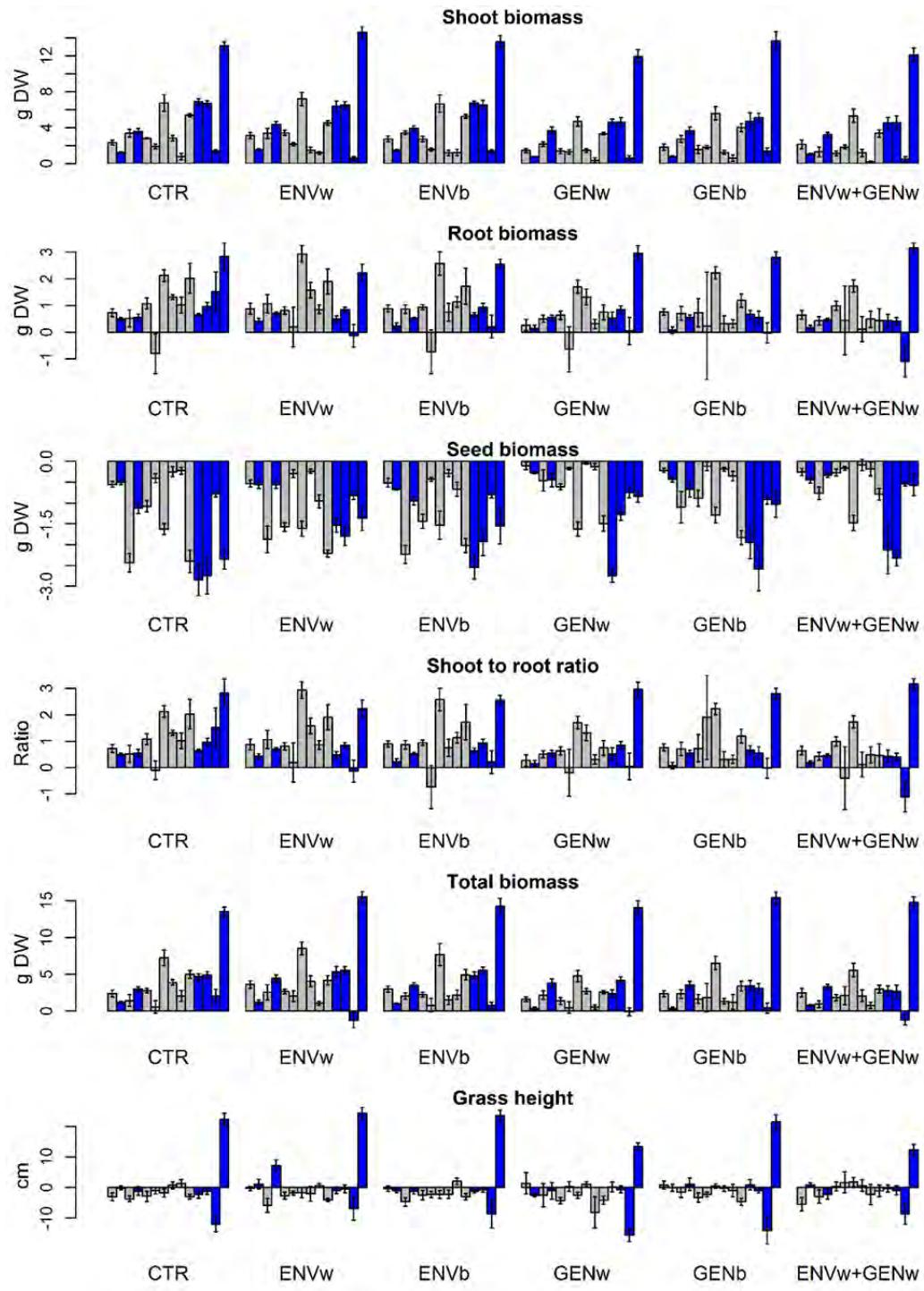
50

51

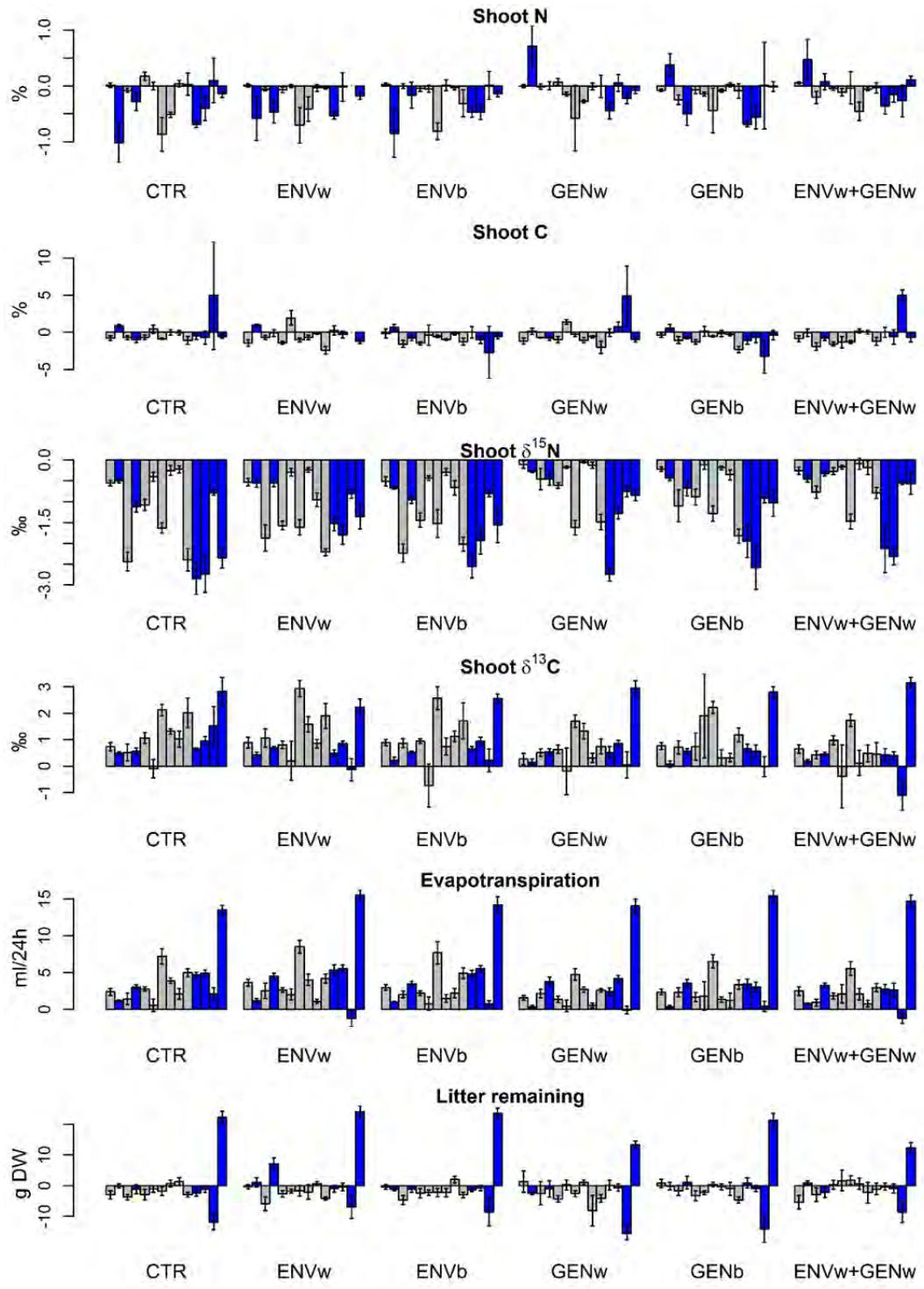
52 **Supplementary Fig. 1 | Response variables as affected by laboratory and SETUP (growth**
 53 **chamber vs. glasshouse treatment).** Grey and blue bars represent laboratories that used growth
 54 chamber and glasshouse setups, respectively. Bars show means by laboratory obtained by
 55 averaging over all CSV treatments, with error bars representing ± 1 s.e.m. ($n = 72$ microcosms
 56 per laboratory).



58 **Supplementary Fig. 2** | Response variables (first six) as affected by CSV, laboratory, and
 59 SETUP. Grey and blue bars indicate laboratories that used growth chamber and glasshouse
 60 setups, respectively. Bars with error bars represent means \pm 1 s.e.m. ($n = 6$ microcosms).

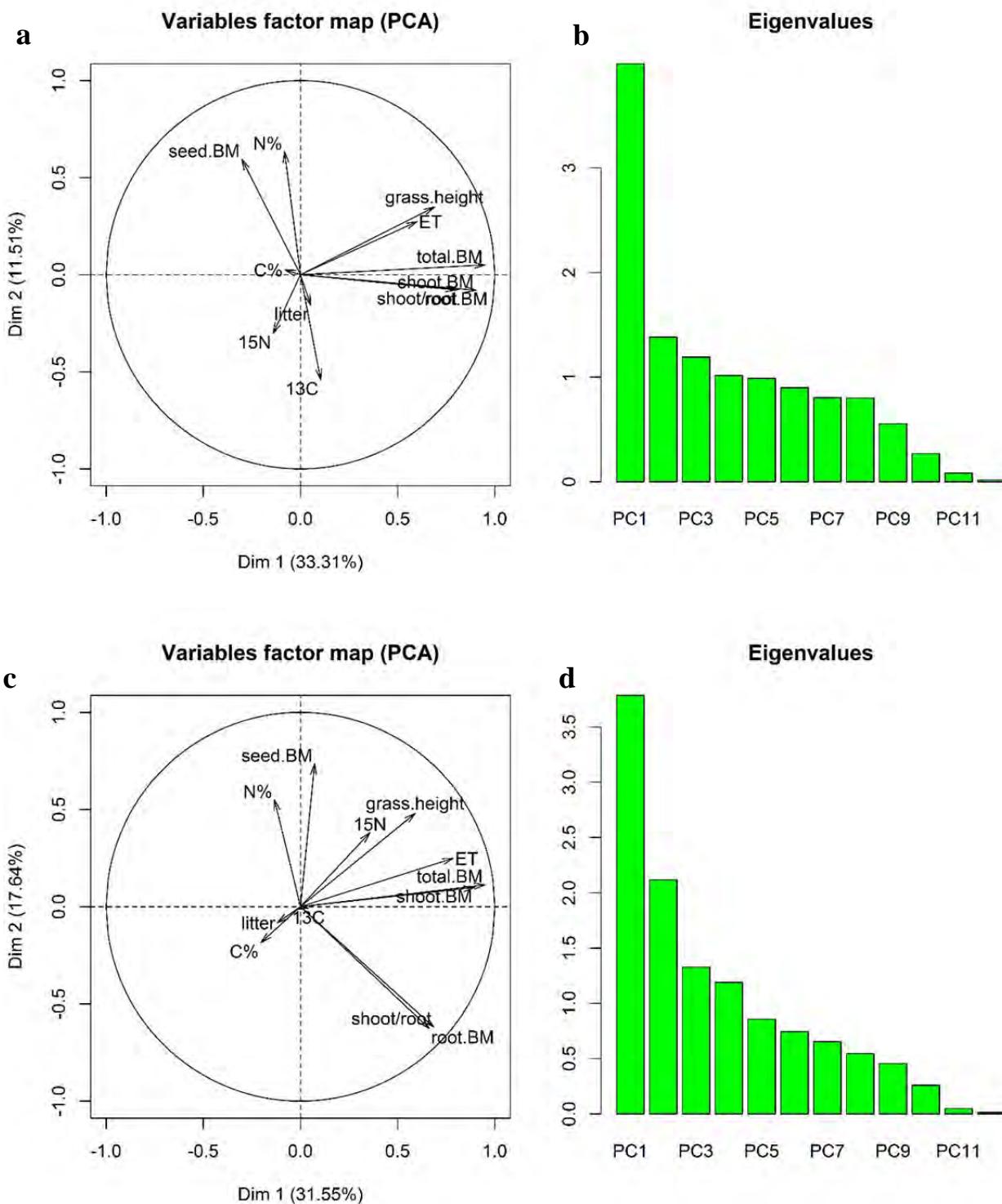


62 **Supplementary Fig. 3** | Response variables (last six) as affected by CSV, laboratory, and
 63 SETUP. Grey and blue bars indicate laboratories that used growth chamber and glasshouse
 64 setups, respectively. Bars with error bars represent means ± 1 s.e.m. ($n = 6$ microcosms).

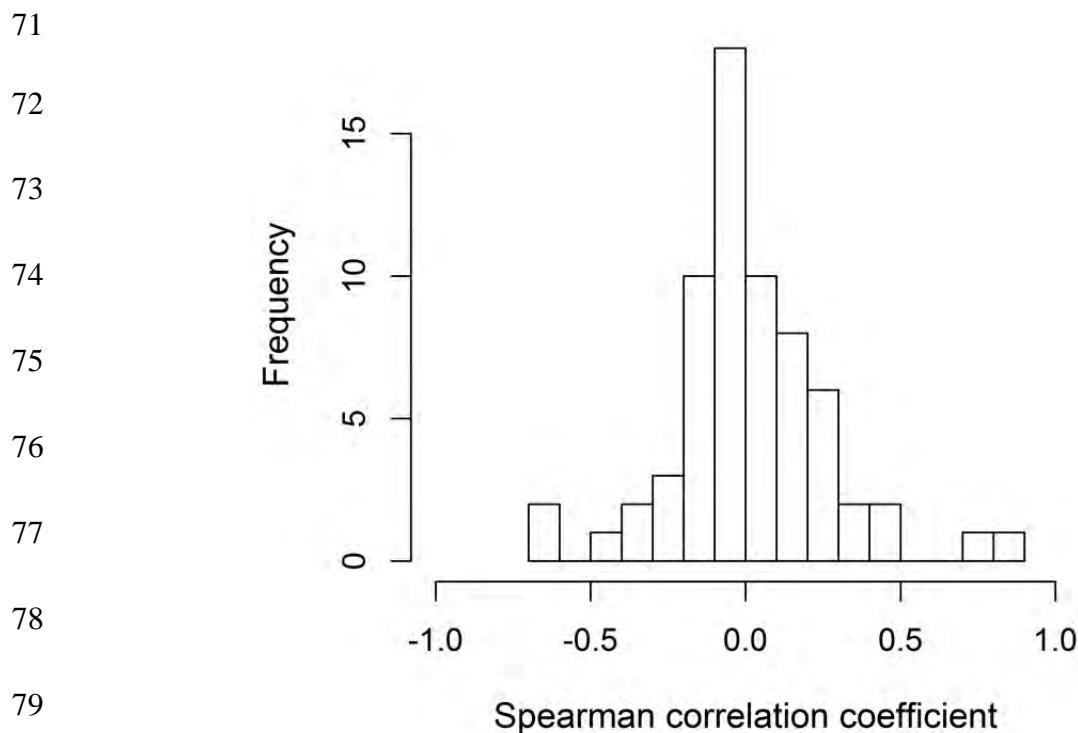


66 **Supplementary Fig. 4 | Results from the principal components analyses for the 12 response
67 variables (top) and for the net legume effect estimated from the 12 variables (bottom).**

68



69 **Supplementary Fig. 5 | Frequency distribution of Spearman's correlation coefficients**
70 **between each pair of the 12 response variables (n = 36 pairs).**



88 **Supplementary Note | Model outputs for the models used to test the effect of experimental**
 89 **treatments on among and within laboratory SD as well as for the model of among-**
 90 **laboratory SD as a function of within-laboratory SD.**

91

92 **Model output for among-laboratory SD**

```
model <- lme(amongSD~csv*setup, random=~setup|variabl e, weights=varI dent(form=~1|variabl e), na.action=na.omit, data=bothSD)
```

anova(model)

	numDF	denDF	F-val ue	p-val ue
(Intercept)	1	121	238.06748	<.0001
csv	5	121	1.21431	0.3065
setup	1	121	13.41761	0.0004
csv: setup	5	121	7.38356	<.0001

Summary (model)

Li near mixed-effects model fit by REML

AIC	BIC	LogLik
1.845438	79.68109	26.07728

Random effects:

Formul a: ~setup | variabl e
 Structure: General positive-definite, Log-Cholesky parametrization
 StdDev Corr
 (Intercept) 0.3015452 (Intr)
 setupgrowth_chamber 0.3261794 -0.904
 Residual 0.1468238

Vari ance function:

Structure: Different standard deviations per stratum
 Formul a: ~1 | variabl e

Parameter estimates:

seedbm	shootbm	rootbm	totalbm	shoot.root	heightB	N%
1.0000000	0.7064977	0.7891088	0.6346943	0.8230489	1.5292827	0.7959960

C%	del taN	del tac	final ET	litter
1.7423080	1.4579229	1.4602126	0.5335987	0.8567412

Fi xed effects: betweenSD ~ csv * setup

	Value	Std. Error	DF	t-val ue	p-val ue
(Intercept)	0.8965986	0.09489334	121	9.448489	0.0000
csvENVw	-0.0222416	0.05078427	121	-0.437962	0.6622
csvENVa	-0.0462239	0.05078427	121	-0.910201	0.3645
csvGENw	0.0497013	0.05078427	121	0.978674	0.3297
csvGENa	0.0409573	0.05078427	121	0.806496	0.4215
csvENVw+GENw	0.0734211	0.05078427	121	1.445745	0.1508
setupgrowth_chamber	-0.2413145	0.10814547	121	-2.231388	0.0275
csvENVw: setupgrowth_chamber	-0.0063497	0.07181981	121	-0.088411	0.9297
csvENVa: setupgrowth_chamber	0.0299276	0.07181981	121	0.416704	0.6776
csvGENw: setupgrowth_chamber	-0.2424468	0.07181981	121	-3.375765	0.0010
csvGENa: setupgrowth_chamber	-0.2124676	0.07181981	121	-2.958343	0.0037
csvENVw+GENw: setupgrowth_chamber	-0.2681373	0.07181981	121	-3.733473	0.0003

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-1.97736204	-0.72183774	0.03459952	0.53585186	2.32685019

Number of Observations: 144
Number of Groups: 12

93 Model output for within-laboratory SD

94 model <- lme(wi thi nSD~csv*setup, random=~setup|vari abl e,
95 wei ghts=varl dent(form=~1|vari abl e), na. acti on=na. omi t, data=bothSD)
96
97 anova(m4)

	numDF	denDF	F-val ue	p-val ue
(Intercept)	1	121	117. 65394	< .0001
csv	5	121	7. 42343	< .0001
setup	1	121	0. 09202	0. 7621
csv: setup	5	121	1. 39108	0. 2324

103
104 summary(model)
105 Linear mixed-effects model fit by REML
106
107 AIC BIC LogLik
108 -103. 5979 -25. 76229 78. 79897
109
110 Random effects:
111 Formula: ~setup | vari able
112 Structure: General positive-definite, Log-Cholesky parametrization
113 StdDev Corr
114 (Intercept) 0. 21316427 (Intr)
115 setupgrowth_chamber 0. 24341650 -0. 536
116 Residual 0. 08340683
117
118 Variance function:
119 Structure: Different standard deviations per stratum
120 Formula: ~1 | vari able
121 Parameter estimates:
122 seedbm shootbm rootbm total bm shoot.root heigh tB N%
123 1. 000000 0. 4270974 0. 9985380 0. 4467339 0. 9999987 1. 5639029 1. 1077805
124 C% del taN del taC final ET litter
125 3. 2391887 1. 0088300 1. 2621380 0. 6040685 1. 8026937
126 Fixed effects: wi thi nSD ~ csv * setup

	Value	Std. Error	DF	t-val ue	p-val ue
(Intercept)	0. 5614479	0. 06526348	121	8. 602788	0. 0000
csvENVw	0. 0196394	0. 02672984	121	0. 734738	0. 4639
csvENVa	-0. 0191756	0. 02672984	121	-0. 717387	0. 4745
csvGENw	0. 0020098	0. 02672984	121	0. 075190	0. 9402
csvGENa	0. 0942525	0. 02672984	121	3. 526117	0. 0006
csvENVw+GENw	0. 0338044	0. 02672984	121	1. 264671	0. 2084
csvENVw: setupgrowth_chamber	-0. 0005847	0. 03780170	121	-0. 015467	0. 9877
csvENVa: setupgrowth_chamber	0. 0525727	0. 03780170	121	1. 390750	0. 1669
csvGENw: setupgrowth_chamber	-0. 0431985	0. 03780170	121	-1. 142766	0. 2554
csvGENa: setupgrowth_chamber	-0. 0180580	0. 03780170	121	-0. 477703	0. 6337
csvENVw+GENw: setupgrowth_chamber	0. 0041737	0. 03780170	121	0. 110409	0. 9123

139 Correl ation:
140 Standardized Wi thi n-Group Residuals:
141 Mi n Q1 Med Q3 Max
142 -2. 04926063 -0. 63398623 -0. 08673377 0. 52628261 2. 48691942
143

```

anova(model)
      numDF denDF   F-value p-value
(Intercept)       1    109 183.31526 <.0001
withinSD          1    109   4.83259  0.0300
csv                5    109   2.68312  0.0251
setup              1    109 13.21629  0.0004
withinSD:csv       5    109   4.84786  0.0005
withinSD:setup     1    109   0.00623  0.9372
csv:setup          5    109 15.17262 <.0001
withinSD:csv:setup 5    109   2.40589  0.0412

```

Number of Observations: 144
 Number of Groups: 12

144 Model output for among-laboratory SD as a function of within-laboratory SD and CSV

```

145 model <- lme(amongSD~withinSD*csv*setup, random=~setup|variable, weights=varIdent(for
146           m = ~1|variable), data=bothSD, na.action=na.omit)
147 summary(model)
148
149 Linear mixed-effects model fit by REML
150   AIC     BIC   LogLik
151 23.15262 131.8648 27.42369
152
153 Random effects:
154 Formula: ~setup | variable
155 Structure: General positive-definite, Log-Cholesky parametrization
156             StdDev   Corr
157 (Intercept) 0.3153546 (Intr)
158 setupgrowth_chamber 0.3256810 -0.885
159 Residual     0.1637205
160
161 Variance function:
162 Structure: Different standard deviations per stratum
163 Formula: ~1 | variable
164 Parameter estimates:
165 seedbm shootbm rootbm totalbm shoot.root heightB N%
166 1.0000000 0.7008668 0.8660312 0.2948917 0.8505491 1.3691757 0.5568015
167
168 C%      deltan      deltaC    finalET    litter
169 1.4064467 1.4398760 1.1425713 0.2992432 0.7962738
170
171 Fixed effects: betweenSD ~ withinSD * csv * setup
172
173
174
175 (Intercept)               Value Std. Error DF t-value p-value
176 withinSD                  0.5902798 0.13732089 109 4.298543 0.0000
177 csvENVw                    0.4932791 0.17311674 109 2.849401 0.0052
178 csvENVa                    0.4983170 0.09666122 109 5.155294 0.0000
179 csvGENw                     0.2320159 0.09541446 109 2.431664 0.0167
180 csvGENa                     0.1903663 0.10854290 109 1.753835 0.0823
181 csvENVw+GENw                0.3592284 0.09943186 109 3.612809 0.0005
182                                         0.4283155 0.10789508 109 3.969740 0.0001

```

```

182 setupgrowth_chamber          0. 0406032 0. 17893949 109 0. 226910 0. 8209
183 wi thi nSD: csvENVw        -0. 8568180 0. 18224967 109 -4. 701342 0. 0000
184 wi thi nSD: csvENVa        -0. 4684887 0. 18382314 109 -2. 548584 0. 0122
185 wi thi nSD: csvGENw        0. 1362548 0. 22132193 109 -0. 615641 0. 5394
186 wi thi nSD: csvGENa        -0. 5051454 0. 17502257 109 -2. 886173 0. 0047
187 wi thi nSD: csvENVw+GENw   -0. 6511553 0. 21015129 109 -3. 098507 0. 0025
188 wi thi nSD: setupgrowth_chamber
189 csvENVw: setupgrowth_chamber
190 csvENVa: setupgrowth_chamber
191 csvGENw: setupgrowth_chamber
192 csvGENa: setupgrowth_chamber
193 csvENVw+GENw: setupgrowth_chamber
194 wi thi nSD: csvENVw: setupgrowth_chamber
195 wi thi nSD: csvENVa: setupgrowth_chamber
196 wi thi nSD: csvGENw: setupgrowth_chamber
197 wi thi nSD: csvGENa: setupgrowth_chamber
198 wi thi nSD: csvENVw+GENw: setupgrowth_chamber 0. 7451687 0. 30808448 109 2. 418716 0. 0172
199
200

```

201 Detailed model outputs from Table 1

202 Model for shoot biomass (shootbm)

```

203 anova(m1)
204
205 (Intercept)      numDF  denDF  F-val ue p-val ue
206 Legumes          1       836    13032.56 <. 0001
207 csv               5       836     4602.95 <. 0001
208 I ab              13      836     15.57 <. 0001
209 Legumes: csv      5       836     1088.67 <. 0001
210 Legumes: I ab    13      836     23.64 <. 0001
211 csv: I ab         65      836     236.00 <. 0001
212 Legumes: csv: I ab 65      836      6.54 <. 0001
213
214 summary(m1)
215 Linear mixed-effects model fit by REML
216 Data: repro
217   AIC   BIC LogLik
218 2220 3152 -913
219
220 Random effects:
221   Formula: ~1 | block
222   (Intercept) Residual
223 StdDev: 0.0255 0.998
224
225 Variance function:
226 Structure: Different standard deviations per stratum
227 Formula: ~1 | I ab * Legumes
228 Parameter estimates:
229 L1*B  L1*BM  L2*B  L2*BM  L3*B  L3*BM  L4*B  L4*BM  L5*B  L5*BM  L6*B
230 1.000  1.553  0.156  0.160  0.969  0.961  0.649  0.699  0.477  0.474  0.301
231 L6*BM  L7*B  L7*BM  L8*B  L8*BM  L9*B  L9*BM  L10*B L10*BM  L11*B L11*BM
232 0.337  0.339  1.757  0.426  0.523  0.215  0.664  0.385  0.580  0.944  0.843
233 L12*B L12*BM L13*B L13*BM L14*B L14*BM
234 1.087  0.874  0.510  0.573  1.322  1.512
235 Fixed effects: shootbm ~ Legumes * csv * I ab

```

		Value	Std. Error	DF	t-value	p-value
236	(Intercept)	2.00	0.408	836	4.90	0.0000
237	I egumesBM	2.32	0.752	836	3.08	0.0021
238	csvENVw	0.06	0.576	836	0.11	0.9134
239	csvENVb	-0.02	0.576	836	-0.04	0.9679
240	csvGENw	-0.08	0.576	836	-0.15	0.8845
241	csvGENb	-0.03	0.576	836	-0.05	0.9562
242	csvENVw+GENw	0.12	0.576	836	0.21	0.8303
243	I abL2	-1.36	0.412	836	-3.29	0.0010
244	I abL3	1.74	0.567	836	3.07	0.0022
245	I abL4	2.76	0.485	836	5.68	0.0000
246	I abL5	0.65	0.451	836	1.44	0.1507
247	I abL6	0.78	0.425	836	1.82	0.0688
248	I abL7	-0.61	0.430	836	-1.41	0.1581
249	I abL8	-0.76	0.443	836	-1.71	0.0876
250	I abL9	0.02	0.417	836	0.05	0.9627
251	I abL10	0.39	0.436	836	0.88	0.3765
252	I abL11	0.59	0.560	836	1.05	0.2933
253	I abL12	0.80	0.602	836	1.34	0.1821
254	I abL13	0.39	0.457	836	0.85	0.3956
255	I abL14	1.40	0.675	836	2.07	0.0388
256	I egumesBM: csvENVw	0.79	1.064	836	0.74	0.4579
257	I egumesBM: csvENVb	0.42	1.064	836	0.39	0.6947
258	I egumesBM: csvGENw	-0.88	1.064	836	-0.82	0.4106
259	I egumesBM: csvGENb	-0.49	1.064	836	-0.46	0.6468
260	I egumesBM: csvENVw+GENw	-0.20	1.064	836	-0.19	0.8529
261	I egumesBM: I abL2	-1.11	0.758	836	-1.46	0.1443
262	I egumesBM: I abL3	1.06	0.935	836	1.14	0.2552
263	I egumesBM: I abL4	1.28	0.846	836	1.51	0.1321
264	I egumesBM: I abL5	0.48	0.800	836	0.60	0.5486
265	I egumesBM: I abL6	-0.42	0.774	836	-0.54	0.5862
266	I egumesBM: I abL7	4.42	1.047	836	4.22	0.0000
267	I egumesBM: I abL8	0.51	0.801	836	0.64	0.5244
268	I egumesBM: I abL9	-1.54	0.804	836	-1.92	0.0558
269	I egumesBM: I abL10	3.06	0.804	836	3.81	0.0001
270	I egumesBM: I abL11	4.56	0.912	836	5.01	0.0000
271	I egumesBM: I abL12	4.39	0.943	836	4.66	0.0000
272	I egumesBM: I abL13	-0.95	0.814	836	-1.17	0.2429
273	I egumesBM: I abL14	10.79	1.111	836	9.71	0.0000
274	csvENVw: I abL2	-0.14	0.583	836	-0.24	0.8094
275	csvENVb: I abL2	-0.01	0.583	836	-0.01	0.9900
276	csvGENw: I abL2	0.57	0.583	836	0.98	0.3257
277	csvGENb: I abL2	0.44	0.583	836	0.76	0.4480
278	csvENVw+GENw: I abL2	0.50	0.583	836	0.86	0.3905
279	csvENVw: I abL3	-0.74	0.802	836	-0.92	0.3557
280	csvENVb: I abL3	-0.43	0.802	836	-0.53	0.5932
281	csvGENw: I abL3	0.69	0.802	836	0.87	0.3872
282	csvGENb: I abL3	0.42	0.802	836	0.52	0.6035
283	csvENVw+GENw: I abL3	0.15	0.802	836	0.19	0.8469
284	csvENVw: I abL4	-2.28	0.686	836	-3.32	0.0009
285	csvENVb: I abL4	-0.67	0.686	836	-0.98	0.3291
286	csvGENw: I abL4	-0.18	0.686	836	-0.27	0.7887
287	csvGENb: I abL4	-0.14	0.686	836	-0.21	0.8341
288	csvENVw+GENw: I abL4	-1.46	0.686	836	-2.12	0.0340
289	csvENVw: I abL5	0.07	0.638	836	0.11	0.9110
290	csvENVb: I abL5	0.22	0.638	836	0.35	0.7251
291	csvGENw: I abL5	1.53	0.638	836	2.40	0.0166
292	csvGENb: I abL5	1.04	0.638	836	1.64	0.1023
293	csvENVw+GENw: I abL5	1.58	0.638	836	2.48	0.0134
294	csvENVw: I abL6	-0.14	0.601	836	-0.23	0.8205
295	csvENVb: I abL6	0.14	0.601	836	0.23	0.8182
296	csvGENw: I abL6	-0.15	0.601	836	-0.25	0.8033
297	csvGENb: I abL6	-0.15	0.601	836	-0.24	0.8068

299	csvENVw+GENw: labL6	-0.18	0.601	836	-0.30	0.7644
300	csvENVw: labL7	0.03	0.608	836	0.05	0.9578
301	csvENVb: labL7	-0.05	0.608	836	-0.08	0.9362
302	csvGENw: labL7	0.43	0.608	836	0.71	0.4803
303	csvGENb: labL7	0.17	0.608	836	0.29	0.7755
304	csvENVw+GENw: labL7	0.34	0.608	836	0.57	0.5720
305	csvENVw: labL8	0.56	0.626	836	0.89	0.3712
306	csvENVb: labL8	0.61	0.626	836	0.98	0.3284
307	csvGENw: labL8	0.05	0.626	836	0.09	0.9309
308	csvGENb: labL8	-0.07	0.626	836	-0.12	0.9051
309	csvENVw+GENw: labL8	0.56	0.626	836	0.90	0.3690
310	csvENVw: labL9	-0.01	0.589	836	-0.01	0.9894
311	csvENVb: labL9	-0.07	0.589	836	-0.12	0.9061
312	csvGENw: labL9	-0.07	0.589	836	-0.13	0.8992
313	csvGENb: labL9	0.02	0.589	836	0.03	0.9765
314	csvENVw+GENw: labL9	0.06	0.589	836	0.10	0.9189
315	csvENVw: labL10	0.24	0.617	836	0.39	0.6991
316	csvENVb: labL10	-0.16	0.617	836	-0.25	0.7997
317	csvGENw: labL10	1.36	0.617	836	2.20	0.0278
318	csvGENb: labL10	1.04	0.617	836	1.68	0.0928
319	csvENVw+GENw: labL10	0.54	0.617	836	0.88	0.3807
320	csvENVw: labL11	-0.11	0.792	836	-0.14	0.8884
321	csvENVb: labL11	0.06	0.792	836	0.07	0.9423
322	csvGENw: labL11	2.19	0.792	836	2.77	0.0058
323	csvGENb: labL11	2.08	0.792	836	2.63	0.0087
324	csvENVw+GENw: labL11	2.16	0.792	836	2.73	0.0065
325	csvENVw: labL12	-0.66	0.851	836	-0.77	0.4389
326	csvENVb: labL12	-0.19	0.851	836	-0.22	0.8250
327	csvGENw: labL12	2.75	0.851	836	3.24	0.0013
328	csvGENb: labL12	1.67	0.851	836	1.97	0.0495
329	csvENVw+GENw: labL12	2.11	0.851	836	2.48	0.0133
330	csvENVw: labL13	-0.28	0.647	836	-0.44	0.6599
331	csvENVb: labL13	-0.27	0.647	836	-0.42	0.6738
332	csvGENw: labL13	0.51	0.647	836	0.79	0.4284
333	csvGENb: labL13	0.07	0.647	836	0.11	0.9116
334	csvENVw+GENw: labL13	0.03	0.647	836	0.04	0.9675
335	csvENVw: labL14	-1.19	0.955	836	-1.25	0.2133
336	csvENVb: labL14	-0.47	0.955	836	-0.49	0.6257
337	csvGENw: labL14	3.03	0.955	836	3.17	0.0016
338	csvGENb: labL14	1.39	0.955	836	1.45	0.1466
339	csvENVw+GENw: labL14	1.71	0.955	836	1.79	0.0736
340	egumesBM: csvENVw: labL2	-0.47	1.071	836	-0.44	0.6587
341	egumesBM: csvENVb: labL2	-0.15	1.071	836	-0.14	0.8883
342	egumesBM: csvGENw: labL2	0.43	1.071	836	0.40	0.6860
343	egumesBM: csvGENb: labL2	0.04	1.071	836	0.04	0.9671
344	egumesBM: csvENVw+GENw: labL2	0.04	1.071	836	0.04	0.9673
345	egumesBM: csvENVw: labL3	-0.82	1.322	836	-0.62	0.5343
346	egumesBM: csvENVb: labL3	-0.37	1.322	836	-0.28	0.7787
347	egumesBM: csvGENw: labL3	-0.36	1.322	836	-0.28	0.7830
348	egumesBM: csvGENb: labL3	-0.16	1.322	836	-0.12	0.9042
349	egumesBM: csvENVw+GENw: labL3	-1.89	1.322	836	-1.43	0.1535
350	egumesBM: csvENVw: labL4	-0.03	1.197	836	-0.02	0.9810
351	egumesBM: csvENVb: labL4	-0.08	1.197	836	-0.07	0.9461
352	egumesBM: csvGENw: labL4	0.91	1.197	836	0.76	0.4480
353	egumesBM: csvGENb: labL4	0.56	1.197	836	0.47	0.6403
354	egumesBM: csvENVw+GENw: labL4	-0.21	1.197	836	-0.18	0.8582
355	egumesBM: csvENVb: labL5	-0.17	1.132	836	-0.15	0.8798
356	egumesBM: csvENVb: labL5	-0.48	1.132	836	-0.42	0.6714
357	egumesBM: csvGENw: labL5	-0.56	1.132	836	-0.49	0.6209
358	egumesBM: csvGENb: labL5	-0.74	1.132	836	-0.66	0.5126
359	egumesBM: csvENVw+GENw: labL5	-1.45	1.132	836	-1.28	0.1992
360	egumesBM: csvENVw: labL6	-0.54	1.095	836	-0.49	0.6233
361	egumesBM: csvENVb: labL6	-0.74	1.095	836	-0.68	0.4980

```

362 | egumesBM: csvGENw: labL6      0. 28      1. 095 836      0. 25      0. 8018
363 | egumesBM: csvGENb: labL6      0. 42      1. 095 836      0. 38      0. 7031
364 | egumesBM: csvENVw+GENw: labL6 0. 14      1. 095 836      0. 12      0. 9018
365 | egumesBM: csvENVw: labL7      -0. 34     1. 481 836      -0. 23     0. 8196
366 | egumesBM: csvENVb: labL7      -0. 51     1. 481 836      -0. 34     0. 7309
367 | egumesBM: csvGENw: labL7      -1. 18     1. 481 836      -0. 80     0. 4241
368 | egumesBM: csvGENb: labL7      -0. 66     1. 481 836      -0. 45     0. 6539
369 | egumesBM: csvENVw+GENw: labL7 -1. 23     1. 481 836      -0. 83     0. 4068
370 | egumesBM: csvENVw: labL8      -1. 94     1. 142 836      -1. 69     0. 0906
371 | egumesBM: csvENVb: labL8      -2. 08     1. 132 836      -1. 84     0. 0666
372 | egumesBM: csvGENw: labL8      -0. 51     1. 132 836      -0. 45     0. 6525
373 | egumesBM: csvGENb: labL8      -1. 10     1. 132 836      -0. 97     0. 3319
374 | egumesBM: csvENVw+GENw: labL8 -1. 46     1. 132 836      -1. 29     0. 1963
375 | egumesBM: csvENVw: labL9      -0. 38     1. 137 836      -0. 33     0. 7413
376 | egumesBM: csvENVb: labL9      0. 04      1. 137 836      0. 03      0. 9745
377 | egumesBM: csvGENw: labL9      0. 45      1. 137 836      0. 40      0. 6900
378 | egumesBM: csvGENb: labL9      0. 31      1. 137 836      0. 27      0. 7850
379 | egumesBM: csvENVw+GENw: labL9 -0. 37     1. 143 836      -0. 33     0. 7450
380 | egumesBM: csvENVw: labL10     -1. 65    1. 137 836      -1. 45     0. 1472
381 | egumesBM: csvENVb: labL10     -0. 55    1. 137 836      -0. 49     0. 6256
382 | egumesBM: csvGENw: labL10     -1. 17    1. 137 836      -1. 03     0. 3046
383 | egumesBM: csvGENb: labL10     -0. 86    1. 137 836      -0. 76     0. 4472
384 | egumesBM: csvENVw+GENw: labL10 -1. 84    1. 137 836      -1. 62     0. 1054
385 | egumesBM: csvENVw: labL11     -1. 28    1. 289 836      -0. 99     0. 3200
386 | egumesBM: csvENVb: labL11     -0. 57    1. 289 836      -0. 45     0. 6560
387 | egumesBM: csvGENw: labL11     -1. 37    1. 289 836      -1. 06     0. 2882
388 | egumesBM: csvGENb: labL11     -1. 66    1. 289 836      -1. 29     0. 1970
389 | egumesBM: csvENVw+GENw: labL11 -2. 19    1. 289 836      -1. 70     0. 0901
390 | egumesBM: csvENVw: labL12     -0. 97    1. 333 836      -0. 73     0. 4649
391 | egumesBM: csvENVb: labL12     -0. 59    1. 333 836      -0. 44     0. 6602
392 | egumesBM: csvGENw: labL12     -1. 22    1. 333 836      -0. 92     0. 3588
393 | egumesBM: csvGENb: labL12     -1. 12    1. 333 836      -0. 84     0. 3993
394 | egumesBM: csvENVw+GENw: labL12 -1. 95    1. 333 836      -1. 46     0. 1438
395 | egumesBM: csvENVw: labL13     -1. 59    1. 152 836      -1. 38     0. 1665
396 | egumesBM: csvENVb: labL13     -0. 42    1. 152 836      -0. 36     0. 7184
397 | egumesBM: csvGENw: labL13     0. 12     1. 152 836      0. 11      0. 9153
398 | egumesBM: csvGENb: labL13     0. 51     1. 152 836      0. 44      0. 6579
399 | egumesBM: csvENVw+GENw: labL13 -0. 69    1. 152 836      -0. 60     0. 5513
400 | egumesBM: csvENVw: labL14     0. 74     1. 571 836      0. 47      0. 6380
401 | egumesBM: csvENVb: labL14     0. 03     1. 571 836      0. 02      0. 9859
402 | egumesBM: csvGENw: labL14     -0. 30    1. 571 836      -0. 19     0. 8510
403 | egumesBM: csvGENb: labL14     1. 02     1. 571 836      0. 65      0. 5171
404 | egumesBM: csvENVw+GENw: labL14 -0. 78    1. 571 836      -0. 50     0. 6179
405
406
407 Standardized Within-Group Residuals:
408   Min      Q1      Med      Q3      Max
409 -2. 8575 -0. 6141 -0. 0245  0. 6276  3. 2740
410
411 Number of Observations: 1005
412 Number of Groups: 2
413

```

414

415 **Model for root biomass (rootbm)**

416 **anova(m2)**

	numDF	denDF	F-value	p-value
(Intercept)	1	820	922.07	<.0001
Legumes	1	820	1131.65	<.0001
csv	5	820	23.93	<.0001

```

421 | ab           13   820  182.53  <.0001
422 | legumes:csv 5    820   4.48  0.0005
423 | legumes:lab 13   820   40.58  <.0001
424 | csv:lab     65   820   3.15  <.0001
425 | legumes:csv:lab 65   820   1.12  0.2462
426

427 summary(m2)
428 Linear mixed-effects model fit by REML
429 Data: repro
430      AIC    BIC   LogLik
431    1635  2563   -620
432
433 Random effects:
434 Formula: ~1 | block
435          (Intercept) Residual
436 StdDev:      0.0468    0.285
437
438 Variance function:
439 Structure: Different standard deviations per stratum
440 Formula: ~1 | lab * legumes
441
442 Parameter estimates:
443 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
444 1.000  1.381  0.705  0.561  1.597  1.553  0.406  0.623  1.548  1.194  7.691
445 L6*BM   L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM   L10*BM  L10*BM  L11*B  L11*BM
446 4.156  1.152  2.112  1.775  2.131  0.994  1.611  3.242  2.304  0.995  0.925
447 L12*B  L12*BM  L13*B  L13*BM  L14*B  L14*BM
448 1.150  1.211  3.864  3.922  0.917  2.876
449
450 Fixed effects: rootbm ~ legumes * csv * lab
451                               Value Std. Error DF t-value p-value
452 (Intercept)             1.410  0.121  820  11.64  0.0000
453 legumesBM              0.729  0.199  820   3.67  0.0003
454 csvENVw                0.029  0.165  820   0.18  0.8595
455 csvENVb                -0.041  0.165  820   -0.25  0.8042
456 csvGENw                0.339  0.165  820   2.06  0.0398
457 csvGENb                0.006  0.165  820   0.03  0.9734
458 csvENVw+GENw           0.205  0.165  820   1.25  0.2128
459 labL2                  -0.927  0.142  820   -6.51  0.0000
460 labL3                  0.225  0.219  820   1.03  0.3043
461 labL4                  -0.837  0.126  820   -6.66  0.0000
462 labL5                  -0.592  0.215  820   -2.76  0.0060
463 labL6                  1.724  0.988  820   1.75  0.0813
464 labL7                  -0.630  0.178  820   -3.55  0.0004
465 labL8                  -0.658  0.237  820   -2.77  0.0057
466 labL9                  -0.661  0.164  820   -4.02  0.0001
467 labL10                 0.207  0.395  820   0.52  0.6013
468 labL11                 -0.860  0.164  820   -5.24  0.0000
469 labL12                 -0.839  0.177  820   -4.73  0.0000
470 labL13                 -0.017  0.465  820   -0.04  0.9714
471 labL14                 -0.850  0.158  820   -5.38  0.0000
472 legumesBM:csvENVw     0.126  0.290  820   0.43  0.6639
473 legumesBM:csvENVb     0.159  0.281  820   0.57  0.5702
474 legumesBM:csvGENw     -0.463  0.281  820   -1.65  0.0995
475 legumesBM:csvGENb     0.035  0.281  820   0.12  0.9013
476 legumesBM:csvENVw+GENw -0.083  0.281  820   -0.29  0.7686
477 legumesBM:labL2       -0.235  0.225  820   -1.05  0.2954
478 legumesBM:labL3       -0.214  0.327  820   -0.66  0.5125
479 legumesBM:labL4       -0.168  0.217  820   -0.77  0.4388
480 legumesBM:labL5       0.341  0.302  820   1.13  0.2596

```

481	egumesBM: abL6	-1. 531	1. 133	820	-1. 35	0. 1767
482	egumesBM: abL7	1. 397	0. 343	820	4. 07	0. 0001
483	egumesBM: abL8	0. 588	0. 379	820	1. 55	0. 1214
484	egumesBM: abL9	0. 204	0. 325	820	0. 63	0. 5304
485	egumesBM: abL10	1. 293	0. 504	820	2. 57	0. 0105
486	egumesBM: abL11	-0. 085	0. 254	820	-0. 33	0. 7384
487	egumesBM: abL12	0. 234	0. 278	820	0. 84	0. 4005
488	egumesBM: abL13	0. 788	0. 671	820	1. 17	0. 2409
489	egumesBM: abL14	2. 103	0. 404	820	5. 21	0. 0000
490	csvENVw: abL2	-0. 036	0. 201	820	-0. 18	0. 8582
491	csvENVb: abL2	0. 070	0. 201	820	0. 35	0. 7265
492	csvGENw: abL2	-0. 039	0. 210	820	-0. 19	0. 8512
493	csvGENb: abL2	0. 204	0. 201	820	1. 02	0. 3104
494	csvENVw+GENw: abL2	-0. 062	0. 201	820	-0. 31	0. 7584
495	csvENVw: abL3	-0. 096	0. 310	820	-0. 31	0. 7583
496	csvENVb: abL3	-0. 035	0. 310	820	-0. 11	0. 9111
497	csvGENw: abL3	0. 298	0. 310	820	0. 96	0. 3379
498	csvGENb: abL3	0. 238	0. 310	820	0. 77	0. 4429
499	csvENVw+GENw: abL3	0. 228	0. 310	820	0. 74	0. 4619
500	csvENVw: abL4	-0. 319	0. 178	820	-1. 80	0. 0729
501	csvENVb: abL4	-0. 048	0. 178	820	-0. 27	0. 7879
502	csvGENw: abL4	-0. 205	0. 178	820	-1. 15	0. 2495
503	csvGENb: abL4	0. 007	0. 178	820	0. 04	0. 9678
504	csvENVw+GENw: abL4	-0. 212	0. 178	820	-1. 19	0. 2344
505	csvENVw: abL5	0. 153	0. 304	820	0. 51	0. 6136
506	csvENVb: abL5	0. 039	0. 304	820	0. 13	0. 8982
507	csvGENw: abL5	0. 315	0. 304	820	1. 04	0. 3000
508	csvGENb: abL5	0. 903	0. 304	820	2. 97	0. 0030
509	csvENVw+GENw: abL5	0. 436	0. 304	820	1. 44	0. 1511
510	csvENVw: abL6	-0. 728	1. 339	820	-0. 54	0. 5866
511	csvENVb: abL6	0. 642	1. 339	820	0. 48	0. 6315
512	csvGENw: abL6	0. 675	1. 339	820	0. 50	0. 6140
513	csvGENb: abL6	-0. 127	1. 397	820	-0. 09	0. 9279
514	csvENVw+GENw: abL6	-0. 314	1. 339	820	-0. 23	0. 8148
515	csvENVw: abL7	0. 109	0. 251	820	0. 44	0. 6631
516	csvENVb: abL7	0. 023	0. 251	820	0. 09	0. 9276
517	csvGENw: abL7	-0. 133	0. 251	820	-0. 53	0. 5963
518	csvGENb: abL7	-0. 105	0. 251	820	-0. 42	0. 6752
519	csvENVw+GENw: abL7	0. 073	0. 251	820	0. 29	0. 7710
520	csvENVw: abL8	0. 863	0. 335	820	2. 57	0. 0103
521	csvENVb: abL8	0. 762	0. 335	820	2. 27	0. 0234
522	csvGENw: abL8	-0. 259	0. 335	820	-0. 77	0. 4403
523	csvGENb: abL8	0. 502	0. 335	820	1. 50	0. 1347
524	csvENVw+GENw: abL8	1. 142	0. 335	820	3. 41	0. 0007
525	csvENVw: abL9	0. 178	0. 232	820	0. 76	0. 4448
526	csvENVb: abL9	0. 078	0. 232	820	0. 34	0. 7375
527	csvGENw: abL9	-0. 155	0. 232	820	-0. 67	0. 5045
528	csvGENb: abL9	0. 281	0. 232	820	1. 21	0. 2270
529	csvENVw+GENw: abL9	0. 280	0. 232	820	1. 21	0. 2276
530	csvENVw: abL10	0. 404	0. 559	820	0. 72	0. 4698
531	csvENVb: abL10	0. 217	0. 559	820	0. 39	0. 6972
532	csvGENw: abL10	0. 635	0. 559	820	1. 14	0. 2557
533	csvGENb: abL10	0. 671	0. 559	820	1. 20	0. 2303
534	csvENVw+GENw: abL10	0. 369	0. 559	820	0. 66	0. 5092
535	csvENVw: abL11	0. 080	0. 232	820	0. 34	0. 7307
536	csvENVb: abL11	0. 041	0. 232	820	0. 18	0. 8594
537	csvGENw: abL11	0. 145	0. 232	820	0. 62	0. 5327
538	csvGENb: abL11	0. 239	0. 232	820	1. 03	0. 3046
539	csvENVw+GENw: abL11	0. 475	0. 232	820	2. 05	0. 0411
540	csvENVw: abL12	-0. 015	0. 251	820	-0. 06	0. 9534
541	csvENVb: abL12	0. 121	0. 251	820	0. 48	0. 6304
542	csvGENw: abL12	0. 199	0. 251	820	0. 79	0. 4270
543	csvGENb: abL12	0. 588	0. 251	820	2. 34	0. 0195

544	csvENVw+GENw: labL12	0. 662	0. 251	820	2. 64	0. 0085
545	csvENVw: labL13	0. 138	0. 687	820	0. 20	0. 8407
546	csvENVb: labL13	-0. 146	0. 657	820	-0. 22	0. 8243
547	csvGENw: labL13	0. 933	0. 657	820	1. 42	0. 1562
548	csvGENb: labL13	1. 143	0. 657	820	1. 74	0. 0823
549	csvENVw+GENw: labL13	1. 143	0. 657	820	1. 74	0. 0823
550	csvENVw: labL14	-0. 279	0. 223	820	-1. 25	0. 2120
551	csvENVb: labL14	-0. 059	0. 223	820	-0. 26	0. 7919
552	csvGENw: labL14	-0. 059	0. 223	820	-0. 26	0. 7919
553	csvGENb: labL14	0. 093	0. 223	820	0. 42	0. 6758
554	csvENVw+GENw: labL14	-0. 042	0. 223	820	-0. 19	0. 8504
555	egumesBM: csvENVw: labL2	-0. 198	0. 326	820	-0. 61	0. 5427
556	egumesBM: csvENVb: labL2	-0. 429	0. 318	820	-1. 35	0. 1767
557	egumesBM: csvGENw: labL2	0. 098	0. 323	820	0. 30	0. 7627
558	egumesBM: csvGENb: labL2	-0. 454	0. 318	820	-1. 43	0. 1536
559	egumesBM: csvENVw+GENw: labL2	-0. 229	0. 318	820	-0. 72	0. 4715
560	egumesBM: csvENVw: labL3	0. 424	0. 468	820	0. 91	0. 3642
561	egumesBM: csvENVb: labL3	0. 189	0. 462	820	0. 41	0. 6825
562	egumesBM: csvGENw: labL3	0. 454	0. 462	820	0. 98	0. 3256
563	egumesBM: csvGENb: labL3	0. 155	0. 462	820	0. 33	0. 7381
564	egumesBM: csvENVw+GENw: labL3	-0. 006	0. 462	820	-0. 01	0. 9891
565	egumesBM: csvENVw: labL4	0. 009	0. 315	820	0. 03	0. 9781
566	egumesBM: csvENVb: labL4	-0. 198	0. 306	820	-0. 65	0. 5187
567	egumesBM: csvGENw: labL4	0. 446	0. 308	820	1. 45	0. 1481
568	egumesBM: csvGENb: labL4	-0. 038	0. 306	820	-0. 12	0. 9013
569	egumesBM: csvENVw+GENw: labL4	-0. 018	0. 306	820	-0. 06	0. 9527
570	egumesBM: csvENVw: labL5	-0. 388	0. 433	820	-0. 90	0. 3710
571	egumesBM: csvENVb: labL5	-0. 286	0. 427	820	-0. 67	0. 5037
572	egumesBM: csvGENw: labL5	0. 027	0. 427	820	0. 06	0. 9493
573	egumesBM: csvGENb: labL5	-0. 370	0. 432	820	-0. 86	0. 3918
574	egumesBM: csvENVw+GENw: labL5	-0. 003	0. 427	820	-0. 01	0. 9938
575	egumesBM: csvENVw: labL6	0. 868	1. 537	820	0. 56	0. 5723
576	egumesBM: csvENVb: labL6	-0. 879	1. 551	820	-0. 57	0. 5712
577	egumesBM: csvGENw: labL6	0. 629	1. 536	820	0. 41	0. 6824
578	egumesBM: csvGENb: labL6	0. 961	1. 602	820	0. 60	0. 5486
579	egumesBM: csvENVw+GENw: labL6	1. 334	1. 536	820	0. 87	0. 3854
580	egumesBM: csvENVw: labL7	0. 686	0. 491	820	1. 40	0. 1625
581	egumesBM: csvENVb: labL7	0. 293	0. 486	820	0. 60	0. 5461
582	egumesBM: csvGENw: labL7	0. 044	0. 486	820	0. 09	0. 9278
583	egumesBM: csvGENb: labL7	0. 064	0. 486	820	0. 13	0. 8949
584	egumesBM: csvENVw+GENw: labL7	-0. 308	0. 486	820	-0. 63	0. 5262
585	egumesBM: csvENVw: labL8	-0. 071	0. 569	820	-0. 13	0. 9002
586	egumesBM: csvENVb: labL8	-0. 733	0. 536	820	-1. 37	0. 1721
587	egumesBM: csvGENw: labL8	0. 469	0. 536	820	0. 87	0. 3822
588	egumesBM: csvGENb: labL8	-1. 037	0. 536	820	-1. 93	0. 0533
589	egumesBM: csvENVw+GENw: labL8	-0. 916	0. 564	820	-1. 62	0. 1048
590	egumesBM: csvENVw: labL9	-0. 203	0. 446	820	-0. 45	0. 6493
591	egumesBM: csvENVb: labL9	0. 047	0. 448	820	0. 10	0. 9165
592	egumesBM: csvGENw: labL9	-0. 162	0. 440	820	-0. 37	0. 7123
593	egumesBM: csvGENb: labL9	-0. 575	0. 448	820	-1. 28	0. 1998
594	egumesBM: csvENVw+GENw: labL9	-0. 365	0. 440	820	-0. 83	0. 4077
595	egumesBM: csvENVw: labL10	-0. 244	0. 716	820	-0. 34	0. 7331
596	egumesBM: csvENVb: labL10	-0. 462	0. 713	820	-0. 65	0. 5171
597	egumesBM: csvGENw: labL10	-0. 815	0. 713	820	-1. 14	0. 2529
598	egumesBM: csvGENb: labL10	-0. 869	0. 713	820	-1. 22	0. 2230
599	egumesBM: csvENVw+GENw: labL10	-1. 496	0. 713	820	-2. 10	0. 0361
600	egumesBM: csvENVw: labL11	-0. 279	0. 366	820	-0. 76	0. 4466
601	egumesBM: csvENVb: labL11	-0. 155	0. 359	820	-0. 43	0. 6651
602	egumesBM: csvGENw: labL11	0. 341	0. 359	820	0. 95	0. 3423
603	egumesBM: csvGENb: labL11	-0. 012	0. 359	820	-0. 03	0. 9730
604	egumesBM: csvENVw+GENw: labL11	-0. 134	0. 359	820	-0. 37	0. 7094
605	egumesBM: csvENVw: labL12	-0. 237	0. 400	820	-0. 59	0. 5536
606	egumesBM: csvENVb: labL12	-0. 188	0. 393	820	-0. 48	0. 6326

```

607 | legumesBM: csvGENw: labL12      0. 349      0. 393 820      0. 89  0. 3745
608 | legumesBM: csvGENb: labL12     -0. 442      0. 393 820     -1. 12  0. 2610
609 | legumesBM: csvENVw+GENw: labL12 -0. 472      0. 393 820     -1. 20  0. 2304
610 | legumesBM: csvENVw: labL13     -1. 969      0. 973 820     -2. 02  0. 0433
611 | legumesBM: csvENVb: labL13     -1. 468      0. 949 820     -1. 55  0. 1224
612 | legumesBM: csvGENw: labL13     -1. 010      0. 949 820     -1. 06  0. 2874
613 | legumesBM: csvGENb: labL13     -1. 576      0. 949 820     -1. 66  0. 0972
614 | legumesBM: csvENVw+GENw: labL13 -2. 539      0. 949 820     -2. 68  0. 0076
615 | legumesBM: csvENVw: labL14     -0. 719      0. 576 820     -1. 25  0. 2119
616 | legumesBM: csvENVb: labL14     -0. 432      0. 571 820     -0. 76  0. 4495
617 | legumesBM: csvGENw: labL14      0. 597      0. 571 820      1. 05  0. 2958
618 | legumesBM: csvGENb: labL14     -0. 068      0. 571 820     -0. 12  0. 9045
619 | legumesBM: csvENVw+GENw: labL14  0. 420      0. 571 820      0. 73  0. 4627
620
621 Standardized Within-Group Residuals:
622   Min      Q1      Med      Q3      Max
623 -3.2331 -0.5866 -0.0851  0.4929  3.7528
624
625 Number of Observations: 989
626 Number of Groups: 2
627

```

Model for seed biomass (seedbm)

[anova\(m3\)](#)

	numDF	denDF	F-value	p-value
(Intercept)	1	828	1019.92	<.0001
legumes	1	828	2186.64	<.0001
csv	5	828	58.01	<.0001
lab	13	828	364.57	<.0001
legumes: csv	5	828	33.62	<.0001
legumes: lab	13	828	78.17	<.0001
csv: lab	65	828	6.93	<.0001
legumes: csv: lab	65	828	2.70	<.0001

[summary\(m3\)](#)

Linear mixed-effects model fit by REML

Data: repro

AIC	BIC	LogLik
813	1743	-209

Random effects:

Formula: ~1 | block
 (Intercept) Residual
 StdDev: 0.0183 0.272

Variance function:

Structure: Different standard deviations per stratum
 Formula: ~1 | lab * legumes

Parameter estimates:

L1*B	L1*BM	L2*B	L2*BM	L3*B	L3*BM	L4*B	L4*BM	L5*B	L5*BM	L6*B	L6*BM
1.000	0.496	0.463	0.161	2.475	1.352	1.214	0.581	1.348	0.699	0.630	0.446
L7*B	L7*BM	L8*B	L8*BM	L9*B	L9*BM	L10*B	L10*BM	L11*B	L11*BM	L12*B	L12*BM
1.596	0.765	0.666	0.741	1.074	0.866	1.406	0.866	2.885	1.811	2.546	1.352
L13*B	L13*BM	L14*B	L14*BM								
0.799	0.343	2.491	1.377								

Fixed effects: seedbm ~ legumes * csv * lab

	Value	Std. Error	DF	t-value	p-value
(Intercept)	0.98	0.122	828	7.98	0.0000
legumesBM	-0.54	0.134	828	-4.02	0.0001
csvENVw	0.06	0.165	828	0.35	0.7259

csvENVb	-0.01	0.183	828	-0.06	0.9488
csvGENw	-0.69	0.165	828	-4.20	0.0000
csvGENb	-0.50	0.165	828	-3.03	0.0025
csvENVw+GENw	-0.60	0.165	828	-3.61	0.0003
abL2	-0.19	0.132	828	-1.46	0.1440
abL3	2.61	0.301	828	8.67	0.0000
abL4	0.68	0.182	828	3.76	0.0002
abL5	1.17	0.193	828	6.06	0.0000
abL6	-0.27	0.140	828	-1.92	0.0552
abL7	1.43	0.215	828	6.65	0.0000
abL8	-0.43	0.143	828	-3.02	0.0026
abL9	0.15	0.171	828	0.87	0.3841
abL10	2.52	0.198	828	12.71	0.0000
abL11	3.25	0.343	828	9.46	0.0000
abL12	3.15	0.308	828	10.21	0.0000
abL13	-0.03	0.151	828	-0.19	0.8517
abL14	3.01	0.327	828	9.22	0.0000
egumesBM: csvENVw	0.01	0.182	828	0.06	0.9519
egumesBM: csvENVb	0.11	0.199	828	0.56	0.5768
egumesBM: csvGENw	0.43	0.182	828	2.37	0.0180
egumesBM: csvGENb	0.33	0.182	828	1.78	0.0748
egumesBM: csvENVw+GENw	0.28	0.182	828	1.56	0.1187
egumesBM: abL2	0.04	0.144	828	0.26	0.7915
egumesBM: abL3	-1.90	0.341	828	-5.58	0.0000
egumesBM: abL4	-0.59	0.201	828	-2.93	0.0035
egumesBM: abL5	-0.53	0.215	828	-2.48	0.0132
egumesBM: abL6	0.14	0.159	828	0.86	0.3903
egumesBM: abL7	-1.09	0.238	828	-4.58	0.0000
egumesBM: abL8	0.29	0.174	828	1.67	0.0944
egumesBM: abL9	0.32	0.203	828	1.56	0.1201
egumesBM: abL10	-1.86	0.227	828	-8.19	0.0000
egumesBM: abL11	-2.31	0.402	828	-5.75	0.0000
egumesBM: abL12	-2.21	0.347	828	-6.35	0.0000
egumesBM: abL13	-0.25	0.165	828	-1.49	0.1354
egumesBM: abL14	-1.76	0.365	828	-4.82	0.0000
csvENVw: abL2	-0.01	0.182	828	-0.07	0.9453
csvENVb: abL2	0.15	0.197	828	0.76	0.4471
csvGENw: abL2	0.37	0.180	828	2.06	0.0396
csvGENb: abL2	0.45	0.180	828	2.50	0.0126
csvENVw+GENw: abL2	0.49	0.180	828	2.72	0.0067
csvENVw: abL3	-1.06	0.422	828	-2.50	0.0126
csvENVb: abL3	-0.46	0.430	828	-1.06	0.2885
csvGENw: abL3	-1.74	0.422	828	-4.12	0.0000
csvGENb: abL3	-1.06	0.422	828	-2.51	0.0122
csvENVw+GENw: abL3	-1.71	0.422	828	-4.04	0.0001
csvENVw: abL4	-0.70	0.252	828	-2.79	0.0054
csvENVb: abL4	-0.27	0.264	828	-1.02	0.3104
csvGENw: abL4	-0.27	0.252	828	-1.08	0.2823
csvGENb: abL4	-0.15	0.252	828	-0.58	0.5628
csvENVw+GENw: abL4	-0.61	0.252	828	-2.42	0.0156
csvENVw: abL5	0.46	0.268	828	1.70	0.0889
csvENVb: abL5	0.34	0.280	828	1.23	0.2179
csvGENw: abL5	-0.40	0.268	828	-1.50	0.1329
csvGENb: abL5	-0.09	0.268	828	-0.35	0.7277
csvENVw+GENw: abL5	-0.67	0.268	828	-2.48	0.0134
csvENVw: abL6	-0.09	0.192	828	-0.46	0.6424
csvENVb: abL6	0.00	0.208	828	0.00	0.9978
csvGENw: abL6	0.28	0.192	828	1.48	0.1405
csvGENb: abL6	0.21	0.192	828	1.10	0.2706
csvENVw+GENw: abL6	0.15	0.192	828	0.78	0.4335
csvENVw: abL7	0.05	0.300	828	0.17	0.8681
csvENVb: abL7	-0.11	0.310	828	-0.34	0.7341
csvGENw: abL7	0.68	0.300	828	2.25	0.0247

csvGENb: I abL7	0. 34	0. 300	828	1. 13	0. 2592
csvENVw+GENw: I abL7	0. 47	0. 300	828	1. 56	0. 1201
csvENVw: I abL8	-0. 09	0. 209	828	-0. 42	0. 6723
csvENVb: I abL8	-0. 07	0. 217	828	-0. 32	0. 7497
csvGENw: I abL8	0. 28	0. 195	828	1. 41	0. 1587
csvGENb: I abL8	0. 22	0. 195	828	1. 15	0. 2521
csvENVw+GENw: I abL8	0. 39	0. 195	828	2. 00	0. 0458
csvENVw: I abL9	0. 67	0. 236	828	2. 83	0. 0048
csvENVb: I abL9	0. 41	0. 249	828	1. 64	0. 1005
csvGENw: I abL9	-0. 06	0. 236	828	-0. 24	0. 8103
csvGENb: I abL9	0. 22	0. 236	828	0. 94	0. 3477
csvENVw+GENw: I abL9	0. 12	0. 236	828	0. 49	0. 6216
csvENVw: I abL10	-0. 29	0. 276	828	-1. 07	0. 2867
csvENVb: I abL10	-0. 24	0. 287	828	-0. 83	0. 4079
csvGENw: I abL10	-0. 38	0. 276	828	-1. 39	0. 1649
csvGENb: I abL10	-0. 25	0. 276	828	-0. 91	0. 3646
csvENVw+GENw: I abL10	-1. 19	0. 276	828	-4. 31	0. 0000
csvENVw: I abL11	-0. 68	0. 483	828	-1. 42	0. 1562
csvENVb: I abL11	0. 13	0. 489	828	0. 26	0. 7945
csvGENw: I abL11	1. 19	0. 483	828	2. 47	0. 0138
csvGENb: I abL11	-0. 04	0. 483	828	-0. 09	0. 9318
csvENVw+GENw: I abL11	0. 54	0. 483	828	1. 11	0. 2658
csvENVw: I abL12	-0. 59	0. 433	828	-1. 37	0. 1708
csvENVb: I abL12	-0. 31	0. 440	828	-0. 72	0. 4744
csvGENw: I abL12	-0. 15	0. 433	828	-0. 36	0. 7212
csvGENb: I abL12	0. 55	0. 433	828	1. 28	0. 2010
csvENVw+GENw: I abL12	0. 75	0. 433	828	1. 74	0. 0821
csvENVw: I abL13	-0. 02	0. 207	828	-0. 08	0. 9398
csvENVb: I abL13	-0. 01	0. 222	828	-0. 06	0. 9505
csvGENw: I abL13	0. 64	0. 207	828	3. 11	0. 0019
csvGENb: I abL13	0. 56	0. 207	828	2. 70	0. 0070
csvENVw+GENw: I abL13	0. 43	0. 207	828	2. 08	0. 0381
csvENVw: I abL14	-1. 35	0. 443	828	-3. 05	0. 0024
csvENVb: I abL14	-1. 02	0. 466	828	-2. 19	0. 0289
csvGENw: I abL14	-2. 02	0. 443	828	-4. 56	0. 0000
csvGENb: I abL14	-1. 63	0. 443	828	-3. 68	0. 0002
csvENVw+GENw: I abL14	-2. 20	0. 443	828	-4. 96	0. 0000
I egumesBM: csvENVw: I abL2	-0. 07	0. 199	828	-0. 36	0. 7179
I egumesBM: csvENVb: I abL2	-0. 28	0. 213	828	-1. 31	0. 1906
I egumesBM: csvGENw: I abL2	-0. 21	0. 198	828	-1. 04	0. 3008
I egumesBM: csvGENb: I abL2	-0. 25	0. 198	828	-1. 28	0. 1993
I egumesBM: csvENVw+GENw: I abL2	-0. 23	0. 198	828	-1. 18	0. 2396
I egumesBM: csvENVw: I abL3	0. 55	0. 479	828	1. 16	0. 2483
I egumesBM: csvENVb: I abL3	0. 09	0. 486	828	0. 19	0. 8456
I egumesBM: csvGENw: I abL3	1. 55	0. 479	828	3. 23	0. 0013
I egumesBM: csvGENb: I abL3	1. 01	0. 479	828	2. 11	0. 0348
I egumesBM: csvENVw+GENw: I abL3	1. 39	0. 479	828	2. 89	0. 0039
I egumesBM: csvENVw: I abL4	0. 56	0. 279	828	2. 01	0. 0446
I egumesBM: csvENVb: I abL4	0. 06	0. 290	828	0. 21	0. 8351
I egumesBM: csvGENw: I abL4	0. 24	0. 279	828	0. 87	0. 3846
I egumesBM: csvGENb: I abL4	0. 13	0. 279	828	0. 46	0. 6469
I egumesBM: csvENVw+GENw: I abL4	0. 51	0. 279	828	1. 84	0. 0664
I egumesBM: csvENVw: I abL5	-0. 51	0. 300	828	-1. 70	0. 0890
I egumesBM: csvENVb: I abL5	-0. 48	0. 310	828	-1. 55	0. 1218
I egumesBM: csvGENw: I abL5	0. 03	0. 300	828	0. 11	0. 9157
I egumesBM: csvGENb: I abL5	-0. 14	0. 300	828	-0. 45	0. 6504
I egumesBM: csvENVw+GENw: I abL5	0. 52	0. 300	828	1. 73	0. 0832
I egumesBM: csvENVw: I abL6	0. 10	0. 219	828	0. 46	0. 6460
I egumesBM: csvENVb: I abL6	-0. 14	0. 233	828	-0. 61	0. 5450
I egumesBM: csvGENw: I abL6	-0. 20	0. 219	828	-0. 92	0. 3570
I egumesBM: csvGENb: I abL6	-0. 04	0. 219	828	-0. 18	0. 8569
I egumesBM: csvENVw+GENw: I abL6	-0. 05	0. 219	828	-0. 23	0. 8206
I egumesBM: csvENVw: I abL7	0. 00	0. 333	828	0. 01	0. 9924

egumesBM: csvENVb: labL7	-0.01	0.342	828	-0.03	0.9730
egumesBM: csvGENw: labL7	-0.43	0.333	828	-1.29	0.1985
egumesBM: csvGENb: labL7	0.02	0.333	828	0.06	0.9517
egumesBM: csvENVw+GENw: labL7	-0.13	0.333	828	-0.40	0.6908
egumesBM: csvENVw: labL8	0.30	0.252	828	1.19	0.2326
egumesBM: csvENVb: labL8	0.03	0.258	828	0.13	0.8946
egumesBM: csvGENw: labL8	-0.23	0.240	828	-0.95	0.3411
egumesBM: csvGENb: labL8	-0.26	0.240	828	-1.09	0.2776
egumesBM: csvENVw+GENw: labL8	-0.12	0.240	828	-0.48	0.6286
egumesBM: csvENVw: labL9	-0.74	0.283	828	-2.62	0.0090
egumesBM: csvENVb: labL9	-0.56	0.294	828	-1.89	0.0593
egumesBM: csvGENw: labL9	-0.33	0.283	828	-1.17	0.2416
egumesBM: csvGENb: labL9	-0.46	0.283	828	-1.61	0.1087
egumesBM: csvENVw+GENw: labL9	-0.25	0.283	828	-0.87	0.3871
egumesBM: csvENVw: labL10	0.18	0.317	828	0.56	0.5760
egumesBM: csvENVb: labL10	0.27	0.327	828	0.81	0.4155
egumesBM: csvGENw: labL10	0.48	0.317	828	1.50	0.1341
egumesBM: csvGENb: labL10	0.25	0.317	828	0.78	0.4328
egumesBM: csvENVw+GENw: labL10	1.32	0.317	828	4.17	0.0000
egumesBM: csvENVw: labL11	1.31	0.566	828	2.32	0.0208
egumesBM: csvENVb: labL11	0.19	0.571	828	0.34	0.7371
egumesBM: csvGENw: labL11	-0.33	0.566	828	-0.58	0.5600
egumesBM: csvGENb: labL11	0.57	0.566	828	1.01	0.3117
egumesBM: csvENVw+GENw: labL11	0.44	0.566	828	0.78	0.4341
egumesBM: csvENVw: labL12	0.94	0.488	828	1.91	0.0559
egumesBM: csvENVb: labL12	0.70	0.495	828	1.42	0.1548
egumesBM: csvGENw: labL12	1.03	0.488	828	2.11	0.0349
egumesBM: csvGENb: labL12	-0.16	0.488	828	-0.33	0.7386
egumesBM: csvENVw+GENw: labL12	0.14	0.488	828	0.28	0.7779
egumesBM: csvENVw: labL13	-0.04	0.228	828	-0.18	0.8607
egumesBM: csvENVb: labL13	-0.13	0.241	828	-0.55	0.5825
egumesBM: csvGENw: labL13	-0.40	0.228	828	-1.75	0.0802
egumesBM: csvGENb: labL13	-0.46	0.228	828	-2.02	0.0435
egumesBM: csvENVw+GENw: labL13	-0.05	0.228	828	-0.21	0.8372
egumesBM: csvENVw: labL14	0.93	0.499	828	1.86	0.0639
egumesBM: csvENVb: labL14	0.66	0.520	828	1.26	0.2071
egumesBM: csvGENw: labL14	1.02	0.499	828	2.04	0.0412
egumesBM: csvGENb: labL14	0.94	0.499	828	1.89	0.0585
egumesBM: csvENVw+GENw: labL14	1.45	0.499	828	2.90	0.0038

Model for total biomass (totalbm)

[anova \(m4\)](#)

	numDF	denDF	F-val ue	p-val ue
(Intercept)	1	839	3534.7	<.0001
legumes	1	839	690.7	<.0001
csv	5	839	1.8	0.1145
lab	13	839	1252.0	<.0001
legumes: csv	5	839	3.5	0.0040
legumes: lab	13	839	116.6	<.0001
csv: lab	65	839	7.3	<.0001
legumes: csv: lab	65	839	1.2	0.1677

[summary\(m4\)](#)

Linear mixed-effects model fit by REML
 Data: repro
 AIC BIC LogLik
 3241 4174 -1424

Random effects:

Formula: ~1 | block
 (Intercept) Residual
 StdDev: 0.114 1.43

Variance function:

Structure: Different standard deviations per stratum

Formula: ~1 | lab * legumes

Parameter estimates:

L1*B	L1*BM	L2*B	L2*BM	L3*B	L3*BM	L4*B	L4*BM	L5*B	L5*BM	L6*B	L6*BM
1.000	1.367	0.261	0.156	1.256	0.906	0.646	0.509	0.551	0.417	2.014	1.603
L7*B	L7*BM	L8*B	L8*BM	L9*B	L9*BM	L10*B	L10*BM	L11*B	L11*BM	L12*B	L12*BM
0.605	1.438	0.616	0.816	0.263	1.073	0.685	0.679	0.764	0.674	1.058	0.639
1.175	1.012	1.227	1.403								
L13*B	L13*BM	L14*B	L14*BM								

Fixed effects: total_bm ~ legumes * csv * lab

	Value	Std. Error	DF	t-value	p-value
(Intercept)	4.48	0.590	839	7.60	0.0000
legumesBM	2.41	0.989	839	2.44	0.0150
csvENVw	0.05	0.826	839	0.06	0.9495
csvENVb	0.03	0.826	839	0.03	0.9726
csvGENw	-0.53	0.826	839	-0.65	0.5180
csvGENb	-0.62	0.826	839	-0.76	0.4503
csvENVw+GENw	-0.36	0.826	839	-0.44	0.6590
labL2	-2.57	0.604	839	-4.26	0.0000
labL3	4.48	0.938	839	4.78	0.0000
labL4	2.51	0.695	839	3.60	0.0003
labL5	1.13	0.667	839	1.69	0.0908
labL6	3.57	1.313	839	2.72	0.0066
labL7	0.10	0.683	839	0.14	0.8892
labL8	-1.94	0.686	839	-2.83	0.0047
labL9	-0.59	0.604	839	-0.98	0.3288
labL10	3.01	0.708	839	4.26	0.0000
labL11	2.88	0.735	839	3.91	0.0001
labL12	3.01	0.850	839	3.54	0.0004
labL13	0.25	0.901	839	0.27	0.7848
labL14	3.60	0.925	839	3.89	0.0001
legumesBM: csvENVw	1.22	1.399	839	0.87	0.3839
legumesBM: csvENVb	0.58	1.399	839	0.42	0.6765
legumesBM: csvGENw	-0.81	1.399	839	-0.58	0.5634
legumesBM: csvGENb	-0.03	1.399	839	-0.02	0.9830
legumesBM: csvENVw+GENw	0.10	1.399	839	0.07	0.9415
legumesBM: labL2	-1.21	1.005	839	-1.20	0.2304
legumesBM: labL3	-0.95	1.341	839	-0.71	0.4779
legumesBM: labL4	0.62	1.100	839	0.56	0.5738
legumesBM: labL5	0.38	1.069	839	0.36	0.7194
legumesBM: labL6	-1.83	1.800	839	-1.02	0.3094
legumesBM: labL7	4.83	1.345	839	3.59	0.0004
legumesBM: labL8	1.49	1.156	839	1.29	0.1988
legumesBM: labL9	-0.31	1.181	839	-0.26	0.7923
legumesBM: labL10	2.60	1.139	839	2.28	0.0229
legumesBM: labL11	2.27	1.155	839	1.96	0.0501
legumesBM: labL12	2.52	1.225	839	2.06	0.0402
legumesBM: labL13	-0.31	1.341	839	-0.23	0.8157
legumesBM: labL14	11.09	1.471	839	7.54	0.0000
csvENVw: labL2	0.08	0.854	839	0.09	0.9257
csvENVb: labL2	0.11	0.854	839	0.13	0.8991
csvGENw: labL2	1.24	0.854	839	1.45	0.1463
csvGENb: labL2	1.19	0.854	839	1.40	0.1620
csvENVw+GENw: labL2	1.03	0.854	839	1.20	0.2296
csvENVw: labL3	-1.80	1.326	839	-1.35	0.1761
csvENVb: labL3	-1.02	1.326	839	-0.77	0.4405
csvGENw: labL3	-0.65	1.326	839	-0.49	0.6240
csvGENb: labL3	-0.31	1.326	839	-0.23	0.8159
csvENVw+GENw: labL3	-1.23	1.326	839	-0.93	0.3550

csvENVw: labL4	-3.21	0.983	839	-3.26	0.0012
csvENVb: labL4	-1.09	0.983	839	-1.11	0.2679
csvGENw: labL4	-0.56	0.983	839	-0.57	0.5675
csvGENb: labL4	-0.18	0.983	839	-0.19	0.8508
csvENVw+GENw: labL4	-2.18	0.983	839	-2.22	0.0267
csvENVw: labL5	0.78	0.943	839	0.83	0.4090
csvENVb: labL5	0.50	0.943	839	0.53	0.5932
csvGENw: labL5	1.54	0.943	839	1.63	0.1028
csvGENb: labL5	1.95	0.943	839	2.07	0.0389
csvENVw+GENw: labL5	1.45	0.943	839	1.54	0.1246
csvENVw: labL6	-2.30	1.857	839	-1.24	0.2163
csvENVb: labL6	-0.76	1.857	839	-0.41	0.6808
csvGENw: labL6	-0.53	1.857	839	-0.29	0.7736
csvGENb: labL6	-0.49	1.857	839	-0.26	0.7913
csvENVw+GENw: labL6	-1.69	1.857	839	-0.91	0.3639
csvENVw: labL7	0.29	0.965	839	0.30	0.7649
csvENVb: labL7	-0.24	0.965	839	-0.24	0.8075
csvGENw: labL7	1.07	0.965	839	1.11	0.2683
csvGENb: labL7	0.50	0.965	839	0.52	0.6015
csvENVw+GENw: labL7	0.98	0.965	839	1.02	0.3095
csvENVw: labL8	1.82	0.970	839	1.87	0.0616
csvENVb: labL8	1.50	0.970	839	1.55	0.1214
csvGENw: labL8	0.17	0.970	839	0.17	0.8621
csvGENb: labL8	0.75	0.970	839	0.77	0.4404
csvENVw+GENw: labL8	2.19	0.970	839	2.26	0.0240
csvENVw: labL9	0.93	0.854	839	1.09	0.2747
csvENVb: labL9	0.31	0.854	839	0.37	0.7140
csvGENw: labL9	-0.19	0.854	839	-0.22	0.8252
csvGENb: labL9	0.62	0.854	839	0.72	0.4703
csvENVw+GENw: labL9	0.55	0.854	839	0.65	0.5164
csvENVw: labL10	0.45	1.001	839	0.45	0.6561
csvENVb: labL10	-0.28	1.001	839	-0.28	0.7793
csvGENw: labL10	1.71	1.001	839	1.71	0.0880
csvGENb: labL10	1.56	1.001	839	1.55	0.1204
csvENVw+GENw: labL10	-0.18	1.001	839	-0.18	0.8567
csvENVw: labL11	-0.62	1.039	839	-0.60	0.5518
csvENVb: labL11	0.12	1.039	839	0.12	0.9067
csvGENw: labL11	3.63	1.039	839	3.49	0.0005
csvGENb: labL11	2.38	1.039	839	2.29	0.0224
csvENVw+GENw: labL11	3.27	1.039	839	3.15	0.0017
csvENVw: labL12	-1.17	1.202	839	-0.97	0.3311
csvENVb: labL12	-0.49	1.202	839	-0.40	0.6863
csvGENw: labL12	2.90	1.202	839	2.41	0.0162
csvGENb: labL12	2.91	1.202	839	2.42	0.0156
csvENVw+GENw: labL12	3.62	1.202	839	3.01	0.0027
csvENVw: labL13	0.56	1.274	839	0.44	0.6626
csvENVb: labL13	-0.54	1.274	839	-0.42	0.6742
csvGENw: labL13	2.19	1.274	839	1.72	0.0865
csvGENb: labL13	1.87	1.274	839	1.47	0.1422
csvENVw+GENw: labL13	1.70	1.274	839	1.33	0.1831
csvENVw: labL14	-2.86	1.308	839	-2.18	0.0292
csvENVb: labL14	-1.43	1.308	839	-1.09	0.2741
csvGENw: labL14	0.91	1.308	839	0.70	0.4858
csvGENb: labL14	-0.19	1.308	839	-0.15	0.8837
csvENVw+GENw: labL14	-0.57	1.308	839	-0.43	0.6640
I egumesBM: csvENVw: labL2	-1.21	1.422	839	-0.85	0.3959
I egumesBM: csvENVb: labL2	-0.75	1.422	839	-0.53	0.5956
I egumesBM: csvGENw: labL2	-0.01	1.422	839	-0.01	0.9943
I egumesBM: csvGENb: labL2	-0.76	1.422	839	-0.54	0.5927
I egumesBM: csvENVw+GENw: labL2	-0.52	1.422	839	-0.36	0.7169
I egumesBM: csvENVw: labL3	-0.14	1.896	839	-0.07	0.9428
I egumesBM: csvENVb: labL3	0.02	1.896	839	0.01	0.9933
I egumesBM: csvGENw: labL3	1.54	1.896	839	0.81	0.4167

egumesBM: csvGENB: labL3	0. 91	1. 896	839	0. 48	0. 6310
egumesBM: csvENVw+GENw: labL3	-0. 61	1. 896	839	-0. 32	0. 7489
egumesBM: csvENVw: labL4	0. 25	1. 556	839	0. 16	0. 8725
egumesBM: csvENVb: labL4	-0. 11	1. 556	839	-0. 07	0. 9413
egumesBM: csvGENw: labL4	1. 60	1. 556	839	1. 03	0. 3047
egumesBM: csvGENB: labL4	0. 55	1. 556	839	0. 35	0. 7229
egumesBM: csvENVw+GENw: labL4	0. 18	1. 556	839	0. 12	0. 9061
egumesBM: csvENVw: labL5	-1. 36	1. 511	839	-0. 90	0. 3674
egumesBM: csvENVb: labL5	-1. 14	1. 511	839	-0. 76	0. 4500
egumesBM: csvGENw: labL5	-0. 60	1. 511	839	-0. 40	0. 6922
egumesBM: csvGENB: labL5	-1. 10	1. 511	839	-0. 73	0. 4652
egumesBM: csvENVw+GENw: labL5	-1. 03	1. 511	839	-0. 68	0. 4938
egumesBM: csvENVw: labL6	0. 25	2. 545	839	0. 10	0. 9217
egumesBM: csvENVb: labL6	-0. 36	2. 545	839	-0. 14	0. 8887
egumesBM: csvGENw: labL6	0. 72	2. 545	839	0. 28	0. 7787
egumesBM: csvGENB: labL6	1. 29	2. 545	839	0. 51	0. 6132
egumesBM: csvENVw+GENw: labL6	1. 43	2. 545	839	0. 56	0. 5736
egumesBM: csvENVw: labL7	0. 06	1. 902	839	0. 03	0. 9750
egumesBM: csvENVb: labL7	-0. 12	1. 902	839	-0. 07	0. 9482
egumesBM: csvGENw: labL7	-1. 67	1. 902	839	-0. 88	0. 3815
egumesBM: csvGENB: labL7	-0. 68	1. 902	839	-0. 36	0. 7219
egumesBM: csvENVw+GENw: labL7	-1. 77	1. 902	839	-0. 93	0. 3531
egumesBM: csvENVw: labL8	-1. 07	1. 634	839	-0. 65	0. 5137
egumesBM: csvENVb: labL8	-2. 98	1. 634	839	-1. 82	0. 0688
egumesBM: csvGENw: labL8	-0. 37	1. 634	839	-0. 23	0. 8220
egumesBM: csvGENB: labL8	-2. 50	1. 634	839	-1. 53	0. 1271
egumesBM: csvENVw+GENw: labL8	-1. 91	1. 634	839	-1. 17	0. 2432
egumesBM: csvENVw: labL9	-2. 22	1. 671	839	-1. 33	0. 1836
egumesBM: csvENVb: labL9	-0. 47	1. 671	839	-0. 28	0. 7799
egumesBM: csvGENw: labL9	-0. 75	1. 671	839	-0. 45	0. 6541
egumesBM: csvGENB: labL9	-0. 82	1. 671	839	-0. 49	0. 6234
egumesBM: csvENVw+GENw: labL9	-1. 39	1. 671	839	-0. 83	0. 4045
egumesBM: csvENVw: labL10	-2. 01	1. 610	839	-1. 25	0. 2127
egumesBM: csvENVb: labL10	-0. 65	1. 610	839	-0. 40	0. 6882
egumesBM: csvGENw: labL10	-1. 60	1. 610	839	-1. 00	0. 3193
egumesBM: csvGENB: labL10	-1. 58	1. 610	839	-0. 98	0. 3261
egumesBM: csvENVw+GENw: labL10	-2. 11	1. 610	839	-1. 31	0. 1894
egumesBM: csvENVw: labL11	-0. 54	1. 633	839	-0. 33	0. 7391
egumesBM: csvENVb: labL11	-0. 43	1. 633	839	-0. 27	0. 7903
egumesBM: csvGENw: labL11	-1. 46	1. 633	839	-0. 89	0. 3726
egumesBM: csvGENB: labL11	-1. 20	1. 633	839	-0. 74	0. 4619
egumesBM: csvENVw+GENw: labL11	-1. 98	1. 633	839	-1. 21	0. 2263
egumesBM: csvENVw: labL12	-0. 57	1. 732	839	-0. 33	0. 7429
egumesBM: csvENVb: labL12	0. 03	1. 732	839	0. 02	0. 9843
egumesBM: csvGENw: labL12	0. 06	1. 732	839	0. 03	0. 9723
egumesBM: csvGENB: labL12	-1. 83	1. 732	839	-1. 06	0. 2917
egumesBM: csvENVw+GENw: labL12	-2. 38	1. 732	839	-1. 38	0. 1693
egumesBM: csvENVw: labL13	-4. 52	1. 897	839	-2. 38	0. 0175
egumesBM: csvENVb: labL13	-1. 91	1. 897	839	-1. 01	0. 3137
egumesBM: csvGENw: labL13	-1. 38	1. 897	839	-0. 73	0. 4658
egumesBM: csvGENB: labL13	-1. 62	1. 897	839	-0. 86	0. 3924
egumesBM: csvENVw+GENw: labL13	-3. 37	1. 897	839	-1. 78	0. 0760
egumesBM: csvENVw: labL14	0. 79	2. 080	839	0. 38	0. 7033
egumesBM: csvENVb: labL14	0. 14	2. 080	839	0. 07	0. 9470
egumesBM: csvGENw: labL14	1. 36	2. 080	839	0. 66	0. 5125
egumesBM: csvGENB: labL14	1. 94	2. 080	839	0. 93	0. 3524
egumesBM: csvENVw+GENw: labL14	1. 12	2. 080	839	0. 54	0. 5898

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-3. 36073	-0. 66483	-0. 00439	0. 58740	3. 00416

Number of Observations: 1008

Number of Groups: 2

628 **Model for shoot to root biomass ratio (shoot.root)**

629 **anova(m5)**

630 numDF denDF F-value p-value

631 (Intercept) 1 815 932 <.0001

632 Legumes 1 815 1137 <.0001

633 csv 5 815 24 <.0001

634 lab 13 815 183 <.0001

635 Legumes: csv 5 815 5 0.0005

636 Legumes: lab 13 815 40 <.0001

637 csv: lab 65 815 3 <.0001

638 Legumes: csv: lab 65 815 1 0.2502

639

640 **summary(m5)**

641 Linear mixed-effects model fit by REML

642 Data: repro

643 AIC BIC LogLik

644 1590 2517 -598

645

646 Random effects:

647 Formula: ~1 | block

648 (Intercept) Residual

649 StdDev: 0.0466 0.284

650

651 Variance function:

652 Structure: Different standard deviations per stratum

653 Formula: ~1 | lab * Legumes

654 Parameter estimates:

655 L1*B L1*BM L2*B L2*BM L3*B L3*BM L4*B L4*BM L5*B L5*BM L6*B
656 1.000 1.385 0.706 0.563 1.602 1.557 0.408 0.625 1.553 1.197 5.762
657 L6*BM L7*B L7*BM L8*B L8*BM L9*B L9*BM L10*B L10*BM L11*B L11*BM
658 3.503 1.156 2.119 1.780 2.139 0.997 1.616 3.251 2.310 0.998 0.928
659 L12*B L12*BM L13*B L13*BM L14*B L14*BM
660 1.154 1.215 3.875 3.935 0.920 2.885

661

662 Fixed effects: shoot.root ~ Legumes * csv * lab

	Value	Std. Error	DF	t-value	p-value
(Intercept)	1.410	0.121	815	11.68	0.0000
LegumesBM	0.728	0.198	815	3.67	0.0003
csvENVw	0.029	0.164	815	0.18	0.8591
csvENVb	-0.041	0.164	815	-0.25	0.8037
csvGENw	0.339	0.164	815	2.07	0.0392
csvGENb	0.005	0.164	815	0.03	0.9733
csvENVw+GENw	0.205	0.164	815	1.25	0.2115
labL2	-0.927	0.142	815	-6.52	0.0000
labL3	0.225	0.219	815	1.03	0.3041
labL4	-0.837	0.125	815	-6.67	0.0000
labL5	-0.592	0.214	815	-2.76	0.0059
labL6	0.685	0.828	815	0.83	0.4084
labL7	-0.630	0.177	815	-3.55	0.0004
labL8	-0.658	0.237	815	-2.78	0.0056
labL9	-0.661	0.164	815	-4.03	0.0001
labL10	0.206	0.395	815	0.52	0.6012
labL11	-0.860	0.164	815	-5.24	0.0000
labL12	-0.840	0.177	815	-4.73	0.0000
labL13	-0.017	0.465	815	-0.04	0.9714
labL14	-0.850	0.158	815	-5.39	0.0000
LegumesBM: csvENVw	0.126	0.290	815	0.44	0.6634
LegumesBM: csvENVb	0.160	0.280	815	0.57	0.5697

686	egumesBM: csvGENw	-0. 463	0. 280	815	-1. 65	0. 0990
687	egumesBM: csvGENb	0. 035	0. 280	815	0. 12	0. 9012
688	egumesBM: csvENVw+GENw	-0. 083	0. 280	815	-0. 29	0. 7683
689	egumesBM: abL2	-0. 235	0. 224	815	-1. 05	0. 2948
690	egumesBM: abL3	-0. 214	0. 327	815	-0. 66	0. 5124
691	egumesBM: abL4	-0. 168	0. 216	815	-0. 78	0. 4383
692	egumesBM: abL5	0. 341	0. 302	815	1. 13	0. 2593
693	egumesBM: abL6	-0. 492	0. 954	815	-0. 52	0. 6062
694	egumesBM: abL7	1. 397	0. 343	815	4. 07	0. 0001
695	egumesBM: abL8	0. 588	0. 379	815	1. 55	0. 1214
696	egumesBM: abL9	0. 204	0. 325	815	0. 63	0. 5302
697	egumesBM: abL10	1. 293	0. 504	815	2. 57	0. 0104
698	egumesBM: abL11	-0. 085	0. 254	815	-0. 33	0. 7382
699	egumesBM: abL12	0. 234	0. 278	815	0. 84	0. 4002
700	egumesBM: abL13	0. 788	0. 671	815	1. 17	0. 2409
701	egumesBM: abL14	2. 103	0. 404	815	5. 21	0. 0000
702	csvENVw: abL2	-0. 036	0. 201	815	-0. 18	0. 8579
703	csvENVb: abL2	0. 071	0. 201	815	0. 35	0. 7259
704	csvGENw: abL2	-0. 039	0. 209	815	-0. 19	0. 8513
705	csvGENb: abL2	0. 205	0. 201	815	1. 02	0. 3093
706	csvENVw+GENw: abL2	-0. 062	0. 201	815	-0. 31	0. 7578
707	csvENVw: abL3	-0. 095	0. 310	815	-0. 31	0. 7582
708	csvENVb: abL3	-0. 035	0. 310	815	-0. 11	0. 9110
709	csvGENw: abL3	0. 297	0. 310	815	0. 96	0. 3377
710	csvGENb: abL3	0. 238	0. 310	815	0. 77	0. 4427
711	csvENVw+GENw: abL3	0. 228	0. 310	815	0. 74	0. 4618
712	csvENVw: abL4	-0. 319	0. 177	815	-1. 80	0. 0722
713	csvENVb: abL4	-0. 048	0. 177	815	-0. 27	0. 7874
714	csvGENw: abL4	-0. 205	0. 177	815	-1. 16	0. 2484
715	csvGENb: abL4	0. 007	0. 177	815	0. 04	0. 9678
716	csvENVw+GENw: abL4	-0. 211	0. 177	815	-1. 19	0. 2333
717	csvENVw: abL5	0. 153	0. 303	815	0. 51	0. 6133
718	csvENVb: abL5	0. 039	0. 303	815	0. 13	0. 8981
719	csvGENw: abL5	0. 315	0. 303	815	1. 04	0. 2995
720	csvGENb: abL5	0. 903	0. 303	815	2. 98	0. 0030
721	csvENVw+GENw: abL5	0. 436	0. 303	815	1. 44	0. 1508
722	csvENVw: abL6	0. 312	1. 071	815	0. 29	0. 7711
723	csvENVb: abL6	0. 892	1. 112	815	0. 80	0. 4226
724	csvGENw: abL6	1. 207	1. 112	815	1. 09	0. 2778
725	csvGENb: abL6	-0. 142	1. 170	815	-0. 12	0. 9031
726	csvENVw+GENw: abL6	0. 726	1. 071	815	0. 68	0. 4978
727	csvENVw: abL7	0. 110	0. 251	815	0. 44	0. 6627
728	csvENVb: abL7	0. 023	0. 251	815	0. 09	0. 9275
729	csvGENw: abL7	-0. 133	0. 251	815	-0. 53	0. 5958
730	csvGENb: abL7	-0. 105	0. 251	815	-0. 42	0. 6748
731	csvENVw+GENw: abL7	0. 073	0. 251	815	0. 29	0. 7707
732	csvENVw: abL8	0. 863	0. 335	815	2. 57	0. 0103
733	csvENVb: abL8	0. 762	0. 335	815	2. 27	0. 0233
734	csvGENw: abL8	-0. 259	0. 335	815	-0. 77	0. 4401
735	csvGENb: abL8	0. 502	0. 335	815	1. 50	0. 1345
736	csvENVw+GENw: abL8	1. 142	0. 335	815	3. 41	0. 0007
737	csvENVw: abL9	0. 178	0. 232	815	0. 77	0. 4441
738	csvENVb: abL9	0. 078	0. 232	815	0. 34	0. 7372
739	csvGENw: abL9	-0. 155	0. 232	815	-0. 67	0. 5040
740	csvGENb: abL9	0. 281	0. 232	815	1. 21	0. 2264
741	csvENVw+GENw: abL9	0. 280	0. 232	815	1. 21	0. 2269
742	csvENVw: abL10	0. 404	0. 559	815	0. 72	0. 4697
743	csvENVb: abL10	0. 218	0. 559	815	0. 39	0. 6971
744	csvGENw: abL10	0. 636	0. 559	815	1. 14	0. 2556
745	csvGENb: abL10	0. 671	0. 559	815	1. 20	0. 2302
746	csvENVw+GENw: abL10	0. 369	0. 559	815	0. 66	0. 5090
747	csvENVw: abL11	0. 080	0. 232	815	0. 34	0. 7303
748	csvENVb: abL11	0. 041	0. 232	815	0. 18	0. 8592

749	csvGENw: labL11	0.145	0.232	815	0.63	0.5321
750	csvGENb: labL11	0.239	0.232	815	1.03	0.3039
751	csvENVw+GENw: labL11	0.475	0.232	815	2.05	0.0409
752	csvENVw: labL12	-0.015	0.251	815	-0.06	0.9534
753	csvENVb: labL12	0.121	0.251	815	0.48	0.6300
754	csvGENw: labL12	0.200	0.251	815	0.80	0.4265
755	csvGENb: labL12	0.588	0.251	815	2.34	0.0193
756	csvENVw+GENw: labL12	0.663	0.251	815	2.64	0.0084
757	csvENVw: labL13	0.138	0.687	815	0.20	0.8406
758	csvENVb: labL13	-0.146	0.657	815	-0.22	0.8242
759	csvGENw: labL13	0.933	0.657	815	1.42	0.1561
760	csvGENb: labL13	1.144	0.657	815	1.74	0.0822
761	csvENVw+GENw: labL13	1.143	0.657	815	1.74	0.0822
762	csvENVw: labL14	-0.279	0.223	815	-1.25	0.2113
763	csvENVb: labL14	-0.059	0.223	815	-0.26	0.7915
764	csvGENw: labL14	-0.059	0.223	815	-0.26	0.7915
765	csvGENb: labL14	0.094	0.223	815	0.42	0.6753
766	csvENVw+GENw: labL14	-0.042	0.223	815	-0.19	0.8502
767	egumesBM: csvENVw: labL2	-0.198	0.325	815	-0.61	0.5421
768	egumesBM: csvENVb: labL2	-0.430	0.317	815	-1.35	0.1762
769	egumesBM: csvGENw: labL2	0.097	0.323	815	0.30	0.7628
770	egumesBM: csvGENb: labL2	-0.454	0.317	815	-1.43	0.1531
771	egumesBM: csvENVw+GENw: labL2	-0.229	0.317	815	-0.72	0.4709
772	egumesBM: csvENVw: labL3	0.424	0.467	815	0.91	0.3641
773	egumesBM: csvENVb: labL3	0.189	0.462	815	0.41	0.6824
774	egumesBM: csvGENw: labL3	0.454	0.462	815	0.98	0.3255
775	egumesBM: csvGENb: labL3	0.154	0.462	815	0.33	0.7380
776	egumesBM: csvENVw+GENw: labL3	-0.006	0.462	815	-0.01	0.9891
777	egumesBM: csvENVw: labL4	0.009	0.314	815	0.03	0.9782
778	egumesBM: csvENVb: labL4	-0.198	0.306	815	-0.65	0.5182
779	egumesBM: csvGENw: labL4	0.446	0.308	815	1.45	0.1476
780	egumesBM: csvGENb: labL4	-0.038	0.306	815	-0.12	0.9012
781	egumesBM: csvENVw+GENw: labL4	-0.018	0.306	815	-0.06	0.9527
782	egumesBM: csvENVw: labL5	-0.388	0.433	815	-0.90	0.3706
783	egumesBM: csvENVb: labL5	-0.286	0.427	815	-0.67	0.5034
784	egumesBM: csvGENw: labL5	0.027	0.427	815	0.06	0.9493
785	egumesBM: csvGENb: labL5	-0.370	0.431	815	-0.86	0.3916
786	egumesBM: csvENVw+GENw: labL5	-0.003	0.427	815	-0.01	0.9938
787	egumesBM: csvENVw: labL6	-0.171	1.252	815	-0.14	0.8912
788	egumesBM: csvENVb: labL6	-1.128	1.298	815	-0.87	0.3850
789	egumesBM: csvGENw: labL6	0.097	1.285	815	0.08	0.9397
790	egumesBM: csvGENb: labL6	0.977	1.348	815	0.72	0.4688
791	egumesBM: csvENVw+GENw: labL6	-0.342	1.263	815	-0.27	0.7869
792	egumesBM: csvENVw: labL7	0.686	0.491	815	1.40	0.1623
793	egumesBM: csvENVb: labL7	0.293	0.486	815	0.60	0.5459
794	egumesBM: csvGENw: labL7	0.044	0.486	815	0.09	0.9278
795	egumesBM: csvGENb: labL7	0.064	0.486	815	0.13	0.8949
796	egumesBM: csvENVw+GENw: labL7	-0.308	0.486	815	-0.63	0.5260
797	egumesBM: csvENVw: labL8	-0.071	0.569	815	-0.13	0.9001
798	egumesBM: csvENVb: labL8	-0.733	0.536	815	-1.37	0.1720
799	egumesBM: csvGENw: labL8	0.469	0.536	815	0.87	0.3821
800	egumesBM: csvGENb: labL8	-1.038	0.536	815	-1.94	0.0533
801	egumesBM: csvENVw+GENw: labL8	-0.916	0.564	815	-1.62	0.1047
802	egumesBM: csvENVw: labL9	-0.203	0.446	815	-0.46	0.6490
803	egumesBM: csvENVb: labL9	0.047	0.448	815	0.10	0.9164
804	egumesBM: csvGENw: labL9	-0.162	0.440	815	-0.37	0.7122
805	egumesBM: csvGENb: labL9	-0.575	0.448	815	-1.28	0.1997
806	egumesBM: csvENVw+GENw: labL9	-0.365	0.440	815	-0.83	0.4075
807	egumesBM: csvENVw: labL10	-0.244	0.716	815	-0.34	0.7330
808	egumesBM: csvENVb: labL10	-0.462	0.712	815	-0.65	0.5170
809	egumesBM: csvGENw: labL10	-0.815	0.712	815	-1.14	0.2528
810	egumesBM: csvGENb: labL10	-0.869	0.712	815	-1.22	0.2228
811	egumesBM: csvENVw+GENw: labL10	-1.496	0.712	815	-2.10	0.0360

```

812 | egumesBM: csvENVw: labL11      -0. 279      0. 366 815      -0. 76 0. 4462
813 | egumesBM: csvENVb: labL11      -0. 156      0. 359 815      -0. 43 0. 6648
814 | egumesBM: csvGENw: labL11      0. 341      0. 359 815      0. 95 0. 3420
815 | egumesBM: csvGENb: labL11      -0. 012      0. 359 815      -0. 03 0. 9730
816 | egumesBM: csvENVw+GENw: labL11 -0. 134      0. 359 815      -0. 37 0. 7092
817 | egumesBM: csvENVw: labL12      -0. 237      0. 399 815      -0. 59 0. 5533
818 | egumesBM: csvENVb: labL12      -0. 188      0. 393 815      -0. 48 0. 6324
819 | egumesBM: csvGENw: labL12      0. 349      0. 393 815      0. 89 0. 3742
820 | egumesBM: csvGENb: labL12      -0. 442      0. 393 815      -1. 13 0. 2607
821 | egumesBM: csvENVw+GENw: labL12 -0. 472      0. 393 815      -1. 20 0. 2301
822 | egumesBM: csvENVw: labL13      -1. 969      0. 973 815      -2. 02 0. 0433
823 | egumesBM: csvENVb: labL13      -1. 468      0. 949 815      -1. 55 0. 1224
824 | egumesBM: csvGENw: labL13      -1. 010      0. 949 815      -1. 06 0. 2874
825 | egumesBM: csvGENb: labL13      -1. 576      0. 949 815      -1. 66 0. 0972
826 | egumesBM: csvENVw+GENw: labL13 -2. 539      0. 949 815      -2. 68 0. 0076
827 | egumesBM: csvENVw: labL14      -0. 719      0. 575 815      -1. 25 0. 2118
828 | egumesBM: csvENVb: labL14      -0. 432      0. 571 815      -0. 76 0. 4494
829 | egumesBM: csvGENw: labL14      0. 597      0. 571 815      1. 05 0. 2957
830 | egumesBM: csvGENb: labL14      -0. 069      0. 571 815      -0. 12 0. 9045
831 | egumesBM: csvENVw+GENw: labL14 0. 419      0. 571 815      0. 73 0. 4627
832
833 Standardized Within-Group Residuals:
834   Min      Q1      Med      Q3     Max
835 -3.2346 -0.5889 -0.0817  0.4892  3.7536
836
837 Number of Observations: 984
838 Number of Groups: 2
839

```

840 Model for Brachipodium distachyon height (heightB)

```

841 anova(m6)
842
843   numDF denDF F-value p-value
844 (Intercept)    1    825 94752.31 <.0001
845 | egumes       1    825   3.33 0.0683
846 | csv          5    825   23.36 <.0001
847 | lab          13   825  317.33 <.0001
848 | egumes:csv  5    825   2.62 0.0231
849 | egumes:lab   13   825   49.89 <.0001
850 | csv:lab      65   825   10.16 <.0001
851 | egumes:csv:lab 65   825    1.45 0.0136
852
853 summary(m6)
854 Linear mixed-effects model fit by REML
855 Data: repro
856   AIC   BIC LogLik
857   4866 5795 -2236
858
859 Random effects:
860   Formula: ~1 | block
861   (Intercept) Residual
862   StdDev: 0.0718 5.27
863
864 Variance function:
865   Structure: Different standard deviations per stratum
866   Formula: ~1 | lab * egumes
867   Parameter estimates:
868   L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
869   1.000  0.890  0.164  0.388  0.504  0.857  0.684  0.948  0.422  0.571  0.479
870   L6*BM   L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM   L10*B  L10*BM  L11*B  L11*BM
871   0.394  0.453  0.540  0.629  0.582  0.754  0.740  0.483  0.374  0.389  0.552

```

871	L12*B	L12*BM	L13*B	L13*BM	L14*B	L14*BM	
872	0.415	0.434	1.201	1.184	0.736	0.641	
873	Fixed effects: heightB ~ Legumes * csv * lab						
874	(Intercept)		Value	Std. Error	DF	t-value	p-value
875		30.57	2.15	825	14.21	0.0000	
876	LegumesBM	-2.97	2.88	825	-1.03	0.3031	
877	csvENVw	-1.01	3.04	825	-0.33	0.7404	
878	csvENVb	-0.73	3.04	825	-0.24	0.8096	
879	csvGENw	-8.13	3.04	825	-2.67	0.0077	
880	csvGENb	-5.32	3.04	825	-1.75	0.0807	
881	csvENVw+GENw	-4.16	3.04	825	-1.37	0.1714	
882	LabL2	-4.84	2.18	825	-2.22	0.0268	
883	LabL3	3.20	2.41	825	1.33	0.1846	
884	LabL4	9.62	2.61	825	3.69	0.0002	
885	LabL5	2.36	2.33	825	1.01	0.3126	
886	LabL6	-2.43	2.39	825	-1.02	0.3096	
887	LabL7	-4.97	2.36	825	-2.11	0.0354	
888	LabL8	-5.98	2.54	825	-2.35	0.0189	
889	LabL9	-4.27	2.69	825	-1.59	0.1129	
890	LabL10	-8.06	2.39	825	-3.37	0.0008	
891	LabL11	2.93	2.31	825	1.27	0.2050	
892	LabL12	2.59	2.33	825	1.11	0.2655	
893	LabL13	1.60	3.36	825	0.48	0.6336	
894	LabL14	4.22	2.67	825	1.58	0.1142	
895	LegumesBM: csvENVw	2.65	4.07	825	0.65	0.5157	
896	LegumesBM: csvENVb	2.59	4.07	825	0.64	0.5256	
897	LegumesBM: csvGENw	4.36	4.07	825	1.07	0.2847	
898	LegumesBM: csvGENb	3.74	4.07	825	0.92	0.3591	
899	LegumesBM: csvENVw+GENw	-2.48	4.07	825	-0.61	0.5425	
900	LegumesBM: LabL2	2.90	3.04	825	0.95	0.3402	
901	LegumesBM: LabL3	-0.71	3.59	825	-0.20	0.8423	
902	LegumesBM: LabL4	1.79	3.82	825	0.47	0.6399	
903	LegumesBM: LabL5	0.08	3.26	825	0.02	0.9803	
904	LegumesBM: LabL6	1.90	3.17	825	0.60	0.5489	
905	LegumesBM: LabL7	1.20	3.25	825	0.37	0.7130	
906	LegumesBM: LabL8	3.70	3.42	825	1.08	0.2790	
907	LegumesBM: LabL9	4.30	3.67	825	1.17	0.2417	
908	LegumesBM: LabL10	0.04	3.16	825	0.01	0.9908	
909	LegumesBM: LabL11	1.03	3.27	825	0.31	0.7532	
910	LegumesBM: LabL12	1.57	3.18	825	0.49	0.6215	
911	LegumesBM: LabL13	-8.88	4.63	825	-1.92	0.0554	
912	LegumesBM: LabL14	25.27	3.56	825	7.09	0.0000	
913	csvENVw: LabL2	-0.45	3.08	825	-0.15	0.8840	
914	csvENVb: LabL2	-0.79	3.08	825	-0.26	0.7967	
915	csvGENw: LabL2	8.01	3.08	825	2.60	0.0095	
916	csvGENb: LabL2	5.76	3.08	825	1.87	0.0619	
917	csvENVw+GENw: LabL2	4.27	3.08	825	1.39	0.1659	
918	csvENVw: LabL3	-0.97	3.41	825	-0.28	0.7766	
919	csvENVb: LabL3	-1.00	3.41	825	-0.29	0.7683	
920	csvGENw: LabL3	9.89	3.41	825	2.91	0.0038	
921	csvGENb: LabL3	7.30	3.41	825	2.14	0.0324	
922	csvENVw+GENw: LabL3	7.31	3.41	825	2.15	0.0322	
923	csvENVw: LabL4	-8.78	3.69	825	-2.38	0.0174	
924	csvENVb: LabL4	-0.24	3.69	825	-0.06	0.9489	
925	csvGENw: LabL4	0.28	3.69	825	0.07	0.9405	
926	csvGENb: LabL4	-0.90	3.69	825	-0.24	0.8071	
927	csvENVw+GENw: LabL4	-5.36	3.69	825	-1.45	0.1466	
928	csvENVw: LabL5	1.06	3.30	825	0.32	0.7486	
929	csvENVb: LabL5	0.47	3.30	825	0.14	0.8870	
930	csvGENw: LabL5	12.12	3.33	825	3.64	0.0003	
931	csvGENb: LabL5	6.67	3.30	825	2.02	0.0438	
932	csvENVw+GENw: LabL5	5.39	3.30	825	1.63	0.1028	

934	csvENVw: labL6	2. 58	3. 37	825	0. 77	0. 4445
935	csvENVb: labL6	1. 28	3. 37	825	0. 38	0. 7043
936	csvGENw: labL6	5. 03	3. 37	825	1. 49	0. 1367
937	csvGENb: labL6	4. 54	3. 37	825	1. 35	0. 1788
938	csvENVw+GENw: labL6	1. 70	3. 40	825	0. 50	0. 6174
939	csvENVw: labL7	1. 99	3. 34	825	0. 60	0. 5516
940	csvENVb: labL7	2. 13	3. 37	825	0. 63	0. 5263
941	csvGENw: labL7	14. 56	3. 34	825	4. 36	0. 0000
942	csvGENb: labL7	6. 72	3. 34	825	2. 01	0. 0443
943	csvENVw+GENw: labL7	8. 97	3. 34	825	2. 69	0. 0073
944	csvENVw: labL8	2. 41	3. 59	825	0. 67	0. 5025
945	csvENVb: labL8	1. 00	3. 59	825	0. 28	0. 7815
946	csvGENw: labL8	0. 31	3. 59	825	0. 09	0. 9310
947	csvGENb: labL8	0. 54	3. 59	825	0. 15	0. 8802
948	csvENVw+GENw: labL8	-2. 49	3. 59	825	-0. 69	0. 4887
949	csvENVw: labL9	-0. 50	3. 81	825	-0. 13	0. 8950
950	csvENVb: labL9	-1. 65	3. 81	825	-0. 43	0. 6644
951	csvGENw: labL9	8. 47	3. 81	825	2. 22	0. 0264
952	csvGENb: labL9	3. 71	3. 88	825	0. 96	0. 3385
953	csvENVw+GENw: labL9	0. 48	3. 81	825	0. 13	0. 9003
954	csvENVw: labL10	3. 30	3. 38	825	0. 98	0. 3288
955	csvENVb: labL10	1. 11	3. 38	825	0. 33	0. 7429
956	csvGENw: labL10	16. 32	3. 38	825	4. 83	0. 0000
957	csvGENb: labL10	10. 68	3. 38	825	3. 16	0. 0016
958	csvENVw+GENw: labL10	13. 25	3. 38	825	3. 92	0. 0001
959	csvENVw: labL11	-1. 12	3. 26	825	-0. 34	0. 7304
960	csvENVb: labL11	-1. 29	3. 26	825	-0. 40	0. 6917
961	csvGENw: labL11	11. 47	3. 26	825	3. 51	0. 0005
962	csvGENb: labL11	7. 20	3. 26	825	2. 21	0. 0276
963	csvENVw+GENw: labL11	6. 19	3. 26	825	1. 90	0. 0582
964	csvENVw: labL12	-0. 80	3. 29	825	-0. 24	0. 8075
965	csvENVb: labL12	0. 36	3. 29	825	0. 11	0. 9134
966	csvGENw: labL12	13. 58	3. 29	825	4. 12	0. 0000
967	csvGENb: labL12	8. 31	3. 29	825	2. 52	0. 0119
968	csvENVw+GENw: labL12	7. 31	3. 29	825	2. 22	0. 0267
969	csvENVw: labL13	4. 08	4. 75	825	0. 86	0. 3906
970	csvENVb: labL13	-1. 67	4. 75	825	-0. 35	0. 7260
971	csvGENw: labL13	17. 28	4. 75	825	3. 63	0. 0003
972	csvGENb: labL13	13. 27	4. 75	825	2. 79	0. 0054
973	csvENVw+GENw: labL13	18. 64	4. 75	825	3. 92	0. 0001
974	csvENVw: labL14	-3. 71	3. 78	825	-0. 98	0. 3267
975	csvENVb: labL14	-0. 91	3. 78	825	-0. 24	0. 8099
976	csvGENw: labL14	7. 56	3. 78	825	2. 00	0. 0455
977	csvGENb: labL14	3. 31	3. 78	825	0. 88	0. 3809
978	csvENVw+GENw: labL14	4. 24	3. 78	825	1. 12	0. 2620
979	I egumesBM: csvENVw: labL2	-1. 47	4. 30	825	-0. 34	0. 7322
980	I egumesBM: csvENVb: labL2	-3. 60	4. 28	825	-0. 84	0. 4004
981	I egumesBM: csvGENw: labL2	-6. 72	4. 28	825	-1. 57	0. 1169
982	I egumesBM: csvGENb: labL2	-3. 77	4. 28	825	-0. 88	0. 3793
983	I egumesBM: csvENVw+GENw: labL2	3. 37	4. 30	825	0. 78	0. 4336
984	I egumesBM: csvENVw: labL3	-4. 80	5. 07	825	-0. 95	0. 3441
985	I egumesBM: csvENVb: labL3	-3. 54	5. 07	825	-0. 70	0. 4850
986	I egumesBM: csvGENw: labL3	-3. 17	5. 07	825	-0. 62	0. 5325
987	I egumesBM: csvGENb: labL3	-1. 60	5. 07	825	-0. 32	0. 7524
988	I egumesBM: csvENVw+GENw: labL3	3. 26	5. 07	825	0. 64	0. 5207
989	I egumesBM: csvENVw: labL4	5. 69	5. 41	825	1. 05	0. 2926
990	I egumesBM: csvENVb: labL4	-2. 61	5. 41	825	-0. 48	0. 6294
991	I egumesBM: csvGENw: labL4	-4. 20	5. 41	825	-0. 78	0. 4378
992	I egumesBM: csvGENb: labL4	-1. 48	5. 41	825	-0. 27	0. 7839
993	I egumesBM: csvENVw+GENw: labL4	1. 48	5. 41	825	0. 27	0. 7847
994	I egumesBM: csvENVw: labL5	-2. 41	4. 61	825	-0. 52	0. 6014
995	I egumesBM: csvENVb: labL5	-2. 17	4. 61	825	-0. 47	0. 6385
996	I egumesBM: csvGENw: labL5	-6. 57	4. 63	825	-1. 42	0. 1559

```

997 | egumesBM: csvGENb: labL5      -3.70      4.64 825    -0.80 0.4253
998 | egumesBM: csvENVw+GENw: labL5 5.68       4.61 825    1.23 0.2185
999 | egumesBM: csvENVw: labL6     -3.35      4.49 825    -0.75 0.4559
1000 | egumesBM: csvENVb: labL6     -3.78      4.49 825    -0.84 0.3995
1001 | egumesBM: csvGENw: labL6     -2.98      4.49 825    -0.66 0.5068
1002 | egumesBM: csvGENb: labL6     -4.92      4.49 825    -1.10 0.2736
1003 | egumesBM: csvENVw+GENw: labL6 4.83       4.53 825    1.07 0.2862
1004 | egumesBM: csvENVw: labL7     -2.51      4.60 825    -0.54 0.5862
1005 | egumesBM: csvENVb: labL7     -3.00      4.62 825    -0.65 0.5168
1006 | egumesBM: csvGENw: labL7     -5.91      4.63 825    -1.28 0.2023
1007 | egumesBM: csvGENb: labL7     -1.49      4.60 825    -0.32 0.7459
1008 | egumesBM: csvENVw+GENw: labL7 5.99       4.60 825    1.30 0.1932
1009 | egumesBM: csvENVw: labL8     -5.41      4.83 825    -1.12 0.2634
1010 | egumesBM: csvENVb: labL8     -5.54      4.83 825    -1.15 0.2518
1011 | egumesBM: csvGENw: labL8     -3.99      4.83 825    -0.83 0.4095
1012 | egumesBM: csvGENb: labL8     -4.79      4.83 825    -0.99 0.3219
1013 | egumesBM: csvENVw+GENw: labL8 2.41       4.83 825    0.50 0.6181
1014 | egumesBM: csvENVw: labL9     -3.34      5.19 825    -0.64 0.5196
1015 | egumesBM: csvENVb: labL9     -1.89      5.19 825    -0.36 0.7159
1016 | egumesBM: csvGENw: labL9     -14.33     5.24 825    -2.74 0.0063
1017 | egumesBM: csvGENb: labL9     -7.25      5.24 825    -1.38 0.1668
1018 | egumesBM: csvENVw+GENw: labL9 -1.13      5.19 825    -0.22 0.8271
1019 | egumesBM: csvENVw: labL10    -3.80      4.47 825    -0.85 0.3960
1020 | egumesBM: csvENVb: labL10    -2.66      4.47 825    -0.59 0.5531
1021 | egumesBM: csvGENw: labL10    -5.58      4.47 825    -1.25 0.2127
1022 | egumesBM: csvGENb: labL10    -5.46      4.47 825    -1.22 0.2229
1023 | egumesBM: csvENVw+GENw: labL10 4.34       4.47 825    0.97 0.3322
1024 | egumesBM: csvENVw: labL11    -1.63      4.59 825    -0.36 0.7225
1025 | egumesBM: csvENVb: labL11    -2.21      4.62 825    -0.48 0.6321
1026 | egumesBM: csvGENw: labL11    -2.21      4.59 825    -0.48 0.6301
1027 | egumesBM: csvGENb: labL11    -0.87      4.59 825    -0.19 0.8489
1028 | egumesBM: csvENVw+GENw: labL11 4.06       4.59 825    0.88 0.3770
1029 | egumesBM: csvENVw: labL12    -1.66      4.48 825    -0.37 0.7105
1030 | egumesBM: csvENVb: labL12    -1.93      4.48 825    -0.43 0.6674
1031 | egumesBM: csvGENw: labL12    -3.59      4.48 825    -0.80 0.4235
1032 | egumesBM: csvGENb: labL12    -3.22      4.48 825    -0.72 0.4732
1033 | egumesBM: csvENVw+GENw: labL12 3.00       4.48 825    0.67 0.5028
1034 | egumesBM: csvENVw: labL13    2.30       6.55 825    0.35 0.7252
1035 | egumesBM: csvENVb: labL13    0.71       6.55 825    0.11 0.9132
1036 | egumesBM: csvGENw: labL13    -8.03      6.55 825    -1.23 0.2203
1037 | egumesBM: csvGENb: labL13    -5.91      6.55 825    -0.90 0.3670
1038 | egumesBM: csvENVw+GENw: labL13 5.78       6.55 825    0.88 0.3777
1039 | egumesBM: csvENVw: labL14    -0.80      5.04 825    -0.16 0.8745
1040 | egumesBM: csvENVb: labL14    -1.40      5.04 825    -0.28 0.7814
1041 | egumesBM: csvGENw: labL14     -13.24     5.04 825    -2.63 0.0088
1042 | egumesBM: csvGENb: labL14     -4.74      5.04 825    -0.94 0.3476
1043 | egumesBM: csvENVw+GENw: labL14 -7.50      5.04 825    -1.49 0.1372
1044
1045 Standardized Within-Group Residuals:
1046   Min Q1 Med Q3 Max
1047 -3.10279 -0.61473 0.00168 0.55965 3.06272
1048
1049 Number of Observations: 994
1050 Number of Groups: 2
1051

```

Model for shoot N% (N.)

```

1053 anova(m7)
1054
1055 (Intercept) 1 839 1961.43 <.0001
1056 Legumes      1 839 449.87 <.0001
1057 csv          5 839  0.78 0.5664

```

```

1058 lab 13 839 335.18 <.0001
1059 legumes:csv 5 839 1.34 0.2449
1060 legumes:lab 13 839 14.12 <.0001
1061 csv:lab 65 839 1.98 <.0001
1062 legumes:csv:lab 65 839 1.71 0.0006
1063
1064 summary(m7)
1065 Linear mixed-effects model fit by REML
1066 Data: reproto
1067 AIC BIC LogLik
1068 523 1456 -64.7
1069
1070 Random effects:
1071 Formula: ~1 | block
1072 (Intercept) Residual
1073 StdDev: 0.0279 0.11
1074
1075 Variance function:
1076 Structure: Different standard deviations per stratum
1077 Formula: ~1 | lab * legumes
1078
1079 Parameter estimates:
1080 L1*B L1*BM L2*B L2*BM L3*B L3*BM L4*B L4*BM L5*B L5*BM L6*B
1081 1.000 0.469 4.991 6.048 2.026 1.610 3.800 2.978 0.966 1.084 0.959
1082 L6*BM L7*B L7*BM L8*B L8*BM L9*B L9*BM L10*B L10*BM L11*B L11*BM
1083 1.013 4.379 3.800 2.162 1.686 1.370 1.070 2.293 2.407 1.508 1.799
1084 L12*B L12*BM L13*B L13*BM L14*B L14*BM
1085 3.219 3.142 5.776 4.602 1.224 0.802
1086
1087 Fixed effects: N. ~ legumes * csv * lab
1088
1089 (Intercept) Value Std. Error DF t-value p-value
1090 legumesBM 0.665 0.049 839 13.51 0.0000
1091 csvENVw 0.012 0.050 839 0.24 0.8097
1092 csvENVb 0.003 0.064 839 0.04 0.9687
1093 csvGENw -0.034 0.064 839 -0.53 0.5959
1094 csvGENb 0.009 0.064 839 0.14 0.8919
1095 csvENVw+GENw 0.053 0.064 839 0.83 0.4047
1096 labL2 0.064 0.064 839 1.01 0.3122
1097 labL3 1.440 0.230 839 6.27 0.0000
1098 labL4 0.167 0.202 839 1.64 0.1024
1099 labL5 0.454 0.102 839 2.56 0.0106
1100 labL6 0.025 0.177 839 0.39 0.6961
1101 labL7 0.383 0.063 839 6.12 0.0000
1102 labL8 1.198 0.063 839 5.91 0.0000
1103 labL9 0.386 0.063 839 6.18 0.0000
1104 labL10 0.050 0.063 839 -0.65 0.5163
1105 labL11 1.613 0.063 839 3.42 0.0007
1106 labL12 0.425 0.063 839 19.76 0.0000
1107 labL13 1.648 0.063 839 10.84 0.0000
1108 labL14 0.386 0.063 839 5.54 0.0000
1109 legumesBM:csvENVw -0.003 0.063 839 -0.04 0.9679
1110 legumesBM:csvENVb 0.014 0.063 839 0.20 0.8388
1111 legumesBM:csvGENw -0.016 0.063 839 -0.22 0.8222
1112 legumesBM:csvGENb -0.090 0.063 839 -1.28 0.2001
1113 legumesBM:csvENVw+GENw -0.064 0.063 839 -0.90 0.3665
1114 legumesBM:labL2 -1.033 0.063 839 -2.89 0.0039
1115 legumesBM:labL3 -0.109 0.127 839 -0.86 0.3915
1116 legumesBM:labL4 -0.298 0.223 839 -1.33 0.1832
1117 legumesBM:labL5 0.160 0.082 839 1.95 0.0519
1118 legumesBM:labL6 -0.077 0.082 839 -0.96 0.3359
1119 legumesBM:labL7 -0.886 0.266 839 -3.33 0.0009
1120 legumesBM:labL8 -0.475 0.133 839 -3.56 0.0004

```

1121	I egumesBM: I abL9	0. 030	0. 093	839	0. 33	0. 7427
1122	I egumesBM: I abL10	0. 017	0. 158	839	0. 11	0. 9143
1123	I egumesBM: I abL11	-0. 703	0. 117	839	-6. 01	0. 0000
1124	I egumesBM: I abL12	-0. 412	0. 209	839	-1. 97	0. 0491
1125	I egumesBM: I abL13	-0. 403	0. 337	839	-1. 20	0. 2318
1126	I egumesBM: I abL14	-0. 162	0. 083	839	-1. 96	0. 0505
1127	csvENVw: I abL2	-0. 145	0. 325	839	-0. 45	0. 6542
1128	csvENVb: I abL2	-0. 162	0. 325	839	-0. 50	0. 6176
1129	csvGENw: I abL2	-1. 330	0. 325	839	-4. 10	0. 0000
1130	csvGENb: I abL2	-1. 011	0. 325	839	-3. 11	0. 0019
1131	csvENVw+GENw: I abL2	-1. 053	0. 325	839	-3. 24	0. 0012
1132	csvENVw: I abL3	-0. 056	0. 144	839	-0. 39	0. 6962
1133	csvENVb: I abL3	-0. 056	0. 144	839	-0. 39	0. 6953
1134	csvGENw: I abL3	-0. 074	0. 144	839	-0. 52	0. 6055
1135	csvGENb: I abL3	-0. 122	0. 144	839	-0. 85	0. 3976
1136	csvENVw+GENw: I abL3	-0. 143	0. 144	839	-0. 99	0. 3215
1137	csvENVw: I abL4	0. 210	0. 251	839	0. 84	0. 4027
1138	csvENVb: I abL4	0. 045	0. 251	839	0. 18	0. 8581
1139	csvGENw: I abL4	0. 286	0. 251	839	1. 14	0. 2550
1140	csvGENb: I abL4	0. 191	0. 251	839	0. 76	0. 4466
1141	csvENVw+GENw: I abL4	-0. 004	0. 251	839	-0. 02	0. 9862
1142	csvENVw: I abL5	0. 181	0. 089	839	2. 04	0. 0420
1143	csvENVb: I abL5	0. 223	0. 089	839	2. 52	0. 0120
1144	csvGENw: I abL5	0. 118	0. 089	839	1. 33	0. 1831
1145	csvGENb: I abL5	0. 158	0. 089	839	1. 78	0. 0755
1146	csvENVw+GENw: I abL5	0. 069	0. 089	839	0. 77	0. 4389
1147	csvENVw: I abL6	-0. 097	0. 088	839	-1. 10	0. 2731
1148	csvENVb: I abL6	-0. 003	0. 088	839	-0. 04	0. 9698
1149	csvGENw: I abL6	0. 089	0. 088	839	1. 01	0. 3127
1150	csvGENb: I abL6	0. 007	0. 088	839	0. 08	0. 9363
1151	csvENVw+GENw: I abL6	0. 030	0. 088	839	0. 34	0. 7322
1152	csvENVw: I abL7	-0. 451	0. 286	839	-1. 57	0. 1159
1153	csvENVb: I abL7	-0. 183	0. 286	839	-0. 64	0. 5227
1154	csvGENw: I abL7	-0. 395	0. 286	839	-1. 38	0. 1680
1155	csvGENb: I abL7	-0. 699	0. 286	839	-2. 44	0. 0150
1156	csvENVw+GENw: I abL7	-0. 889	0. 286	839	-3. 10	0. 0020
1157	csvENVw: I abL8	-0. 007	0. 152	839	-0. 04	0. 9648
1158	csvENVb: I abL8	-0. 131	0. 152	839	-0. 86	0. 3893
1159	csvGENw: I abL8	0. 077	0. 152	839	0. 51	0. 6111
1160	csvGENb: I abL8	0. 082	0. 152	839	0. 54	0. 5883
1161	csvENVw+GENw: I abL8	0. 120	0. 152	839	0. 79	0. 4315
1162	csvENVw: I abL9	0. 139	0. 108	839	1. 29	0. 1979
1163	csvENVb: I abL9	0. 082	0. 108	839	0. 76	0. 4505
1164	csvGENw: I abL9	0. 095	0. 108	839	0. 88	0. 3775
1165	csvGENb: I abL9	0. 096	0. 108	839	0. 89	0. 3750
1166	csvENVw+GENw: I abL9	0. 046	0. 108	839	0. 42	0. 6741
1167	csvENVw: I abL10	-0. 103	0. 160	839	-0. 64	0. 5201
1168	csvENVb: I abL10	0. 080	0. 160	839	0. 50	0. 6181
1169	csvGENw: I abL10	-0. 175	0. 160	839	-1. 10	0. 2730
1170	csvGENb: I abL10	-0. 153	0. 160	839	-0. 96	0. 3382
1171	csvENVw+GENw: I abL10	-0. 187	0. 160	839	-1. 17	0. 2413
1172	csvENVw: I abL11	-0. 061	0. 115	839	-0. 53	0. 5983
1173	csvENVb: I abL11	-0. 089	0. 115	839	-0. 77	0. 4434
1174	csvGENw: I abL11	-0. 333	0. 115	839	-2. 89	0. 0040
1175	csvGENb: I abL11	-0. 202	0. 115	839	-1. 75	0. 0802
1176	csvENVw+GENw: I abL11	-0. 188	0. 115	839	-1. 63	0. 1031
1177	csvENVw: I abL12	-0. 362	0. 215	839	-1. 69	0. 0923
1178	csvENVb: I abL12	-0. 211	0. 215	839	-0. 98	0. 3275
1179	csvGENw: I abL12	-0. 431	0. 215	839	-2. 00	0. 0455
1180	csvGENb: I abL12	-0. 164	0. 215	839	-0. 76	0. 4448
1181	csvENVw+GENw: I abL12	-0. 286	0. 215	839	-1. 33	0. 1838
1182	csvENVw: I abL13	0. 273	0. 374	839	0. 73	0. 4660
1183	csvENVb: I abL13	0. 340	0. 374	839	0. 91	0. 3631

1184	csvGENw: I abL13	0. 063	0. 374	839	0. 17	0. 8655
1185	csvGENb: I abL13	-0. 267	0. 374	839	-0. 71	0. 4760
1186	csvENVw+GENw: I abL13	-0. 248	0. 374	839	-0. 66	0. 5077
1187	csvENVw: I abL14	0. 003	0. 101	839	0. 03	0. 9800
1188	csvENVb: I abL14	0. 000	0. 101	839	0. 00	0. 9971
1189	csvGENw: I abL14	-0. 051	0. 101	839	-0. 50	0. 6145
1190	csvGENb: I abL14	-0. 161	0. 101	839	-1. 60	0. 1099
1191	csvENVw+GENw: I abL14	-0. 278	0. 101	839	-2. 76	0. 0060
1192	I egumesBM: csvENVw: I abL2	0. 438	0. 505	839	0. 87	0. 3863
1193	I egumesBM: csvENVb: I abL2	0. 156	0. 505	839	0. 31	0. 7568
1194	I egumesBM: csvGENw: I abL2	1. 747	0. 505	839	3. 46	0. 0006
1195	I egumesBM: csvGENb: I abL2	1. 487	0. 505	839	2. 94	0. 0033
1196	I egumesBM: csvENVw+GENw: I abL2	1. 557	0. 505	839	3. 08	0. 0021
1197	I egumesBM: csvENVw: I abL3	0. 047	0. 179	839	0. 26	0. 7944
1198	I egumesBM: csvENVb: I abL3	0. 146	0. 179	839	0. 81	0. 4160
1199	I egumesBM: csvGENw: I abL3	0. 100	0. 179	839	0. 56	0. 5770
1200	I egumesBM: csvGENb: I abL3	-0. 062	0. 179	839	-0. 34	0. 7303
1201	I egumesBM: csvENVw+GENw: I abL3	-0. 043	0. 179	839	-0. 24	0. 8104
1202	I egumesBM: csvENVw: I abL4	-0. 179	0. 316	839	-0. 57	0. 5722
1203	I egumesBM: csvENVb: I abL4	0. 105	0. 316	839	0. 33	0. 7393
1204	I egumesBM: csvGENw: I abL4	0. 301	0. 316	839	0. 95	0. 3404
1205	I egumesBM: csvGENb: I abL4	-0. 130	0. 316	839	-0. 41	0. 6808
1206	I egumesBM: csvENVw+GENw: I abL4	0. 423	0. 316	839	1. 34	0. 1811
1207	I egumesBM: csvENVw: I abL5	-0. 242	0. 116	839	-2. 08	0. 0374
1208	I egumesBM: csvENVb: I abL5	-0. 236	0. 116	839	-2. 03	0. 0425
1209	I egumesBM: csvGENw: I abL5	-0. 086	0. 116	839	-0. 74	0. 4600
1210	I egumesBM: csvGENb: I abL5	-0. 151	0. 116	839	-1. 30	0. 1952
1211	I egumesBM: csvENVw+GENw: I abL5	-0. 159	0. 116	839	-1. 37	0. 1712
1212	I egumesBM: csvENVw: I abL6	0. 107	0. 113	839	0. 94	0. 3483
1213	I egumesBM: csvENVb: I abL6	0. 017	0. 113	839	0. 15	0. 8804
1214	I egumesBM: csvGENw: I abL6	-0. 068	0. 113	839	-0. 60	0. 5466
1215	I egumesBM: csvGENb: I abL6	0. 075	0. 113	839	0. 66	0. 5105
1216	I egumesBM: csvENVw+GENw: I abL6	0. 023	0. 113	839	0. 20	0. 8427
1217	I egumesBM: csvENVw: I abL7	0. 170	0. 376	839	0. 45	0. 6517
1218	I egumesBM: csvENVb: I abL7	0. 044	0. 376	839	0. 12	0. 9066
1219	I egumesBM: csvGENw: I abL7	0. 332	0. 376	839	0. 88	0. 3778
1220	I egumesBM: csvGENb: I abL7	0. 690	0. 376	839	1. 83	0. 0672
1221	I egumesBM: csvENVw+GENw: I abL7	0. 777	0. 376	839	2. 06	0. 0393
1222	I egumesBM: csvENVw: I abL8	0. 054	0. 189	839	0. 29	0. 7744
1223	I egumesBM: csvENVb: I abL8	0. 459	0. 189	839	2. 43	0. 0152
1224	I egumesBM: csvGENw: I abL8	0. 328	0. 189	839	1. 74	0. 0822
1225	I egumesBM: csvGENb: I abL8	0. 466	0. 189	839	2. 47	0. 0136
1226	I egumesBM: csvENVw+GENw: I abL8	0. 156	0. 189	839	0. 83	0. 4094
1227	I egumesBM: csvENVw: I abL9	-0. 160	0. 131	839	-1. 22	0. 2243
1228	I egumesBM: csvENVb: I abL9	-0. 091	0. 131	839	-0. 69	0. 4894
1229	I egumesBM: csvGENw: I abL9	0. 053	0. 131	839	0. 40	0. 6890
1230	I egumesBM: csvGENb: I abL9	-0. 033	0. 131	839	-0. 25	0. 7996
1231	I egumesBM: csvENVw+GENw: I abL9	-0. 032	0. 131	839	-0. 25	0. 8055
1232	I egumesBM: csvENVw: I abL10	-0. 056	0. 223	839	-0. 25	0. 8022
1233	I egumesBM: csvENVb: I abL10	-0. 285	0. 223	839	-1. 28	0. 2025
1234	I egumesBM: csvGENw: I abL10	-0. 022	0. 223	839	-0. 10	0. 9204
1235	I egumesBM: csvGENb: I abL10	-0. 088	0. 223	839	-0. 40	0. 6929
1236	I egumesBM: csvENVw+GENw: I abL10	-0. 060	0. 223	839	-0. 27	0. 7897
1237	I egumesBM: csvENVw: I abL11	0. 159	0. 165	839	0. 96	0. 3364
1238	I egumesBM: csvENVb: I abL11	0. 209	0. 165	839	1. 26	0. 2077
1239	I egumesBM: csvGENw: I abL11	0. 231	0. 165	839	1. 40	0. 1628
1240	I egumesBM: csvGENb: I abL11	0. 095	0. 165	839	0. 58	0. 5647
1241	I egumesBM: csvENVw+GENw: I abL11	0. 394	0. 165	839	2. 38	0. 0174
1242	I egumesBM: csvENVw: I abL12	0. 443	0. 295	839	1. 50	0. 1337
1243	I egumesBM: csvENVb: I abL12	0. 001	0. 295	839	0. 00	0. 9969
1244	I egumesBM: csvGENw: I abL12	0. 330	0. 295	839	1. 12	0. 2638
1245	I egumesBM: csvGENb: I abL12	-0. 188	0. 295	839	-0. 64	0. 5242
1246	I egumesBM: csvENVw+GENw: I abL12	0. 308	0. 295	839	1. 04	0. 2980

```

1247 | egumesBM: csvENVw: labL13      -0.785    0.476 839   -1.65  0.0996
1248 | egumesBM: csvENVb: labL13      -0.435    0.476 839   -0.91  0.3612
1249 | egumesBM: csvGENw: labL13      -0.288    0.476 839   -0.61  0.5453
1250 | egumesBM: csvGENb: labL13      0.394    0.476 839   0.83   0.4083
1251 | egumesBM: csvENVw+GENw: labL13 0.447    0.476 839   0.94   0.3477
1252 | egumesBM: csvENVw: labL14      -0.025    0.117 839   -0.21  0.8306
1253 | egumesBM: csvENVb: labL14      -0.006    0.117 839   -0.05  0.9623
1254 | egumesBM: csvGENw: labL14      0.087    0.117 839   0.75   0.4547
1255 | egumesBM: csvGENb: labL14      0.181    0.117 839   1.55   0.1213
1256 | egumesBM: csvENVw+GENw: labL14 0.319    0.117 839   2.73   0.0065
1257
1258 Standardized Within-Group Residuals:
1259   Min     Q1     Med     Q3     Max
1260 -2.7004 -0.6720 -0.0372  0.5961  4.5580
1261
1262 Number of Observations: 1008
1263 Number of Groups: 2
1264

```

1265 Model for shoot C% (C.)

```

1266 anova(m8)
1267
1268   numDF denDF F-value p-value
1269 (Intercept)       1     839 2288364 <.0001
1270 Legumes          1     839    111 <.0001
1271 csv               5     839     0  0.9782
1272 lab              13    839    174 <.0001
1273 Legumes:csv      5     839     3  0.0267
1274 Legumes:lab       13    839    12 <.0001
1275 csv:lab           65    839     2  0.0011
1276 Legumes:csv:lab  65    839     1  0.0449
1277
1278 summary(m8)
1279 Linear mixed-effects model fit by REML
1280 Data: reprotoz
1281   AIC   BIC LogLik
1282 2718 3650 -1162
1283
1284 Random effects:
1285   Formula: ~1 | block
1286   (Intercept) Residual
1287 StdDev:        0.0296  0.73
1288
1289 Variance function:
1290 Structure: Different standard deviations per stratum
1291 Formula: ~1 | lab * Legumes
1292 Parameter estimates:
1293 L1*B  L1*BM  L2*B  L2*BM  L3*B  L3*BM  L4*B  L4*BM  L5*B  L5*BM  L6*B
1294 1.000  1.022  0.711  1.010  1.238  0.969  1.068  0.838  0.970  0.590  2.252
1295 L6*BM  L7*B  L7*BM  L8*B  L8*BM  L9*B  L9*BM  L10*B L10*BM  L11*B L11*BM
1296 1.929  0.440  0.592  0.989  0.802  0.550  0.445  1.652  1.362  0.977  1.424
1297 L12*B L12*BM L13*B L13*BM L14*B L14*BM
1298 1.417  1.691  5.870  4.150  0.906  0.971
1299 Fixed effects: C. ~ Legumes * csv * lab
1300
1301   Value Std. Error DF t-value p-value
1302 (Intercept) 46.0    0.299 839  153.8  0.0000
1303 LegumesBM   -0.8    0.426 839   -1.9  0.0635
1304 csvENVw     0.4    0.422 839    1.0  0.3012
1305 csvENVb     -0.4   0.422 839   -0.9  0.3915
1306 csvGENw     -0.1   0.422 839   -0.1  0.8891
1307 csvGENb     -0.4   0.422 839   -0.9  0.3658
1308 csvENVw+GENw -0.1   0.422 839   -0.4  0.7248
1309 labL2       -3.0   0.366 839   -8.2  0.0000

```

1308	abL3	-0. 2	0. 474	839	-0. 4	0. 7225
1309	abL4	-3. 5	0. 436	839	-8. 1	0. 0000
1310	abL5	-1. 7	0. 415	839	-4. 0	0. 0001
1311	abL6	-2. 6	0. 735	839	-3. 5	0. 0004
1312	abL7	-2. 7	0. 326	839	-8. 3	0. 0000
1313	abL8	-2. 1	0. 419	839	-4. 9	0. 0000
1314	abL9	-1. 6	0. 340	839	-4. 8	0. 0000
1315	abL10	-3. 4	0. 576	839	-5. 9	0. 0000
1316	abL11	-2. 7	0. 417	839	-6. 4	0. 0000
1317	abL12	-3. 8	0. 517	839	-7. 4	0. 0000
1318	abL13	-7. 5	1. 776	839	-4. 2	0. 0000
1319	abL14	-2. 9	0. 402	839	-7. 1	0. 0000
1320	egumesBM: csvENVw	-0. 7	0. 603	839	-1. 1	0. 2732
1321	egumesBM: csvENVb	0. 6	0. 603	839	1. 0	0. 3001
1322	egumesBM: csvGENw	-0. 4	0. 603	839	-0. 6	0. 5443
1323	egumesBM: csvGENb	0. 4	0. 603	839	0. 7	0. 4994
1324	egumesBM: csvENVw+GENw	-0. 1	0. 603	839	-0. 1	0. 9271
1325	egumesBM: abL2	1. 6	0. 563	839	2. 9	0. 0039
1326	egumesBM: abL3	-0. 4	0. 634	839	-0. 6	0. 5589
1327	egumesBM: abL4	-0. 6	0. 588	839	-0. 9	0. 3433
1328	egumesBM: abL5	0. 1	0. 544	839	0. 2	0. 8080
1329	egumesBM: abL6	1. 3	0. 981	839	1. 4	0. 1712
1330	egumesBM: abL7	0. 0	0. 480	839	0. 1	0. 9367
1331	egumesBM: abL8	0. 8	0. 571	839	1. 4	0. 1549
1332	egumesBM: abL9	0. 9	0. 475	839	1. 8	0. 0732
1333	egumesBM: abL10	-0. 3	0. 768	839	-0. 4	0. 6893
1334	egumesBM: abL11	0. 2	0. 668	839	0. 3	0. 7355
1335	egumesBM: abL12	0. 1	0. 784	839	0. 1	0. 9157
1336	egumesBM: abL13	5. 9	2. 186	839	2. 7	0. 0075
1337	egumesBM: abL14	0. 2	0. 582	839	0. 4	0. 7026
1338	csvENVw: abL2	-0. 3	0. 517	839	-0. 6	0. 5285
1339	csvENVb: abL2	0. 7	0. 517	839	1. 3	0. 1972
1340	csvGENw: abL2	0. 4	0. 517	839	0. 8	0. 4352
1341	csvGENb: abL2	0. 6	0. 517	839	1. 1	0. 2543
1342	csvENVw+GENw: abL2	0. 7	0. 517	839	1. 4	0. 1599
1343	csvENVw: abL3	-0. 9	0. 671	839	-1. 4	0. 1580
1344	csvENVb: abL3	0. 3	0. 671	839	0. 5	0. 6186
1345	csvGENw: abL3	-0. 4	0. 671	839	-0. 6	0. 5816
1346	csvGENb: abL3	-0. 2	0. 671	839	-0. 3	0. 7578
1347	csvENVw+GENw: abL3	0. 1	0. 671	839	0. 2	0. 8322
1348	csvENVw: abL4	-1. 4	0. 617	839	-2. 3	0. 0201
1349	csvENVb: abL4	0. 2	0. 617	839	0. 3	0. 7989
1350	csvGENw: abL4	-0. 1	0. 617	839	-0. 1	0. 8931
1351	csvGENb: abL4	0. 0	0. 617	839	-0. 1	0. 9417
1352	csvENVw+GENw: abL4	-0. 8	0. 617	839	-1. 4	0. 1772
1353	csvENVw: abL5	0. 1	0. 587	839	0. 1	0. 9295
1354	csvENVb: abL5	0. 9	0. 587	839	1. 5	0. 1300
1355	csvGENw: abL5	0. 1	0. 587	839	0. 1	0. 9261
1356	csvGENb: abL5	0. 6	0. 587	839	1. 1	0. 2821
1357	csvENVw+GENw: abL5	0. 4	0. 587	839	0. 6	0. 5318
1358	csvENVw: abL6	-1. 1	1. 039	839	-1. 1	0. 2844
1359	csvENVb: abL6	0. 8	1. 039	839	0. 7	0. 4684
1360	csvGENw: abL6	0. 3	1. 039	839	0. 3	0. 7964
1361	csvGENb: abL6	-0. 5	1. 039	839	-0. 5	0. 6394
1362	csvENVw+GENw: abL6	0. 2	1. 039	839	0. 2	0. 8625
1363	csvENVw: abL7	-0. 4	0. 461	839	-0. 8	0. 4186
1364	csvENVb: abL7	0. 3	0. 461	839	0. 6	0. 5527
1365	csvGENw: abL7	0. 3	0. 461	839	0. 6	0. 5766
1366	csvGENb: abL7	0. 6	0. 461	839	1. 3	0. 1959
1367	csvENVw+GENw: abL7	0. 4	0. 461	839	1. 0	0. 3302
1368	csvENVw: abL8	0. 5	0. 593	839	0. 9	0. 3862
1369	csvENVb: abL8	1. 2	0. 593	839	2. 1	0. 0359
1370	csvGENw: abL8	0. 4	0. 593	839	0. 6	0. 5197

1371	csvGENb: labL8	0.2	0.593	839	0.3	0.7274
1372	csvENVw+GENw: labL8	0.4	0.593	839	0.7	0.5119
1373	csvENVw: labL9	-0.1	0.481	839	-0.2	0.8278
1374	csvENVb: labL9	0.3	0.481	839	0.6	0.5304
1375	csvGENw: labL9	0.2	0.481	839	0.5	0.6288
1376	csvGENb: labL9	0.4	0.481	839	0.9	0.3604
1377	csvENVw+GENw: labL9	0.0	0.481	839	-0.1	0.9409
1378	csvENVw: labL10	-0.4	0.814	839	-0.6	0.5824
1379	csvENVb: labL10	0.2	0.814	839	0.3	0.8013
1380	csvGENw: labL10	0.3	0.814	839	0.3	0.7320
1381	csvGENb: labL10	0.6	0.814	839	0.7	0.4714
1382	csvENVw+GENw: labL10	0.3	0.814	839	0.4	0.6805
1383	csvENVw: labL11	-1.0	0.589	839	-1.6	0.1054
1384	csvENVb: labL11	0.4	0.589	839	0.8	0.4516
1385	csvGENw: labL11	0.9	0.589	839	1.6	0.1173
1386	csvGENb: labL11	1.1	0.589	839	1.9	0.0608
1387	csvENVw+GENw: labL11	0.9	0.589	839	1.5	0.1245
1388	csvENVw: labL12	-0.7	0.731	839	-1.0	0.3180
1389	csvENVb: labL12	0.4	0.731	839	0.5	0.6094
1390	csvGENw: labL12	-0.5	0.731	839	-0.7	0.4993
1391	csvGENb: labL12	0.7	0.731	839	1.0	0.3180
1392	csvENVw+GENw: labL12	0.4	0.731	839	0.5	0.5885
1393	csvENVw: labL13	10.6	2.511	839	4.2	0.0000
1394	csvENVb: labL13	4.7	2.511	839	1.9	0.0635
1395	csvGENw: labL13	1.3	2.511	839	0.5	0.6139
1396	csvGENb: labL13	5.2	2.511	839	2.1	0.0377
1397	csvENVw+GENw: labL13	3.3	2.511	839	1.3	0.1923
1398	csvENVw: labL14	-0.4	0.569	839	-0.6	0.5309
1399	csvENVb: labL14	0.5	0.569	839	0.8	0.4227
1400	csvGENw: labL14	0.6	0.569	839	1.0	0.3012
1401	csvGENb: labL14	0.2	0.569	839	0.4	0.7184
1402	csvENVw+GENw: labL14	0.1	0.569	839	0.2	0.8610
1403	IegumesBM: csvENVw: labL2	0.8	0.797	839	1.0	0.3356
1404	IegumesBM: csvENVb: labL2	-0.8	0.797	839	-1.0	0.3005
1405	IegumesBM: csvGENw: labL2	-0.4	0.797	839	-0.5	0.6502
1406	IegumesBM: csvGENb: labL2	-1.0	0.797	839	-1.3	0.1994
1407	IegumesBM: csvENVw+GENw: labL2	-0.8	0.797	839	-1.0	0.3419
1408	IegumesBM: csvENVw: labL3	0.1	0.896	839	0.2	0.8700
1409	IegumesBM: csvENVb: labL3	-1.8	0.896	839	-2.0	0.0506
1410	IegumesBM: csvGENw: labL3	-0.3	0.896	839	-0.3	0.7554
1411	IegumesBM: csvGENb: labL3	0.0	0.896	839	0.1	0.9556
1412	IegumesBM: csvENVw+GENw: labL3	-0.7	0.896	839	-0.8	0.4431
1413	IegumesBM: csvENVw: labL4	1.9	0.831	839	2.3	0.0214
1414	IegumesBM: csvENVb: labL4	0.0	0.831	839	0.0	0.9640
1415	IegumesBM: csvGENw: labL4	0.6	0.831	839	0.7	0.4839
1416	IegumesBM: csvGENb: labL4	0.2	0.831	839	0.2	0.8396
1417	IegumesBM: csvENVw+GENw: labL4	0.6	0.831	839	0.8	0.4451
1418	IegumesBM: csvENVw: labL5	-0.1	0.770	839	-0.1	0.9066
1419	IegumesBM: csvENVb: labL5	-1.4	0.770	839	-1.8	0.0648
1420	IegumesBM: csvGENw: labL5	0.1	0.770	839	0.1	0.9382
1421	IegumesBM: csvGENb: labL5	-1.0	0.770	839	-1.3	0.1802
1422	IegumesBM: csvENVw+GENw: labL5	-0.8	0.770	839	-1.1	0.2725
1423	IegumesBM: csvENVw: labL6	1.2	1.388	839	0.8	0.4003
1424	IegumesBM: csvENVb: labL6	-1.5	1.388	839	-1.1	0.2935
1425	IegumesBM: csvGENw: labL6	0.4	1.388	839	0.3	0.7674
1426	IegumesBM: csvGENb: labL6	-0.7	1.388	839	-0.5	0.6133
1427	IegumesBM: csvENVw+GENw: labL6	-1.8	1.388	839	-1.3	0.1869
1428	IegumesBM: csvENVw: labL7	0.5	0.678	839	0.8	0.4349
1429	IegumesBM: csvENVb: labL7	-0.4	0.678	839	-0.6	0.5225
1430	IegumesBM: csvGENw: labL7	0.5	0.678	839	0.7	0.4641
1431	IegumesBM: csvGENb: labL7	-0.2	0.678	839	-0.3	0.7840
1432	IegumesBM: csvENVw+GENw: labL7	-0.4	0.678	839	-0.5	0.5971
1433	IegumesBM: csvENVw: labL8	-0.1	0.807	839	-0.1	0.9475

```

1434 | egumesBM: csvENVb: I abL8      -1. 6    0. 807 839    -2. 0   0. 0494
1435 | egumesBM: csvGENw: I abL8      -0. 7    0. 807 839    -0. 9   0. 3836
1436 | egumesBM: csvGENb: I abL8      -0. 6    0. 807 839    -0. 7   0. 4733
1437 | egumesBM: csvENVw+GENw: I abL8  0. 2    0. 807 839    0. 3   0. 7864
1438 | egumesBM: csvENVw: I abL9      0. 4    0. 672 839    0. 6   0. 5468
1439 | egumesBM: csvENVb: I abL9      -0. 7    0. 672 839    -1. 0   0. 3121
1440 | egumesBM: csvGENw: I abL9      -0. 3    0. 672 839    -0. 4   0. 6709
1441 | egumesBM: csvGENb: I abL9      -0. 7    0. 672 839    -1. 1   0. 2762
1442 | egumesBM: csvENVw+GENw: I abL9  0. 0    0. 672 839    0. 0   0. 9606
1443 | egumesBM: csvENVw: I abL10     -0. 6    1. 086 839    -0. 6   0. 5614
1444 | egumesBM: csvENVb: I abL10     -0. 5    1. 086 839    -0. 5   0. 6476
1445 | egumesBM: csvGENw: I abL10     -0. 6    1. 086 839    -0. 5   0. 6121
1446 | egumesBM: csvGENb: I abL10     -1. 6    1. 086 839    -1. 5   0. 1409
1447 | egumesBM: csvENVw+GENw: I abL10  0. 0    1. 086 839    0. 0   0. 9696
1448 | egumesBM: csvENVw: I abL11     1. 5    0. 945 839    1. 6   0. 1158
1449 | egumesBM: csvENVb: I abL11     -0. 1    0. 945 839    -0. 1   0. 9468
1450 | egumesBM: csvGENw: I abL11     0. 5    0. 945 839    0. 5   0. 5932
1451 | egumesBM: csvGENb: I abL11     -0. 9    0. 945 839    -1. 0   0. 3354
1452 | egumesBM: csvENVw+GENw: I abL11  0. 6    0. 945 839    0. 7   0. 5127
1453 | egumesBM: csvENVw: I abL12     1. 1    1. 109 839    1. 0   0. 3297
1454 | egumesBM: csvENVb: I abL12     -0. 9    1. 109 839    -0. 8   0. 4022
1455 | egumesBM: csvGENw: I abL12     2. 0    1. 109 839    1. 8   0. 0705
1456 | egumesBM: csvGENb: I abL12     -0. 4    1. 109 839    -0. 4   0. 7100
1457 | egumesBM: csvENVw+GENw: I abL12  0. 2    1. 109 839    0. 1   0. 8913
1458 | egumesBM: csvENVw: I abL13     -10. 4   3. 091 839    -3. 4   0. 0008
1459 | egumesBM: csvENVb: I abL13     -6. 6    3. 091 839    -2. 1   0. 0335
1460 | egumesBM: csvGENw: I abL13     -0. 1    3. 091 839    0. 0   0. 9696
1461 | egumesBM: csvGENb: I abL13     -5. 6    3. 091 839    -1. 8   0. 0682
1462 | egumesBM: csvENVw+GENw: I abL13  -3. 2   3. 091 839    -1. 0   0. 3050
1463 | egumesBM: csvENVw: I abL14     0. 1    0. 823 839    0. 1   0. 8843
1464 | egumesBM: csvENVb: I abL14     -0. 6    0. 823 839    -0. 7   0. 4604
1465 | egumesBM: csvGENw: I abL14     -0. 1    0. 823 839    -0. 1   0. 9312
1466 | egumesBM: csvGENb: I abL14     -0. 2    0. 823 839    -0. 2   0. 8056
1467 | egumesBM: csvENVw+GENw: I abL14  0. 0    0. 823 839    0. 0   0. 9886
1468
1469 Standardized Within-Group Residuals:
1470   Min      Q1      Med      Q3      Max
1471 -3. 213 -0. 550  0. 014   0. 614   3. 326
1472
1473 Number of Observations: 1008
1474 Number of Groups: 2
1475

```

Model for foliar delta ¹⁵N (deltaN)

```

1476
1477 anova(m9)
1478
1479   numDF denDF F-value p-value
1480 (Intercept)      1    794 10217. 6 <. 0001
1481 Legumes          1    794   14. 4 2e-04
1482 csv               5    794    8. 9 <. 0001
1483 I ab             13   794   258. 3 <. 0001
1484 Legumes: csv      5    794    6. 5 <. 0001
1485 Legumes: I ab    13   794   16. 8 <. 0001
1486 csv: I ab        65   794    4. 4 <. 0001
1487 Legumes: csv: I ab 65   794    1. 8 1e-04
1488
1489 summary(m9)
1490 Linear mixed-effects model fit by REML
1491 Data: repro
1492   AIC   BIC LogLik
1493   2222 3144 -914
1494 Random effects:
```

```

1495 Formula: ~1 | block
1496 (Intercept) Residual
1497 StdDev: 0.0365 0.687
1498
1499 Variance function:
1500 Structure: Different standard deviations per stratum
1501 Formula: ~1 | lab * legumes
1502
1503 Parameter estimates:
1504 L1*B L1*BM L2*B L2*BM L3*B L3*BM L4*B L4*BM L5*B L5*BM L6*B
1505 1.000 0.949 0.548 0.516 6.240 5.814 0.817 0.911 0.569 0.612 0.740
1506 L6*BM L7*B L7*BM L8*B L8*BM L9*B L9*BM L10*B L10*BM L11*B L11*BM
1507 0.706 0.915 1.429 1.012 1.356 0.725 0.891 0.312 0.424 0.885 0.732
1508 L12*B L12*BM L13*B L13*BM L14*B L14*BM
1509 1.031 0.491 0.949 0.978 1.655 1.275
1510
1511 Fixed effects: deltaN ~ legumes * csv * lab
1512
1513 (Intercept) Value Std. Error DF t-value p-value
1514 legumesBM 1.49 0.28 794 5.31 0.0000
1515 csvENVw -0.38 0.39 794 -0.97 0.3316
1516 csvENVb 0.35 0.40 794 0.88 0.3795
1517 csvGENw 0.24 0.40 794 0.60 0.5503
1518 csvGENb 0.07 0.40 794 0.18 0.8572
1519 csvENVw+GENw -0.20 0.40 794 -0.51 0.6134
1520 labL2 0.49 0.42 794 1.17 0.2427
1521 labL3 0.50 0.33 794 1.54 0.1233
1522 labL4 5.40 1.94 794 2.79 0.0054
1523 labL5 1.36 0.32 794 3.75 0.0002
1524 labL6 1.86 0.35 794 5.78 0.0000
1525 labL7 0.20 0.40 794 0.57 0.5664
1526 labL8 0.66 0.40 794 1.67 0.0952
1527 labL9 1.41 0.40 794 3.54 0.0004
1528 labL10 0.54 0.35 794 1.56 0.1181
1529 labL11 0.58 0.29 794 5.37 0.0000
1530 labL12 2.62 0.37 794 7.01 0.0000
1531 labL13 2.26 0.40 794 5.61 0.0000
1532 labL14 3.46 0.39 794 8.96 0.0000
1533 labL15 5.52 0.54 794 10.19 0.0000
1534 legumesBM: csvENVw 0.02 0.56 794 0.04 0.9720
1535 legumesBM: csvENVb 0.42 0.55 794 0.76 0.4451
1536 legumesBM: csvGENw 0.31 0.55 794 0.57 0.5692
1537 legumesBM: csvGENb 0.48 0.55 794 0.88 0.3796
1538 legumesBM: csvENVw+GENw 0.01 0.56 794 0.02 0.9865
1539 legumesBM: labL2 -0.09 0.45 794 -0.20 0.8439
1540 legumesBM: labL3 0.69 2.54 794 0.27 0.7876
1541 legumesBM: labL4 0.18 0.52 794 0.35 0.7235
1542 legumesBM: labL5 0.10 0.45 794 0.22 0.8275
1543 legumesBM: labL6 0.61 0.48 794 1.27 0.2042
1544 legumesBM: labL7 0.07 0.62 794 0.11 0.9132
1545 legumesBM: labL8 0.57 0.61 794 0.94 0.3488
1546 legumesBM: labL9 0.65 0.50 794 1.29 0.1990
1547 legumesBM: labL10 -0.13 0.41 794 -0.31 0.7580
1548 legumesBM: labL11 0.92 0.50 794 1.83 0.0674
1549 legumesBM: labL12 1.31 0.50 794 2.62 0.0091
1550 legumesBM: labL13 -0.93 0.58 794 -1.61 0.1069
1551 legumesBM: labL14 -1.73 0.70 794 -2.46 0.0141
1552 csvENVw: labL2 -0.05 0.46 794 -0.11 0.9141
1553 csvENVb: labL2 -0.07 0.46 794 -0.15 0.8799
1554 csvGENw: labL2 0.26 0.46 794 0.56 0.5761
1555 csvGENb: labL2 0.01 0.46 794 0.03 0.9772
1556 csvENVw+GENw: labL2 0.38 0.47 794 0.81 0.4206
1557 csvENVb: labL3 2.83 2.74 794 1.03 0.3022
1558 csvENVb: labL3 3.38 2.62 794 1.29 0.1975

```

1558	csvGENw: labL3	1. 13	2. 62	794	0. 43	0. 6663
1559	csvGENb: labL3	0. 87	2. 62	794	0. 33	0. 7392
1560	csvENVw+GENw: labL3	2. 51	2. 63	794	0. 95	0. 3403
1561	csvENVw: labL4	0. 10	0. 51	794	0. 19	0. 8495
1562	csvENVb: labL4	0. 07	0. 51	794	0. 14	0. 8876
1563	csvGENw: labL4	0. 00	0. 51	794	0. 00	0. 9961
1564	csvGENb: labL4	-0. 06	0. 51	794	-0. 11	0. 9103
1565	csvENVw+GENw: labL4	-0. 45	0. 53	794	-0. 86	0. 3910
1566	csvENVw: labL5	0. 44	0. 46	794	0. 97	0. 3310
1567	csvENVb: labL5	-0. 04	0. 46	794	-0. 09	0. 9258
1568	csvGENw: labL5	-0. 02	0. 46	794	-0. 05	0. 9612
1569	csvGENb: labL5	0. 48	0. 46	794	1. 05	0. 2926
1570	csvENVw+GENw: labL5	0. 17	0. 47	794	0. 35	0. 7239
1571	csvENVw: labL6	0. 77	0. 49	794	1. 57	0. 1165
1572	csvENVb: labL6	0. 53	0. 49	794	1. 08	0. 2814
1573	csvGENw: labL6	0. 32	0. 49	794	0. 64	0. 5220
1574	csvGENb: labL6	0. 92	0. 49	794	1. 86	0. 0638
1575	csvENVw+GENw: labL6	0. 41	0. 51	794	0. 81	0. 4163
1576	csvENVw: labL7	0. 41	0. 55	794	0. 75	0. 4558
1577	csvENVb: labL7	-0. 07	0. 55	794	-0. 12	0. 9039
1578	csvGENw: labL7	-0. 43	0. 61	794	-0. 71	0. 4807
1579	csvGENb: labL7	0. 16	0. 55	794	0. 29	0. 7715
1580	csvENVw+GENw: labL7	-0. 18	0. 58	794	-0. 32	0. 7488
1581	csvENVw: labL8	0. 57	0. 56	794	1. 01	0. 3140
1582	csvENVb: labL8	0. 07	0. 56	794	0. 13	0. 8984
1583	csvGENw: labL8	0. 31	0. 58	794	0. 54	0. 5874
1584	csvGENb: labL8	0. 33	0. 58	794	0. 56	0. 5736
1585	csvENVw+GENw: labL8	-0. 52	0. 61	794	-0. 85	0. 3928
1586	csvENVw: labL9	0. 76	0. 49	794	1. 55	0. 1225
1587	csvENVb: labL9	1. 01	0. 49	794	2. 06	0. 0394
1588	csvGENw: labL9	0. 27	0. 49	794	0. 56	0. 5747
1589	csvGENb: labL9	0. 55	0. 49	794	1. 12	0. 2620
1590	csvENVw+GENw: labL9	0. 62	0. 51	794	1. 23	0. 2203
1591	csvENVw: labL10	-0. 49	0. 42	794	-1. 17	0. 2428
1592	csvENVb: labL10	-0. 25	0. 42	794	-0. 60	0. 5454
1593	csvGENw: labL10	-0. 17	0. 42	794	-0. 40	0. 6870
1594	csvGENb: labL10	0. 35	0. 42	794	0. 85	0. 3935
1595	csvENVw+GENw: labL10	0. 29	0. 43	794	0. 66	0. 5104
1596	csvENVw: labL11	-1. 23	0. 53	794	-2. 33	0. 0202
1597	csvENVb: labL11	-0. 81	0. 53	794	-1. 53	0. 1255
1598	csvGENw: labL11	1. 36	0. 53	794	2. 57	0. 0103
1599	csvGENb: labL11	1. 27	0. 53	794	2. 40	0. 0166
1600	csvENVw+GENw: labL11	-0. 35	0. 54	794	-0. 64	0. 5251
1601	csvENVw: labL12	-0. 89	0. 58	794	-1. 53	0. 1275
1602	csvENVb: labL12	-0. 51	0. 57	794	-0. 90	0. 3705
1603	csvGENw: labL12	0. 80	0. 57	794	1. 41	0. 1595
1604	csvGENb: labL12	0. 53	0. 57	794	0. 93	0. 3517
1605	csvENVw+GENw: labL12	-0. 16	0. 60	794	-0. 27	0. 7880
1606	csvENVw: labL13	-1. 51	0. 55	794	-2. 76	0. 0060
1607	csvENVb: labL13	-0. 01	0. 58	794	-0. 03	0. 9799
1608	csvGENw: labL13	0. 01	0. 61	794	0. 01	0. 9893
1609	csvGENb: labL13	-1. 25	0. 66	794	-1. 89	0. 0590
1610	csvENVw+GENw: labL13	-2. 10	0. 62	794	-3. 39	0. 0007
1611	csvENVw: labL14	-0. 22	0. 77	794	-0. 29	0. 7706
1612	csvENVb: labL14	-0. 82	0. 77	794	-1. 07	0. 2860
1613	csvGENw: labL14	-0. 55	0. 77	794	-0. 71	0. 4751
1614	csvGENb: labL14	0. 54	0. 77	794	0. 70	0. 4824
1615	csvENVw+GENw: labL14	-0. 74	0. 78	794	-0. 95	0. 3404
1616	IegumesBM: csvENVw: labL2	0. 25	0. 64	794	0. 39	0. 6953
1617	IegumesBM: csvENVb: labL2	-0. 18	0. 63	794	-0. 29	0. 7710
1618	IegumesBM: csvGENw: labL2	-0. 11	0. 63	794	-0. 18	0. 8572
1619	IegumesBM: csvGENb: labL2	0. 06	0. 63	794	0. 10	0. 9196
1620	IegumesBM: csvENVw+GENw: labL2	-0. 17	0. 64	794	-0. 27	0. 7894

1621	egumesBM: csvENVw: labL3	-3. 10	3. 60	794	-0. 86	0. 3899
1622	egumesBM: csvENVb: labL3	-0. 61	3. 70	794	-0. 17	0. 8689
1623	egumesBM: csvGENw: labL3	0. 36	3. 51	794	0. 10	0. 9180
1624	egumesBM: csvGENb: labL3	-0. 62	3. 51	794	-0. 18	0. 8591
1625	egumesBM: csvENVw+GENw: labL3	1. 35	3. 51	794	0. 38	0. 7020
1626	egumesBM: csvENVw: labL4	-0. 63	0. 74	794	-0. 85	0. 3952
1627	egumesBM: csvENVb: labL4	-0. 42	0. 73	794	-0. 58	0. 5646
1628	egumesBM: csvGENw: labL4	-0. 50	0. 73	794	-0. 69	0. 4935
1629	egumesBM: csvGENb: labL4	0. 13	0. 73	794	0. 18	0. 8574
1630	egumesBM: csvENVw+GENw: labL4	0. 41	0. 74	794	0. 55	0. 5837
1631	egumesBM: csvENVw: labL5	-0. 69	0. 65	794	-1. 06	0. 2911
1632	egumesBM: csvENVb: labL5	-0. 62	0. 64	794	-0. 97	0. 3328
1633	egumesBM: csvGENw: labL5	0. 10	0. 64	794	0. 16	0. 8730
1634	egumesBM: csvGENb: labL5	-0. 47	0. 64	794	-0. 74	0. 4579
1635	egumesBM: csvENVw+GENw: labL5	-0. 43	0. 65	794	-0. 65	0. 5127
1636	egumesBM: csvENVw: labL6	-0. 61	0. 69	794	-0. 88	0. 3796
1637	egumesBM: csvENVb: labL6	-0. 95	0. 68	794	-1. 40	0. 1627
1638	egumesBM: csvGENw: labL6	-0. 45	0. 68	794	-0. 67	0. 5046
1639	egumesBM: csvGENb: labL6	-1. 06	0. 68	794	-1. 56	0. 1181
1640	egumesBM: csvENVw+GENw: labL6	-0. 25	0. 69	794	-0. 36	0. 7169
1641	egumesBM: csvENVw: labL7	-0. 01	0. 88	794	-0. 01	0. 9895
1642	egumesBM: csvENVb: labL7	0. 24	0. 87	794	0. 28	0. 7831
1643	egumesBM: csvGENw: labL7	0. 47	0. 91	794	0. 51	0. 6077
1644	egumesBM: csvGENb: labL7	-0. 37	0. 89	794	-0. 42	0. 6759
1645	egumesBM: csvENVw+GENw: labL7	0. 15	0. 91	794	0. 17	0. 8653
1646	egumesBM: csvENVw: labL8	-1. 10	0. 87	794	-1. 26	0. 2080
1647	egumesBM: csvENVb: labL8	-1. 11	0. 87	794	-1. 28	0. 2016
1648	egumesBM: csvGENw: labL8	-0. 57	0. 87	794	-0. 65	0. 5171
1649	egumesBM: csvGENb: labL8	-0. 85	0. 87	794	-0. 97	0. 3322
1650	egumesBM: csvENVw+GENw: labL8	0. 17	0. 90	794	0. 19	0. 8455
1651	egumesBM: csvENVw: labL9	-0. 44	0. 72	794	-0. 61	0. 5426
1652	egumesBM: csvENVb: labL9	-0. 93	0. 71	794	-1. 30	0. 1930
1653	egumesBM: csvGENw: labL9	-1. 10	0. 71	794	-1. 55	0. 1222
1654	egumesBM: csvGENb: labL9	-0. 82	0. 71	794	-1. 15	0. 2498
1655	egumesBM: csvENVw+GENw: labL9	-0. 07	0. 72	794	-0. 09	0. 9260
1656	egumesBM: csvENVw: labL10	0. 09	0. 60	794	0. 15	0. 8845
1657	egumesBM: csvENVb: labL10	-0. 69	0. 59	794	-1. 18	0. 2379
1658	egumesBM: csvGENw: labL10	-0. 64	0. 58	794	-1. 09	0. 2755
1659	egumesBM: csvGENb: labL10	-1. 26	0. 58	794	-2. 15	0. 0321
1660	egumesBM: csvENVw+GENw: labL10	-1. 27	0. 60	794	-2. 11	0. 0353
1661	egumesBM: csvENVw: labL11	0. 25	0. 72	794	0. 35	0. 7244
1662	egumesBM: csvENVb: labL11	0. 19	0. 71	794	0. 26	0. 7930
1663	egumesBM: csvGENw: labL11	-1. 33	0. 72	794	-1. 86	0. 0636
1664	egumesBM: csvGENb: labL11	-1. 09	0. 72	794	-1. 51	0. 1307
1665	egumesBM: csvENVw+GENw: labL11	-0. 59	0. 72	794	-0. 81	0. 4168
1666	egumesBM: csvENVw: labL12	0. 13	0. 73	794	0. 18	0. 8555
1667	egumesBM: csvENVb: labL12	-0. 63	0. 71	794	-0. 89	0. 3715
1668	egumesBM: csvGENw: labL12	-0. 82	0. 71	794	-1. 15	0. 2509
1669	egumesBM: csvGENb: labL12	-0. 79	0. 71	794	-1. 11	0. 2662
1670	egumesBM: csvENVw+GENw: labL12	-0. 90	0. 73	794	-1. 23	0. 2189
1671	egumesBM: csvENVw: labL13	-0. 09	0. 80	794	-0. 11	0. 9146
1672	egumesBM: csvENVb: labL13	-0. 96	0. 81	794	-1. 18	0. 2370
1673	egumesBM: csvGENw: labL13	-0. 63	0. 84	794	-0. 74	0. 4568
1674	egumesBM: csvGENb: labL13	0. 51	0. 89	794	0. 57	0. 5673
1675	egumesBM: csvENVw+GENw: labL13	0. 85	0. 85	794	1. 00	0. 3164
1676	egumesBM: csvENVw: labL14	0. 64	1. 00	794	0. 64	0. 5219
1677	egumesBM: csvENVb: labL14	0. 89	0. 99	794	0. 90	0. 3693
1678	egumesBM: csvGENw: labL14	1. 44	0. 99	794	1. 45	0. 1482
1679	egumesBM: csvGENb: labL14	0. 07	0. 99	794	0. 07	0. 9470
1680	egumesBM: csvENVw+GENw: labL14	0. 73	1. 00	794	0. 73	0. 4638

1681 Standardized Within-Group Residuals:

1682 Min Q1 Med Q3

Max

```

1684 -2.90315 -0.63626 -0.00634 0.63610 2.82546
1685
1686 Number of Observations: 963
1687 Number of Groups: 2
1688

1689 Model for foliar delta 13C (deltaC)

1690 anova(m10)
1691
1692 (Intercept) 1 804 434648 <.0001
1693 Legumes 1 804 27 <.0001
1694 csv 5 804 76 <.0001
1695 lab 13 804 888 <.0001
1696 Legumes: csv 5 804 5 0.0001
1697 Legumes: lab 13 804 3 0.0021
1698 csv: lab 65 804 5 <.0001
1699 Legumes: csv: lab 65 804 1 0.1081
1700
1701 summary(m10)
1702 Linear mixed-effects model fit by REML
1703 Data: reprod
1704 AIC BIC LogLik
1705 1750 2682 -678
1706
1707 Random effects:
1708 Formula: ~1 | block
1709 (Intercept) Residual
1710 StdDev: 0.0415 0.437
1711
1712 Variance function:
1713 Structure: Different standard deviations per stratum
1714 Formula: ~1 | lab * Legumes
1715 Parameter estimates:
1716 L1*B L1*BM L2*B L2*BM L3*B L3*BM L4*B L4*BM L5*B L5*BM L6*B
1717 1.000 1.788 0.652 0.991 0.685 1.131 0.771 0.854 1.112 0.992 1.127
1718 L6*BM L7*B L7*BM L8*B L8*BM L9*B L9*BM L10*B L10*BM L11*B L11*BM
1719 1.095 1.819 1.490 0.920 0.823 0.883 0.900 0.590 0.913 1.184 1.002
1720 L12*B L12*BM L13*B L13*BM L14*B L14*BM
1721 1.198 1.167 0.989 1.637 1.529 0.952
1722
1723 Fixed effects: deltaC ~ Legumes * csv * lab
1724
1725 (Intercept) Value Std. Error DF t-value p-value
1726 LegumesBM -30.02 0.181 839 -166.1 0.0000
1727 csvENVw 0.57 0.365 839 1.5 0.1216
1728 csvENVb 0.19 0.252 839 0.7 0.4630
1729 csvGENw 0.20 0.252 839 0.8 0.4203
1730 csvGENb 0.83 0.252 839 3.3 0.0010
1731 csvENVw+GENw 0.48 0.252 839 1.9 0.0576
1732 csvENVw+GENw 0.79 0.252 839 3.1 0.0018
1733 labL2 -1.57 0.213 839 -7.4 0.0000
1734 labL3 -3.65 0.216 839 -16.9 0.0000
1735 labL4 -2.04 0.225 839 -9.0 0.0000
1736 labL5 -1.37 0.267 839 -5.1 0.0000
1737 labL6 -3.82 0.269 839 -14.2 0.0000
1738 labL7 -4.33 0.370 839 -11.7 0.0000
1739 labL8 -3.67 0.242 839 -15.1 0.0000
1740 labL9 -2.50 0.238 839 -10.5 0.0000
1741 labL10 0.07 0.207 839 0.3 0.7312
1742 labL11 -2.23 0.276 839 -8.1 0.0000
1743 labL12 -2.41 0.278 839 -8.7 0.0000
1744 labL13 -1.24 0.251 839 -4.9 0.0000
1744 labL14 -2.71 0.326 839 -8.3 0.0000

```

1745	egumesBM: csvENVw	-0. 59	0. 517	839	-1. 1	0. 2521
1746	egumesBM: csvENVb	-0. 72	0. 517	839	-1. 4	0. 1615
1747	egumesBM: csvGENw	-1. 59	0. 517	839	-3. 1	0. 0021
1748	egumesBM: csvGENb	0. 07	0. 517	839	0. 1	0. 8989
1749	egumesBM: csvENVw+GENw	-0. 62	0. 517	839	-1. 2	0. 2335
1750	egumesBM: abL2	-0. 37	0. 422	839	-0. 9	0. 3806
1751	egumesBM: abL3	-0. 25	0. 435	839	-0. 6	0. 5634
1752	egumesBM: abL4	-0. 38	0. 419	839	-0. 9	0. 3704
1753	egumesBM: abL5	-0. 55	0. 452	839	-1. 2	0. 2271
1754	egumesBM: abL6	-0. 39	0. 460	839	-0. 9	0. 3928
1755	egumesBM: abL7	-0. 42	0. 556	839	-0. 8	0. 4523
1756	egumesBM: abL8	0. 18	0. 427	839	0. 4	0. 6754
1757	egumesBM: abL9	-0. 53	0. 429	839	-1. 2	0. 2160
1758	egumesBM: abL10	-0. 51	0. 414	839	-1. 2	0. 2169
1759	egumesBM: abL11	-0. 25	0. 458	839	-0. 6	0. 5817
1760	egumesBM: abL12	0. 00	0. 472	839	0. 0	0. 9927
1761	egumesBM: abL13	-0. 07	0. 500	839	-0. 1	0. 8960
1762	egumesBM: abL14	0. 11	0. 487	839	0. 2	0. 8140
1763	csvENVw: abL2	-0. 10	0. 301	839	-0. 3	0. 7390
1764	csvENVb: abL2	-0. 34	0. 301	839	-1. 1	0. 2654
1765	csvGENw: abL2	-0. 08	0. 301	839	-0. 3	0. 7829
1766	csvGENb: abL2	-0. 01	0. 301	839	0. 0	0. 9660
1767	csvENVw+GENw: abL2	0. 47	0. 301	839	1. 6	0. 1186
1768	csvENVw: abL3	-0. 27	0. 306	839	-0. 9	0. 3805
1769	csvENVb: abL3	-0. 23	0. 306	839	-0. 8	0. 4503
1770	csvGENw: abL3	-0. 08	0. 306	839	-0. 2	0. 8058
1771	csvGENb: abL3	0. 08	0. 306	839	0. 3	0. 7852
1772	csvENVw+GENw: abL3	0. 01	0. 306	839	0. 0	0. 9613
1773	csvENVw: abL4	-0. 55	0. 318	839	-1. 7	0. 0832
1774	csvENVb: abL4	-0. 43	0. 318	839	-1. 4	0. 1762
1775	csvGENw: abL4	-0. 47	0. 318	839	-1. 5	0. 1393
1776	csvGENb: abL4	-0. 07	0. 318	839	-0. 2	0. 8190
1777	csvENVw+GENw: abL4	-0. 77	0. 318	839	-2. 4	0. 0161
1778	csvENVw: abL5	-0. 18	0. 377	839	-0. 5	0. 6421
1779	csvENVb: abL5	-0. 40	0. 377	839	-1. 1	0. 2870
1780	csvGENw: abL5	-0. 20	0. 377	839	-0. 5	0. 6026
1781	csvGENb: abL5	-0. 15	0. 377	839	-0. 4	0. 7001
1782	csvENVw+GENw: abL5	0. 01	0. 377	839	0. 0	0. 9739
1783	csvENVw: abL6	-0. 15	0. 380	839	-0. 4	0. 6941
1784	csvENVb: abL6	0. 24	0. 380	839	0. 6	0. 5264
1785	csvGENw: abL6	-0. 40	0. 380	839	-1. 0	0. 2965
1786	csvGENb: abL6	-0. 11	0. 380	839	-0. 3	0. 7633
1787	csvENVw+GENw: abL6	-0. 23	0. 380	839	-0. 6	0. 5525
1788	csvENVw: abL7	-0. 06	0. 524	839	-0. 1	0. 9161
1789	csvENVb: abL7	-0. 07	0. 524	839	-0. 1	0. 9002
1790	csvGENw: abL7	0. 40	0. 524	839	0. 8	0. 4439
1791	csvGENb: abL7	-0. 13	0. 524	839	-0. 2	0. 8057
1792	csvENVw+GENw: abL7	0. 04	0. 524	839	0. 1	0. 9464
1793	csvENVw: abL8	0. 57	0. 343	839	1. 7	0. 0940
1794	csvENVb: abL8	0. 63	0. 343	839	1. 8	0. 0683
1795	csvGENw: abL8	-0. 11	0. 343	839	-0. 3	0. 7498
1796	csvGENb: abL8	0. 06	0. 343	839	0. 2	0. 8573
1797	csvENVw+GENw: abL8	0. 23	0. 343	839	0. 7	0. 4996
1798	csvENVw: abL9	-0. 21	0. 336	839	-0. 6	0. 5320
1799	csvENVb: abL9	-0. 33	0. 336	839	-1. 0	0. 3220
1800	csvGENw: abL9	-0. 08	0. 336	839	-0. 2	0. 8105
1801	csvGENb: abL9	-0. 02	0. 336	839	-0. 1	0. 9431
1802	csvENVw+GENw: abL9	0. 02	0. 336	839	0. 1	0. 9589
1803	csvENVw: abL10	-0. 66	0. 293	839	-2. 2	0. 0250
1804	csvENVb: abL10	-0. 52	0. 293	839	-1. 8	0. 0756
1805	csvGENw: abL10	-0. 77	0. 293	839	-2. 6	0. 0091
1806	csvGENb: abL10	-0. 45	0. 293	839	-1. 5	0. 1230
1807	csvENVw+GENw: abL10	-1. 07	0. 293	839	-3. 6	0. 0003

1808	csvENVw: labL11	-0.46	0.391	839	-1.2	0.2414
1809	csvENVb: labL11	-0.17	0.391	839	-0.4	0.6631
1810	csvGENw: labL11	0.17	0.391	839	0.4	0.6591
1811	csvGENb: labL11	0.23	0.391	839	0.6	0.5544
1812	csvENVw+GENw: labL11	0.36	0.391	839	0.9	0.3559
1813	csvENVw: labL12	-0.13	0.394	839	-0.3	0.7368
1814	csvENVb: labL12	-0.28	0.394	839	-0.7	0.4812
1815	csvGENw: labL12	-0.07	0.394	839	-0.2	0.8506
1816	csvGENb: labL12	0.31	0.394	839	0.8	0.4240
1817	csvENVw+GENw: labL12	0.60	0.394	839	1.5	0.1284
1818	csvENVw: labL13	-0.90	0.355	839	-2.5	0.0117
1819	csvENVb: labL13	-0.41	0.355	839	-1.1	0.2519
1820	csvGENw: labL13	-1.06	0.355	839	-3.0	0.0029
1821	csvGENb: labL13	-0.85	0.355	839	-2.4	0.0173
1822	csvENVw+GENw: labL13	-1.48	0.355	839	-4.2	0.0000
1823	csvENVw: labL14	0.13	0.461	839	0.3	0.7779
1824	csvENVb: labL14	-0.18	0.461	839	-0.4	0.6897
1825	csvGENw: labL14	0.73	0.461	839	1.6	0.1144
1826	csvGENb: labL14	0.90	0.461	839	1.9	0.0519
1827	csvENVw+GENw: labL14	0.94	0.461	839	2.0	0.0419
1828	egumesBM: csvENVw: labL2	0.76	0.597	839	1.3	0.2025
1829	egumesBM: csvENVb: labL2	1.20	0.597	839	2.0	0.0449
1830	egumesBM: csvGENw: labL2	1.61	0.597	839	2.7	0.0070
1831	egumesBM: csvGENb: labL2	-0.10	0.597	839	-0.2	0.8668
1832	egumesBM: csvENVw+GENw: labL2	0.41	0.597	839	0.7	0.4908
1833	egumesBM: csvENVw: labL3	0.58	0.615	839	0.9	0.3497
1834	egumesBM: csvENVb: labL3	1.20	0.615	839	2.0	0.0511
1835	egumesBM: csvGENw: labL3	1.07	0.615	839	1.7	0.0815
1836	egumesBM: csvGENb: labL3	-0.43	0.615	839	-0.7	0.4796
1837	egumesBM: csvENVw+GENw: labL3	0.11	0.615	839	0.2	0.8527
1838	egumesBM: csvENVw: labL4	0.69	0.593	839	1.2	0.2431
1839	egumesBM: csvENVb: labL4	0.43	0.593	839	0.7	0.4713
1840	egumesBM: csvGENw: labL4	1.34	0.593	839	2.3	0.0243
1841	egumesBM: csvGENb: labL4	-0.33	0.593	839	-0.6	0.5763
1842	egumesBM: csvENVw+GENw: labL4	0.38	0.593	839	0.6	0.5206
1843	egumesBM: csvENVw: labL5	0.92	0.639	839	1.4	0.1501
1844	egumesBM: csvENVb: labL5	0.96	0.639	839	1.5	0.1337
1845	egumesBM: csvGENw: labL5	1.38	0.639	839	2.2	0.0313
1846	egumesBM: csvGENb: labL5	-0.27	0.639	839	-0.4	0.6672
1847	egumesBM: csvENVw+GENw: labL5	0.33	0.639	839	0.5	0.6109
1848	egumesBM: csvENVw: labL6	0.64	0.651	839	1.0	0.3285
1849	egumesBM: csvENVb: labL6	0.61	0.651	839	0.9	0.3521
1850	egumesBM: csvGENw: labL6	0.92	0.651	839	1.4	0.1573
1851	egumesBM: csvGENb: labL6	-0.54	0.651	839	-0.8	0.4108
1852	egumesBM: csvENVw+GENw: labL6	-0.11	0.651	839	-0.2	0.8689
1853	egumesBM: csvENVw: labL7	0.58	0.787	839	0.7	0.4612
1854	egumesBM: csvENVb: labL7	0.52	0.787	839	0.7	0.5093
1855	egumesBM: csvGENw: labL7	0.97	0.787	839	1.2	0.2190
1856	egumesBM: csvGENb: labL7	-0.04	0.787	839	0.0	0.9618
1857	egumesBM: csvENVw+GENw: labL7	0.27	0.787	839	0.3	0.7301
1858	egumesBM: csvENVw: labL8	0.15	0.603	839	0.2	0.8048
1859	egumesBM: csvENVb: labL8	-0.39	0.603	839	-0.6	0.5200
1860	egumesBM: csvGENw: labL8	0.90	0.603	839	1.5	0.1356
1861	egumesBM: csvGENb: labL8	-0.92	0.603	839	-1.5	0.1291
1862	egumesBM: csvENVw+GENw: labL8	-0.07	0.603	839	-0.1	0.9081
1863	egumesBM: csvENVw: labL9	0.63	0.607	839	1.0	0.2995
1864	egumesBM: csvENVb: labL9	0.67	0.607	839	1.1	0.2698
1865	egumesBM: csvGENw: labL9	1.56	0.607	839	2.6	0.0103
1866	egumesBM: csvGENb: labL9	-0.11	0.607	839	-0.2	0.8542
1867	egumesBM: csvENVw+GENw: labL9	0.72	0.607	839	1.2	0.2351
1868	egumesBM: csvENVw: labL10	0.54	0.585	839	0.9	0.3556
1869	egumesBM: csvENVb: labL10	0.56	0.585	839	1.0	0.3384
1870	egumesBM: csvGENw: labL10	1.47	0.585	839	2.5	0.0124

```

1871 | egumesBM: csvGENb: labL10    -0.17    0.585 839    -0.3  0.7682
1872 | egumesBM: csvENVw+GENw: labL10  0.65    0.585 839    1.1  0.2698
1873 | egumesBM: csvENVw: labL11     1.34    0.648 839    2.1  0.0386
1874 | egumesBM: csvENVb: labL11     0.69    0.648 839    1.1  0.2849
1875 | egumesBM: csvGENw: labL11     1.34    0.648 839    2.1  0.0386
1876 | egumesBM: csvGENb: labL11     -0.48   0.648 839    -0.7  0.4591
1877 | egumesBM: csvENVw+GENw: labL11  0.81    0.648 839    1.2  0.2130
1878 | egumesBM: csvENVw: labL12     0.47    0.667 839    0.7  0.4798
1879 | egumesBM: csvENVb: labL12     0.98    0.667 839    1.5  0.1402
1880 | egumesBM: csvGENw: labL12     1.48    0.667 839    2.2  0.0272
1881 | egumesBM: csvGENb: labL12     -0.55   0.667 839    -0.8  0.4084
1882 | egumesBM: csvENVw+GENw: labL12  0.23    0.667 839    0.3  0.7279
1883 | egumesBM: csvENVw: labL13     0.52    0.707 839    0.7  0.4633
1884 | egumesBM: csvENVb: labL13     0.60    0.707 839    0.8  0.3970
1885 | egumesBM: csvGENw: labL13     1.11    0.707 839    1.6  0.1171
1886 | egumesBM: csvGENb: labL13     -0.38   0.707 839    -0.5  0.5927
1887 | egumesBM: csvENVw+GENw: labL13  0.64    0.707 839    0.9  0.3665
1888 | egumesBM: csvENVw: labL14     0.42    0.688 839    0.6  0.5457
1889 | egumesBM: csvENVb: labL14     0.82    0.688 839    1.2  0.2325
1890 | egumesBM: csvGENw: labL14     0.55    0.688 839    0.8  0.4213
1891 | egumesBM: csvGENb: labL14     -1.04   0.688 839    -1.5  0.1324
1892 | egumesBM: csvENVw+GENw: labL14  -0.44   0.688 839    -0.6  0.5264
1893
1894 Standardized Within-Group Residuals:
1895   Min      Q1      Med      Q3      Max
1896 -3.8010 -0.5813  0.0341  0.6093  2.9884
1897
1898 Number of Observations: 1008
1899 Number of Groups: 2
1900

```

1901 Model for microcosm evapotranspiration before the final harvest (finalET)

```

1902
1903   numDF denDF F-value p-value
1904 (Intercept)       1     833 693.67 <.0001
1905 | egumes          1     833 1269.93 <.0001
1906 | csv              5     833  9.37 <.0001
1907 | lab              13    833  748.66 <.0001
1908 | egumes:csv       5     833  1.24 0.2884
1909 | egumes:lab        13    833  172.74 <.0001
1910 | csv:lab           65    833  21.69 <.0001
1911 | egumes:csv:lab    65    833  1.53 0.0056
1912
1913 summary(m11)
1914 Linear mixed-effects model fit by REML
1915 Data: repro
1916   AIC   BIC LogLik
1917 7942 8873 -3774
1918
1919 Random effects:
1920 Formula: ~1 | block
1921   (Intercept) Residual
1922 StdDev:       6.49    25.9
1923
1924 Variance function:
1925 Structure: Different standard deviations per stratum
1926 Formula: ~1 | lab * egumes
1927 Parameter estimates:
1928 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
1929 1.000  1.366  0.244  0.236  0.732  0.824  0.301  1.396  0.570  0.793  0.422
1930 L6*BM  L7*BM  L7*BM  L8*B   L8*BM  L9*B   L9*BM  L10*B  L10*BM  L11*B  L11*BM
1931 0.771  1.085  1.104  0.680  0.962  0.375  0.589  0.558  0.670  1.728  1.472
1932 L12*B  L12*BM L13*B  L13*BM L14*B  L14*BM

```

1932 1. 931 2. 157 0. 238 0. 235 0. 844 1. 035

1933

1934

1935 Fixed effects: final ET ~ Legumes * csv * lab

	Value	Std. Error	DF	t-value	p-value
(Intercept)	121.7	11.5	833	10.56	0.0000
LegumesBM	43.7	17.9	833	2.44	0.0149
csvENVw	-1.2	15.0	833	-0.08	0.9386
csvENVb	4.7	15.0	833	0.31	0.7552
csvGENw	-10.9	15.0	833	-0.73	0.4670
csvGENb	-11.0	15.0	833	-0.73	0.4629
csvENVw+GENw	-8.9	15.0	833	-0.60	0.5504
labL2	-50.5	10.9	833	-4.64	0.0000
labL3	-1.8	13.1	833	-0.13	0.8927
labL4	-29.4	11.0	833	-2.66	0.0079
labL5	-7.7	12.2	833	-0.63	0.5272
labL6	2.0	11.5	833	0.17	0.8650
labL7	-16.5	15.6	833	-1.06	0.2897
labL8	-24.4	12.8	833	-1.91	0.0570
labL9	3.5	11.3	833	0.31	0.7569
labL10	19.1	12.1	833	1.58	0.1152
labL11	98.6	21.1	833	4.67	0.0000
labL12	49.8	23.0	833	2.17	0.0306
labL13	8.7	10.9	833	0.80	0.4233
labL14	-7.0	13.8	833	-0.50	0.6148
LegumesBM: csvENVw	28.8	25.3	833	1.14	0.2551
LegumesBM: csvENVb	12.6	25.3	833	0.50	0.6188
LegumesBM: csvGENw	1.2	25.3	833	0.05	0.9611
LegumesBM: csvGENb	8.0	25.3	833	0.32	0.7516
LegumesBM: csvENVw+GENw	21.7	25.3	833	0.86	0.3909
LegumesBM: labL2	-40.4	18.3	833	-2.21	0.0271
LegumesBM: labL3	154.7	21.4	833	7.24	0.0000
LegumesBM: labL4	30.9	23.4	833	1.32	0.1877
LegumesBM: labL5	35.7	20.7	833	1.73	0.0845
LegumesBM: labL6	-6.0	20.2	833	-0.30	0.7654
LegumesBM: labL7	15.7	24.3	833	0.65	0.5172
LegumesBM: labL8	-4.2	21.8	833	-0.19	0.8489
LegumesBM: labL9	-25.7	19.4	833	-1.33	0.1850
LegumesBM: labL10	-50.9	20.1	833	-2.53	0.0117
LegumesBM: labL11	26.4	29.9	833	0.88	0.3789
LegumesBM: labL12	11.3	35.5	833	0.32	0.7503
LegumesBM: labL13	-24.2	18.2	833	-1.33	0.1845
LegumesBM: labL14	141.1	22.8	833	6.19	0.0000
csvENVw: labL2	7.9	15.4	833	0.51	0.6068
csvENVb: labL2	-5.0	15.4	833	-0.32	0.7478
csvGENw: labL2	11.2	15.4	833	0.73	0.4673
csvGENb: labL2	10.1	15.4	833	0.66	0.5100
csvENVw+GENw: labL2	15.9	15.4	833	1.03	0.3020
csvENVw: labL3	1.0	18.5	833	0.05	0.9562
csvENVb: labL3	-7.9	18.5	833	-0.43	0.6702
csvGENw: labL3	37.6	18.5	833	2.03	0.0429
csvGENb: labL3	36.4	18.5	833	1.97	0.0497
csvENVw+GENw: labL3	36.8	18.5	833	1.98	0.0478
csvENVw: labL4	-16.1	15.6	833	-1.03	0.3042
csvENVb: labL4	-12.5	15.6	833	-0.80	0.4240
csvGENw: labL4	3.0	15.6	833	0.19	0.8489
csvGENb: labL4	3.6	15.6	833	0.23	0.8173
csvENVw+GENw: labL4	-8.3	15.6	833	-0.53	0.5968
csvENVw: labL5	1.0	17.2	833	0.06	0.9559
csvENVb: labL5	1.1	17.2	833	0.06	0.9505
csvGENw: labL5	13.0	17.2	833	0.75	0.4521
csvGENb: labL5	24.5	17.2	833	1.42	0.1548
csvENVw+GENw: labL5	25.8	17.2	833	1.50	0.1339

1995	csvENVw: labL6	6. 4	16. 2	833	0. 39	0. 6946
1996	csvENVb: labL6	-5. 4	16. 2	833	-0. 33	0. 7395
1997	csvGENw: labL6	-3. 0	16. 2	833	-0. 18	0. 8557
1998	csvGENb: labL6	4. 2	16. 2	833	0. 26	0. 7955
1999	csvENVw+GENw: labL6	-6. 2	16. 2	833	-0. 38	0. 7015
2000	csvENVw: labL7	0. 3	22. 1	833	0. 01	0. 9893
2001	csvENVb: labL7	14. 2	22. 1	833	0. 65	0. 5188
2002	csvGENw: labL7	10. 2	22. 1	833	0. 46	0. 6425
2003	csvGENb: labL7	30. 5	22. 7	833	1. 34	0. 1791
2004	csvENVw+GENw: labL7	-5. 9	22. 1	833	-0. 27	0. 7904
2005	csvENVw: labL8	3. 3	18. 1	833	0. 18	0. 8548
2006	csvENVb: labL8	-5. 7	18. 1	833	-0. 32	0. 7508
2007	csvGENw: labL8	-16. 3	18. 1	833	-0. 90	0. 3686
2008	csvGENb: labL8	-11. 7	18. 1	833	-0. 65	0. 5175
2009	csvENVw+GENw: labL8	-9. 1	18. 1	833	-0. 50	0. 6139
2010	csvENVw: labL9	5. 7	16. 0	833	0. 36	0. 7206
2011	csvENVb: labL9	0. 6	16. 0	833	0. 04	0. 9697
2012	csvGENw: labL9	-7. 1	16. 0	833	-0. 45	0. 6546
2013	csvGENb: labL9	6. 4	16. 0	833	0. 40	0. 6901
2014	csvENVw+GENw: labL9	5. 1	16. 0	833	0. 32	0. 7518
2015	csvENVw: labL10	137. 3	17. 1	833	8. 01	0. 0000
2016	csvENVb: labL10	-3. 5	17. 1	833	-0. 20	0. 8383
2017	csvGENw: labL10	131. 4	17. 1	833	7. 67	0. 0000
2018	csvGENb: labL10	4. 1	17. 1	833	0. 24	0. 8099
2019	csvENVw+GENw: labL10	130. 6	17. 1	833	7. 62	0. 0000
2020	csvENVw: labL11	-20. 0	29. 9	833	-0. 67	0. 5023
2021	csvENVb: labL11	-17. 0	29. 9	833	-0. 57	0. 5704
2022	csvGENw: labL11	83. 6	29. 9	833	2. 80	0. 0052
2023	csvGENb: labL11	72. 0	29. 9	833	2. 41	0. 0162
2024	csvENVw+GENw: labL11	51. 9	29. 9	833	1. 74	0. 0828
2025	csvENVw: labL12	-0. 3	32. 5	833	-0. 01	0. 9937
2026	csvENVb: labL12	-15. 7	32. 5	833	-0. 48	0. 6293
2027	csvGENw: labL12	98. 3	32. 5	833	3. 02	0. 0026
2028	csvGENb: labL12	87. 6	32. 5	833	2. 69	0. 0072
2029	csvENVw+GENw: labL12	74. 0	32. 5	833	2. 28	0. 0231
2030	csvENVw: labL13	-2. 0	15. 4	833	-0. 13	0. 8961
2031	csvENVb: labL13	-8. 9	15. 4	833	-0. 58	0. 5641
2032	csvGENw: labL13	17. 0	15. 4	833	1. 10	0. 2695
2033	csvGENb: labL13	11. 6	15. 4	833	0. 75	0. 4525
2034	csvENVw+GENw: labL13	11. 1	15. 4	833	0. 72	0. 4718
2035	csvENVw: labL14	-17. 0	19. 6	833	-0. 87	0. 3852
2036	csvENVb: labL14	-13. 1	19. 6	833	-0. 67	0. 5037
2037	csvGENw: labL14	14. 4	19. 6	833	0. 74	0. 4622
2038	csvGENb: labL14	8. 1	19. 6	833	0. 41	0. 6807
2039	csvENVw+GENw: labL14	6. 8	19. 6	833	0. 35	0. 7285
2040	I egumesBM: csvENVw: labL2	-20. 9	25. 8	833	-0. 81	0. 4192
2041	I egumesBM: csvENVb: labL2	3. 8	25. 8	833	0. 15	0. 8817
2042	I egumesBM: csvGENw: labL2	6. 1	25. 8	833	0. 24	0. 8140
2043	I egumesBM: csvGENb: labL2	0. 2	25. 8	833	0. 01	0. 9948
2044	I egumesBM: csvENVw+GENw: labL2	-4. 7	25. 8	833	-0. 18	0. 8558
2045	I egumesBM: csvENVw: labL3	-25. 2	30. 2	833	-0. 84	0. 4038
2046	I egumesBM: csvENVb: labL3	-26. 3	30. 2	833	-0. 87	0. 3843
2047	I egumesBM: csvGENw: labL3	-52. 6	30. 2	833	-1. 74	0. 0821
2048	I egumesBM: csvGENb: labL3	-64. 0	30. 2	833	-2. 12	0. 0344
2049	I egumesBM: csvENVw+GENw: labL3	-65. 8	30. 2	833	-2. 18	0. 0298
2050	I egumesBM: csvENVw: labL4	-22. 8	33. 1	833	-0. 69	0. 4917
2051	I egumesBM: csvENVb: labL4	12. 0	33. 1	833	0. 36	0. 7173
2052	I egumesBM: csvGENw: labL4	6. 9	33. 1	833	0. 21	0. 8361
2053	I egumesBM: csvGENb: labL4	8. 8	33. 1	833	0. 26	0. 7914
2054	I egumesBM: csvENVw+GENw: labL4	-17. 7	33. 1	833	-0. 53	0. 5933
2055	I egumesBM: csvENVw: labL5	-13. 8	29. 2	833	-0. 47	0. 6362
2056	I egumesBM: csvENVb: labL5	-7. 0	29. 2	833	-0. 24	0. 8099
2057	I egumesBM: csvGENw: labL5	-2. 6	29. 2	833	-0. 09	0. 9291

```

2058 | egumesBM: csvGENb: I abL5    -30. 5    29. 2  833   -1. 04  0. 2973
2059 | egumesBM: csvENVw+GENw: I abL5  -32. 8    29. 2  833   -1. 12  0. 2622
2060 | egumesBM: csvENVw: I abL6    -29. 7    28. 5  833   -1. 04  0. 2975
2061 | egumesBM: csvENVb: I abL6    -25. 5    28. 5  833   -0. 89  0. 3720
2062 | egumesBM: csvGENw: I abL6     3. 0     28. 5  833   0. 11  0. 9158
2063 | egumesBM: csvGENb: I abL6    -5. 4     28. 5  833   -0. 19  0. 8499
2064 | egumesBM: csvENVw+GENw: I abL6  -5. 5     28. 8  833   -0. 19  0. 8470
2065 | egumesBM: csvENVw: I abL7    -11. 1    34. 3  833   -0. 32  0. 7474
2066 | egumesBM: csvENVb: I abL7    -52. 1    34. 3  833   -1. 52  0. 1290
2067 | egumesBM: csvGENw: I abL7     2. 4     34. 3  833   0. 07  0. 9441
2068 | egumesBM: csvGENb: I abL7    -35. 2    35. 1  833   -1. 00  0. 3161
2069 | egumesBM: csvENVw+GENw: I abL7  -16. 7    34. 3  833   -0. 49  0. 6255
2070 | egumesBM: csvENVw: I abL8    -33. 8    30. 8  833   -1. 09  0. 2740
2071 | egumesBM: csvENVb: I abL8     4. 3     30. 8  833   0. 14  0. 8901
2072 | egumesBM: csvGENw: I abL8    20. 0     30. 8  833   0. 65  0. 5163
2073 | egumesBM: csvGENb: I abL8     3. 6     30. 8  833   0. 12  0. 9076
2074 | egumesBM: csvENVw+GENw: I abL8  -2. 0     30. 8  833   -0. 06  0. 9483
2075 | egumesBM: csvENVw: I abL9    -21. 3    27. 7  833   -0. 77  0. 4438
2076 | egumesBM: csvENVb: I abL9    -13. 9    27. 4  833   -0. 51  0. 6124
2077 | egumesBM: csvGENw: I abL9     -6. 7    27. 4  833   -0. 24  0. 8076
2078 | egumesBM: csvGENb: I abL9    -12. 6    27. 4  833   -0. 46  0. 6455
2079 | egumesBM: csvENVw+GENw: I abL9  -27. 5    27. 4  833   -1. 01  0. 3151
2080 | egumesBM: csvENVw: I abL10   -18. 7    28. 5  833   -0. 66  0. 5112
2081 | egumesBM: csvENVb: I abL10   -4. 5     28. 5  833   -0. 16  0. 8747
2082 | egumesBM: csvGENw: I abL10   22. 7     28. 5  833   0. 80  0. 4248
2083 | egumesBM: csvGENb: I abL10   18. 0     28. 5  833   0. 63  0. 5278
2084 | egumesBM: csvENVw+GENw: I abL10  -19. 1    28. 5  833   -0. 67  0. 5031
2085 | egumesBM: csvENVw: I abL11   -46. 8     42. 3  833   -1. 11  0. 2693
2086 | egumesBM: csvENVb: I abL11   -14. 5     42. 3  833   -0. 34  0. 7320
2087 | egumesBM: csvGENw: I abL11   -53. 4     42. 9  833   -1. 24  0. 2136
2088 | egumesBM: csvGENb: I abL11   -51. 1     42. 3  833   -1. 21  0. 2283
2089 | egumesBM: csvENVw+GENw: I abL11  -56. 6     42. 3  833   -1. 34  0. 1814
2090 | egumesBM: csvENVw: I abL12   -58. 2     50. 2  833   -1. 16  0. 2462
2091 | egumesBM: csvENVb: I abL12   -43. 6     50. 2  833   -0. 87  0. 3847
2092 | egumesBM: csvGENw: I abL12   -85. 1     50. 2  833   -1. 70  0. 0900
2093 | egumesBM: csvGENb: I abL12   -38. 6     50. 2  833   -0. 77  0. 4422
2094 | egumesBM: csvENVw+GENw: I abL12  -75. 8     50. 2  833   -1. 51  0. 1312
2095 | egumesBM: csvENVw: I abL13   -40. 3     25. 8  833   -1. 56  0. 1188
2096 | egumesBM: csvENVb: I abL13   -12. 6     25. 8  833   -0. 49  0. 6263
2097 | egumesBM: csvGENw: I abL13   -12. 0     25. 8  833   -0. 46  0. 6433
2098 | egumesBM: csvGENb: I abL13   -7. 7      25. 8  833   -0. 30  0. 7656
2099 | egumesBM: csvENVw+GENw: I abL13  -34. 3     25. 8  833   -1. 33  0. 1840
2100 | egumesBM: csvENVw: I abL14   -11. 9     32. 2  833   -0. 37  0. 7129
2101 | egumesBM: csvENVb: I abL14   -8. 0      32. 2  833   -0. 25  0. 8038
2102 | egumesBM: csvGENw: I abL14   -1. 9      32. 2  833   -0. 06  0. 9523
2103 | egumesBM: csvGENb: I abL14   4. 5       32. 2  833   0. 14  0. 8894
2104 | egumesBM: csvENVw+GENw: I abL14  -18. 0     32. 2  833   -0. 56  0. 5759
2105
2106 Model for teabag litter remaining (teabag)

```

```

2107 anova(m12)
2108
2109   numDF denDF F-val ue p-val ue
2110 (Intercept) 1 805 49915. 31 < .0001
2111 | egumes 1 805 1. 81 0. 1784
2112 | csv 5 805 1. 05 0. 3881
2113 | ab 13 805 117. 34 < .0001
2114 | egumes: csv 5 805 1. 77 0. 1156
2115 | egumes: ab 13 805 2. 05 0. 0149
2116 | csv: ab 65 805 2. 97 < .0001
2117 | egumes: csv: ab 65 805 1. 17 0. 1800

```

```

2118 Model for PC1 (PC1)

```

```

2119 anova(mpc1)
2120
2121 (Intercept) numDF denDF F-val ue p-val ue
2122 Legumes 1 839 175.72 <.0001
2123 csv 5 839 1242.53 <.0001
2124 lab 13 839 920.65 <.0001
2125 Legumes: csv 5 839 12.87 <.0001
2126 Legumes: lab 13 839 118.12 <.0001
2127 csv: lab 65 839 7.23 <.0001
2128 Legumes: csv: lab 65 839 0.94 0.6133
2129
2130 summary(m12)
2131 Linear mixed-effects model fit by REML
2132 Data: repro
2133 AIC BIC LogLik
2134 -935 -10.5 664
2135
2136 Random effects:
2137 Formula: ~1 | block
2138 (Intercept) Residual
2139 StdDev: 0.000226 0.0777
2140
2141 Variance function:
2142 Structure: Different standard deviations per stratum
2143 Formula: ~1 | lab * Legumes
2144 Parameter estimates:
2145 L1*B L1*BM L2*B L2*BM L3*B L3*BM L4*B L4*BM L5*B L5*BM L6*B
2146 1.000 1.175 0.892 1.162 1.295 1.214 1.058 1.035 1.346 0.974 1.236
2147 L6*BM L7*B L7*BM L8*B L8*BM L9*B L9*BM L10*B L10*BM L11*B L11*BM
2148 0.849 3.316 2.370 1.447 0.989 1.212 1.793 1.374 1.346 1.042 0.934
2149 L12*B L12*BM L13*B L13*BM L14*B L14*BM
2150 1.200 1.430 0.540 0.515 0.854 0.882
2151
2152 Fixed effects: teabag ~ Legumes * csv * lab
2153
2154 (Intercept) Value Std. Error DF t-value p-value
2155 LegumesBM 0.524 0.0317 805 16.53 0.0000
2156 csvENVw 0.076 0.0517 805 1.47 0.1429
2157 csvENVb -0.045 0.0449 805 -1.01 0.3107
2158 csvGENw -0.042 0.0449 805 -0.93 0.3513
2159 csvGENb 0.000 0.0449 805 0.00 0.9970
2160 csvENVw+GENw 0.016 0.0449 805 0.35 0.7242
2161 csvENVw+GENb -0.029 0.0449 805 -0.65 0.5181
2162 abL2 0.223 0.0425 805 5.25 0.0000
2163 abL3 -0.006 0.0519 805 -0.13 0.9003
2164 abL4 0.071 0.0486 805 1.46 0.1450
2165 abL5 -0.158 0.0532 805 -2.98 0.0030
2166 abL6 -0.018 0.0504 805 -0.35 0.7237
2167 abL7 0.222 0.1099 805 2.02 0.0441
2168 abL8 0.314 0.0558 805 5.63 0.0000
2169 abL9 0.231 0.0498 805 4.63 0.0000
2170 abL10 0.061 0.0573 805 1.06 0.2904
2171 abL11 0.008 0.0458 805 0.18 0.8557
2172 abL12 0.147 0.0495 805 2.97 0.0031
2173 abL13 -0.081 0.0361 805 -2.25 0.0249
2174 abL14 0.068 0.0417 805 1.63 0.1043
2175 LegumesBM: csvENVw -0.048 0.0712 805 -0.67 0.5049
2176 LegumesBM: csvENVb -0.021 0.0712 805 -0.29 0.7681
2177 LegumesBM: csvGENw -0.051 0.0712 805 -0.71 0.4783
2178 LegumesBM: csvGENb -0.077 0.0712 805 -1.08 0.2808
2179 LegumesBM: csvENVw+GENw -0.061 0.0712 805 -0.86 0.3905
2180 LegumesBM: labL2 -0.076 0.0695 805 -1.10 0.2725
2181 LegumesBM: labL3 0.053 0.0764 805 0.70 0.4855
2182 LegumesBM: labL4 0.031 0.0751 805 0.42 0.6758

```

2182	egumesBM: abL5	-0. 046	0. 0738	805	-0. 63	0. 5305
2183	egumesBM: abL6	-0. 086	0. 0702	805	-1. 22	0. 2230
2184	egumesBM: abL7	-0. 024	0. 1432	805	-0. 17	0. 8686
2185	egumesBM: abL8	-0. 023	0. 0759	805	-0. 30	0. 7620
2186	egumesBM: abL9	-0. 215	0. 0859	805	-2. 50	0. 0126
2187	egumesBM: abL10	0. 002	0. 0877	805	0. 02	0. 9807
2188	egumesBM: abL11	-0. 095	0. 0682	805	-1. 40	0. 1630
2189	egumesBM: abL12	-0. 200	0. 0786	805	-2. 54	0. 0112
2190	egumesBM: abL13	-0. 075	0. 0569	805	-1. 32	0. 1876
2191	egumesBM: abL14	-0. 033	0. 0659	805	-0. 51	0. 6122
2192	csvENVw: abL2	-0. 082	0. 0601	805	-1. 36	0. 1747
2193	csvENVb: abL2	-0. 086	0. 0601	805	-1. 43	0. 1537
2194	csvGENw: abL2	0. 073	0. 0601	805	1. 21	0. 2260
2195	csvGENb: abL2	-0. 034	0. 0601	805	-0. 57	0. 5718
2196	csvENVw+GENw: abL2	-0. 117	0. 0601	805	-1. 95	0. 0513
2197	csvENVw: abL3	0. 131	0. 0756	805	1. 73	0. 0841
2198	csvENVb: abL3	0. 115	0. 0756	805	1. 52	0. 1296
2199	csvGENw: abL3	0. 006	0. 0734	805	0. 08	0. 9367
2200	csvGENb: abL3	-0. 029	0. 0734	805	-0. 39	0. 6978
2201	csvENVw+GENw: abL3	0. 132	0. 0734	805	1. 80	0. 0724
2202	csvENVw: abL4	0. 058	0. 0670	805	0. 87	0. 3856
2203	csvENVb: abL4	0. 138	0. 0670	805	2. 06	0. 0395
2204	csvGENw: abL4	-0. 036	0. 0670	805	-0. 53	0. 5947
2205	csvGENb: abL4	0. 026	0. 0687	805	0. 38	0. 7054
2206	csvENVw+GENw: abL4	0. 113	0. 0670	805	1. 68	0. 0926
2207	csvENVw: abL5	0. 076	0. 0752	805	1. 01	0. 3115
2208	csvENVb: abL5	0. 097	0. 0752	805	1. 29	0. 1991
2209	csvGENw: abL5	0. 041	0. 0752	805	0. 55	0. 5828
2210	csvGENb: abL5	0. 072	0. 0752	805	0. 95	0. 3410
2211	csvENVw+GENw: abL5	0. 090	0. 0752	805	1. 20	0. 2318
2212	csvENVw: abL6	0. 107	0. 0713	805	1. 50	0. 1338
2213	csvENVb: abL6	0. 090	0. 0713	805	1. 27	0. 2056
2214	csvGENw: abL6	0. 018	0. 0713	805	0. 25	0. 7990
2215	csvGENb: abL6	0. 015	0. 0734	805	0. 21	0. 8336
2216	csvENVw+GENw: abL6	0. 078	0. 0713	805	1. 09	0. 2764
2217	csvENVw: abL7	0. 276	0. 1554	805	1. 78	0. 0757
2218	csvENVb: abL7	0. 233	0. 1554	805	1. 50	0. 1338
2219	csvGENw: abL7	-0. 021	0. 1554	805	-0. 14	0. 8917
2220	csvGENb: abL7	-0. 117	0. 1623	805	-0. 72	0. 4717
2221	csvENVw+GENw: abL7	0. 070	0. 1554	805	0. 45	0. 6501
2222	csvENVw: abL8	-0. 014	0. 0789	805	-0. 18	0. 8575
2223	csvENVb: abL8	0. 011	0. 0789	805	0. 14	0. 8875
2224	csvGENw: abL8	-0. 004	0. 0789	805	-0. 05	0. 9613
2225	csvGENb: abL8	0. 038	0. 0789	805	0. 49	0. 6272
2226	csvENVw+GENw: abL8	-0. 046	0. 0789	805	-0. 58	0. 5643
2227	csvENVw: abL9	-0. 169	0. 0705	805	-2. 40	0. 0168
2228	csvENVb: abL9	-0. 234	0. 0705	805	-3. 32	0. 0009
2229	csvGENw: abL9	-0. 257	0. 0705	805	-3. 64	0. 0003
2230	csvGENb: abL9	-0. 151	0. 0705	805	-2. 14	0. 0325
2231	csvENVw+GENw: abL9	-0. 141	0. 0705	805	-2. 00	0. 0461
2232	csvENVw: abL10	0. 040	0. 0787	805	0. 51	0. 6080
2233	csvENVb: abL10	0. 021	0. 0787	805	0. 26	0. 7925
2234	csvGENw: abL10	-0. 041	0. 0787	805	-0. 52	0. 5998
2235	csvGENb: abL10	-0. 077	0. 0787	805	-0. 98	0. 3261
2236	csvENVw+GENw: abL10	-0. 001	0. 0787	805	-0. 02	0. 9851
2237	csvENVw: abL11	0. 027	0. 0665	805	0. 40	0. 6891
2238	csvENVb: abL11	0. 076	0. 0648	805	1. 18	0. 2391
2239	csvGENw: abL11	0. 021	0. 0648	805	0. 32	0. 7479
2240	csvGENb: abL11	-0. 020	0. 0648	805	-0. 30	0. 7635
2241	csvENVw+GENw: abL11	0. 001	0. 0648	805	0. 02	0. 9856
2242	csvENVw: abL12	0. 028	0. 0701	805	0. 40	0. 6895
2243	csvENVb: abL12	-0. 013	0. 0721	805	-0. 17	0. 8624
2244	csvGENw: abL12	-0. 082	0. 0701	805	-1. 17	0. 2441

2245	csvGENb: I abL12	-0.102	0.0721	805	-1.41	0.1585
2246	csvENVw+GENw: I abL12	-0.005	0.0721	805	-0.07	0.9432
2247	csvENVw: I abL13	0.096	0.0510	805	1.89	0.0592
2248	csvENVb: I abL13	0.080	0.0510	805	1.57	0.1170
2249	csvGENw: I abL13	-0.023	0.0510	805	-0.46	0.6473
2250	csvGENb: I abL13	0.023	0.0510	805	0.45	0.6520
2251	csvENVw+GENw: I abL13	0.046	0.0510	805	0.90	0.3690
2252	csvENVw: I abL14	0.046	0.0590	805	0.78	0.4358
2253	csvENVb: I abL14	0.038	0.0602	805	0.63	0.5301
2254	csvGENw: I abL14	-0.022	0.0590	805	-0.37	0.7114
2255	csvGENb: I abL14	-0.007	0.0590	805	-0.11	0.9101
2256	csvENVw+GENw: I abL14	0.018	0.0590	805	0.30	0.7647
2257	I egumesBM: csvENVw: I abL2	0.099	0.0969	805	1.02	0.3072
2258	I egumesBM: csvENVb: I abL2	0.075	0.0969	805	0.77	0.4422
2259	I egumesBM: csvGENw: I abL2	-0.027	0.0969	805	-0.28	0.7793
2260	I egumesBM: csvGENb: I abL2	0.089	0.0969	805	0.91	0.3613
2261	I egumesBM: csvENVw+GENw: I abL2	0.043	0.0969	805	0.44	0.6598
2262	I egumesBM: csvENVw: I abL3	-0.057	0.1117	805	-0.51	0.6106
2263	I egumesBM: csvENVb: I abL3	0.012	0.1084	805	0.11	0.9089
2264	I egumesBM: csvGENw: I abL3	0.000	0.1068	805	0.00	0.9975
2265	I egumesBM: csvGENb: I abL3	0.059	0.1068	805	0.56	0.5787
2266	I egumesBM: csvENVw+GENw: I abL3	0.016	0.1082	805	0.15	0.8800
2267	I egumesBM: csvENVw: I abL4	0.050	0.1012	805	0.49	0.6208
2268	I egumesBM: csvENVb: I abL4	-0.110	0.1012	805	-1.09	0.2755
2269	I egumesBM: csvGENw: I abL4	-0.040	0.1012	805	-0.40	0.6909
2270	I egumesBM: csvGENb: I abL4	-0.065	0.1023	805	-0.63	0.5282
2271	I egumesBM: csvENVw+GENw: I abL4	-0.139	0.1012	805	-1.38	0.1692
2272	I egumesBM: csvENVw: I abL5	0.047	0.1031	805	0.46	0.6474
2273	I egumesBM: csvENVb: I abL5	0.027	0.1040	805	0.26	0.7937
2274	I egumesBM: csvGENw: I abL5	0.116	0.1040	805	1.12	0.2635
2275	I egumesBM: csvGENb: I abL5	0.048	0.1031	805	0.47	0.6416
2276	I egumesBM: csvENVw+GENw: I abL5	0.032	0.1031	805	0.31	0.7563
2277	I egumesBM: csvENVw: I abL6	0.021	0.0979	805	0.22	0.8276
2278	I egumesBM: csvENVb: I abL6	-0.016	0.0979	805	-0.16	0.8716
2279	I egumesBM: csvGENw: I abL6	0.110	0.0979	805	1.13	0.2602
2280	I egumesBM: csvGENb: I abL6	0.080	0.0995	805	0.80	0.4241
2281	I egumesBM: csvENVw+GENw: I abL6	0.042	0.0987	805	0.43	0.6690
2282	I egumesBM: csvENVw: I abL7	-0.200	0.2019	805	-0.99	0.3214
2283	I egumesBM: csvENVb: I abL7	-0.038	0.2060	805	-0.19	0.8532
2284	I egumesBM: csvGENw: I abL7	0.099	0.1991	805	0.49	0.6208
2285	I egumesBM: csvGENb: I abL7	0.137	0.2046	805	0.67	0.5019
2286	I egumesBM: csvENVw+GENw: I abL7	-0.005	0.2060	805	-0.02	0.9801
2287	I egumesBM: csvENVw: I abL8	0.057	0.1061	805	0.54	0.5889
2288	I egumesBM: csvENVb: I abL8	-0.106	0.1061	805	-1.00	0.3194
2289	I egumesBM: csvGENw: I abL8	-0.016	0.1061	805	-0.15	0.8814
2290	I egumesBM: csvGENb: I abL8	-0.071	0.1061	805	-0.67	0.5054
2291	I egumesBM: csvENVw+GENw: I abL8	-0.099	0.1061	805	-0.94	0.3485
2292	I egumesBM: csvENVw: I abL9	0.190	0.1204	805	1.58	0.1153
2293	I egumesBM: csvENVb: I abL9	0.181	0.1231	805	1.47	0.1408
2294	I egumesBM: csvGENw: I abL9	0.181	0.1269	805	1.42	0.1548
2295	I egumesBM: csvGENb: I abL9	0.090	0.1204	805	0.74	0.4575
2296	I egumesBM: csvENVw+GENw: I abL9	0.156	0.1204	805	1.29	0.1959
2297	I egumesBM: csvENVw: I abL10	0.021	0.1175	805	0.18	0.8556
2298	I egumesBM: csvENVb: I abL10	-0.054	0.1175	805	-0.46	0.6472
2299	I egumesBM: csvGENw: I abL10	0.033	0.1175	805	0.28	0.7797
2300	I egumesBM: csvGENb: I abL10	0.084	0.1175	805	0.72	0.4729
2301	I egumesBM: csvENVw+GENw: I abL10	-0.009	0.1175	805	-0.07	0.9404
2302	I egumesBM: csvENVw: I abL11	0.152	0.0961	805	1.58	0.1142
2303	I egumesBM: csvENVb: I abL11	-0.025	0.0949	805	-0.27	0.7896
2304	I egumesBM: csvGENw: I abL11	0.027	0.0949	805	0.28	0.7761
2305	I egumesBM: csvGENb: I abL11	0.118	0.0949	805	1.24	0.2149
2306	I egumesBM: csvENVw+GENw: I abL11	0.197	0.0958	805	2.06	0.0399
2307	I egumesBM: csvENVw: I abL12	0.171	0.1099	805	1.56	0.1202

```

2308 | egumesBM: csvENVb: labL12      0. 178    0. 1112 805    1. 60    0. 1109
2309 | egumesBM: csvGENw: labL12      0. 201    0. 1099 805    1. 83    0. 0674
2310 | egumesBM: csvGENb: labL12      0. 254    0. 1112 805    2. 29    0. 0225
2311 | egumesBM: csvENVw+GENw: labL12 0. 243    0. 1112 805    2. 19    0. 0289
2312 | egumesBM: csvENVw: labL13      0. 037    0. 0787 805    0. 47    0. 6368
2313 | egumesBM: csvENVb: labL13      -0. 025   0. 0787 805   -0. 32    0. 7492
2314 | egumesBM: csvGENw: labL13      0. 092    0. 0787 805    1. 16    0. 2452
2315 | egumesBM: csvGENb: labL13      0. 032    0. 0787 805    0. 41    0. 6843
2316 | egumesBM: csvENVw+GENw: labL13 0. 106    0. 0787 805    1. 35    0. 1790
2317 | egumesBM: csvENVw: labL14      0. 018    0. 0909 805    0. 20    0. 8436
2318 | egumesBM: csvENVb: labL14      -0. 039   0. 0917 805   -0. 43    0. 6675
2319 | egumesBM: csvGENw: labL14      0. 098    0. 0909 805    1. 08    0. 2791
2320 | egumesBM: csvGENb: labL14      0. 047    0. 0909 805    0. 51    0. 6083
2321 | egumesBM: csvENVw+GENw: labL14 0. 009    0. 0909 805    0. 10    0. 9232
2322
2323 Standardized Within-Group Residuals:
2324     Min      Q1      Med      Q3      Max
2325 -2. 1971 -0. 6441 -0. 0995  0. 5854  2. 6829
2326
2327 Number of Observations: 974
2328 Number of Groups: 2
2329

```

2330 Model for PC2 (PC2)

[anova\(mpc2\)](#)

	numDF	denDF	F-value	p-value
(Intercept)	1	839	6. 03	0. 0143
legumes	1	839	988. 88	<. 0001
csv	5	839	22. 56	<. 0001
lab	13	839	513. 83	<. 0001
legumes: csv	5	839	11. 79	<. 0001
legumes: lab	13	839	28. 22	<. 0001
csv: lab	65	839	2. 77	<. 0001
legumes: csv: lab	65	839	1. 65	0. 0014

[summary\(mpc2\)](#)

Linear mixed-effects model fit by REML
 Data: reprod
 AIC BIC LogLik
 1965 2897 -785

Random effects:

Formula: ~1 | block
 (Intercept) Residual
 StdDev: 0. 036 0. 358

Variance function:

Structure: Different standard deviations per stratum

Formula: ~1 | lab * legumes

Parameter estimates:

L1*B	L1*BM	L2*B	L2*BM	L3*B	L3*BM	L4*B	L4*BM	L5*B	L5*BM	L6*B	L6*BM
1. 000	0. 845	1. 288	1. 355	1. 415	1. 397	1. 149	0. 882	1. 202	1. 152	3. 578	2. 197
L9*B	L9*BM	L10*B	L10*BM	L11*B	L11*BM	L12*B	L12*BM	L13*B	L13*BM	L14*B	L14*BM
1. 203	1. 384	1. 299	1. 405	1. 046	1. 239	2. 230	1. 673	1. 169	0. 990	1. 302	1. 228
L7*B	L7*BM	L8*B	L8*BM								
3. 623	2. 622	1. 576	1. 995								

Fixed effects: PC2 ~ legumes * csv * lab

	Value	Std. Error	DF	t-value	p-value
(Intercept)	-0. 80	0. 148	839	-5. 40	0. 0000
legumesBM	-0. 77	0. 191	839	-4. 04	0. 0001
csvENVw	-0. 03	0. 207	839	-0. 15	0. 8802
csvENVb	0. 07	0. 207	839	0. 35	0. 7281
csvGENw	-0. 96	0. 207	839	-4. 64	0. 0000

csvGENb	-0.48	0.207	839	-2.31	0.0213
csvENVw+GENw	-0.50	0.207	839	-2.41	0.0163
abL2	1.39	0.238	839	5.85	0.0000
abL3	1.91	0.253	839	7.53	0.0000
abL4	2.07	0.223	839	9.32	0.0000
abL5	1.49	0.229	839	6.54	0.0000
abL6	-0.54	0.543	839	-0.99	0.3244
abL7	1.86	0.229	839	8.13	0.0000
abL8	0.60	0.240	839	2.51	0.0122
abL9	0.45	0.212	839	2.13	0.0335
abL10	1.34	0.357	839	3.74	0.0002
abL11	4.08	0.225	839	18.15	0.0000
abL12	3.91	0.240	839	16.29	0.0000
abL13	2.03	0.549	839	3.70	0.0002
abL14	3.15	0.273	839	11.55	0.0000
egumesBM: csvENVw	0.31	0.271	839	1.14	0.2548
egumesBM: csvENVb	0.09	0.271	839	0.33	0.7414
egumesBM: csvGENw	0.81	0.271	839	2.99	0.0029
egumesBM: csvGENb	0.30	0.271	839	1.10	0.2699
egumesBM: csvENVw+GENw	0.11	0.271	839	0.41	0.6815
egumesBM: abL2	-0.59	0.334	839	-1.78	0.0761
egumesBM: abL3	-0.22	0.348	839	-0.63	0.5261
egumesBM: abL4	-0.05	0.285	839	-0.18	0.8535
egumesBM: abL5	-0.25	0.310	839	-0.81	0.4208
egumesBM: abL6	0.83	0.643	839	1.29	0.1984
egumesBM: abL7	-1.87	0.329	839	-5.69	0.0000
egumesBM: abL8	-0.43	0.339	839	-1.27	0.2048
egumesBM: abL9	0.23	0.305	839	0.76	0.4455
egumesBM: abL10	-1.79	0.450	839	-3.98	0.0001
egumesBM: abL11	-1.01	0.294	839	-3.43	0.0006
egumesBM: abL12	-0.94	0.324	839	-2.89	0.0040
egumesBM: abL13	-1.94	0.681	839	-2.84	0.0046
egumesBM: abL14	-0.69	0.418	839	-1.65	0.0998
csvENVw: abL2	0.01	0.337	839	0.03	0.9790
csvENVb: abL2	-0.20	0.337	839	-0.58	0.5612
csvGENw: abL2	-0.38	0.337	839	-1.12	0.2627
csvGENb: abL2	-0.36	0.337	839	-1.07	0.2860
csvENVw+GENw: abL2	-0.18	0.337	839	-0.53	0.5984
csvENVw: abL3	-0.21	0.358	839	-0.58	0.5641
csvENVb: abL3	0.08	0.358	839	0.23	0.8160
csvGENw: abL3	-0.29	0.358	839	-0.80	0.4259
csvGENb: abL3	-0.12	0.358	839	-0.33	0.7430
csvENVw+GENw: abL3	-0.35	0.358	839	-0.97	0.3343
csvENVw: abL4	-0.32	0.315	839	-1.02	0.3072
csvENVb: abL4	-0.19	0.315	839	-0.62	0.5384
csvGENw: abL4	0.28	0.315	839	0.89	0.3752
csvGENb: abL4	0.03	0.315	839	0.09	0.9248
csvENVw+GENw: abL4	-0.46	0.315	839	-1.47	0.1407
csvENVw: abL5	0.30	0.323	839	0.93	0.3501
csvENVb: abL5	0.18	0.323	839	0.57	0.5694
csvGENw: abL5	0.21	0.323	839	0.65	0.5148
csvGENb: abL5	-0.24	0.323	839	-0.75	0.4548
csvENVw+GENw: abL5	-0.29	0.323	839	-0.89	0.3742
csvENVw: abL6	0.21	0.768	839	0.27	0.7895
csvENVb: abL6	-0.65	0.768	839	-0.85	0.3942
csvGENw: abL6	-0.30	0.768	839	-0.39	0.6947
csvGENb: abL6	0.58	0.768	839	0.75	0.4531
csvENVw+GENw: abL6	-0.12	0.768	839	-0.16	0.8712
csvENVw: abL7	-0.30	0.323	839	-0.93	0.3511
csvENVb: abL7	-0.24	0.323	839	-0.74	0.4583
csvGENw: abL7	0.83	0.323	839	2.57	0.0104
csvGENb: abL7	0.16	0.323	839	0.49	0.6234
csvENVw+GENw: abL7	-0.15	0.323	839	-0.46	0.6459

csvENVw: labL8	-0.36	0.339	839	-1.08	0.2823
csvENVb: labL8	-0.65	0.339	839	-1.91	0.0565
csvGENw: labL8	0.37	0.339	839	1.10	0.2717
csvGENb: labL8	-0.21	0.339	839	-0.62	0.5377
csvENVw+GENw: labL8	-0.81	0.339	839	-2.39	0.0172
csvENVw: labL9	0.43	0.299	839	1.45	0.1479
csvENVb: labL9	0.28	0.299	839	0.92	0.3571
csvGENw: labL9	0.63	0.299	839	2.12	0.0341
csvGENb: labL9	0.25	0.299	839	0.83	0.4063
csvENVw+GENw: labL9	0.02	0.299	839	0.08	0.9373
csvENVw: labL10	-0.05	0.505	839	-0.11	0.9142
csvENVb: labL10	-0.26	0.505	839	-0.51	0.6090
csvGENw: labL10	0.28	0.505	839	0.56	0.5747
csvGENb: labL10	-0.17	0.505	839	-0.34	0.7352
csvENVw+GENw: labL10	-0.04	0.505	839	-0.08	0.9336
csvENVw: labL11	-0.59	0.318	839	-1.84	0.0655
csvENVb: labL11	-0.30	0.318	839	-0.95	0.3405
csvGENw: labL11	1.09	0.318	839	3.43	0.0006
csvGENb: labL11	0.32	0.318	839	1.01	0.3126
csvENVw+GENw: labL11	0.11	0.318	839	0.34	0.7318
csvENVw: labL12	-0.61	0.339	839	-1.79	0.0745
csvENVb: labL12	-0.51	0.339	839	-1.49	0.1355
csvGENw: labL12	0.59	0.339	839	1.74	0.0827
csvGENb: labL12	0.39	0.339	839	1.14	0.2566
csvENVw+GENw: labL12	0.15	0.339	839	0.45	0.6548
csvENVw: labL13	-0.70	0.777	839	-0.90	0.3661
csvENVb: labL13	-0.23	0.777	839	-0.30	0.7630
csvGENw: labL13	0.29	0.777	839	0.37	0.7118
csvGENb: labL13	-0.71	0.777	839	-0.91	0.3636
csvENVw+GENw: labL13	-0.51	0.777	839	-0.65	0.5153
csvENVw: labL14	-0.45	0.386	839	-1.16	0.2481
csvENVb: labL14	-0.59	0.386	839	-1.54	0.1246
csvGENw: labL14	-0.32	0.386	839	-0.83	0.4094
csvGENb: labL14	-0.44	0.386	839	-1.15	0.2493
csvENVw+GENw: labL14	-0.81	0.386	839	-2.09	0.0366
egumesBM: csvENVw: labL2	0.08	0.472	839	0.17	0.8668
egumesBM: csvENVb: labL2	0.21	0.472	839	0.45	0.6514
egumesBM: csvGENw: labL2	0.83	0.472	839	1.76	0.0786
egumesBM: csvGENb: labL2	1.11	0.472	839	2.35	0.0191
egumesBM: csvENVw+GENw: labL2	1.28	0.472	839	2.71	0.0070
egumesBM: csvENVw: labL3	-0.75	0.492	839	-1.52	0.1298
egumesBM: csvENVb: labL3	-0.49	0.492	839	-1.01	0.3150
egumesBM: csvGENw: labL3	0.12	0.492	839	0.24	0.8106
egumesBM: csvGENb: labL3	-0.11	0.492	839	-0.22	0.8229
egumesBM: csvENVw+GENw: labL3	0.67	0.492	839	1.36	0.1747
egumesBM: csvENVw: labL4	-0.05	0.403	839	-0.12	0.9058
egumesBM: csvENVb: labL4	0.16	0.403	839	0.40	0.6860
egumesBM: csvGENw: labL4	-0.39	0.403	839	-0.96	0.3359
egumesBM: csvGENb: labL4	-0.03	0.403	839	-0.07	0.9457
egumesBM: csvENVw+GENw: labL4	0.59	0.403	839	1.47	0.1430
egumesBM: csvENVw: labL5	-0.46	0.438	839	-1.04	0.2970
egumesBM: csvENVb: labL5	-0.26	0.438	839	-0.59	0.5525
egumesBM: csvGENw: labL5	-0.39	0.438	839	-0.89	0.3718
egumesBM: csvGENb: labL5	-0.08	0.438	839	-0.18	0.8535
egumesBM: csvENVw+GENw: labL5	0.25	0.438	839	0.56	0.5753
egumesBM: csvENVw: labL6	-0.63	0.909	839	-0.69	0.4918
egumesBM: csvENVb: labL6	0.54	0.909	839	0.60	0.5512
egumesBM: csvGENw: labL6	-0.75	0.909	839	-0.82	0.4111
egumesBM: csvGENb: labL6	-0.93	0.909	839	-1.02	0.3057
egumesBM: csvENVw+GENw: labL6	0.01	0.909	839	0.01	0.9955
egumesBM: csvENVw: labL7	-0.63	0.466	839	-1.36	0.1753
egumesBM: csvENVb: labL7	-0.31	0.466	839	-0.67	0.5037
egumesBM: csvGENw: labL7	-0.40	0.466	839	-0.86	0.3893

egumesBM: csvGENb: labL7	0.20	0.466	839	0.44	0.6607
egumesBM: csvENVw+GENw: labL7	0.97	0.466	839	2.08	0.0378
egumesBM: csvENVw: labL8	-0.15	0.479	839	-0.31	0.7554
egumesBM: csvENVb: labL8	0.51	0.479	839	1.06	0.2881
egumesBM: csvGENw: labL8	-0.41	0.479	839	-0.86	0.3903
egumesBM: csvGENb: labL8	0.70	0.479	839	1.47	0.1418
egumesBM: csvENVw+GENw: labL8	1.14	0.479	839	2.39	0.0172
egumesBM: csvENVw: labL9	-0.82	0.431	839	-1.90	0.0579
egumesBM: csvENVb: labL9	-0.57	0.431	839	-1.32	0.1866
egumesBM: csvGENw: labL9	-0.81	0.431	839	-1.88	0.0608
egumesBM: csvGENb: labL9	-0.28	0.431	839	-0.66	0.5113
egumesBM: csvENVw+GENw: labL9	-0.07	0.431	839	-0.16	0.8696
egumesBM: csvENVw: labL10	-0.09	0.637	839	-0.14	0.8890
egumesBM: csvENVb: labL10	0.15	0.637	839	0.24	0.8085
egumesBM: csvGENw: labL10	0.51	0.637	839	0.80	0.4226
egumesBM: csvGENb: labL10	0.40	0.637	839	0.63	0.5316
egumesBM: csvENVw+GENw: labL10	1.68	0.637	839	2.63	0.0086
egumesBM: csvENVw: labL11	0.42	0.416	839	1.01	0.3110
egumesBM: csvENVb: labL11	0.26	0.416	839	0.62	0.5330
egumesBM: csvGENw: labL11	-0.83	0.416	839	-1.99	0.0474
egumesBM: csvGENb: labL11	-0.05	0.416	839	-0.11	0.9113
egumesBM: csvENVw+GENw: labL11	0.33	0.416	839	0.80	0.4264
egumesBM: csvENVw: labL12	0.40	0.458	839	0.87	0.3872
egumesBM: csvENVb: labL12	0.18	0.458	839	0.40	0.6916
egumesBM: csvGENw: labL12	-0.35	0.458	839	-0.76	0.4460
egumesBM: csvGENb: labL12	-0.32	0.458	839	-0.71	0.4802
egumesBM: csvENVw+GENw: labL12	0.29	0.458	839	0.64	0.5231
egumesBM: csvENVw: labL13	1.50	0.963	839	1.55	0.1205
egumesBM: csvENVb: labL13	1.23	0.963	839	1.28	0.2022
egumesBM: csvGENw: labL13	0.00	0.963	839	0.00	0.9999
egumesBM: csvGENb: labL13	1.45	0.963	839	1.51	0.1317
egumesBM: csvENVw+GENw: labL13	2.65	0.963	839	2.75	0.0061
egumesBM: csvENVw: labL14	0.66	0.591	839	1.12	0.2624
egumesBM: csvENVb: labL14	0.65	0.591	839	1.10	0.2723
egumesBM: csvGENw: labL14	-0.60	0.591	839	-1.02	0.3074
egumesBM: csvGENb: labL14	0.24	0.591	839	0.41	0.6840
egumesBM: csvENVw+GENw: labL14	0.05	0.591	839	0.08	0.9332

Standardized Within-Group Residuals:

Min	Q1	Median	Q3	Max
-3.2963	-0.5815	0.0528	0.6596	3.1293

Number of Observations: 1008

Number of Groups: 2

2331 [Detailed model outputs from Supplementary Table S3](#)

2332 [Model for shoot biomass \(shootbm\)](#)

	numDF	denDF	F-value	p-value
2334 anova(m1)				
2335 (Intercept)	1	955	76.70	<.0001
2336 mi xture	1	955	1843.37	<.0001
2337 het	5	955	9.10	<.0001
2338 setup	1	12	2.99	0.1094
2339 mi xture: het	5	955	12.41	<.0001
2340 mi xture: setup	1	955	209.81	<.0001
2341 het: setup	5	955	23.31	<.0001
2342 mi xture: het: setup	5	955	7.34	<.0001

```

2344 summary(m1)
2345 Linear mixed-effects model fit by REML
2346 Data: repro
2347   AIC   BIC LogLik
2348 2868 3132 -1380
2349
2350 Random effects:
2351   Formula: ~1 | lab
2352             (Intercept)
2353 StdDev:      1.66
2354
2355   Formula: ~1 | block %in% lab
2356             (Intercept) Residual
2357 StdDev:      0.442   0.165
2358
2359 Variance function:
2360 Structure: Different standard deviations per stratum
2361 Formula: ~1 | lab * mixture
2362
2363 Parameter estimates:
2364   L1*B    L1*BM   L2*B    L2*BM   L3*B    L3*BM   L4*B    L4*BM   L5*B    L5*BM   L6*B
2365 1.000   5.483   0.979   18.348   5.569   6.876   6.235   4.325   4.737   3.093   1.941
2366 L6*BM   L7*B    L7*BM   L8*B    L8*BM   L9*B    L9*BM   L10*B   L10*BM   L11*B   L11*BM
2367 2.175   1.831   27.137   2.977   4.069   1.253   8.022   3.997   14.183   10.006   5.615
2368 L12*B   L12*BM  L13*B   L13*BM  L14*B   L14*BM
2369 11.360   5.856   18.913   2.602   10.150   54.072
2370
2371 Fixed effects: shootbm ~ mixture * het * setup
2372                                         Value Std. Error DF t-value p-value
2373 (Intercept)                   2.79   0.701 955  3.98  0.0001
2374 mixtureBM                    4.71   0.195 955  24.21 0.0000
2375 hetENVw                      -0.14   0.091 955  -1.55 0.1204
2376 hetENVb                      -0.05   0.091 955  -0.57 0.5712
2377 hetGENw                      0.52   0.091 955  5.77  0.0000
2378 hetGENb                      0.43   0.091 955  4.72  0.0000
2379 hetENVw+GENw                 0.61   0.091 955  6.77  0.0000
2380 setupgrowth_chamber          -0.30   0.923 12   -0.32 0.7524
2381 mixtureBM: hetENVw           -0.87   0.206 955  -4.23 0.0000
2382 mixtureBM: hetENVb           -0.24   0.206 955  -1.15 0.2488
2383 mixtureBM: hetGENw           -0.70   0.206 955  -3.41 0.0007
2384 mixtureBM: hetGENb           -0.42   0.206 955  -2.04 0.0413
2385 mixtureBM: hetENVw+GENw     -1.37   0.206 955  -6.66 0.0000
2386 mixtureBM: setupgrowth_chamber -2.51   0.225 955  -11.16 0.0000
2387 hetENVw: setupgrowth_chamber  0.21   0.109 955  1.96  0.0501
2388 hetENVb: setupgrowth_chamber  0.04   0.109 955  0.38  0.7014
2389 hetGENw: setupgrowth_chamber -0.52   0.109 955  -4.73 0.0000
2390 hetGENb: setupgrowth_chamber -0.40   0.109 955  -3.68 0.0002
2391 hetENVw+GENw: setupgrowth_chamber -0.38   0.109 955  -3.50 0.0005
2392 mixtureBM: hetENVw: setupgrowth_chamber  1.03   0.258 955  4.01  0.0001
2393 mixtureBM: hetENVb: setupgrowth_chamber  0.06   0.257 955  0.22  0.8260
2394 mixtureBM: hetGENw: setupgrowth_chamber -0.01   0.257 955  -0.05 0.9576
2395 mixtureBM: hetGENb: setupgrowth_chamber -0.06   0.257 955  -0.24 0.8127
2396 mixtureBM: hetENVw+GENw: setupgrowth_chamber  0.85   0.257 955  3.31  0.0010
2397
2398 Standardized Within-Group Residuals:
2399   Min     Q1     Med     Q3     Max
2400 -2.9236 -0.7399  0.0667  0.8455  3.6711
2401
2402 Number of Observations: 1005
2403 Number of Groups:
2404   lab block %in% lab
2405      14            28
2406

```

2407 **Model for shoot biomass (rootbm)**

```

2408 anova(m2)
2409 numDF denDF F-value p-value
2410 (Intercept) 1 939 114.19 <.0001
2411 mixture 1 939 705.35 <.0001
2412 het 5 939 20.91 <.0001
2413 setup 1 12 7.35 0.0189
2414 mixture:het 5 939 3.30 0.0059
2415 mixture:setup 1 939 30.33 <.0001
2416 het:setup 5 939 5.59 <.0001
2417 mixture:het:setup 5 939 1.03 0.3993
2418
2419 summary(m2)
2420 Linear mixed-effects model fit by REML
2421 Data: repro
2422   AIC BIC LogLik
2423 1633 1896 -763
2424
2425 Random effects:
2426 Formula: ~1 | lab
2427   (Intercept)
2428 StdDev: 0.52
2429
2430 Formula: ~1 | block %in% lab
2431   (Intercept) Residual
2432 StdDev: 0.15 0.23
2433
2434 Variance function:
2435 Structure: Different standard deviations per stratum
2436 Formula: ~1 | lab * mixture
2437 Parameter estimates:
2438 L1*B L1*BM L2*B L2*BM L3*B L3*BM L4*B L4*BM L5*B L5*BM L6*B L
2439 1.00 1.34 1.08 0.92 1.81 2.00 0.55 0.76 2.12 1.84 9.85 L
2440 6*BM L7*B L7*BM L8*B L8*BM L9*B L9*BM L10*B L10*BM L11*B L11*BM
2441 5.12 1.41 6.57 2.71 2.79 1.23 2.09 3.85 3.49 1.38 1.26
2442 L12*B L12*BM L13*B L13*BM L14*B L14*BM
2443 1.78 1.51 4.69 5.13 0.96 10.27
2444
2445 Fixed effects: rootbm ~ mixture * het * setup
2446                                         Value Std. Error DF t-value p-value
2447 (Intercept) 0.83 0.223 939 3.7 0.0002
2448 mixtureBM 0.58 0.061 939 9.4 0.0000
2449 hetENVw -0.19 0.054 939 -3.5 0.0004
2450 hetENVb -0.06 0.054 939 -1.1 0.2759
2451 hetGENw 0.24 0.055 939 4.3 0.0000
2452 hetGENb 0.11 0.054 939 2.1 0.0360
2453 hetENVw+GENw 0.16 0.054 939 2.9 0.0035
2454 setupgrowth_chamber 0.54 0.298 12 1.8 0.0964
2455 mixtureBM:hetENVw 0.07 0.086 939 0.8 0.4455
2456 mixtureBM:hetENVb -0.07 0.086 939 -0.9 0.3845
2457 mixtureBM:hetGENw -0.10 0.087 939 -1.2 0.2332
2458 mixtureBM:hetGENb -0.11 0.086 939 -1.3 0.1952
2459 mixtureBM:hetENVw+GENw -0.16 0.086 939 -1.8 0.0683
2460 mixtureBM:setupgrowth_chamber 0.27 0.114 939 2.4 0.0189
2461 hetENVw:setupgrowth_chamber 0.33 0.095 939 3.5 0.0006
2462 hetENVb:setupgrowth_chamber 0.08 0.095 939 0.9 0.3865
2463 hetGENw:setupgrowth_chamber 0.11 0.096 939 1.1 0.2690
2464 hetGENb:setupgrowth_chamber 0.07 0.095 939 0.7 0.4548
2465 hetENVw+GENw:setupgrowth_chamber 0.24 0.095 939 2.6 0.0109
2466 mixtureBM:hetENVw:setupgrowth_chamber 0.04 0.160 939 0.2 0.8078
2467 mixtureBM:hetENVb:setupgrowth_chamber 0.15 0.159 939 1.0 0.3297
2468 mixtureBM:hetGENw:setupgrowth_chamber -0.19 0.159 939 -1.2 0.2370

```

```

2469 mixtureBM: hetGENB: setupgrowth_chamber      0.05      0.159 939      0.3  0.7714
2470 mixtureBM: hetENVw+GENw: setupgrowth_chamber -0.04      0.159 939      -0.3  0.7933
2471
2472 Standardized Within-Group Residuals:
2473   Min     Q1     Med     Q3     Max
2474 -2.968 -0.678 -0.028  0.692  4.380
2475
2476 Number of Observations: 989
2477 Number of Groups:
2478   Lab block %in% Lab
2479       14          28
2480

```

2481 Model for shoot biomass (seedbm)

```

2482
2483   numDF denDF F-value p-value
2484 (Intercept)    1    947   28.74 <.0001
2485 mixture        1    947   729.57 <.0001
2486 het             5    947   39.52 <.0001
2487 setup          1     12    1.34  0.2696
2488 mixture: het   5    947   21.51 <.0001
2489 mixture: setup 1    947   87.11 <.0001
2490 het: setup     5    947   22.70 <.0001
2491 mixture: het: setup 5    947   0.82  0.5347
2492
2493 summary(m3)
2494 Linear mixed-effects model fit by REML
2495 Data: repro
2496   AIC   BIC LogLik
2497 1047 1311 -470
2498
2499 Random effects:
2500   Formula: ~1 | Lab
2501   (Intercept)
2502 StdDev: 0.59
2503
2504 Formula: ~1 | block %in% Lab
2505   (Intercept) Residual
2506 StdDev: 0.071 0.19
2507
2508 Variance function:
2509 Structure: Different standard deviations per stratum
2510 Formula: ~1 | Lab * mixture
2511
2512 Parameter estimates:
2513   L1*B  L1*BM  L2*B  L2*BM  L3*B  L3*BM  L4*B  L4*BM  L5*B  L5*BM  L6*B
2514 1.00   0.53   1.26   0.21   7.29   2.05   2.21   1.00   4.19   1.17   1.02
2515 L6*BM  L7*B  L7*BM  L8*B  L8*BM  L9*B  L9*BM  L10*B L10*BM  L11*B L11*BM
2516 0.69   6.42   1.32   1.27   1.19   2.00   1.34   7.91   1.23   9.03   2.84
2517 L12*B L12*BM L13*B L13*BM L14*B L14*BM
2518 8.05   2.24   1.18   0.56   5.99   2.95
2519
2520 Fixed effects: seedbm ~ mixture * het * setup
2521
2522   (Intercept) Value Std. Error DF t-value p-value
2523 mixtureBM      1.76   0.25  947   7.1  0.0000
2524 hetENVw        -0.77   0.06  947  -12.1 0.0000
2525 hetENVb        -0.06   0.09  947  -0.7  0.4776
2526 hetGENw        -0.01   0.09  947  -0.1  0.9036
2527

```

```

2527 hetGENb -0.11 0.09 947 -1.3 0.2068
2528 hetENVw+GENw -0.31 0.09 947 -3.6 0.0004
2529 setupgrowth_chamber -0.57 0.33 12 -1.7 0.1096
2530 mi xtureBM: hetENVw 0.05 0.09 947 0.6 0.5566
2531 mi xtureBM: hetENVb -0.02 0.09 947 -0.2 0.8256
2532 mi xtureBM: hetGENw 0.23 0.09 947 2.5 0.0113
2533 mi xtureBM: hetGENb 0.11 0.09 947 1.2 0.2155
2534 mi xtureBM: hetENVw+GENw 0.26 0.09 947 2.9 0.0035
2535 mi xtureBM: setupgrowth_chamber 0.32 0.08 947 3.8 0.0002
2536 hetENVw: setupgrowth_chamber 0.17 0.11 947 1.5 0.1257
2537 hetENVb: setupgrowth_chamber 0.05 0.11 947 0.5 0.6219
2538 hetGENw: setupgrowth_chamber -0.25 0.11 947 -2.3 0.0229
2539 hetGENb: setupgrowth_chamber -0.26 0.11 947 -2.4 0.0156
2540 hetENVw+GENw: setupgrowth_chamber -0.17 0.11 947 -1.6 0.1164
2541 mi xtureBM: hetENVw: setupgrowth_chamber -0.10 0.12 947 -0.8 0.3989
2542 mi xtureBM: hetENVb: setupgrowth_chamber 0.00 0.12 947 0.0 0.9681
2543 mi xtureBM: hetGENw: setupgrowth_chamber 0.06 0.12 947 0.5 0.5952
2544 mi xtureBM: hetGENb: setupgrowth_chamber 0.11 0.12 947 1.0 0.3318
2545 mi xtureBM: hetENVw+GENw: setupgrowth_chamber -0.04 0.12 947 -0.4 0.7064
2546
2547
2548 Model for shoot biomass (totalbm)

```

```

2549 summary(m4)
2550 Linear mixed-effects model fit by REML
2551 Data: repro
2552   AIC   BIC LogLik
2553 3736 4000 -1814
2554
2555 Random effects:
2556 Formula: ~1 | lab
2557           (Intercept)
2558 StdDev:      2.64
2559
2560 Formula: ~1 | block %in% lab
2561           (Intercept) Residual
2562 StdDev:      0.786   0.362
2563
2564 Variance function:
2565 Structure: Different standard deviations per stratum
2566 Formula: ~1 | lab * mixture
2567 Parameter estimates:
2568 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
2569 1.000  2.915  1.078  0.676  4.465  3.862  7.152  3.382  2.568  1.760  7.745
2570 L6*BM   L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM   L10*B  L10*BM  L11*B  L11*BM
2571 5.606  2.353  12.988 3.091  4.315  1.288  5.097  3.742  3.770  8.312  2.815
2572 L12*B  L12*BM  L13*B  L13*BM  L14*B  L14*BM
2573 10.039 2.986  3.333  4.700  4.710  37.184
2574 Fixed effects: totalbm ~ mixture * het * setup
2575                                         Value Std. Error DF t-value p-value
2576 (Intercept)          7.20    1.112 958  6.48  0.0000
2577 mi xtureBM          1.33    0.173 958  7.67  0.0000
2578 hetENVw            -0.04    0.205 958  -0.18  0.8550
2579 hetENVb            -0.01    0.205 958  -0.07  0.9462
2580 hetGENw             0.79    0.205 958  3.85  0.0001
2581 hetGENb             0.58    0.205 958  2.81  0.0051
2582 hetENVw+GENw        0.65    0.205 958  3.15  0.0017
2583 setupgrowth_chamber -1.60    1.469 12  -1.09  0.2984
2584 mi xtureBM: hetENVw  0.04    0.243 958  0.16  0.8708
2585 mi xtureBM: hetENVb -0.05    0.243 958  -0.19  0.8487
2586 mi xtureBM: hetGENw -0.79    0.243 958  -3.26  0.0011
2587 mi xtureBM: hetGENb -0.74    0.243 958  -3.02  0.0026
2588 mi xtureBM: hetENVw+GENw -0.45    0.243 958  -1.85  0.0640

```

```

2589 mi xtureBM: setupgrowth_chamber      1. 31    0. 273 958    4. 82    0. 0000
2590 hetENVw: setupgrowth_chamber        0. 47    0. 249 958    1. 88    0. 0602
2591 hetENVb: setupgrowth_chamber        0. 18    0. 249 958    0. 71    0. 4754
2592 hetGENw: setupgrowth_chamber       -1. 14    0. 249 958   -4. 55    0. 0000
2593 hetGENb: setupgrowth_chamber       -0. 78    0. 249 958   -3. 11    0. 0019
2594 hetENVw+GENw: setupgrowth_chamber  -0. 62    0. 249 958   -2. 47    0. 0136
2595 mi xtureBM: hetENVw: setupgrowth_chamber  0. 09    0. 376 958    0. 25    0. 8049
2596 mi xtureBM: hetENVb: setupgrowth_chamber -0. 16    0. 376 958   -0. 42    0. 6748
2597 mi xtureBM: hetGENw: setupgrowth_chamber  0. 26    0. 376 958    0. 69    0. 4935
2598 mi xtureBM: hetGENb: setupgrowth_chamber  0. 61    0. 376 958    1. 63    0. 1030
2599 mi xtureBM: hetENVw+GENw: setupgrowth_chamber -0. 09    0. 376 958   -0. 25    0. 8013
2600

```

```

2601 Standardized Within-Group Residuals:
2602   Min     Q1     Med     Q3     Max
2603 -3.4575 -0.7405 -0.0443  0.7257  3.4425
2604

```

```

2605 Number of Observations: 1008
2606 Number of Groups:
2607   Lab block %in% Lab
2608     14           28

```

Model for shoot to root biomass ratio (shoot.root)

```

2610 anova(m5)
2611
2612   numDF denDF F-value p-value
2613 (Intercept)      1    934 120.46 <.0001
2614 mixture          1    934 706.29 <.0001
2615 het               5    934 21.00 <.0001
2616 setup             1    12   7.52  0.0178
2617 mixture:het       5    934  3.32  0.0056
2618 mixture:setup     1    934 30.37 <.0001
2619 het:setup         5    934  5.57  <.0001
2620 mixture:het:setup 5    934  1.00  0.4140

```

```

2620 summary(m5)
Linear mixed-effects model fit by REML
  Data: repro
  AIC   BIC LogLik
1583 1846 -737

```

Random effects:

```

  Formula: ~1 | Lab
            (Intercept)
  StdDev:      0.51

```

```

  Formula: ~1 | block %in% Lab
            (Intercept) Residual
  StdDev:      0.14      0.23

```

Variance function:

```

  Structure: Different standard deviations per stratum
  Formula: ~1 | Lab * mixture

```

Parameter estimates:

L1*B	L1*BM	L2*B	L2*BM	L3*B	L3*BM	L4*B	L4*BM	L5*B	L5*BM	L6*B	L6*BM
1.00	1.35	1.08	0.92	1.81	1.99	0.55	0.76	2.12	1.84	7.17	4.40
L7*B	L7*BM	L8*B	L8*BM	L9*B	L9*BM	L10*B	L10*BM	L11*B	L11*BM	L12*B	L12*BM
1.41	6.57	2.71	2.80	1.23	2.09	3.85	3.48	1.38	1.26	1.77	1.51
L13*B	L13*BM	L14*B	L14*BM								
4.72	5.12	0.96	10.26								

Fixed effects: shoot.root ~ mixture * het * setup

	Value	Std. Error	DF	t-value	p-value
(Intercept)	0.83	0.215	934	3.9	0.0001
mi xtureBM	0.58	0.061	934	9.4	0.0000
hetENVw	-0.19	0.054	934	-3.5	0.0004
hetENVb	-0.06	0.054	934	-1.1	0.2761
hetGENw	0.24	0.055	934	4.3	0.0000
hetGENb	0.11	0.054	934	2.1	0.0361
hetENVw+GENw	0.16	0.054	934	2.9	0.0035
setupgrowth_chamber	0.52	0.289	12	1.8	0.0979
mi xtureBM: hetENVw	0.07	0.086	934	0.8	0.4452
mi xtureBM: hetENVb	-0.07	0.086	934	-0.9	0.3843
mi xtureBM: hetGENw	-0.10	0.087	934	-1.2	0.2335
mi xtureBM: hetGENb	-0.11	0.086	934	-1.3	0.1955
mi xtureBM: hetENVw+GENw	-0.16	0.086	934	-1.8	0.0684
mi xtureBM: setupgrowth_chamber	0.27	0.114	934	2.4	0.0181
hetENVw: setupgrowth_chamber	0.33	0.095	934	3.5	0.0005
hetENVb: setupgrowth_chamber	0.08	0.095	934	0.9	0.3741
hetGENw: setupgrowth_chamber	0.11	0.096	934	1.1	0.2518
hetGENb: setupgrowth_chamber	0.07	0.095	934	0.7	0.4593
hetENVw+GENw: setupgrowth_chamber	0.25	0.095	934	2.6	0.0093
mi xtureBM: hetENVw: setupgrowth_chamber	0.04	0.159	934	0.2	0.8238
mi xtureBM: hetENVb: setupgrowth_chamber	0.15	0.158	934	1.0	0.3408
mi xtureBM: hetGENw: setupgrowth_chamber	-0.18	0.159	934	-1.1	0.2554
mi xtureBM: hetGENb: setupgrowth_chamber	0.05	0.159	934	0.3	0.7345
mi xtureBM: hetENVw+GENw: setupgrowth_chamber	-0.06	0.158	934	-0.4	0.7150

Standardized Within-Group Residuals:

Min	Q1	Med	Q3	Max
-2.967	-0.690	-0.026	0.685	4.382

Number of Observations: 984

Number of Groups:

Lab	Block	%in%	Lab
14			28

2621 Model for Brachypodium distachyon height (heightB)

```
2622 anova(m6)
2623
2624 (Intercept) 1 944 827.30 <.0001
2625 mi xture 1 944 30.90 <.0001
2626 het 5 944 20.16 <.0001
2627 setup 1 12 5.28 0.0404
2628 mi xture: het 5 944 1.70 0.1318
2629 mi xture: setup 1 944 10.92 0.0010
2630 het: setup 5 944 3.37 0.0051
2631 mi xture: het: setup 5 944 2.58 0.0251
```

2632

```
2633 summary(m6)
2634 Linear mixed-effects model fit by REML
```

2635 Data: repro

```
2636 AIC BIC LogLik
2637 5659 5922 -2775
```

2638

2639 Random effects:

2640 Formula: ~1 | lab

2641 (Intercept)

2642 StdDev: 3.6

```

2644 Formula: ~1 | block %in% lab
2645             (Intercept) Residual
2646 StdDev:      1.6       5.1
2647
2648 Variance function:
2649 Structure: Different standard deviations per stratum
2650 Formula: ~1 | lab * mixture
2651
2652 Parameter estimates:
2653 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
2654 1.00    0.92    0.19    0.48    0.49    1.10    1.03    1.32    0.44    0.56    0.69
2655 L6*BM   L7*B    L7*BM   L8*B    L8*BM   L9*B    L9*BM   L10*B   L10*BM  L11*B   L11*BM
2656 0.43    0.51    0.71    1.12    0.81    0.78    1.00    0.71    0.83    0.40    0.58
2657 L12*B   L12*BM  L13*B   L13*BM  L14*B   L14*BM
2658 0.52    0.51    1.84    1.85    0.64    4.00
2659
2660
2661 Fixed effects: heightB ~ mixture * het * setup
2662                                         Value Std. Error DF t-value p-value
2663 (Intercept)                      33     1.60 944   20.4  0.0000
2664 mixtureBM                         -2     0.73 944   -2.2  0.0299
2665 hetENVw                           -2     0.45 944   -4.3  0.0000
2666 hetENVb                           -2     0.45 944   -3.3  0.0010
2667 hetGENw                           1     0.45 944   1.7   0.0902
2668 hetGENb                           1     0.45 944   1.4   0.1537
2669 hetENVw+GENw                     1     0.45 944   1.2   0.2228
2670 setupgrowth_chamber              -5     2.14 12    -2.5  0.0299
2671 mixtureBM:hetENVw                1     1.00 944   1.3   0.1959
2672 mixtureBM:hetENVb                0     1.00 944   0.3   0.7301
2673 mixtureBM:hetGENw                1     0.99 944   1.4   0.1567
2674 mixtureBM:hetGENb                2     0.99 944   1.7   0.0820
2675 mixtureBM:hetENVw+GENw          2     1.00 944   1.7   0.0840
2676 mixtureBM:setupgrowth_chamber   0     1.01 944   0.4   0.6987
2677 hetENVw:setupgrowth_chamber     2     0.79 944   2.5   0.0113
2678 hetENVb:setupgrowth_chamber     1     0.79 944   1.5   0.1264
2679 hetGENw:setupgrowth_chamber     2     0.80 944   2.0   0.0504
2680 hetGENb:setupgrowth_chamber     0     0.79 944   0.3   0.7690
2681 hetENVw+GENw:setupgrowth_chamber 1     0.79 944   1.5   0.1217
2682 mixtureBM:hetENVw:setupgrowth_chamber -1    1.40 944   -0.8  0.4122
2683 mixtureBM:hetENVb:setupgrowth_chamber 0     1.40 944   -0.3  0.7501
2684 mixtureBM:hetGENw:setupgrowth_chamber -4    1.40 944   -3.0  0.0032
2685 mixtureBM:hetGENb:setupgrowth_chamber -3    1.39 944   -2.1  0.0322
2686 mixtureBM:hetENVw+GENw:setupgrowth_chamber -2    1.40 944   -1.4  0.1493
2687
2688 Standardized Within-Group Residuals:
2689      Min      Q1      Med      Q3      Max
2690 -2.898 -0.750  0.063  0.752  2.517
2691
2692 Number of Observations: 994
2693 Number of Groups:
2694     lab block %in% lab
2695      14           28
2696
2697 Model for shoot N% (N.)
2698
2699 anova(m7)
2700                                         numDF denDF F-value p-value
2701 (Intercept)                      1     958 194.788 <.0001
2702 mixture                           1     958 54.143 <.0001
2703 het                                5     958  0.754 0.5831
2704 setup                               1     12  15.130 0.0021

```

```

2704 mixture: het      5   958   1. 283  0. 2690
2705 mixture: setup    1   958   35. 934 <. 0001
2706 het: setup       5   958   0. 911  0. 4729
2707 mixture: het: setup 5   958   3. 768  0. 0022
2708

2709 summary(m7)
2710 Linear mixed-effects model fit by REML
2711 Data: reproz
2712   AIC   BIC LogLik
2713 128 393 -10
2714
2715 Random effects:
2716 Formula: ~1 | lab
2717             (Intercept)
2718 StdDev:        0. 3
2719
2720 Formula: ~1 | block %in% lab
2721             (Intercept) Residual
2722 StdDev:        0. 15     0. 11
2723
2724 Variance function:
2725 Structure: Different standard deviations per stratum
2726 Formula: ~1 | lab * mixture
2727
2728 Parameter estimates:
2729 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
2730 1. 00   0. 47   6. 17   5. 89   0. 69   1. 55   3. 39   3. 22   1. 07   1. 10   1. 04
2731 L6*BM   L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM   L10*B  L10*BM  L11*B  L11*BM
2732 1. 00   5. 77   3. 64   2. 41   2. 45   1. 37   1. 09   1. 96   2. 46   1. 58   2. 97
2733 L12*B  L12*BM  L13*B  L13*BM  L14*B  L14*BM
2734 3. 14   3. 18   4. 79   5. 05   1. 63   0. 87
2735
2736 Fixed effects: N. ~ mixture * het * setup
2737
2738 (Intercept)           Value  Std. Error DF t-value p-value
2739 mixtureBM            -0. 32   0. 057  958  -5. 7  0. 0000
2740 hetENVw               -0. 03   0. 062  958  -0. 5  0. 6242
2741 hetENVb               -0. 07   0. 062  958  -1. 2  0. 2273
2742 hetGENw               -0. 19   0. 062  958  -3. 0  0. 0024
2743 hetGENb               -0. 12   0. 062  958  -2. 0  0. 0510
2744 hetENVw+GENw          -0. 17   0. 062  958  -2. 8  0. 0048
2745 setupgrowth_chamber  -0. 86   0. 178  12   -4. 8  0. 0004
2746 mixtureBM:hetENVw    0. 02   0. 078  958   0. 2  0. 8120
2747 mixtureBM:hetENVb    0. 05   0. 078  958   0. 7  0. 4972
2748 mixtureBM:hetGENw    0. 23   0. 078  958   3. 0  0. 0032
2749 mixtureBM:hetGENb    0. 09   0. 078  958   1. 1  0. 2729
2750 mixtureBM:hetENVw+GENw 0. 26   0. 078  958   3. 3  0. 0010
2751 mixtureBM:setupgrowth_chamber 0. 29   0. 062  958   4. 7  0. 0000
2752 hetENVw:setupgrowth_chamber 0. 03   0. 067  958   0. 4  0. 6533
2753 hetENVb:setupgrowth_chamber 0. 06   0. 067  958   0. 9  0. 3733
2754 hetGENw:setupgrowth_chamber 0. 20   0. 067  958   3. 0  0. 0025
2755 hetGENb:setupgrowth_chamber 0. 16   0. 067  958   2. 3  0. 0201
2756 hetENVw+GENw:setupgrowth_chamber 0. 20   0. 067  958   3. 0  0. 0032
2757 mixtureBM:hetENVw:setupgrowth_chamber -0. 03   0. 086  958  -0. 4  0. 7110
2758 mixtureBM:hetENVb:setupgrowth_chamber -0. 05   0. 086  958  -0. 6  0. 5403
2759 mixtureBM:hetGENw:setupgrowth_chamber -0. 23   0. 086  958  -2. 7  0. 0080
2760 mixtureBM:hetGENb:setupgrowth_chamber -0. 14   0. 086  958  -1. 7  0. 0925
2761 mixtureBM:hetENVw+GENw:setupgrowth_chamber -0. 29   0. 086  958  -3. 4  0. 0006
2762
2763
2764 Standardized Within-Group Residuals:
2765   Min     Q1     Med     Q3     Max

```

2766 -2.454 -0.735 -0.054 0.591 4.755

2767

2768 Number of Observations: 1008

2769 Number of Groups:

2770 Lab block %in% Lab

2771 14 28

2772

2773 **Model for shoot C% (C.)**

2774 **anova(m8)**

	numDF	denDF	F-value	p-value
(Intercept)	1	958	27558.9	<.0001
mixture	1	958	197.3	<.0001
het	5	958	0.0	0.9998
setup	1	12	5.0	0.0456
mixture: het	5	958	2.3	0.0425
mixture: setup	1	958	11.6	0.0007
het: setup	5	958	2.0	0.0699
mixture: het: setup	5	958	0.6	0.6643

2784

2785 **summary(m8)**

2786 Linear mixed-effects model fit by REML

2787 Data: reproz

2788 AIC BIC LogLik
2789 2769 3033 -1331

2790

2791 Random effects:

2792 Formula: ~1 | Lab
2793 (Intercept)
2794 StdDev: 0.95

2795

2796 Formula: ~1 | block %in% Lab
2797 (Intercept) Residual
2798 StdDev: 0.25 0.71

2799

2800 Variance function:

2801 Structure: Different standard deviations per stratum

2802 Formula: ~1 | Lab * mixture

2803

2804 Parameter estimates:

L1*B	L1*BM	L2*B	L2*BM	L3*B	L3*BM	L4*B	L4*BM	L5*B	L5*BM	L6*B
1.000	0.962	0.774	1.394	1.408	1.259	1.187	0.931	1.053	0.641	2.364
L6*BM	L7*B	L7*BM	L8*B	L8*BM	L9*B	L9*BM	L10*B	L10*BM	L11*B	L11*BM
2.177	0.425	0.646	1.053	0.886	0.815	0.522	1.235	1.895	1.089	1.513
L12*B	L12*BM	L13*B	L13*BM	L14*B	L14*BM					
1.459	1.725	7.686	4.144	0.935	1.022					

2811

2812 Fixed effects: C. ~ mixture * het * setup

2813

	Value	Std. Error	DF	t-value	p-value
(Intercept)	42.77	0.4212	958	101.56	0.0000
mixtureBM	-0.36	0.2041	958	-1.77	0.0770
hetENVw	-0.17	0.1848	958	-0.92	0.3579
hetENVb	0.13	0.1848	958	0.69	0.4879
hetGENw	0.32	0.1848	958	1.75	0.0801
hetGENb	0.14	0.1848	958	0.78	0.4344
hetENVw+GENw	0.21	0.1848	958	1.14	0.2548
setupgrowth_chamber	1.36	0.5499	12	2.46	0.0298
mixtureBM: hetENVw	0.21	0.2865	958	0.73	0.4631
mixtureBM: hetENVb	0.07	0.2865	958	0.25	0.8025
mixtureBM: hetGENw	-0.08	0.2865	958	-0.30	0.7672
mixtureBM: hetGENb	-0.09	0.2865	958	-0.32	0.7465

```

2826 mi xtureBM: hetENVw+GENw           -0. 21   0. 2865 958   -0. 74   0. 4585
2827 mi xtureBM: setupgrowth_chamber  -0. 10   0. 2373 958   -0. 41   0. 6810
2828 hetENVw: setupgrowth_chamber      0. 37    0. 2213 958   1. 66    0. 0982
2829 hetENVb: setupgrowth_chamber      -0. 10   0. 2213 958   -0. 46   0. 6441
2830 hetGENw: setupgrowth_chamber      -0. 18   0. 2213 958   -0. 83   0. 4040
2831 hetGENb: setupgrowth_chamber      -0. 09   0. 2213 958   -0. 39   0. 6955
2832 hetENVw+GENw: setupgrowth_chamber -0. 05   0. 2213 958   -0. 23   0. 8152
2833 mi xtureBM: hetENVw: setupgrowth_chamber -0. 53   0. 3327 958   -1. 60   0. 1097
2834 mi xtureBM: hetENVb: setupgrowth_chamber -0. 22   0. 3327 958   -0. 66   0. 5066
2835 mi xtureBM: hetGENw: setupgrowth_chamber -0. 38   0. 3327 958   -1. 15   0. 2490
2836 mi xtureBM: hetGENb: setupgrowth_chamber -0. 12   0. 3327 958   -0. 36   0. 7168
2837 mi xtureBM: hetENVw+GENw: setupgrowth_chamber -0. 22   0. 3327 958   -0. 65   0. 5159
2838
2839 Standardized Within-Group Residuals:
2840 Min Q1 Med Q3 Max
2841 -3. 106 -0. 653 0. 024 0. 696 2. 988
2842
2843 Number of Observations: 1008
2844 Number of Groups:
2845     Lab block %in% Lab
2846     14          28
2847

```

2848 Model for shoot delta ^{15}N (deltaN)

```

2849 anova(m9)
2850
2851             numDF denDF F-value p-value
2852 (Intercept)       1    913 49. 368 <. 0001
2853 mi xture         1    913 56. 153 <. 0001
2854 het               5    913 8. 067 <. 0001
2855 setup             1    12  0. 316 0. 5843
2856 mi xture: het     5    913 6. 384 <. 0001
2857 mi xture: setup   1    913 4. 615 0. 0320
2858 het: setup        5    913 6. 760 <. 0001
2859 mi xture: het: setup 5    913 1. 565 0. 1674
2859

```

```

2860 summary(m9)
2861 Linear mixed-effects model fit by REML
2862 Data: repro
2863     AIC   BIC LogLik
2864 2304 2566 -1098
2865
2866 Random effects:
2867 Formula: ~1 | Lab
2868     (Intercept)
2869 StdDev: 1. 8
2870
2871 Formula: ~1 | block %in% Lab
2872     (Intercept) Residual
2873 StdDev: 0. 83   0. 51
2874
2875 Variance function:
2876 Structure: Different standard deviations per stratum
2877 Formula: ~1 | Lab * mixture
2878
2879 Parameter estimates:
2880 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
2881 1. 00   1. 10   0. 81   0. 89   5. 63   6. 21   1. 12   1. 11   0. 75   0. 79   1. 02
2882 L6*BM   L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM   L10*B  L10*BM  L11*B  L11*BM
2883 0. 94   1. 23   1. 85   1. 11   1. 56   1. 08   1. 47   0. 91   0. 95   2. 09   1. 06
2884 L12*B  L12*BM  L13*B  L13*BM  L14*B  L14*BM

```

```

2885 2.04 0.80 2.52 1.41 3.01 1.62
2886
2887 Fixed effects: deltan ~ mixture * het * setup
2888                                         Value Std. Error DF t-value p-value
2889 (Intercept)                   3.9   0.79 913  4.9 0.0000
2890 mixtureBM                  -0.1   0.16 913 -0.9 0.3798
2891 hetENVw                      0.1   0.18 913  0.6 0.5518
2892 hetENVb                      0.1   0.17 913  0.3 0.7707
2893 hetGENw                      0.3   0.17 913  1.7 0.0875
2894 hetGENb                      -0.1   0.17 913 -0.8 0.4252
2895 hetENVw+GENw                 0.4   0.17 913  2.3 0.0226
2896 setupgrowth_chamber        -0.7   1.04 12  -0.7 0.5045
2897 mixtureBM: hetENVw          -0.2   0.22 913 -1.1 0.2512
2898 mixtureBM: hetENVb          0.0   0.22 913  0.0 0.9850
2899 mixtureBM: hetGENw          0.1   0.22 913  0.3 0.7642
2900 mixtureBM: hetGENb          0.4   0.22 913  1.8 0.0670
2901 mixtureBM: hetENVw+GENw     -0.4   0.22 913 -1.9 0.0533
2902 mixtureBM: setupgrowth_chamber 0.0   0.19 913 -0.1 0.9372
2903 hetENVw: setupgrowth_chamber 0.6   0.21 913  2.8 0.0054
2904 hetENVb: setupgrowth_chamber 0.3   0.20 913  1.7 0.0935
2905 hetGENw: setupgrowth_chamber -0.2   0.21 913 -0.8 0.4319
2906 hetGENb: setupgrowth_chamber 0.4   0.20 913  1.8 0.0744
2907 hetENVw+GENw: setupgrowth_chamber 0.3   0.21 913  1.5 0.1416
2908 mixtureBM: hetENVw: setupgrowth_chamber -0.2   0.27 913 -0.6 0.5798
2909 mixtureBM: hetENVb: setupgrowth_chamber -0.2   0.27 913 -0.8 0.4190
2910 mixtureBM: hetGENw: setupgrowth_chamber 0.0   0.27 913 -0.2 0.8575
2911 mixtureBM: hetGENb: setupgrowth_chamber -0.6   0.27 913 -2.3 0.0246
2912 mixtureBM: hetENVw+GENw: setupgrowth_chamber 0.0   0.27 913  0.2 0.8703
2913
2914 Standardized Within-Group Residuals:
2915      Min       Q1       Med       Q3      Max
2916 -2.90862 -0.68204  0.00092  0.63948  3.52505
2917
2918 Number of Observations: 963
2919 Number of Groups:
2920           Lab block %in% Lab
2921             14            28
2922

```

2923 Model for shoot delta ^{13}C (deltaC)

```

2924 anova(m10)
2925                                         numDF denDF F-value p-value
2926 (Intercept)                   1    923 8224.3 <.0001
2927 mixture                     1    923  22.2 <.0001
2928 het                          5    923  77.5 <.0001
2929 setup                        1    12   0.6  0.4710
2930 mixture:het                  5    923  6.5 <.0001
2931 mixture:setup                1    923  17.0 <.0001
2932 het:setup                    5    923  9.9 <.0001
2933 mixture:het:setup            5    923  1.0  0.4279
2934
2935 summary(m10)
2936 Linear mixed-effects model fit by REML
2937 Data: repro
2938   AIC   BIC LogLik
2939 1328 1590 -610
2940
2941 Random effects:
2942   Formula: ~1 | Lab
2943   (Intercept)
2944 StdDev:      1.31

```

```

2945
2946 Formula: ~1 | block %in% lab
2947     (Intercept) Residual
2948 StdDev:      0.224    0.295
2949
2950 Variance function:
2951 Structure: Different standard deviations per stratum
2952 Formula: ~1 | lab * mixture
2953 Parameter estimates:
2954 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
2955 1.000  1.633  1.005  1.092  0.952  0.915  1.639  1.721  1.260  0.998  1.399
2956 L6*BM   L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM   L10*B  L10*BM  L11*B  L11*BM
2957 1.679  1.159  1.302  1.645  1.398  1.223  1.511  1.081  0.988  1.714  1.537
2958 L12*B  L12*BM  L13*B  L13*BM  L14*B  L14*BM
2959 1.747  1.678  2.280  2.968  2.279  1.368
2960
2961 Fixed effects: dataC ~ mixture * het * setup
2962                                         Value Std. Error DF t-value p-value
2963 e
2964 (Intercept)                   -32.07    0.542 923  -59.12  0.0000
2965 mixtureBM                    0.31     0.108 923   2.85  0.0045
2966 hetENVw                      -0.08    0.109 923   -0.77  0.4409
2967 hetENVb                      -0.11    0.110 923   -0.96  0.3367
2968 hetGENw                      0.76     0.111 923   6.76  0.0000
2969 hetGENb                      0.58     0.112 923   5.20  0.0000
2970 hetENVw+GENw                 1.01     0.111 923   9.03  0.0000
2971 setupgrowth_chamber          -0.33    0.716 12   -0.47  0.6493
2972 mixtureBM: hetENVw           0.19     0.152 923   1.23  0.2201
2973 mixtureBM: hetENVb           0.18     0.153 923   1.16  0.2480
2974 mixtureBM: hetGENw           -0.18    0.155 923   -1.17  0.2409
2975 mixtureBM: hetGENb           -0.29    0.154 923   -1.87  0.0619
2976 mixtureBM: hetENVw+GENw     -0.15    0.155 923   -0.99  0.3223
2977 mixtureBM: setupgrowth_chamber -0.07   0.130 923   -0.51  0.6115
2978 hetENVw: setupgrowth_chamber 0.10     0.130 923   0.75  0.4554
2979 hetENVb: setupgrowth_chamber 0.16     0.131 923   1.23  0.2179
2980 hetGENw: setupgrowth_chamber -0.15    0.133 923   -1.10  0.2704
2981 hetGENb: setupgrowth_chamber -0.19    0.132 923   -1.47  0.1421
2982 hetENVw+GENw: setupgrowth_chamber -0.44   0.132 923   -3.34  0.0009
2983 mixtureBM: hetENVw: setupgrowth_chamber -0.24   0.183 923   -1.29  0.1960
2984 mixtureBM: hetENVb: setupgrowth_chamber -0.33   0.185 923   -1.79  0.0744
2985 mixtureBM: hetGENw: setupgrowth_chamber -0.19   0.186 923   -1.02  0.3062
2986 mixtureBM: hetGENb: setupgrowth_chamber -0.01   0.185 923   -0.06  0.9547
2987 mixtureBM: hetENVw+GENw: setupgrowth_chamber -0.18   0.186 923   -0.96  0.3396
2988
2989 Standardized Within-Group Residuals:
2990      Min      Q1      Med      Q3      Max
2991 -3.0753 -0.6545  0.0148  0.6620  3.0739
2992
2993 Number of Observations: 973
2994 Number of Groups:
2995     lab block %in% lab
2996      14          28
2997
2998 Model for evapotranspiration (finalET)

```

```

2999 anova(m11)
3000                                         numDF denDF F-value p-value
3001 (Intercept)                   1     952 106.13 <.0001
3002 mixture                     1     952 650.80 <.0001
3003 het                          5     952  1.20  0.3049
3004 setup                        1     12   0.09  0.7744
3005 mixture:het                  5     952  0.50  0.7771
3006 mixture:setup                1     952 281.93 <.0001

```

```

3007 het: setup      5   952    12.44 <.0001
3008 mixture:het: setup     5   952     4.31 0.0007
3009
3010 summary(m11)
3011 Linear mixed-effects model fit by REML
3012 Data: repro
3013   AIC   BIC LogLik
3014 9374 9638 -4633
3015
3016 Random effects:
3017 Formula: ~1 | lab
3018           (Intercept)
3019 StdDev:      51
3020
3021 Formula: ~1 | block %in% lab
3022           (Intercept) Residual
3023 StdDev:      17.6    7.94
3024
3025 Variance function:
3026 Structure: Different standard deviations per stratum
3027 Formula: ~1 | lab * mixture
3028 Parameter estimates:
3029 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
3030 1.000  2.152  0.635  1.392  3.086  14.650  1.281  9.628  2.923  2.238  1.267
3031 L6*BM  L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM  L10*B  L10*BM  L11*B  L11*BM
3032 2.882  3.643  3.443  2.394  2.855  1.271  4.684  9.252  8.621  7.314  5.047
3033 6.550  6.628  0.784  0.873  2.068  22.086
3034 L12*B  L12*BM  L13*B  L13*BM  L14*B  L14*BM
3035
3036 Fixed effects: final ET ~ mixture * het * setup
3037 (Intercept)          Value   Std. Error   DF t-value p-value
3038                               144.91  21.519  952  6.734  0.0000
3039 mixtureBM              15.43   2.798  952  5.514  0.0000
3040 hetENVw                 -0.71   2.053  952 -0.344  0.7311
3041 hetENVb                 -2.96   2.053  952 -1.444  0.1491
3042 hetGENw                  2.02   2.053  952  0.986  0.3245
3043 hetGENb                 -0.68   2.053  952 -0.332  0.7401
3044 hetENVw+GENw             2.42   2.053  952  1.177  0.2393
3045 setupgrowth_chamber     -16.89  28.507  12 -0.592  0.5645
3046 mixtureBM:hetENVw       -6.63   3.906  952 -1.696  0.0901
3047 mixtureBM:hetENVb       3.76   3.906  952  0.962  0.3364
3048 mixtureBM:hetGENw       -2.81   3.909  952 -0.719  0.4725
3049 mixtureBM:hetGENb       4.27   3.906  952  1.094  0.2742
3050 mixtureBM:hetENVw+GENw -2.90   3.906  952 -0.741  0.4586
3051 mixtureBM:setupgrowth_chamber 30.32  5.029  952  6.030  0.0000
3052 hetENVw:setupgrowth_chamber 3.20   3.453  952  0.926  0.3546
3053 hetENVb:setupgrowth_chamber 6.28   3.453  952  1.820  0.0691
3054 hetGENw:setupgrowth_chamber -13.40  3.453  952 -3.879  0.0001
3055 hetGENb:setupgrowth_chamber -5.39   3.456  952 -1.559  0.1193
3056 hetENVw+GENw:setupgrowth_chamber -9.29  3.453  952 -2.690  0.0073
3057 mixtureBM:hetENVw:setupgrowth_chamber 20.90  7.020  952  2.977  0.0030
3058 mixtureBM:hetENVb:setupgrowth_chamber -1.16   7.002  952 -0.166  0.8680
3059 mixtureBM:hetGENw:setupgrowth_chamber 10.70   7.003  952  1.528  0.1267
3060 mixtureBM:hetGENb:setupgrowth_chamber -4.70   7.020  952 -0.670  0.5032
3061 mixtureBM:hetENVw+GENw:setupgrowth_chamber 15.56  7.026  952  2.215  0.0270
3062
3063 Standardized Within-Group Residuals:
3064   Min      Q1      Med      Q3      Max
3065 -2.7957 -0.6881  0.0316  0.8653  2.9818
3066
3067 Number of Observations: 1002
3068 Number of Groups:
3069   Lab block %in% lab

```

3070 14
3071

28

3072 **Model for teabag litter decomposition (teabag)**

3073 **anova(m12)**

	numDF	denDF	F-val ue	p-val ue
(Intercept)	1	924	388.72	<.0001
mi xture	1	924	3.63	0.0570
het	5	924	0.79	0.5601
setup	1	12	0.03	0.8578
mi xture: het	5	924	2.08	0.0662
mi xture: setup	1	924	1.04	0.3092
het: setup	5	924	1.38	0.2279
mi xture: het: setup	5	924	1.24	0.2863

3074

3075

3076

3077

3078

3079

3080

3081

3082

3083

3084 **summary(m12)**

3085 Linear mixed-effects model fit by REML

3086 Data: repro

AIC	BIC	LogLik
-1547	-1285	828

3087

3088

3089

3090 Random effects:

3091 Formula: ~1 | lab

(Intercept)
StdDev: 0.112

3092

3093

3094

3095 Formula: ~1 | block %in% lab

(Intercept)	Residual
StdDev: 0.017	0.0775

3096

3097

3098

3099 Variance function:

3100 Structure: Different standard deviations per stratum

3101 Formula: ~1 | lab * mixture

3102 Parameter estimates:

L1*B	L1*BM	L2*B	L2*BM	L3*B	L3*BM	L4*B	L4*BM	L5*B	L5*BM	L6*B
1.000	1.074	1.439	1.400	1.434	1.414	1.124	1.203	1.300	1.011	1.172
L6*BM	L7*B	L7*BM	L8*B	L8*BM	L9*B	L9*BM	L10*B	L10*BM	L11*B	L11*BM
0.882	3.364	2.152	1.440	1.292	1.635	1.796	1.290	1.323	1.011	0.949
L12*B	L12*BM	L13*B	L13*BM	L14*B	L14*BM					
1.189	1.429	0.519	0.538	0.797	0.959					

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3111 Fixed effects: teabag ~ mi xture * het * setup

	Value	Std. Error	DF	t-value	p-value
(Intercept)	0.585	0.047	924	12.32	0.000
mi xtureBM	0.001	0.016	924	0.07	0.942
hetENVw	0.013	0.015	924	0.83	0.407
hetENVb	0.018	0.016	924	1.17	0.244
hetGENw	-0.019	0.016	924	-1.21	0.226
hetGENb	0.015	0.016	924	0.94	0.349
hetENVw+GENw	-0.002	0.016	924	-0.12	0.901
setupgrowth_chamber	0.016	0.064	12	0.25	0.804
mi xtureBM: hetENVw	0.021	0.023	924	0.92	0.355
mi xtureBM: hetENVb	-0.032	0.023	924	-1.38	0.168
mi xtureBM: hetGENw	0.026	0.023	924	1.15	0.251
mi xtureBM: hetGENb	-0.015	0.023	924	-0.67	0.502
mi xtureBM: hetENVw+GENw	0.027	0.023	924	1.16	0.244
mi xtureBM: setupgrowth_chamber	0.021	0.026	924	0.80	0.422
hetENVw: setupgrowth_chamber	-0.021	0.026	924	-0.77	0.441
hetENVb: setupgrowth_chamber	-0.030	0.027	924	-1.13	0.258
hetGENw: setupgrowth_chamber	-0.001	0.027	924	-0.02	0.984

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```

3130 hetGENb: setupgrowth_chamber -0. 011 0. 026 924 -0. 41 0. 685
3131 hetENVw+GENw: setupgrowth_chamber -0. 003 0. 027 924 -0. 11 0. 910
3132 mi xtureBM: hetENVw: setupgrowth_chamber -0. 027 0. 037 924 -0. 73 0. 464
3133 mi xtureBM: hetENVb: setupgrowth_chamber 0. 026 0. 037 924 0. 70 0. 487
3134 mi xtureBM: hetGENw: setupgrowth_chamber 0. 003 0. 037 924 0. 08 0. 935
3135 mi xtureBM: hetGENb: setupgrowth_chamber -0. 004 0. 037 924 -0. 10 0. 919
3136 mi xtureBM: hetENVw+GENw: setupgrowth_chamber -0. 059 0. 037 924 -1. 58 0. 114
3137
3138 Standardized Within-Group Residuals:
3139      Min      Q1      Med      Q3      Max
3140 -2. 3845 -0. 7307 -0. 0867  0. 6559  3. 6548
3141
3142 Number of Observations: 974
3143 Number of Groups:
3144      Lab block %in% Lab
3145        14             28
3146

```

3147 Model for PC1 (PC1)

```

3148 anova(mpc1)
3149
3150 (Intercept) numDF denDF F-value p-value
3151 mi xture      1     958    0.74  0.3904
3152 het            5     958   1002.71 <.0001
3153 setup          1     12     0.00  0.9456
3154 mi xture: het  5     958    2.84  0.0150
3155 mi xture: setup 1     958    2.31  0.1285
3156 het: setup     5     958   15.65 <.0001
3157 mi xture: het: setup 5     958   10.03 <.0001
3158 summary(mpc1)
3159 Linear mixed-effects model fit by REML
3160 Data: reprod
3161   AIC   BIC LogLik
3162 2440 2704 -1166
3163
3164 Random effects:
3165 Formula: ~1 | Lab
3166   (Intercept)
3167 StdDev: 1.22
3168
3169 Formula: ~1 | block %in% Lab
3170   (Intercept) Residual
3171 StdDev: 0.404 0.273
3172
3173 Variance function:
3174 Structure: Different standard deviations per stratum
3175 Formula: ~1 | Lab * mi xture
3176 Parameter estimates:
3177 L1*B  L1*BM  L2*B  L2*BM  L3*B  L3*BM  L4*B  L4*BM  L5*B  L5*BM  L6*B
3178 1.000  2.080  4.275  0.625  2.832  2.355  2.812  2.075  2.121  1.191  5.095
3179 L6*BM  L7*B  L7*BM  L8*B  L8*BM  L9*B  L9*BM  L10*B L10*BM  L11*B L11*BM
3180 2.909  1.649  7.677  2.450  2.589  0.908  3.260  3.604  2.383  2.286  2.172
3181 L12*B  L12*BM L13*B  L13*BM L14*B  L14*BM
3182 2.583  2.442  2.757  6.640  2.124  19.900
3183
3184 Fixed effects: PC1 ~ mi xture * het * setup
3185
3186      Value Std. Error DF t-value p-value
3187 (Intercept) -1.189  0.527 958 -2.25  0.0244
3188 mi xtureBM   1.740  0.146 958 11.94  0.0000
3189 hetENVw    -0.607  0.169 958 -3.60  0.0003

```

```

3190 hetENVb -0.330 0.169 958 -1.95 0.0509
3191 hetGENw 0.967 0.169 958 5.73 0.0000
3192 hetGENb 0.591 0.169 958 3.51 0.0005
3193 hetENVw+GENw 0.755 0.169 958 4.48 0.0000
3194 setupgrowth_chamber 0.096 0.693 12 0.14 0.8922
3195 mixtureBM: hetENVw 0.577 0.190 958 3.03 0.0025
3196 mixtureBM: hetENVb 0.240 0.190 958 1.26 0.2072
3197 mixtureBM: hetGENw -0.961 0.190 958 -5.05 0.0000
3198 mixtureBM: hetGENb -0.612 0.190 958 -3.21 0.0014
3199 mixtureBM: hetENVw+GENw -0.585 0.190 958 -3.07 0.0022
3200 mixtureBM: setupgrowth_chamber -0.348 0.184 958 -1.90 0.0579
3201 hetENVw: setupgrowth_chamber 0.868 0.190 958 4.56 0.0000
3202 hetENVb: setupgrowth_chamber 0.478 0.190 958 2.51 0.0122
3203 hetGENw: setupgrowth_chamber -0.859 0.190 958 -4.51 0.0000
3204 hetGENb: setupgrowth_chamber -0.522 0.190 958 -2.74 0.0062
3205 hetENVw+GENw: setupgrowth_chamber -0.419 0.190 958 -2.20 0.0280
3206 mixtureBM: hetENVw: setupgrowth_chamber -0.440 0.243 958 -1.81 0.0703
3207 mixtureBM: hetENVb: setupgrowth_chamber -0.348 0.243 958 -1.43 0.1518
3208 mixtureBM: hetGENw: setupgrowth_chamber 0.880 0.243 958 3.63 0.0003
3209 mixtureBM: hetGENb: setupgrowth_chamber 0.597 0.243 958 2.46 0.0142
3210 mixtureBM: hetENVw+GENw: setupgrowth_chamber 0.529 0.243 958 2.18 0.0294
3211
3212
3213 Standardized Within-Group Residuals:
3214   Min Q1 Median Q3 Max
3215 -3.1176 -0.6583 0.0607 0.7984 3.1556
3216
3217 Number of Observations: 1008
3218 Number of Groups:
3219   Lab Block %in% Lab
3220     14          28
3221

```

3222 Model for PC2 (PC2)

```

3223 anova(mpc2)
3224
3225   numDF denDF F-value p-value
3226 (Intercept) 1 958 0.03 0.8607
3227 mixture 1 958 588.49 <.0001
3228 het 5 958 28.11 <.0001
3229 setup 1 12 12.27 0.0044
3230 mixture: het 5 958 10.12 <.0001
3231 mixture: setup 1 958 6.59 0.0104
3232 het: setup 5 958 1.42 0.2141
3233 mixture: het: setup 5 958 1.42 0.2161
3234 summary(mpc2)
3235 Linear mixed-effects model fit by REML
3236 Data: reproz
3237   AIC BIC LogLik
3238 2029 2293 -960
3239 Random effects:
3240 Formula: ~1 | Lab
3241   (Intercept)
3242 StdDev: 0.816
3243
3244 Formula: ~1 | Block %in% Lab
3245   (Intercept) Residual
3246 StdDev: 0.187 0.324
3247
3248 Variance function:
3249 Structure: Different standard deviations per stratum

```

```

3250 Formula: ~1 | lab * mixture
3251 Parameter estimates:
3252 L1*B   L1*BM   L2*B   L2*BM   L3*B   L3*BM   L4*B   L4*BM   L5*B   L5*BM   L6*B
3253 1. 000  0. 994  1. 800  1. 697  1. 504  1. 574  1. 450  1. 023  1. 456  1. 125  4. 277
3254 L6*BM   L7*B   L7*BM   L8*B   L8*BM   L9*B   L9*BM   L10*B  L10*BM  L11*B  L11*BM
3255 2. 543  1. 633  5. 074  1. 580  1. 642  1. 149  1. 295  2. 701  3. 178  2. 325  1. 012
3256 L12*B  L12*BM  L13*B  L13*BM  L14*B  L14*BM
3257 1. 927  1. 446  3. 265  3. 265  1. 657  2. 717
3258
3259 Fixed effects: PC2 ~ mixture * het * setup
3260                                         Value Std. Error DF t-value p-value
3261 e
3262 (Intercept)                      1. 897  0. 353  958  5. 38  0. 0000
3263 mixtureBM                         -1. 443  0. 128  958 -11. 23  0. 0000
3264 hetENVw                           -0. 414  0. 144  958 -2. 89  0. 0040
3265 hetENVb                           -0. 272  0. 144  958 -1. 89  0. 0585
3266 hetGENw                           -0. 789  0. 144  958 -5. 50  0. 0000
3267 hetGENb                           -0. 573  0. 144  958 -3. 99  0. 0001
3268 hetENVw+GENw                     -0. 825  0. 144  958 -5. 75  0. 0000
3269 setupgrowth_chamber              -1. 843  0. 463  12  -3. 98  0. 0018
3270 mixtureBM: hetENVw               0. 531  0. 180  958  2. 96  0. 0032
3271 mixtureBM: hetENVb               0. 393  0. 180  958  2. 19  0. 0291
3272 mixtureBM: hetGENw               0. 748  0. 180  958  4. 16  0. 0000
3273 mixtureBM: hetGENb               0. 596  0. 180  958  3. 32  0. 0009
3274 mixtureBM: hetENVw+GENw        0. 856  0. 180  958  4. 76  0. 0000
3275 mixtureBM: setupgrowth_chamber 0. 529  0. 163  958  3. 25  0. 0012
3276 hetENVw: setupgrowth_chamber   0. 417  0. 174  958  2. 40  0. 0165
3277 hetENVb: setupgrowth_chamber   0. 320  0. 174  958  1. 84  0. 0662
3278 hetGENw: setupgrowth_chamber   0. 088  0. 174  958  0. 51  0. 6114
3279 hetGENb: setupgrowth_chamber   0. 097  0. 174  958  0. 56  0. 5757
3280 hetENVw+GENw: setupgrowth_chamber 0. 146  0. 174  958  0. 84  0. 4021
3281 mixtureBM: hetENVw: setupgrowth_chamber -0. 558  0. 228  958 -2. 45  0. 0146
3282 mixtureBM: hetENVb: setupgrowth_chamber -0. 424  0. 228  958 -1. 86  0. 0632
3283 mixtureBM: hetGENw: setupgrowth_chamber -0. 312  0. 228  958 -1. 37  0. 1722
3284 mixtureBM: hetGENb: setupgrowth_chamber -0. 357  0. 228  958 -1. 57  0. 1176
3285 mixtureBM: hetENVw+GENw: setupgrowth_chamber -0. 456  0. 228  958 -2. 00  0. 0458
3286
3287 Standardized Within-Group Residuals:
3288      Min       Q1       Med       Q3      Max
3289 -3. 96848 -0. 67233 -0. 00268  0. 67480  3. 44045
3290
3291 Number of Observations: 1008
3292 Number of Groups:
3293     Lab block %in% Lab
3294          14           28
3295
3296
3297
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3299
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3301
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