4.3.1.1.1 Cuttings Experiment 1A

Of the 295 cuttings planted in September 2013, only two-thirds survived five months later, following an overwatering regime that took place in December 2013. Both treatments (intact liverworts, resynthesized with fungus, and fungus isolates) were shown to strongly impact survival of the *Erica* plants, compared to the control (Fig. 21).

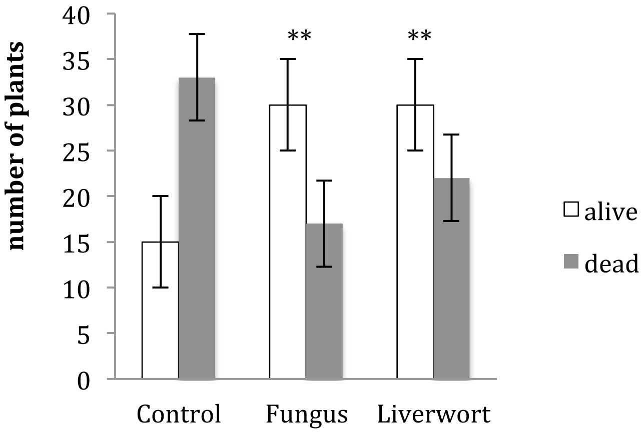

Fig. 21 - Experiment 1A *Erica* survival at 20 wk, following 21 d stress. Treatments shown on horizontal axis: 'Control', no treatment; 'Fungus', isolate of axenically-grown *Pezoloma ericae*; and, 'Liverwort' (bearing ericoid inoculum). Fungal isolate treatment (n = 30:17) compared with the control (n = 15:33), alive:dead respectively, *P*-value < 0.01); liverwort treatment, (n = 30:22) compared with the control, *P*-value < 0.01 using proportion data with a two-sample test for equality of proportions (with continuity correction); error bars ±1 S.E.M.

Calluna was less sensitive to experimental inundation and there was not a statistically significant difference in survivorship.

4.3.1.1.2 Cuttings Experiment 1B

Root establishment was examined several weeks before survival data were collected; this was not examined in Experiment 1A. The results were significant when comparing treatment and control groups for both *Erica* (*P*-value < 0.005) and *Calluna* (*P*-value < 0.02), using proportion data analyses. Proportion data for survival categories also yielded statistically significant results for both taxa after three months. *Erica* was significantly more sensitive to treatment than *Calluna*, although both taxa benefitted (Fig. 22).

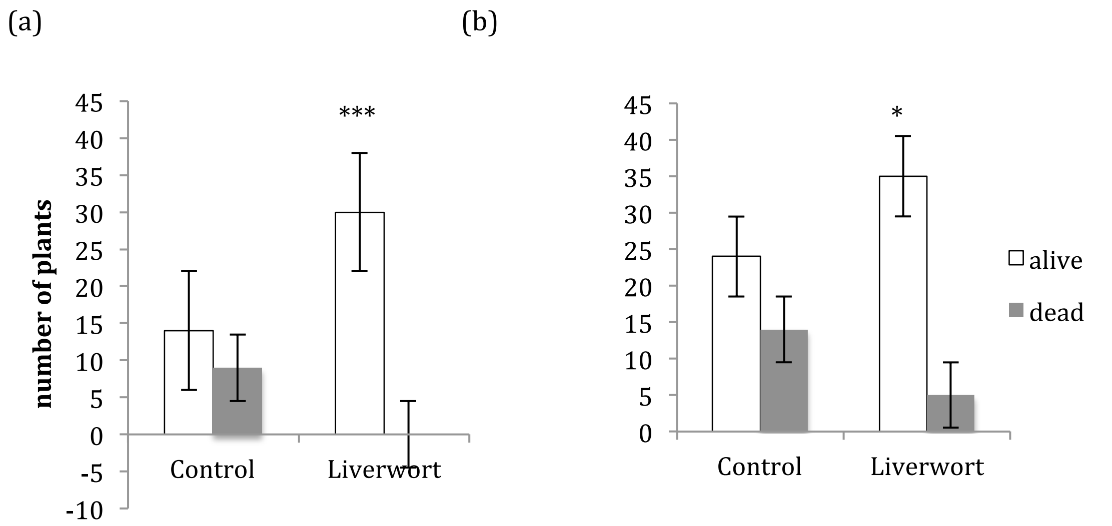

Fig. 22 - Experiment 1B survival at 12 wk. (a) *Erica tetralix*, *P*-value < 0.001; (b) *Calluna, P*-value < 0.05, calculated using binomial proportion data with a two-sample test for equality of proportions (with continuity correction) and Chi-square tests; error bars ±1 S.E.M.

4.3.1.1.3 Experiment 1C

Proportion data for survival yielded statistically significant results for *Calluna* but not *Erica tetralix* after 14 weeks of treatment (Fig. 23). About 20 percent of the overall population of *Erica* died, both with and without treatment.

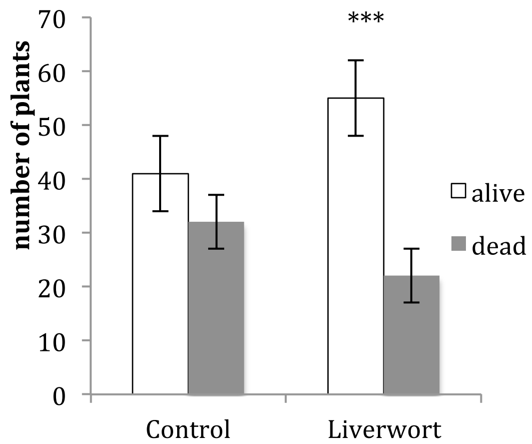

Fig. 23 - Survival of Experiment 1C plants at 14 wk. Treatments shown on horizontal axis: 'Control', no treatment; 'Liverwort' (bearing ericoid inoculum). *Calluna*, *P* – value < 0.001 calculated using binomial proportion data with a two-sample test for equality of proportions (with continuity correction) and Chi-square tests. Error bars ±1 S.E.M.

The survival rates for *Calluna* contrast with the results for Experiments 1A and 1B whereby *Erica*'s survival rate was significantly more sensitive to treatment than *Calluna*. However, within 12 weeks, the leafy liverworts appeared to overwhelm the base of most of the *Erica* cuttings (Fig. 24); this was not as prevalent in the *Calluna* cuttings tubes. As condensation levels appeared the same within the bags and maintenance regimes were otherwise the same, the cause for this difference was not detectable. Perhaps the multi-stem nature of the *Calluna* influenced the growth, or some other ecological factor.

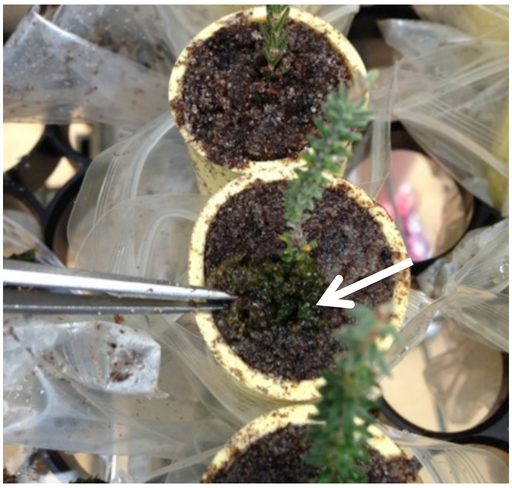

Fig. 24. Liverwort stems initially placed next to *Erica* cutting (L) and (R) growth after one year (liverworts shown with arrow).

4.3.1.1.4 Seedling germination

There was no statistically significant difference between the inoculated and control groups in terms of germination, however, *Erica* was more successful germinating (21% and 26%) than *Calluna* (15% and 18%), in Experiment 2 and 2A, respectively. In Experiment 2A, the overall germination rate was slightly higher than the first.

In Experiment 3, germination rates improved markedly for both taxa, and there was a reversal of the two previous seedling experiments whereby *Calluna* germinated more readily than *Erica* (Appendix 12) as a percentage of seeds sown.

4.3.1.2 Colonization of roots

4.3.1.2.1 Cuttings Experiments

In controlled nursery settings designed to simulate field conditions, the fungi originating from the liverwort rhizoids successfully colonized ericaceous plant roots, from both cuttings and seedlings.

Approximately five months after treatment, a subsample of hair roots was harvested (n = 10) from inoculated and non-treated control plants, and examined to determine if the heathers had been colonized by *Pezoloma ericae*. The samples of hair roots were selected from each group by randomizing their plant numbers. Nine of ten treated plants' roots showed considerable colonization of typical ErM and all of the controls remained uncolonized (Fig. 25).

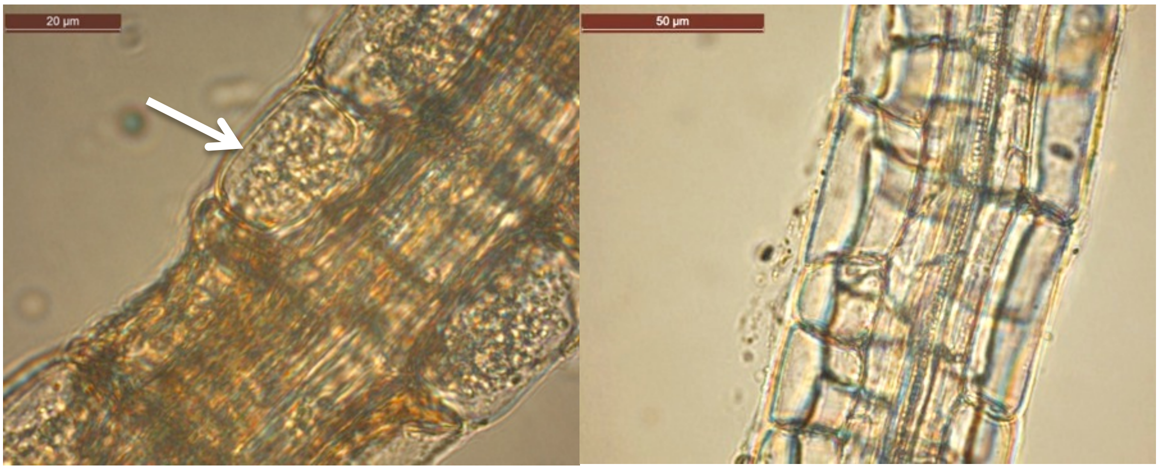

Fig. 25. Epidermal cells of hair root contrasting inoculated (L) and control (R) plants at 20 wk. Arrow points to ericoid mycorrhiza hyphal coils.

The hyphae colonized the epidermal cells, at times contiguously and otherwise skipping every other or every third. These results were repeated in arbitrary samples from Cuttings Experiments 1A, 1B and 1C (n = 5 in all) and Seedling Experiments 2, 2A and 3 (n = 3 in all).

4.3.1.3 Growth response measurements

For the nursery experiments, height was used as a proxy for biomass as the same plants were later planted for the field experiments and therefore could not be harvested for dry weights at this stage. However, comparisons between height and weight were measured using nursery trial plants and a strong correlation was found between height and dry weight, in both single and multi-stem *Erica tetralix* plants c. one-year old, *P*-value < 0.0001 and < 0.001, respectively (Appendix 9).

4.3.1.3.1 Cuttings Experiment 1A

The t-tests comparing the height of *Calluna* controls with inoculated plants show the controls were statistically significantly taller by 7% (*P*-value < 0.05, n=46 and 47) than T1 plants (intact liverworts), 16 weeks post-planting. However, by 32 weeks, there was no significant difference in height between the two. There was no statistical difference between the T2 plants (fungal isolate) and the control at 16 or 32 weeks. *Erica* plants' maximum heights were significantly taller but when including all branches for a total height measure, by 32 weeks this difference was nullified.

4.3.1.3.2 Cuttings Experiment 1B

By week 11, there was a strong statistically significant difference measured in new growth between treated and control plants for both *Erica* and *Calluna* (using proportion tests). As seen below (Fig. 26), by week 27, all of the biomass proxy measures yielded strong statistically significant results in both taxa, pointing to a treatment effect (Appendix 11, for Rstudio transcript).

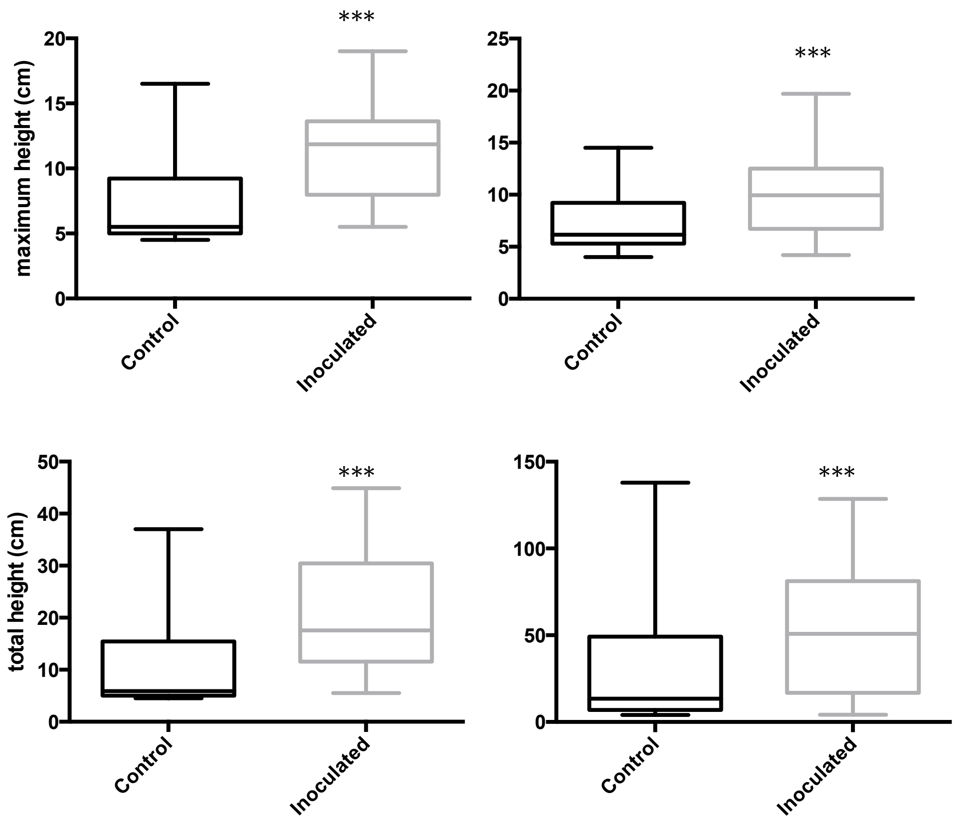

Fig. 26. Experiment 1B maximum and total heights at 27 wk. Treatments shown on horizontal axis: 'Control', no treatment; 'Inoculated', liverworts bearing ericoid inoculum. (upper left) *Erica tetralix*, *P*-value < 0.001 (n = 30, 34); (upper right) *Calluna* vulgaris, *P*–value < 0.01 (n = 38, 44). (lower left) *E. tetralix*, *P*-value < 0.0001 (n = 34, 30); (lower right) *C. vulgaris*, *P*–value < 0.0001 (n = 38, 44).

The analysis of both maximum and total height (maximum height plus the sum of all branch lengths), the most comprehensive gauge of aboveground biomass, yielded statistically significant results.

Branching is another indication of plant vigor. The t-tests comparing the number of branches yielded statistically significant results from both taxa when comparing the inoculated plants and controls; *Calluna* (*P*-value < 0.02) and *Erica* (*P*-value < 0.05)(Appendix 11).

4.3.1.3.3 Cuttings Experiment 1C

At 11 weeks maximum height in inoculated *Calluna* plants was statistically significantly shorter than the control plants (Fig. 27a). There was no significant difference in *Erica* maximum height. However, when looking at total height (which adds all the branches for a more accurate measure of aboveground growth), the *Erica* treatment group is significantly smaller than the control (Fig. 27b). Total height was not taken for *Calluna* as there were too many miniscule branches rendering a count impractical.

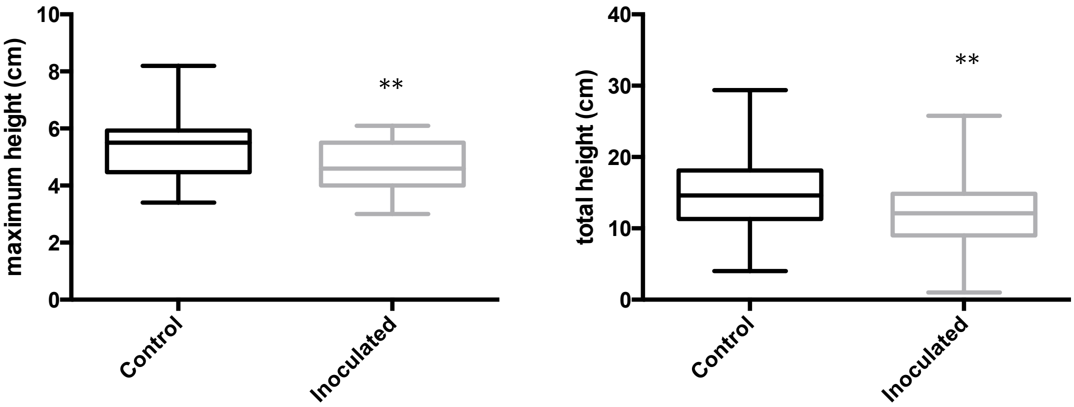

Fig. 27. Experiment 1C height measures at 11 wk. Treatments shown on horizontal axis: 'Control', no treatment; 'Inoculated', liverworts bearing ericoid inoculum. (a) *Calluna vulgaris*, P-value = 0.001 (n = 42, 54); (b) *Erica tetralix*, P-value < 0.05 (n = 47, 46) calculated using Mann-Whitney; means are shown as ±1 S.E.M.

4.3.1.3.4 Seedlings Experiment 2

There was a statistically significant difference in the mean heights of *Erica* control and inoculated plants at 11 wk (Fig. 28a), but t-tests yielded no significant difference between the *Calluna* plant groups (Fig. 28b), a non-parametric Wilcoxon-Rank test was performed.

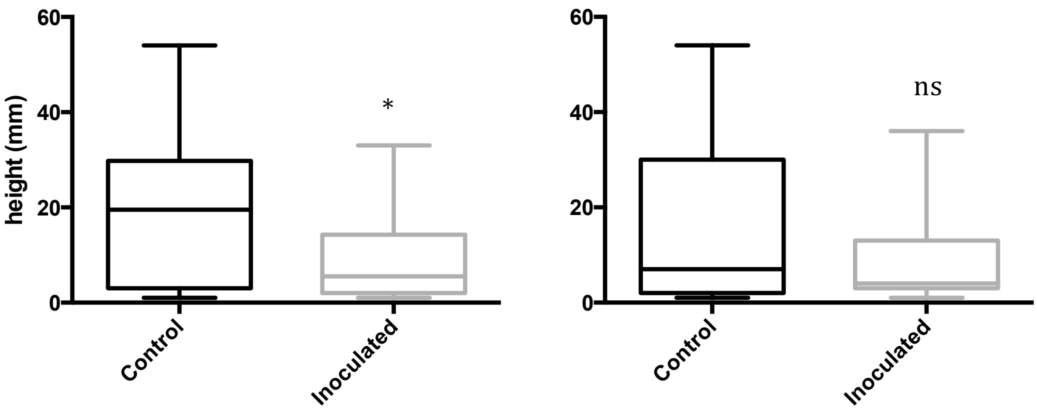

Fig. 28 - Seedlings height measurements at 11 wk. Treatments shown on horizontal axis: 'Control', no treatment; 'Inoculated', liverworts bearing ericoid inoculum. (L) *Erica tetralix*, *P*-value < 0.05 (n = 36, 34); (R) *Calluna*, *P*-value > 0.05 (n = 31, 15); means are shown as ±1 S.E.M.

4.3.1.3.5 Seedlings Experiment 2A

At 22 weeks the seedlings heights were measured. While there was no patent significance statistically, in either *Calluna* or *Erica*, as a function of inoculation, the *P*-value equaled 0.05 for *Erica* plants, suggesting there may be an early sign of impact occurring, certainly ecological. Height was not checked again in the nursery before going to the field.

Survival rate analyses as a function of treatment (before going to the field at one year) yielded nothing significant within taxa as a function of inoculation. However, *Erica* plants, regardless of treatment, were more resilient than *Calluna* (P-value < 0.05).

4.3.1.3.6 Seedlings Experiment 3

Using a t-test, there was no statistically significant difference in the heights or leaf counts when comparing all treatments against each other within a taxon.

4.4 Discussion

These nursery experiments provided considerable progress towards answering the second research question: Can leafy liverworts act as an inoculum delivery mechanism providing a mycorrhizal benefit to vascular plants, and if so, are there advantages or disadvantages to introducing these before seed germination or with cuttings (testing various stages of establishment). Other practical considerations e.g. application rate and mode (i.e. slurry of macerated liverworts or intact individuals) were assessed. The most significant results - that Ericaceae plant cuttings' establishment can be influenced by inoculation with liverworts (particularly under stress) – can now be put to further tests using other strains of *P. ericae* and Ericaceae plants. This knowledge may also be instructive for other liverwort vascular plant combinations (where there is a shared fungal symbiont) and larger scale experiments for either site restoration or difficult *ex situ* conservation projects in wet habitats where it is established that the mycorrhizal component is not present.

These nursery experiments provide unequivocal evidence that the ericoid mycorrhizal fungus (ErM) - emanating from leafy liverworts - is able to colonize Ericaceae plant roots when co-planted closely together. This is the first time an ErM inoculum (in this case *Pezoloma ericae*) has been delivered in controlled conditions to vascular plants in general, and Ericaceae in particular, through liverworts; thereby imitating a biological transfer which has probably been occurring for millions of years. This occurred with both treatment types – 1) isolated liverwort-derived ErM strains in culture; and, 2) via the intact leafy liverworts (resynthesized with the fungal isolate) – regardless of whether the plant originated as a seedling or cutting. Previously, this had been studied using Ericaceae root-derived ErM isolates only, either in autoclaved peat compost or *in vitro* (Stribley *et al.*, 1975, Vosatka *et al.*, 1999, Strandberg and Johansson, 1999, Jansa and Vosatka, 2000, Villarreal-Ruiz *et al.*, 2012, Kowal *et al.*, 2015).

Villarreal-Ruiz *et al.* (2012) introduced two *P. ericae* related strains to Ericaceae host plant seeds (*C. vulgaris, V. myrtillus*, *V. vitis-idaea* and *V. macrocarpon)*, *in vitro.* All four of their tested plants were successfully colonized by eight weeks. This compares to 11 weeks in the nursery seedling experiments undertaken for this project and considerably longer for the cuttings.

Benefit to the inoculated plants, particularly establishment success, was most pronounced when they were subjected to stress. In Experiment 1A, where overwatering was introduced for a three-week period, the *Erica tetralix* plants which were pretreated survived significantly more than the untreated plants. Interestingly, there was no notable response in *Calluna*, suggesting *E. tetralix* is more sensitive to the presence of ErM than *Calluna*. Perhaps *E. tetralix* is only successful with ErM in its more restricted wet habitat than *Calluna*, which has evolved to be more adaptable, hence its more widespread distribution in both dry and wet heathlands. Vosatka *et al.* (1999) tested drought stress on *Rhododendron* sp. with and without ErM fungi inoculation. While no significant differences in mortality were recorded, there were significant differences in mycelium growth responses under stress versus non-stress, although not as a result of inoculation; their assumption being that the enhanced mycorrhizal growth is facilitating water uptake (under drought conditions). Only one fungal isolate (of four tested ErM strains) caused a significant growth response i.e. number of leaves and leaf area.

Even without experimentally introduced stress, there were statistically significant results in survival rates when comparing inoculated and control groups in both taxa in Experiment 1B. Environmental stress was present nonetheless (temperatures had risen to 30°C for several consecutive days) prompting a move to a more controllable glasshouse. Once moved, again there were several days where temperatures were higher than recommended for nursery propagation, but more akin to real world fluctuations and stress levels.

Experiment 1C's survival results differed from the previous two cuttings experiments as here only *Calluna* was significantly responsive to treatment. The *Calluna* cuttings repeatedly developed a more branched root system, and faster, than *E. tetralix*. A possible cause is the already noted rapid liverwort growth in the *E. tetralix* tubes (Fig.

24) (perhaps a function of the application rate combined with *E. tetralix's* transpiration under glasshouse conditions). This would have introduced a barrier to *E. tetralix* establishment and therefore survival success. Further studies should alter the liverwort application density to test this possibility. Incidentally, approximately 20 % of the *E. tetralix* died, regardless of treatment status.

Looking at growth response variables, some of the experiments demonstrated ErM treatment induced greater growth while others showed growth was initially suppressed, but then stabilized. Perhaps the plant pays an initial 'cost' of colonization, as the fungus grows into its epidermal cells ie. the transfer of photosynthates to the fungus may be suppressing cellular metabalism? Once the mycorrhiza is functional, the plant prospers by accessing additional nutrients unavailable without the fungus. Villarreal-Ruiz *et al.* (2012) also noted an unknown strain of the *P. ericae* aggregate suppressed the growth of some Ericaceae plants (*C. vulgaris, V. myrtillus*, and *V. vitis-idaea*, but not *V. macrocarpon*), despite the presence of intracellular hyphal coils in epidermal cells of all of the host plants. Although these interactions all occurred *in vitro*, and the life span was arguably short (dry weights were taken at eight weeks), the study still serves as a positive reference and highlights the need to further study individual ErM strains. Similarly, Vosatka *et al.* (1999) found only three of twelve ErM-related strains of 'dark sterile mycelia' and *Oidiodendron* spp. facilitated healthier *Rhododendron* sp. and growth responses as a result of treatment, while some had a negative effect on growth. Jansa and Vosatka (2000) found ten percent of the 200 fungal strains tested resulted in positive growth in Ericales plants (transferred to peat-based compost after inoculation *in vitro*); none were found to suppress growth. In contrast, Strandberg and Johansson (1999), (Duclos and Fortin, 1983) found no biomass growth responses as a result of inoculation. There were however some notable findings with respect to nutrient transfers. This is discussed in Chapter 5. Duclos and Fortin (1983) tested 15 potential ErM symbionts and found no difference in growth between the fungus-free control plants and inoculated *Vaccinium* plants.

The study experiments where suppression of initial growth was measured as a result of treatment (*Calluna* in Experiments 1A and 1C and both taxa in Experiment 2A), were short lived in the nursery and therefore the possibility that treatment eventually enhanced growth could not be evaluated before relocating the plants to the field. However, as discussed in Chapter 5, harvested field measurements of Experiments 1A and 1C show significant differences in growth due to treatment diminished after one year. In Experiment 1A, which compared fungal isolate with the intact liverworts (as an

ErM inoculation device), only the liverwort treatment group was significantly different from the control group. It is unclear if this is due to suspension dilution rate of the fungal isolate or other methodological matters. Clarification of this point is not crucial as the study focused on the viability of the liverwort as a delivery mechanism, not a fungal isolate drench. Similarly Experiment 3 lacked any significant findings. It is unclear whether this is due to its short nursery life or methods. There was also a lack of any significant measureable difference in germination due to inoculation; it may have been expected to trigger an edaphic response creating a more conducive environment for germination. Nonetheless, notably, ErM inoculation caused a statistically significant boost in all growth measures undertaken in Experiment 1B, the largest cuttings experiment.

In terms of experimental design, the use of uncolonized axenically-grown liverworts were also considered as a control. However, the resynthesized liverworts used herein more closely mimic nature; over 90% of liverworts examined from wild collections were found to be colonized (section 2.2.3) with the uncolonized liverworts either young or at the top of the colony. To exploit this function, i.e. determine if there is a practical role in restoration, there were only two realistic possibilities in nature, either the liverworts are present (with their fungal symbiont) or they are not (the negative control). Introducing sterile liverworts as a positive control is not realistic in nature (nor is there any prior indication in the literature that they may be an influential independent variable), and was therefore deemed unnecessarily theoretical.

From a practical perspective, it may also be asked, would it not be easier to apply a sludge of the ErM fungal isolate to a pasteurized soil medium (and in a restorative setting, to the field), rather than using wild liverworts when restoring habitats? There are several reasons why the liverwort is preferable to a direct fungal slurry application. Liverworts have special physiological properties allowing them to dry out for significant time periods and rehydrate, making them the perfect instrument in habitats experiencing climatic extremes. Isolating fungi and maintaining live axenic cultures is costly, time-consuming and prone to contamination. It is also known that ErM roots are present close to the soil horizon surface (Leake *et al.*, 1990b, Read, 1996), where the liverworts are positioned. As such, using liverworts avoids a potential leaching effect, especially in sandy soils.

5 Chapter Five – Returning to nature: efficacy of inoculation in the nursery as measured in the field

5.1 Introduction

Leafy liverworts colonized by ericoid mycorrhizal fungus (ErM) were tested as an inoculation mechanism for Ericaceae plant establishment in restoration, habitat creation or *ex situ* conservation work. These liverworts were established to harbour the same ErM fungus (*Pezoloma ericae*) as British heathers (Chapters Two and Three).

The plants surviving the nursery experiments (presented in Chapter Four) were planted at two sites, The Delft, Norfolk ('the Delft') and Thursley Common, Surrey ('Thursley'), each in a fully randomized factorial experimental design. A subsample of inoculated and control plants were examined before planting and confirmed colonized and uncolonized, respectively.

Originally it was conceived that both sites would receive plants from the same nursery experiments at the same time, leaving local edaphic conditions, climate and land use considerations as influential factors. This did not occur as site conditions at the Delft made simultaneous planting unfeasible and the low survival rate of some of the nursery plants rendered the statistical power too low to divide the sample sizes between two sites. Rather than postponing the planting at Thursley by another season, it was decided to plant out one of the nursery experiments at Thursley according to the original schedule.

In addition to receiving plants from different experiments, the two sites are notably dissimilar in terms of land use. The Delft is an underproductive agricultural site in transition to heathland, and Thursley is an existing heathland recovering from large-scale wildfire. As mentioned in Chapter Four, Diaz *et al.* (2006) found a correlation between heather root colonization and plant growth. They also suggested restoration may be improved by finding ways to accelerate colonization. Liverworts colonized by ErM, as the field experiments described below demonstrate, are a novel and ecologically sound mechanism to hasten colonization.

5.2 Description of the field sites

5.2.1 The Delft

This former agricultural site adjacent to an existing heathland, Roydon Common, Norfolk (Figs. 1 and 23) was scraped of its nutrient rich topsoil in 2013 to prepare for creation of heathland, a priority habitat for Norfolk Wildlife Trust (NWT), the manager of the site.

Fig. 29 – Picture of the Delft after topsoil removal November 2013 (L); One of three plots at Thursley, seen inundated at harvest (R).

The NWT has invested a significant amount of time and staff resources to convert this land to an ecologically diverse landscape and habitat for threatened species. This research fit well with NWT's conservation goals and therefore they agreed to allocate a portion of the plot to the restoration experiments explored herein.

5.2.2 Thursley Common

Thursley comprises a 325-hectare mosaic of dry sandy heathlands, wet heathlands, open water, valley mire, peat bogs with sphagnum lawns and pine groves. Sited on a former military training site now managed as a National Nature Reserve, it is home to many rare species of insects, invertebrates, reptiles, breeding birds and vegetation, some only found in these specific habitats. Several Thursley habitats have internationally recognized designations including Ramsar, EU Special Area of Conservation, Special Protection Area (Natura 2000), and Site of Special Scientific Interest, for the UK. Due to its important conservation status, when a major fire struck in the Summer of 2006, efforts to restore the heathland commenced soon thereafter particularly from a wildlife perspective. The areas used for experimental plots were selected as they had their topsoil scraped by the reserve manager the year prior to study resident *Bombus*, amongst other beetles and invertebrates (Fig. 29). This provided optimal field conditions for the experimental design given the lack of vegetation competition and reduced input from existing ericoid mycorrhizal fungus propagules given the combination of fire and topsoil removal.

5.2.3 Methods

While in the plant nurseries, the cuttings and seedlings were kept in randomized patterns, alternating benches, proximity to windows or ventilation sources, whenever the plants were watered. Watering regimes were the same for all plants (section 4.2).

Prior to planting in the field, all plants were measured for baseline height measures. Approximately one year later, plant establishment, root colonization and growth responses (height and biomass) were measured for all experiments at both field sites. To determine whether the controls had been colonized during the time in the field, a random sample of inoculated and control plant roots was removed using a hand-spade, bagged and brought back to the laboratory for rinsing and analysis. Microscopic examination (x40 - x60) was used to examine absence or presence of ericoid mycorrhizal fungus in the hair roots. Survival counts and height measures were taken *in situ*. Plants deemed alive were cut at the base and collected in individual bags and freeze-dried for dry-weight biomass analyses. R-studio was used to determine statistical significance (Rscript located in Appendix 15).

5.2.3.1 Design of The Delft field experiment

Three plots were measured to accommodate the placement of 405 heather plants from nursery trials 1B, 1C and 2 (Table 5), and allocated ½ m^2 per plant. A subgroup of

Table 5 – The Delft total number of plants, randomly distributed by experiment, taxa and treatment

		Calluna		*Erica*	
	cutting or seedling	control	inoculated	control	inoculated
Plot 1					
Experiment 1B	cutting	11	18	13	13
Experiment 1C	cutting	15	24	11	11
Experiment 2	seedling	11	14	12	12
Plot 2					
Experiment 1B	cutting	10	15	0	17
Experiment 1C	cutting	14	17	21	26
Experiment 2	seedling	11	7	14	22
Plot 3*					
Experiment 1B	cutting	1	2	0	0
Experiment 1C	cutting	14	15	16	17
Experiment 2	seedling	0	0	0	1
Totals		87	112	87	119

* A few plants from Experiment 1B and 2 were accidentally planted here during the planting randomization routine, hence the small quantity.

Calluna and *Erica* plants from the nursery (section 4.2.1.2), were planted in the field a year earlier to test site conditions, including grazing pressures. Although the trial allowed one m^2 per plant, it was decided ½ m^2 per plant was sufficient given the smaller size of the actual experimental plants (half the size of the trial plants). Planting at this field site occurred in early-November 2014. Plot 1 (TF 567244 321211) measured 13m long and between 8m and 11.5m wide; Plot 2 (TF 567235 321188), had the same dimensions as Plot 1, and Plot 3 (TF 567 249 321222), was 11m long and 3.5m wide. A strip of approximately 1 m separated the plots. The entire area was fenced off after planting to inhibit grazing disturbance, particularly cattle or ponies which may be introduced in the next year.

5.2.3.2 Design of Thursley field experiment

A total of three plots consisting of 11 subplots were created (Table 6).

Table 6 – Thursley total number of plants, randomly distributed by taxa and treatment

	Calluna			*Erica*		
Subplot	control	fungus	liverwort	control	fungus	liverwort
1	n/a	n/a	n/a	4	2	4
2	n/a	n/a	n/a	4	2	2
3	n/a	n/a	n/a	2	3	6
4	n/a	n/a	n/a	2	6	7
5	n/a	n/a	n/a	3	8	6
6	n/a	n/a	n/a	4	7	4
7	12	10	8	n/a	n/a	n/a
8	9	9	6	n/a	n/a	n/a
9	9	6	6	1	n/a	n/a
10	7	10	7	n/a	n/a	n/a
11	9	7	14	n/a	n/a	n/a
Totals	46	42	41	20	29	29

Note: Shading reflects the three main plots.

The plot sizes were predetermined as a function of the previously scraped areas, roughly measured as $15m^2$, $24m^2$ and $65m^2$ (SU 900416), plots 1-3, respectively. Plants were spaced approximately ½ m^2 and all came from one glasshouse cuttings experiment, Experiment 1A. The total plants actually planted in the field are considerably less than originally planned due to unanticipated glasshouse conditions (mentioned earlier), significantly reducing the experimental population.

(Originally, the nursery plants from Experiment 1A were to be planted at The Delft in May 2014, but due to a rare pair of nesting birds, this was postponed to November 2014. The 1A plants needed to be planted out in the Summer as the glasshouse became infested with a caterpillar moth and were stressed from overheating. Thus, these Experiment 1A plants were instead planted in July 2014 at the pre-scraped plots at Thursley.)

5.2.4 Results

5.2.4.1 The Delft

5.2.4.1.1 Colonization of control plants one year later

Seven of the ten control heather root systems harvested one year after planting had become mycorrhizal while in the field.

5.2.4.1.2 Survival

A higher percentage of inoculated plants, by taxa, survived compared with the controls (Table 7), but this was not statistically significant. Some of the plots had high numbers of missing plants; Plot 2, in particular, experienced flash flooding with seasonal turbulence. A detailed breakdown by plot can be seen in Appendix 14.

Table 7 - The Delft survival rates, one year later

	Erica				*Calluna*			
	control		inoculated		control		inoculated	
Totals	87		119		87		112	
Alive	54	62%	90	76%	69	79%	93	83%
Dead	12	14%	10	8%	7	8%	9	8%
Not found	21	24%	19	16%	11	12%	10	9%

Not found - there was no label at all or clearly associated with a plant; Dead – sticks with labels were firmly in place, even though a plant stem was not always found. Several dead brittle stems were seen lying next to the plant label.

5.2.4.1.3 Growth response variables

5.2.4.1.3.1 Total height

Experiment 1B's *Erica* plants experienced a significant increase in growth when plants were inoculated compared with the controls, *P-value* < 0.05 (Appendix 13). The initial linear model run in R included a block effect diluting the significance. As the plots were narrowly separated and there was no block effect noted, this term was removed from the R-script to simplify the model. There was not a significant difference in growth between *Calluna* inoculated and control plants. No treatment effect was seen for Experiments 1C and 2, with respect to height for both *Erica* and *Calluna* (Appendix 13 and Appendix 15).

5.2.4.1.3.2 Aboveground biomass (measured by dry weight)

The Experiment 1B *Calluna* plants which were co-planted with inoculated liverworts grew significantly more than the controls as measured by dry weight, *P-value* < 0.001, despite there being no difference in total height (Fig. 30)

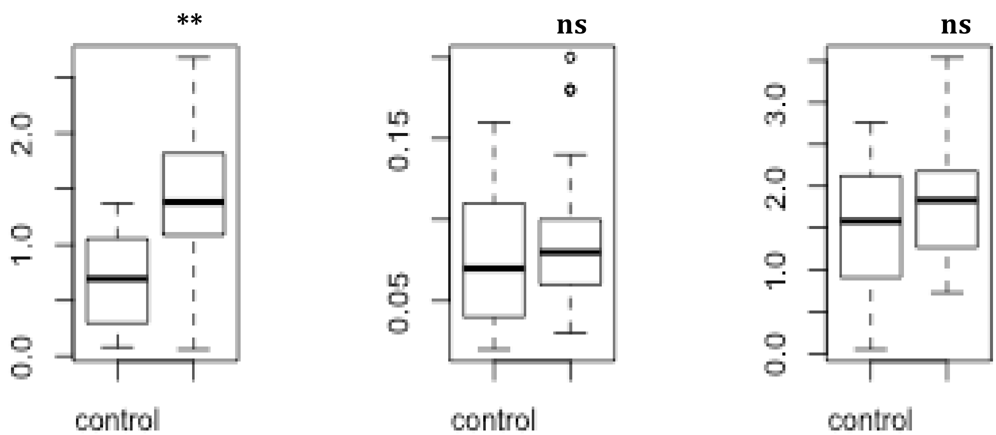

Fig. 30 - *Calluna* biomass (gr), Experiment 1B, 1C, 2 (left to right), control compared with treatment of inoculated liverworts.

Conversely, there was not a significant difference in dry weight between *Erica* inoculated and control plants, even though there was a significant difference in height. No treatment effect was seen in dry weight measurements for Experiments 1C and 2, for both *Erica* and *Calluna*.

5.2.4.2 Thursley

5.2.4.2.1 Colonization of control plants one year later

Two of the ten control heather root systems harvested one year after planting had become mycorrhizal while in the field.

5.2.4.2.2 Survival

Strictly speaking, when comparing dead:alive, neither *Calluna* nor *Erica* plants showed a benefit from inoculation treatment in terms of survival at harvest, after one year in the

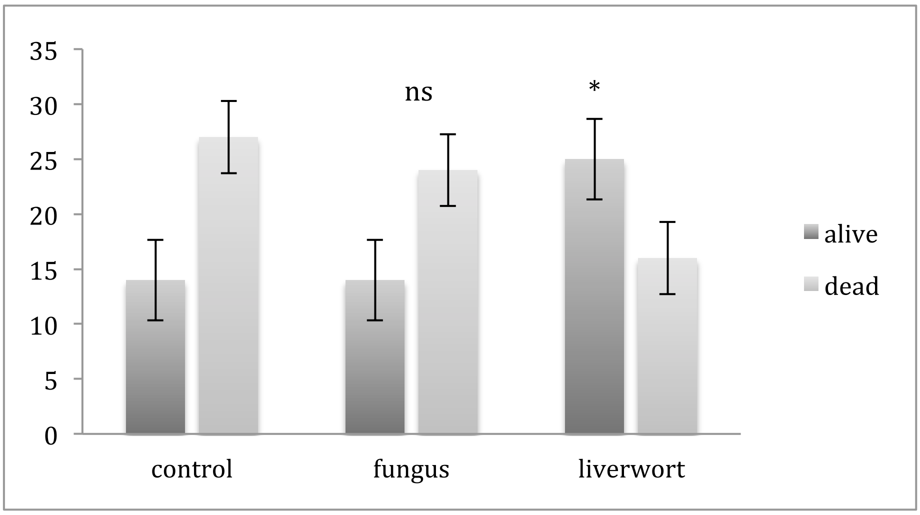

Fig. 31 – Number of *Calluna* plants which survived after one-year in the field.

field. The *P*-value is 0.07 for *Calluna* planted with inoculated liverworts compared with the control and fungal slurry inoculation groups. However, when the missing plants revert to dead status, the *P*-value is < 0.05 and therefore significant, as seen in Fig. 31. Regardless, this suggests an ecological trend may be developing in the field. The differences seen in the nursery phase amongst *Erica* plant groups were no longer evident at harvest in the field.

5.2.4.2.3 Growth response variables

Initial measures comparing growth measured by total height of *Calluna* treatment and control groups, after seven weeks in the field suggest a change in growth may be occurring due to treatment. Although not strictly 'statistically significant', as the *P*-value is slightly above 0.05 (Fig. 32), it may be ecologically significant and reflect initial growth suppression (continuing from the nursery) as the hyphae are incorporated in the plant's root system. The liverwort treatment group grew less than both the control and fungus treatment groups. The *Erica* plant groups continued markedly different growth patterns as in the nursery (Fig. 32).

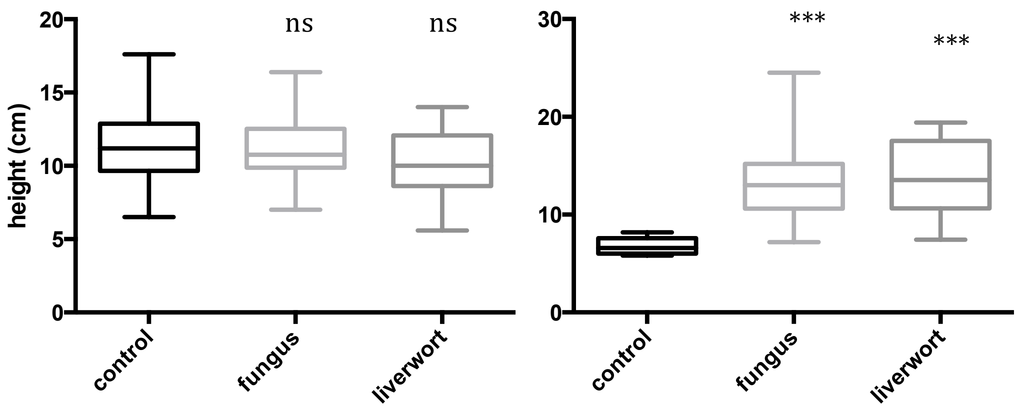

Fig. 32 - Height from field data, after seven weeks. *Calluna* (L)(P-value = 0.056, ANOVA) and *Erica* (R)(P-value < 0.001 using Kruskal-Wallis).

There was no significant difference measured in height between the inoculated and control plant groups after one year in the field for both *Erica* and *Calluna* and there was no treatment effect established for aboveground biomass measurements (dry weight) when the inoculated and control groups were compared. Appendix 13 summarizes all results from the first set of measurements taken in July 2014 (seven weeks after planting out in the field), which established a baseline for future data collections. As can be seen in the histograms, there is an uneven and bimodal distribution in height for *Erica* but not *Calluna*. It was therefore necessary to use different statistical tests to assess significance.

5.2.5 Discussion

This is the first time to my knowledge where a field experiment tested the efficacy of ericoid mycorrhizal fungus inoculation techniques by pre-treating plants in a nursery. Further, the use of leafy liverworts as the inoculum delivery mechanism is novel. Given the unpredictable plant deaths in the nursery, the design of the experiment was not ideal in terms of a full-factorial experiment with statistical power. Still there were some notable results and gleanings laying groundwork for further testing.

Most encouraging were continuing benefits to plant survival measured after one year in the field (at one of the two field sites, with one taxon). These results are, however, subject to interpretation as many plants could not be located. There were also significant benefits in plant growth for some of the experiments. However, many of the controls were tested as colonized after one year *in situ* possibly reducing visible signs of inoculation benefit but also showing possible effectiveness and simplicity of this pre-treatment. Still, atmospheric spores or soil sourced ErM propagules cannot be ruled out given mycorrhizal fungi persist even after disturbances such as tilling, mining and severe fires; noting the burn to their biomass partners hinders fungal growth. (Neary et al., 1999). Thus follow-up field studies should employ more vigorous control mechanisms and designs to interpret the catalyst for these results .

5.2.5.1 Colonization

Unexpectedly, there was a higher rate of ericoid mycorrhizal colonization observed in the Norfolk sample group compared with plant roots from Thursley. As this was a commercial monocrop agricultural site without a trace of heather before topsoil scraping and soil amendment commenced, and Thursley is an existing heathland with potential ericoid mycorrhizal fungal propagules, the opposite may have been predicted as it is generally accepted that semi-natural ecosystems (Thursley) produce more belowground fungal biomass than agricultural ecosystems (Norfolk) (van der Wal *et al.*, 2006). However, when considering the effect of fire on the heathland humus, we know that ericoid mycorrhizal fungi, at least *in vitro*, were unable to colonize new roots after one month without organic matter (Duclos *et al.*, 1983). The low colonization rate at Thursley thus makes more sense, particularly coupled with the topsoil removal for the experimental plots. The only known field study focusing on ErM in heathlands post-fire found a presence of *P. ericae* in burnt areas, one year after fire (Green *et al.*, 2013).

Burning intensity, ground moisture and previous land use all play a major role in belowground ecology recovery (Neary *et al.*, 1999). The possibility that Thursley's fire and resulting production of charcoal may have assisted colonization of heathers as seen *in vitro* with *Vaccinium* spp. by *Pezoloma ericae* (Duclos and Fortin, 1983), is likely cancelled out by the intensity of fire at Thursley hindering ErM hyphal development.

The differences in colonization of plant roots between the two sites may also be linked to the season of planting – late-autumn (The Delft) compared with early-summer (Thursley) – affecting optimal temperatures and/or moisture conducive to hyphal growth or sporulation (Compant *et al.*, 2013, Carvalho *et al.*, 2015). Local edaphic and environmental conditions e.g. flooding, may have also stirred and relocated nearby colonized liverworts to extend their hyphae in new locations. Also possibly relevant was the excess water from Roydon Common (the heathland adjacent to The Delft), which was channeled to the Norfolk site to reduce soil pH.

While it is likely the fungus came from pretreated plants and/or the co-planted liverworts, it remains possible that the field controls developed mycorrhizal partners from pre-existing propagules (although highly improbable at Norfolk). In this case, the pre-treated plants become another unintended tool to disseminate mycorrhizal fungi.

Molecular testing of the roots' fungus post harvest would not have confirmed the source of the fungus, only its identification. In retrospect, it would have been useful to plant non-treated control plants in the field when the nursery experiments commenced to see if they would have 'picked up' propagules from the environment before inoculated plants were planted out.

5.2.5.2 Survival

Although not statistically significant, Experiment 1A's survival results for *Calluna* suggest a trend towards an impact when pretreated with the inoculated liverworts. A larger sample group potentially may have produced significant results, particularly when considering the impact of colonized controls which may have also enhanced resilience. The treatment impact for survival amongst *Erica* was seen during the nursery stage but the resilience was not sustained in the field. This was similar for both taxa in Experiment B. Again, the colonization of controls may have influenced the results. Experiment 1C had many plants 'not found' significantly reducing the total sample population rendering the statistical results weak. Ideally, the field study should have been repeated with a larger population and more secure field labels, however time restrictions on the PhD limited this test.

5.2.5.3 Growth response variables

Only Experiment 1B (planted at The Delft) signals a continuing impact in growth due to early nursery treatment, despite the high rate of colonization found in the controls after one year in the field. Interestingly, however, is that *Erica* plants had measured a significant difference in height, between treated and control groups, but not in biomass (measured by dry-weight), and *Calluna* had a significant difference in biomass, but not height. It could be that the linear relationship between height and biomass, as seen in the young nursery experiment results with *Erica* plants (Appendix 9) is beginning to change as the plants mature and develop multi-branched structures. The *Calluna* was observed branching in early weeks but *Erica* seedlings usually project branches months later and fewer in general. As can be seen in the raw branch count data for Nursery Experiment 2 (Appendix 15), the average branch count for *Calluna* after a few months was 13 whereas *Erica* was only 5. It also may reflect high colonization rate amongst the controls, which would also explain why the other experiments are also not demonstrating a significant difference in either height or biomass.

6 Thesis Overview and Synthesis

The British heathland landscapes romantically evoked by Thomas Hardy have been severely altered over the last 150 years - 80% have disappeared. Once used as economic repositories for traditional husbandry and commoner practices (Rotherham and Bradley, 2009) their refuge for numerous rare fauna, which only thrive with the associated vegetation, has become increasingly under focus by land use policy makers both in the UK and EU. British lowland wet heathlands, dominated by ericaceous plants, are amongst the most important and intact in the world holding about 20% of the world's resource on an island, which covers only about 1/1000 of the earth's surface. As such, their status has been elevated to a priority habitat in the UK Biodiversity Action Plan; Thursley Common has several ecological designations to protect its rare flora and fauna (e.g. RAMSAR, national nature reserve, Site of Special Scientific Interest). Given anthropogenic pressures curtailing their natural succession, efforts to enhance their health and resurgence after e.g. fire are studied and coordinated amongst site managers and conservation agencies. Ecological observations which have provided insights for vegetation restoration (Diaz *et al.*, 2006) recorded a correlation between ericoid mycorrhizal fungus (ErM) and ericaceous plant root colonization, and general plant growth and resilience. Nutritional exchange research whereby ErM enhances a plant's ability to take up soil nutrients and water in exchange for plant photosynthates (Perotto *et al.*, 2012, Strandberg and Johansson, 1999) support these physical observations as well as earlier *in vitro* studies demonstrating Koch's postulates between vascular and non-vascular plants with ErM (Duckett and Read, 1995, Upson *et al.*, 2007). Fungal isolate experiments on ericaceous plants *i.e. Rhododendron* and *Vaccinium*, respectively (Vosatka *et al.*, 1999, Scagel, 2005, Kosola *et al.*, 2007) had also measured benefits with some strains of ErM.

My research sought to fill a gap in the knowledge between the *in vitro* fungal resynthesis experiments and field observations of ErM colonization following restoration. This involved testing a novel landscape restoration tool, utilizing the ascomycete ErM fungus *Pezoloma ericae*, which associates with both vascular and non-vascular plants in nature. Non-vascular liverworts resynthesized with *P. ericae* were co-planted with cuttings and seedlings of their vascular counterparts to test their inoculation efficacy. Liverworts were selected as they are relatively easy to obtain in the wild (full of *P. ericae*) without disturbing the vegetation, easy to bulk up for large-scale distribution and their physical properties lend themselves to adaptation in very dry and wet landscapes. Liverworts are poikilohydric (Wood, 2007, Proctor *et al.*, 2007), thus they can survive for long periods of time in a dry state waiting for the right opportunity to revive metabolic functions; likely aided by oil bodies, (He *et al.*, 2013), although functional studies have yet to be conducted. Most liverworts can withstand long periods of moisture without compromising cell structure.

Whether or not these leafy liverworts form a mutually beneficial association with the fungus they harbour in their rhizoids was tested for the first time. The experiments described in Chapter 3, unequivocally demonstrate that these non-vascular plants can be considered mycorrhizal-like *sensu stricto* as there is a mutual benefit to both the fungus and the liverwort they inhabit. Chapters Four and Five explored whether these leafy liverworts are viable as inoculants by pretreating vascular plants in the nursery before planting in nature for habitat creation or restoration. The model habitat for this thesis being lowland heathland. The two vascular plant taxa tested were successfully colonized by fungi originating from the inoculated liverwort within 12 weeks. The glasshouse experiments simulating climate and soil conditions showed plants with inoculation via the liverworts performed better in terms of both growth and survival under stress induced conditions. After one year in nature (Chapter 5) some significant differences between the liverwort treatment group and the controls continued (in terms of resilience and growth) but upon inspection following harvest, a large proportion of control plant roots had been colonized by ericoid mycorrhizal fungi rendering the results less significant, but still important ecologically.

These experiments generated many further questions. In no particular order, the most intriguing are as follows.

1) In isolating the fungus from wild-sourced liverworts and Ericaceae plant roots (Chapter 2) several strains of *Pezoloma ericae* were identified through molecular analyses. If time had permitted, it would have been beneficial to test them against one another to determine if one strain was more effective as a growth or survival enhancer. How diverse are these strains and in particular are there significant differences between the liverwort-derived and the *Erica*-derived fungus?
2) It is now known that ^{33}P transferred to the liverworts via the fungus (Chapter 3). Although it may be assumed the ^{15}N was also transferred, this has not yet been assessed. Neither has the impact of N on leafy liverwort growth.
3) Determining how much of the field experimental controls were colonized due to the addition of inoculated plants (via the liverworts) or what existed already in the soil-bed prior to the field experiments is important to understand for future

designs. This will differ between heathland restoration and new creation sites as was seen by proxy with controls at Thursley and The Delft (Chapter 5). Molecular testing of genets prior to planting will help clarify this point. This will also help to design a suitable distribution of either pre-inoculated plants in terms of bulk per e.g. hundred cuttings or liverworts per x number of plants. These two scenarios should be tested in nature to determine the most efficient means to inoculate field sites for large-scale restoration and creation.

4) Methods of bulking up and distributing the inoculum require further testing to find the most efficient combination. This can be designed for further control experiments in the nursery but this technology is ready for testing in nature with soft and hard cuttings and direct seed broadcasts. My research aimed to test whether leafy liverworts and their associated fungi can offer a more effective treatment for habitat restoration than previous attempts to inoculate soil with fungal isolates from plant roots as in Jansa and Vosatka (2000). However, because all the inoculation pre-treatments have been carried out in the nursery, this approach may prove prohibitively expensive for a substantial restoration project. To test the efficacy of this approach on a large scale, the next step would be to apply the liverwort treatment *in-situ* with a cost effective slurry application technique. It should work well in combination with a broadcast of thatch cuttings with seed, commonly employed as a restoration technique today. Temporal impact should be expected and monitored both in terms of plant establishment and mycelial growth.
5) Finally determining the impact of nitrogen deposition on these lowland heathland restoration techniques as compared with less polluted environs e.g. Norway, Northern Spain, are important to understand where to apply these techniques. No direct influence of nitrogen on ErM in *Calluna* heathlands was found in Denmark (Johansson, 2000) although we know other mycorrhizal fungi are effected by nitrogen in lowland heathlands (Collier and Bidartondo, 2009).

It is hoped that this ecological triptych model, vascular plant - fungus - non-vascular plant, can be tested for restoration and creation in other vegetation systems where there is a mycorrhizal fungal link between vascular and nonvascular plants. Field *et al.* (2015a) have shown representatives of all four symbiotic fungal groups present in extant liverworts - Mucoromycotina, Glomeromycota, Basidomycota and Ascomycota - associate with conifers, and all but the Mucoromycotina group, with angiosperms. There is tremendous potential here to explore these ecological links in other habitats where liverworts dwell, for example cloud forests, tundra and rainforests. The presence or introduction of certain liverworts in wet heath communities can offer ecologists an additional tool for expediting heathland habitat recovery, especially useful where (a) due to under-management as a result of limited resources, they are under stress of encroachment by trees or bracken scrub, or (b) mycorrhizal fungal reserves have been rendered unavailable due to fire or land use change.

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Appendices

Appendix 1 - Summary table of 500+ culture medium trials for this project

JK	Cleaning preparation	Growth medium	No. of plates
1	2 minutes in 1% bleach, rinse w/ distilled H20	H^20 w/ 0.01 nutr.	9
2	1 minute in 1% bleach	H^20 w/ 0.01 nutr.	7
4	30 s in 1% ʻʼ		15
5	1 min but diluted the hydrochloride 5:1 versus 4:1		15
6	Surface sterilzed in 0.5% hydrochloride @ 1 min, rinse in ster. Water	1.5% Phytagel - 0 nut	15+26+15
7	Surf. ster. 0.25% " 1 min, "	"	22
8	Surf. ster. 0.5% " 30 s, "	"	15
9	Surf. ster. 0.5% " 45 s, "	"	14
12	30 min under cold tap; 2.5 L deionized water, 5-10s in 0.5% hydrochloride (half in dark storage)	" and .01%	36
13 13a	Above but just rhizoids and surf ster. in 1% ʻʼ but surf ster for 5s in 1% hydrochloride	"	5 3
14 14a	1 hour under tap, then same as 12, 5 s surf ster. Above plus 5s surf ster.	"	6 8
15	Same as 14	Malt + antibiot	10
16	Tap 50 min, stir 5x @ 1 min, clean after each spin, in ster. dist. water 5-10 s in 0.5% hydrochloride	1% Phytagel	4
17	Tap for 3 hours, spins 5x @ 1 min each, no surf ster.	"	18
18	As above but 0.5% hydrochloride	"	27
18a	As 18 but only rhizoids	"	3
19*	*Odontoschisma* w/ 0.5% hydrochloride	"	16
	*all others *Cephalozia* spp.		
20	35 min under tap, then 5 min distilled	Mix of 0% and .01%	15
20a	0.5% hydrochloride for 5 s	"	15
20b	0.5% hydrochloride for 10s	"	15
21a	0.25% hydr for 5 s	"	20
21b	0.25% hydr for 10s	"	20
22	0.10% hydr for 5 s	"	10
22	0.10% hydr for 10 s	"	10

23	0.5% hydr for 5s	“ antibiotics	12
24	0.25% hydr for 5s	“ antibiotics	12
25	0.10% hydr for 10 s	“ antibiotics	15
26	Distilled and sterilized water		15
27	Above with 2s in 0.1% hydrochloride		15

Appendix 2 – Liverwort growth with and without fungus

a) Growth 2_13_14-3_24_14

		T1 (mm2)	T2 (mm2)	growth (%)
c1	control	5.19	11.4	119.65%
c2	control	1.86	2.06	10.75%
c3	control	5.91	12.953	119.17%
c4	control	8.09	8.276	2.30%
c5	control	8.03	14.7	83.06%
c6	control	5.04	11.99	137.90%
c7	control	6.67	7.58	13.64%
c8	control	5.93	12.988	119.02%
c9	control	2.07	2.9	40.10%
c10	control	8.64	12.04	39.35%
c11	control	4.72	10.64	125.42%
c12	control	6.38	7.093	11.18%
c13	control	2.77	10.04	262.45%
c14	control	4.52	6.265	38.61%
36	control	6.9	28.97	319.86%
39	control	5.51	13.53	145.55%
37	not rinsed	15.26	23.07	51.18%
38	not rinsed	12.22	36.6	199.51%
40	not rinsed	23.08	40.2	74.18%
41	not rinsed	8.74	16.7	91.08%
42	not rinsed	12.79	34.22	167.55%
43	not rinsed	2.49	11.074	344.74%
44	not rinsed	3.01	9.73	223.26%
45	not rinsed	25.54	75.67	196.28%
46	not rinsed	54.13	68.513	26.57%
47	not rinsed	18.48	43.89	137.50%
48	not rinsed	4.24	9.86	132.55%
49	not rinsed	3.98	12.17	205.78%
50	not rinsed	4.78	18.07	278.03%
51	not rinsed	2.88	10.4	261.11%
52	not rinsed	36.53	66.41	81.80%
53	not rinsed	13.76	46.305	236.52%
54	not rinsed	14.32	47.74	233.38%
55	not rinsed	13.65	41	200.37%
56	not rinsed	10.88	44.94	313.05%
57	not rinsed	19.5	28.74	47.38%
58	not rinsed	3.96	20.05	406.31%
66	not rinsed	13.66	65.373	378.57%
4	rinsed	10.15	20.134	98.36%
5	rinsed	19.77	22.4	13.30%
7	rinsed	15.07	23.89	58.53%
9	rinsed	4.9	25.84	427.35%

10	rinsed	11.44	17.6	53.85%
11	rinsed	9.89	31.4	217.49%
14	rinsed	1.87	8.952	378.72%
15	rinsed	16.28	21.284	30.74%
16	rinsed	26.64	31.53	18.36%
17	rinsed	18.64	44.26	137.45%
20	rinsed	21.78	46.28	112.49%
21	rinsed	2.22	9.03	306.76%
22	rinsed	6.65	18.86	183.61%
23	rinsed	7.7	21.22	175.58%

b) Dryweight after 6 months

liverwort only	liverwort with fungus
0.0740	0.069
0.0470	0.089
0.0730	0.081
0.0600	0.090
0.0490	0.089
0.0370	0.085
Average	
0.0567	0.0838

Appendix 3 - Fungal and plant culture media

(all per 1L diluted water and autoclaved 15 minutes at 120c)

Parker medium

15g Phytagel BioReagent, plant cell culture tested, powder (SIGMA Life Science Lot SLBD1697V), plus:

10 ml nutrient stock to be diluted in water for '0.01' medium: (prepared 200ml of the following measures (L))

2ml (10ml/L) chelated iron solution

400ul (2ml/L) Calcium Chloride (10g/L)

2ml (10ml/L) 'micronutrients'

2.4ml (12ml/L) Magnesium Sulphate (10g/L)

1ml (5ml/L) Ammonium Nitrate (25g/L)

5 ml (25ml/L) Potassium Phosphate (20g/L)

Malt agar – 10g/L

Modified Melin-Norkran's agar (MMN)

recipe:

10g glucose

0.5g KH_4PO_4

0.28g NH_4 Cl

0.15 g $MgSO_4$; H_20

0.5ml 1% $FeCl_3$ (we use ferric citrate solution)

0.05g Ca Cl_2

0.025Na Cl

100 ug thiamine Hcl (100ul)

acidified to pH 4.5 w10% HCl; divide by 10 (to 100g)

20 g agar

Potato Dextrose Agar (PDA) – Oxoid CM0139, concentration per instructions on container

Hagem's (modified by Modess (and then modified again by Pressel-Rimington)):

5g glucose

12.5g malt extract (we used malt agar, so added 20.83g (12.5g malt, 6.25g agar and 2.08g mycological peptone)

0.5g KH_2PO_4

0.5g $MgSO_4.7H_2O$

0.5g NH_4Cl

0.5ml 1% Ferric citrate solution

20g agar (we used 13.75g to account for use of malt agar, see above)

After autoclaving, the following were added:

50mg/L streptomycin; 50mg/L ampicillin

Appendix 4 - Experiment 3 - seedling germination

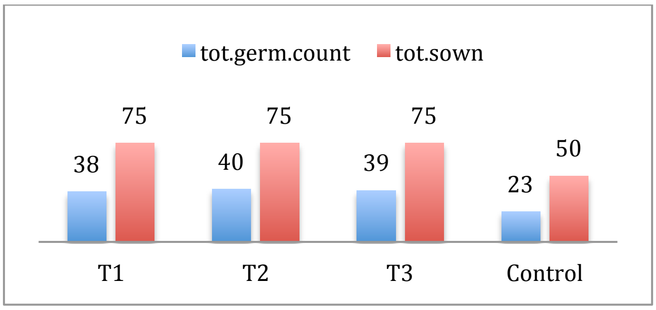


Fig. 33 – Number of *Calluna* seeds germinated at 12 wk, compared to total sown.

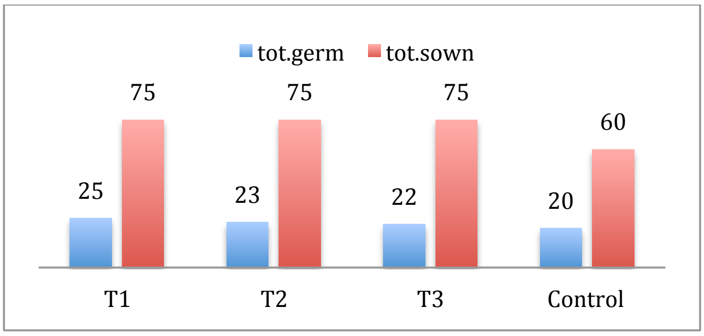


Fig. 34 - Number of *Erica* seeds germinated at 12 wk, compared to total sown.

Table 8 - Comparison between *Calluna* and *Erica* germination rates (% of seeds sown)

Treatment	*Calluna*	*Erica*
T1	51	33
T2	53	30
T3	52	29
Control	46	33

Appendix 5 - Geiger readings, 11/7/14

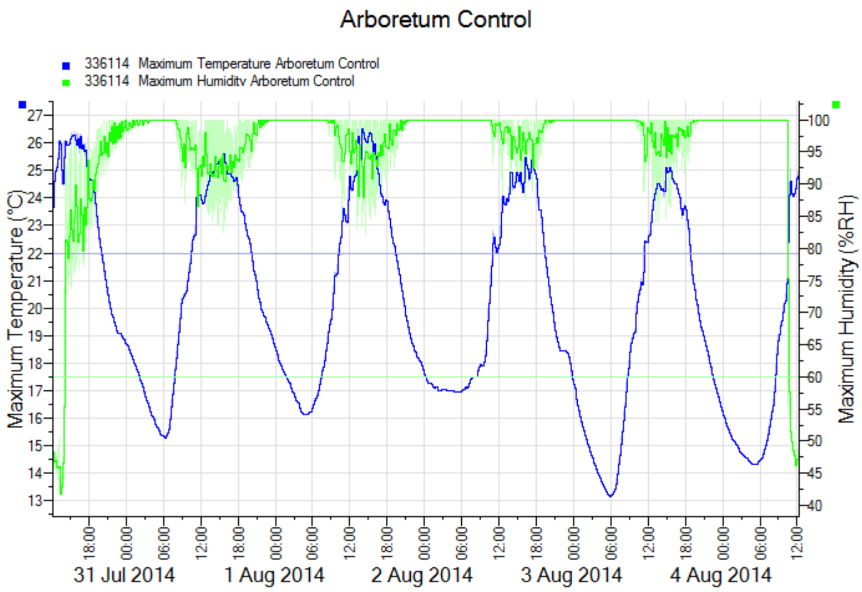
num	treatment.status	cps	fungus	barrier	contam	qualifying notes
C18	negative control	<1	n	Y	n	background noise only
C19	negative control	<1	n	y	n	background noise only
C10	positive control	10.0	n	n	n	vigorous growth
C13	positive control	3.0	n	n	n	smaller than above
C4a	positive control	10.0	n	n	n	large plant
C4b	positive control	12.0	n	n	n	large plant
C7	positive control	6.0	n	n	n	large plant
C2	positive control	9.0	n	n	n	
C8	positive control	20.0	n	n	n	cps surrounding much lower; vigorous plant growth
60	treated	1.0	Y	Y	n	hyphae havent crossed but water droplets persed; maybe control
61	treated	1.5	Y	y	n	‘’
54	treated	2.0	Y	Y	n	hyphae crossed;water droplets dispersed
55	treated	1.5	Y	Y	n	‘’
30	treated	1.5	y	Y	n	hyphae crossed, decent network;water droplets dispersed
31	treated	2.0	Y	Y	n	‘’
50	treated	1.5	y	Y	n	very small plants
51	treated	2.0	Y	Y	n	''
24	treated	1.5	Y	Y	n	tiny plant but good connections over barrier
25	treated	1.0	Y	Y	n	bit larger than above
5	treated	<1	Y	y	Y	huge plant
4	treated	<1	Y	Y	y	tiny plant (may be dead); strong connectivity
62	treated	2.0	Y	Y	n	big plant, connection strong
63	treated	<1	Y	y	n	no connections to eye
8	treated	<1	Y	y	n	small plant; strong crossover barrier
9	treated	1.5	Y	y	n	bigger and greener; strong cross over barrier
26	treated	1.0	Y	Y	?	large plant; good connection
27	treated	3.0	Y	Y	n	large plant; good connection; much 'hotter'
10	treated	<1	Y	Y	y	patchy connection
11	treated	1.5	Y	Y	N	bigger plant; patchy connection
14	treated	1.0	Y	Y	Y	contam. Both sides; 14 smaller, 15 hotter
15	treated	1.5	Y	y	Y	
16	treated	2.0	Y	y	y	contam but extensive network
17	treated	2.0	Y	Y	y	
64	treated	<1	Y	Y	n	patchy hyphae,prob water drops; plants avg size
65	treated	1.0	Y	Y	n	
58	treated	1.0	Y	Y	n	58 avg size, 59 massive and strong connections across barrier and into well
59	treated	1.5	Y	Y	n	
6	treated	1.0	Y	Y	n	happy plants, good network
7	treated	1.5	Y	Y	n	
28	treated	<1	y	Y	n	small network, no contam
29	treated	2.0	y	Y	n	
20	treated	1.0	Y	Y	n	good hyphae networks
21	treated	1.0	y	y	n	

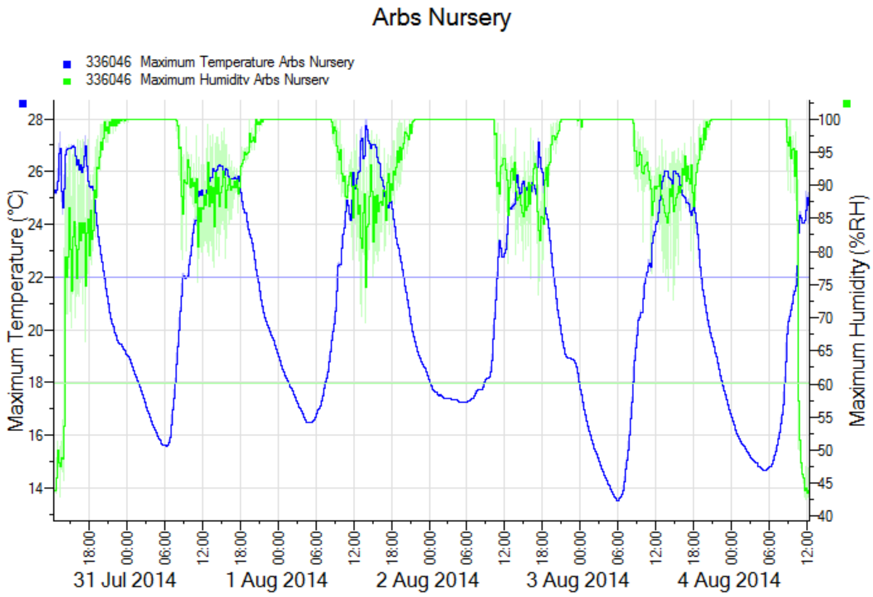
Appendix 6 – P and C budgets

Appendix 7 - Pre-trials for glasshouse experiments

There were a series pre-trials conducted for the cuttings and the seedlings experiments to test some of the design questions, particularly concerning the liverwort treatments. The cuttings pre-trial included several phases of cuttings ('A' – 'F', depending on age), set up to demonstrate repeatability and best practices for inoculation timing. In total, there were 528 plants, half *Erica tetralix* and half *Calluna vulgaris*, beginning in November 2011. All pots were covered with cling film, placed in shallow trays and watered on an as needed basis to keep the compost damp with periods of dry, simulating the wet heath environment. Wild liverworts were introduced to rooted cuttings (six months to one year old) as inoculum. These were randomly dispersed to the plantlets using a complete block design with eight replicates. There were two treatments: 1) colonized liverworts sourced in the wild; 2) same liverworts as 1, but serially washed (20 times in sterilized distilled water after ½ hour under a medium flow of tap water) and, a negative control group, whereby nothing was added to the cutting. Initially, the intention was to re-synthesize fungal isolates from wild liverworts with axenically-grown liverworts and subculture this population harboring the fungi for introduction to the vascular ericaceous plants. This theoretically 'pure' liverwort, containing only identified fungal symbionts, was to be compared with naturally sourced (or wild) liverworts to study whether there is a net gain to the vascular plants with one treatment versus the other. As isolation of the fungal symbiont proved more time consuming than originally planned, crude cross colonization tests began instead with naturally sourced liverworts containing the fungus of interest, *Pezoloma ericae*, in their rhizoids (verified through DNA extraction as described in Chapter Two). This was followed on with the 'pure' liverworts for the later Experiment 1A, B and C treatments. The plants height and spread were measured at time of treatment. As there was a normal distribution and no statistically significant difference in variance within and amongst groups A-F, after five months of treatment, the groups were merged into one experimental group. Growth response and qualitative data were collected, and an arbitrary sample of hair roots was harvested for examination of colonization and control success. After six months however, there was an abundance of mortalities recorded (over 200 plants of 528), mainly due to human error and the learning curve involved with growing these temperate plants in a sheltered environment. This first pre-trial was aborted after eighteen months in the nursery due to an oversight in compost pasteurization procedures, which resulted in a statistically compromising number of controls becoming colonized by ErM, likely originating from the peat compost.

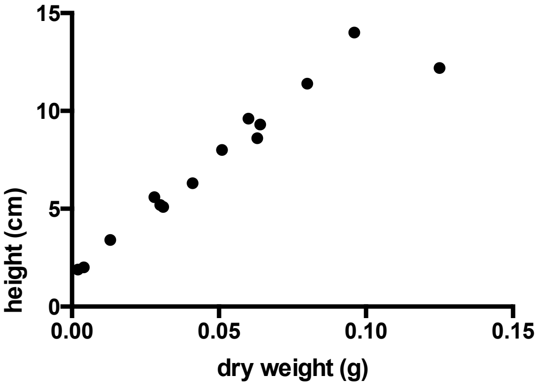
Appendix 8 – Experiment 1B relative humidity and temperature readings (using Tinytag monitors)



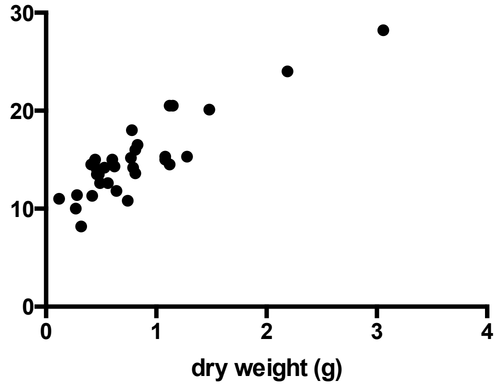


The above Tinytag output shows temperature was the same over the five-day period. Relative humidity (RH) differed, but not significantly; the treatment side recovery to the nursery settings target (RH 90% or above), lagged about an hour behind the control side, resulting in slightly lower RH overall. An additional sponge moisture absorption test supported this with no significant difference between the collective weight of the sponges from either side of the misting unit.

Appendix 9 - Correlation between *Erica tetralix* height and dry weight



(a)



(b)

Appendix 10 - Copy of Kowal *et al.* (2015)*

Appendix 11 - Rstudio transcripts, cuttings experiments

Cuttings Experiment 1A

2-sample test for equality of proportions with continuity correction

data: c(14, 29) out of c(48, 47);

X-squared = 8.8755, df = 1, ***P*-value = 0.00289**

alternative hypothesis: two.sided

95 percent confidence interval:

-0.5357455 -0.1149637

sample estimates:

prop 1 prop 2

0.2916667 0.6170213

prop.test(c(14,30),c(48,52))

data: c(14, 30) out of c(48, 52)

X-squared = 7.1258, df = 1, ***P*-value = 0.007598****

alternative hypothesis: two.sided

95 percent confidence interval:

-0.49120641 -0.07930641

sample estimates:

prop 1 prop 2

0.2916667 0.5769231

Cuttings Experiment 1B

***Erica* alive**

prop.test(c(34,44),c(72,83))

X-squared = 0.3113, df = 1, *P*-value = 0.5769

alternative hypothesis: two.sided

***Erica* with ok health**

prop.test(c(33,43),c(34,44))

X-squared = 0, df = 1, *P*-value = 1

alternative hypothesis: two.sided

Warning message:

In prop.test(c(33, 43), c(34, 44)) :

Chi-squared approximation may be incorrect

***Erica* with good roots**

prop.test(c(19,37),c(34,44))

X-squared = 6.208, df = 1, ***P*-value = 0.01272***

alternative hypothesis: two.sided

***Erica* with new growth**

prop.test(c(17,38),c(34,44))

X-squared = 10.5113, df = 1, P-value = 0.001186**

alternative hypothesis: two.sided

***Calluna* alive**

prop.test(c(38,30),c(72,71))

X-squared = 1.1937, df = 1, P-value = 0.2746

alternative hypothesis: two.sided

***Calluna* ok health**

prop.test(c(36,28),c(38,30))

X-squared = 0, df = 1, P-value = 1

alternative hypothesis: two.sided

***Calluna* with good roots**

prop.test(c(24,27),c(38,30))

X-squared = 5.0901, df = 1, ***P*-value = 0.02406***

alternative hypothesis: two.sided

***Calluna* with new growth**

prop.test(c(28,30),c(38,30))

X-squared = 7.2768, df = 1, ***P*-value = 0.006985****

alternative hypothesis: two.sided

Warning message:

In prop.test(c(28, 30), c(38, 30)) :

Chi-squared approximation may be incorrect

Chisq.test results

***Erica* alive**

X-squared = 0.3113, df = 1, P-value = 0.5769

***Erica* with ok health**

X-squared = 0, df = 1, P-value = 1

***Erica* with good roots**

P-value = 0.01272

***Erica* with new growth**

X-squared = 10.5113, df = 1, **P-value = 0.001186****

***Calluna* alive**

X-squared = 1.1937, df = 1, P-value = 0.2746

***Calluna* ok health**

X-squared = 0, df = 1, P-value = 1

***Calluna* with good roots**

X-squared = 3.8313, df = 1, P-value = 0.0503

***Calluna* with new growth**

X-squared = 7.2768, df = 1, **P-value = 0.006985****

Mheight = maximum height (the highest point on the plant)

Theight= total height (the maximum height + the branch lengths)

Branch**=** number of branches

<u>Transcript</u>

***<u>Erica</u>* <u>maximum height</u>**

var.test(cc_mheight,tc_mheight)

F = 0.6079, num df = 37, denom df = 43, P-value = 0.1249

alternative hypothesis: true ratio of variances is not equal to 1

t.test(cc_mheight,tc_mheight)

t = -3.2936, df = 79.222, P-value = 0.00148**

alternative hypothesis: true difference in means is not equal to 0

***<u>Calluna</u>* <u>maximum height</u>**

var.test(ce_mheight,te_mheight)

F = 0.5997, num df = 33, denom df = 29, P-value = 0.1565

alternative hypothesis: true ratio of variances is not equal to 1

t.test(ce_mheight,te_mheight)

t = -4.5343, df = 54.42, P-value = 3.215e-05***

alternative hypothesis: true difference in means is not equal to 0

***<u>Calluna</u>* <u>total height</u>**

var.test(cc_theight,tc_theight)

F = 0.7726, num df = 37, denom df = 43, P-value = 0.4256

alternative hypothesis: true ratio of variances is not equal to

t.test(cc_theight,tc_theight**)****

t = -2.8074, df = 79.97, **P-value = 0.006273**

alternative hypothesis: true difference in means is not equal to 0

***<u>Erica</u>* <u>total height</u>**

var.test(ce_theight,te_theight)

F = 0.6205, num df = 33, denom df = 29, P-value = 0.1857

alternative hypothesis: true ratio of variances is not equal to 1

t.test(ce_theight,te_theight)

t = -3.6375, df = 54.968, **P-value = 0.0006083*****

alternative hypothesis: true difference in means is not equal to 0

***<u>Calluna</u>* <u>branches</u>**

var.test(cc_branch,tc_branch)

F = 0.8161, num df = 37, denom df = 43, P-value = 0.5309

alternative hypothesis: true ratio of variances is not equal to 1

t.test(cc_branch,tc_branch)

t = -2.4412, df = 79.825, **P-value = 0.01685***

alternative hypothesis: true difference in means is not equal to 0

***<u>Erica</u>* <u>branches</u>**

var.test(ce_branch,te_branch)

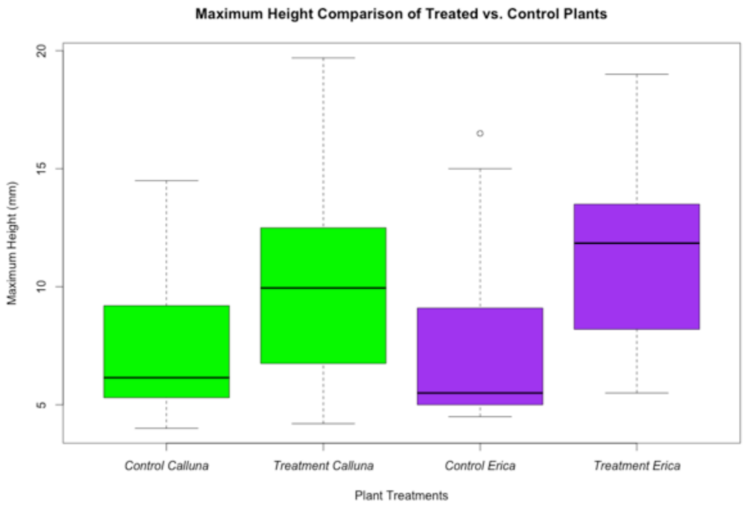
F = 0.9785, num df = 33, denom df = 29, P-value = 0.9461

alternative hypothesis: true ratio of variances is not equal to 1

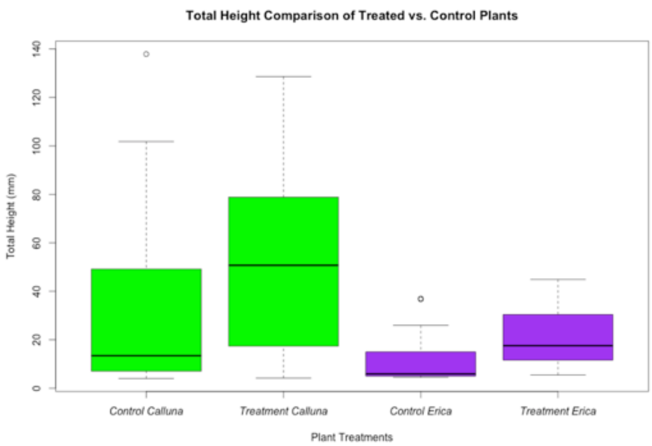
t.test(ce_branch,te_branch**)**

t = -2.2062, df = 60.84, P-value = 0.03116* alternative hypothesis: true difference in means is not equal to 0

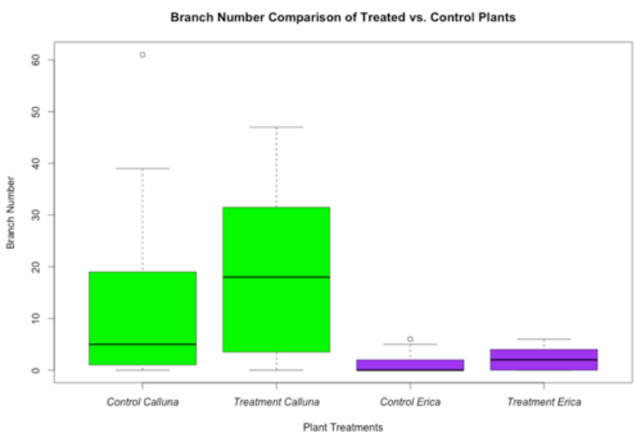
Graphs



boxplot(cc_mheight,tc_mheight,ce_mheight,te_mheight,main="Maximum Height Comparison of Treated vs. Control Plants",ylab="Maximum Height (mm)",xlab="Plant Treatments",col=c("green","green","purple","purple"),names=c(expression(italic("Control Calluna"),italic("Treatment Calluna"),italic("Control Erica"),italic("Treatment Erica"))))



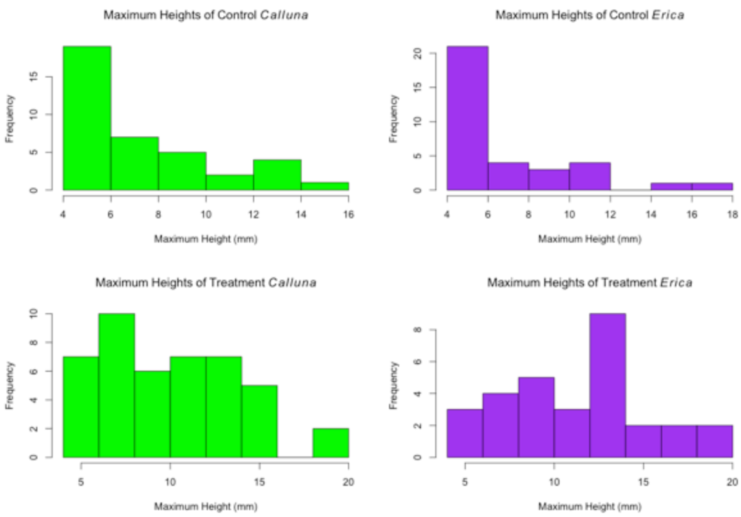
boxplot(cc_theight,tc_theight,ce_theight,te_theight,main="Total Height Comparison of Treated vs. Control Plants",ylab="TotalHeight(mm)",xlab="PlantTreatments",col=c("green","green","purple","purple"),names=c (expression(italic("Control Calluna"),italic("Treatment Calluna"),italic("Control Erica"),italic("Treatment Erica"))))



```
boxplot(cc_branch,tc_branch,ce_branch,te_branch,main="Branch Number Comparison of Treated vs. Control Plants",ylab="BranchNumber",xlab="PlantTreatments",col=c("green","green","purple","purple"),names=c(expression(italic("Control Calluna"),italic("Treatment Calluna"),italic("Control Erica"),italic("Treatment Erica"))))
```

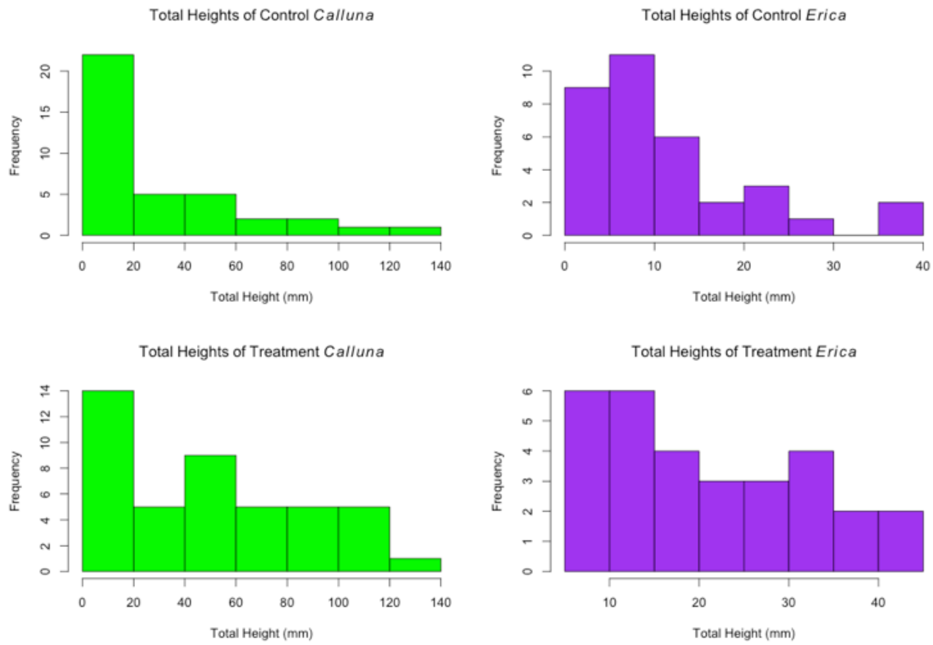
Maximum Height

```
par(mfrow=c(2,2))

hist(cc_mheight,main=expression(Maximum~Heights~of~Control~italic(Calluna)),ylab="Frequency",xlab="Maximum Height (mm)",col=c("green"))

hist(ce_mheight,main=expression(Maximum~Heights~of~Control~italic(Erica)),ylab="Frequency",xlab="Maximum Height (mm)",col=c("purple"))

hist(tc_mheight,main=expression(Maximum~Heights~of~Treatment~italic(Calluna)),ylab="Frequency",xlab="Maximum Height (mm)",col=c("green"))

hist(te_mheight,main=expression(Maximum~Heights~of~Treatment~italic(Erica)),ylab="Frequency",xlab="Maximum Height (mm)",col=c("purple"))
```



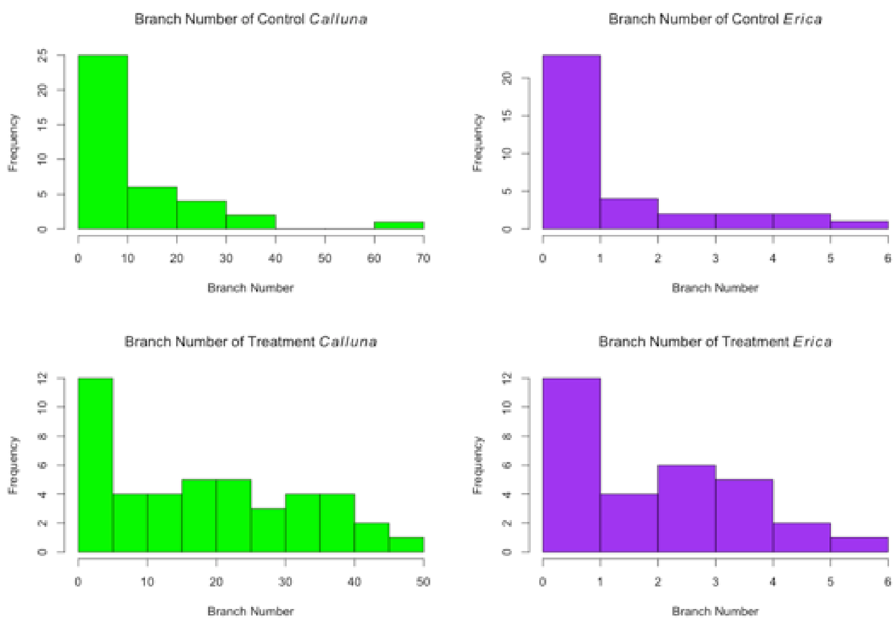
Total height

```
par(mfrow=c(2,2))

hist(cc_theight,main=expression(Total~Heights~of~Control~italic(Calluna)),ylab="Frequency",xlab="Total Height (mm)",col=c("green"))

hist(ce_theight,main=expression(Total~Heights~of~Control~italic(Erica)),ylab="Frequency",xlab="Total Height (mm)",col=c("purple"))

hist(tc_theight,main=expression(Total~Heights~of~Treatment~italic(Calluna)),ylab="Frequency",xlab="Total Height (mm)",col=c("green"))

hist(te_theight,main=expression(Total~Heights~of~Treatment~italic(Erica)),ylab="Frequency",xlab="Total Height (mm)",col=c("purple"))
```



Branch number

```
 par(mfrow=c(2,2))

hist(cc_branch,main=expression(Branch~Number~of~Control~italic(Calluna)),ylab="Frequency",xlab="Branch Number”,col=c("green"))

hist(ce_branch,main=expression(Branch~Number~of~Control~italic(Erica)),ylab="Frequency",xlab="Branch Number",col=c("purple"))

hist(tc_branch,main=expression(Branch~Number~of~Treatment~italic(Calluna)),ylab="Frequency",xlab="Branch Number",col=c("green"))

hist(te_branch,main=expression(Branch~Number~of~Treatment~italic(Erica)),ylab="Frequency",xlab="Branch Number",col=c("purple"))
```



Test on the Change in Max height between the two groups

> var.test(ce_change,te_change)

F test to compare two variances

data: ce_change and te_change

F = 0.4854, num df = 22, denom df = 22, P-value = 0.09728

alternative hypothesis: true ratio of variances is not equal to 1

95 percent confidence interval: 0.2058839 1.1446331

sample estimates: ratio of variances

0.4854498

> t.test(ce_change,te_change)

Welch Two Sample t-test

data: ce_change and te_change

t = -2.6553, df = 39.286, P-value = 0.01139*

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-5.3689845 -0.7266677

sample estimates:

mean of x mean of y

2.586957 5.634783

> var.test(cc_change,tc_change)

F test to compare two variances

data: cc_change and tc_change

F = 0.7959, num df = 23, denom df = 34, P-value = 0.5735

alternative hypothesis: true ratio of variances is not equal to 1

95 percent confidence interval:

0.3811988 1.7588210

sample estimates:

ratio of variances

0.795912

> t.test(cc_change,tc_change)

Welch Two Sample t-test

data: cc_change and tc_change

t = -1.351, df = 53.06, P-value = 0.1824

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-2.5863982 0.5044934

sample estimates:

mean of x mean of y

3.133333 4.174286

Summary of tests and results

Prop.test vs. chisq.test

	Vitality		Health		Rooting		New growth	
	Erica	*Calluna*	*Erica*	*Calluna*	*Erica*	*Calluna*	*Erica*	*Calluna*
Prop.test *P-value*	0.5769	0.2746	1	1	0.01	0.02	0.001	0.007
Chi.sq test *P-value*	0.5769	0.2746	1	1	0.01	0.05	0.001	0.007

T.test/Wilcox.test

Value	**Species**	**Test**	***P-value***
Maximum height	*Erica*	t.test	0.001**
	Calluna	t.test	3.215e-05***
Total Height	*Erica*	t.test	0.0006***
	Calluna	t.test	0.006**
Branch Number	*Erica*	t.test	0.03*
	Calluna	t.test	0.01*
Maximum Height change	*Erica*	t.test	0.01*
	Calluna	t.test	0.1824

Sample size

Erica control n = 34; *Erica* treatment n = 44; *Calluna* control n = 38; *Calluna* treatment n = 30

Appendix 12 - Rstudio transcript seedlings experiment

Seedlings at 11 weeks:

Heights: .txt file "Exp2_w11_height"

Name	Control *Erica*	Treatment *Erica*	Control *Calluna*	Treatment *Calluna*
Mean	18.58	9.18	15.74	8.867
Median	19.50	5.50	7.00	4.00
n	36	34	31	15

Var.test and t/Wilcox tests

The variance in the *Erica* samples is statistically significantly different.
A Wilcox test revealed that there is a statistically significant difference between the heights of the treatment and control groups. This is shown by *P*-value = 0.01493*

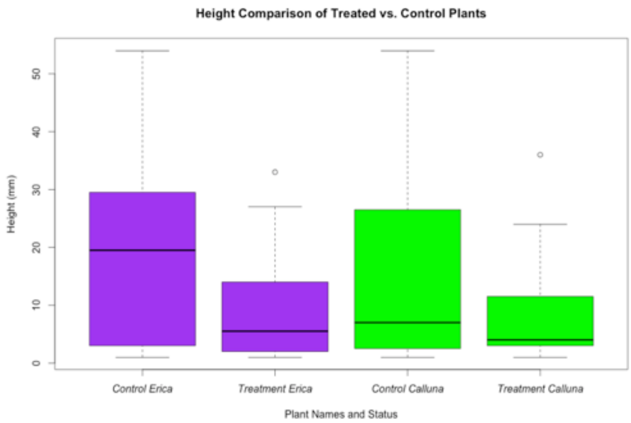
The variance in the *Calluna* samples is not statistically significantly different.
A t-test revealed that there is no statistically significant difference between the heights of the treatment and control groups. This is shown by *P*-value = 0.07457

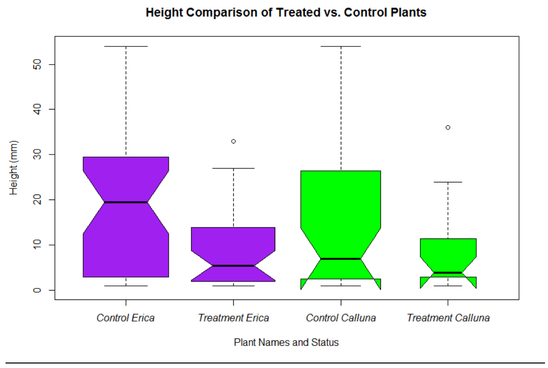
Transcript

```
> var.test(E,TE)
        F test to compare two variances
data:  E and TE
F = 2.8107, num df = 35, denom df = 33, P-value = 0.003614**
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 1.413382 5.550767
sample estimates:
ratio of variances           2.810691
> wilcox.test(E,TE)
        Wilcoxon rank sum test with continuity
        correction
data:  E and TE
W = 819, P-value = 0.01493
alternative hypothesis: true location shift is not equal to 0
Warning message:
In wilcox.test.default(E, TE) : cannot compute exact P-value with ties
> var.test(C,TC)
        F test to compare two variances
data:  C and TC
F = 2.4979, num df = 30, denom df = 14, P-value = 0.07287
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.9142006 5.8396217
sample estimates:
ratio of variances
          2.49794
> t.test(C,TC)
        Welch Two Sample t-test
data:  C and TC
t = 1.8302, df = 40.61, P-value = 0.07457
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.7134657 14.4640034
sample estimates:
mean of x mean of y
15.741935  8.866667
```

Boxplots

boxplot(Data,main="Height Comparison of Treated vs. Control Plants",ylab="Height (mm)",xlab="Plant Names and Status",col=c("purple","purple","green","green"),names=c(expression(italic("Control Erica"),italic("Treatment Erica"),italic("Control Calluna"),italic("Treatment Calluna"))))





This diagram indicates that there is a significant difference in the medians when comparing treatment and control *Erica.* Left to right: n=36, n=34, P-value = 0.01493* (for the difference in means between these two groups (shown by a wilcoxon test); the n=31, n=15 and the difference in mean between the two groups is shown by a t-test and has P-value = 0.07457

<u>Histograms</u>

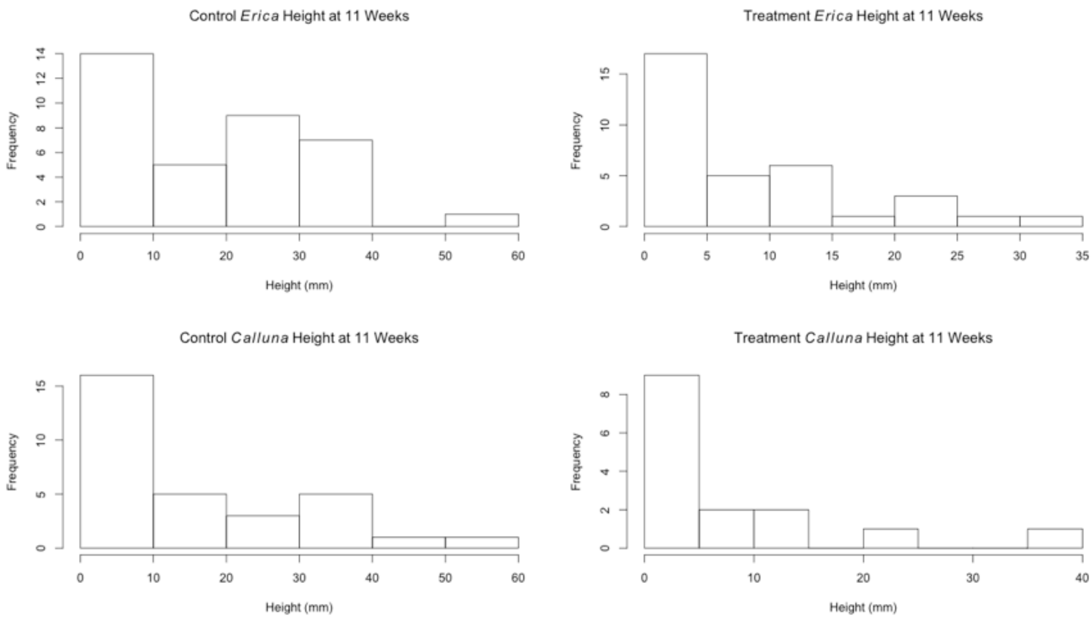
par(mfrow=c(2,2))

hist(E,main=expression(Control~italic(Erica)~Height~at~11~Weeks),ylab="Frequency",xlab="Height (mm)")

hist(TE,main=(Treatment~italic(Erica)~Height~at~11~Weeks),ylab="Frequency",xlab="Height (mm)")

hist(C,main=expression(Control~italic(Calluna)~Height~at~11~Weeks),ylab="Frequency",xlab="Height (mm)")

hist(TC,main=(Treatment~italic(Calluna)~Height~at~11~Weeks),ylab="Frequency",xlab="Height (mm)")

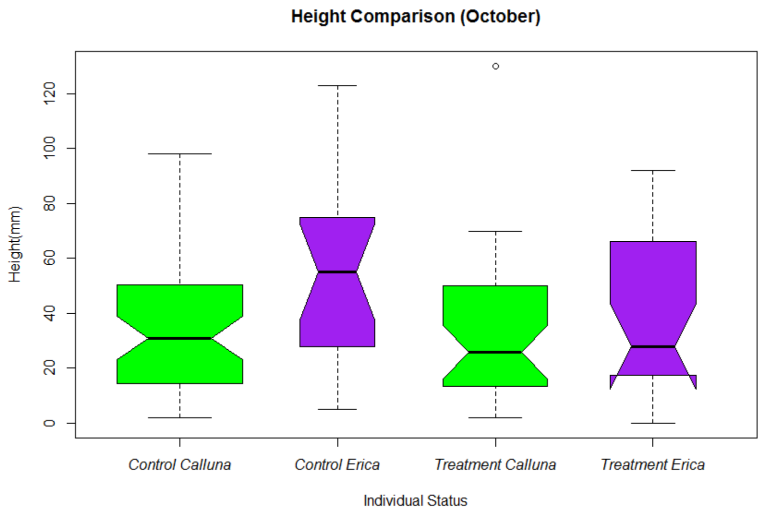


Seedlings at 28 weeks

use: .txt file 'Exp2_oct_height'

Boxplot

```
boxplot(Data,notch=TRUE,varwidth=TRUE, main="Height Comparison (October)",ylab="Height(mm)",xlab="Individual Status",col=c("green","purple","green","purple"),names=c(expression(italic("Control Calluna"),italic("Control Erica"),italic("Treatment Calluna"),italic("Treatment Erica"))))
```

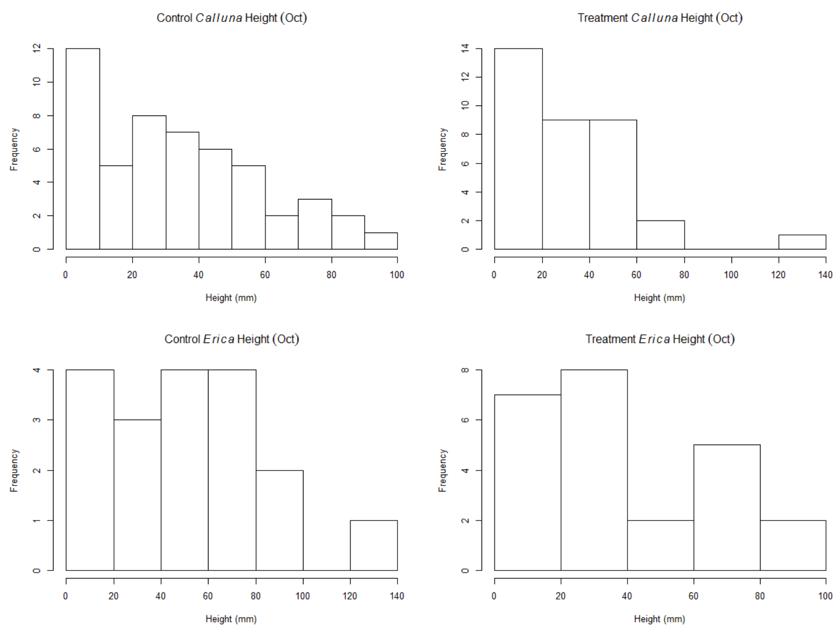


*In contrast to 11 weeks, the notches all overlap here (within species) so there is no significant difference

Control *Calluna* n=51, Control *Erica* n= 18, Treatment *Calluna* n= 35, Treatment *Erica* n= 24

<u>Histogram</u>

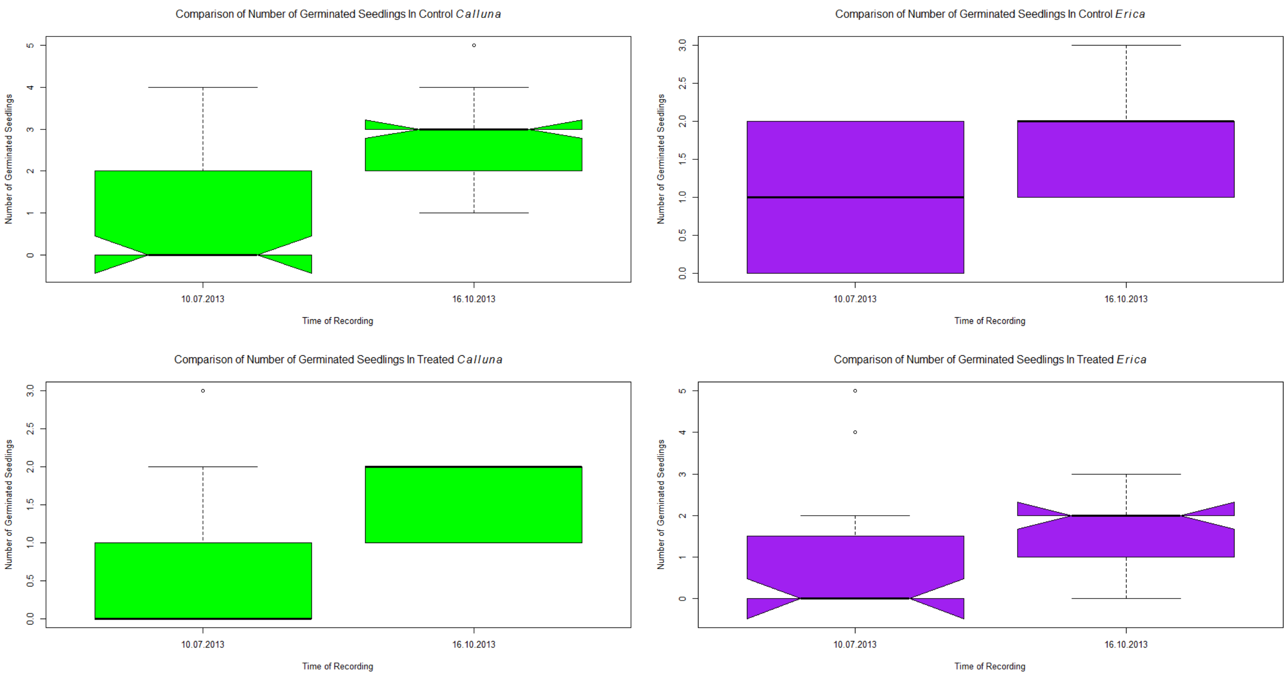
```
par(mfrow=c(2,2))
hist(cc_height, main=expression(Control~italic(Calluna)~Height~(Oct)),ylab="Frequency",xlab="Height (mm)")
hist(tc_height, main=expression(Treatment~italic(Calluna)~Height~(Oct)),ylab="Frequency",xlab="Height (mm)")
hist(ce_height, main=expression(Control~italic(Erica)~Height~(Oct)),ylab="Frequency",xlab="Height (mm)")
hist(te_height, main=expression(Treatment~italic(Erica)~Height~(Oct)),ylab="Frequency",xlab="Height (mm)")
```



Germination rates use: Exp2_oct_germ

Boxplots comparing early to late germination

```
> par(mfrow=c(2,2))
> boxplot(cc_germ1,cc_germ2,notch=TRUE,varwidth=TRUE,main=expression(Compari
son~of~Number~of~Germinated~Seedlings~In~Control~italic(Calluna)),ylab="Numb
er of Germinated Seedlings",xlab="Time of Recording",col=c("green"),names=c(
"10.07.2013","16.10.2013"))
> boxplot(ce_germ1,ce_germ2,nocth=TRUE,varwidth=TRUE,main=expression(Compari
son~of~Number~of~Germinated~Seedlings~In~Control~italic(Erica)),ylab="Number
 of Germinated Seedlings",xlab="Time of Recording",col=c("purple"),names=c("
10.07.2013","16.10.2013"))
> boxplot(tc_germ1,tc_germ2,nocth=TRUE,varwidth=TRUE,main=expression(Compari
son~of~Number~of~Germinated~Seedlings~In~Treated~italic(Calluna)),ylab="Numb
er of Germinated Seedlings",xlab="Time of Recording",col=c("green"),names=c(
"10.07.2013","16.10.2013"))
> boxplot(te_germ1,te_germ2,notch=TRUE,varwidth=TRUE,main=expression(Compari
son~of~Number~of~Germinated~Seedlings~In~Treated~italic(Erica)),ylab="Number
 of Germinated Seedlings",xlab="Time of Recording",col=c("purple"),names=c("
10.07.2013","16.10.2013"))
```



*No notch overalp therefore there is not significant difference between the means

Control *Calluna* early germination n = 51 late germination n= 51

Control *Erica* early germination n = 18 late germination n= 18

Treatment *Calluna* early germination n = 35 late germination n = 35

Treatment *Erica* early germination n = 24 late germination n = 24

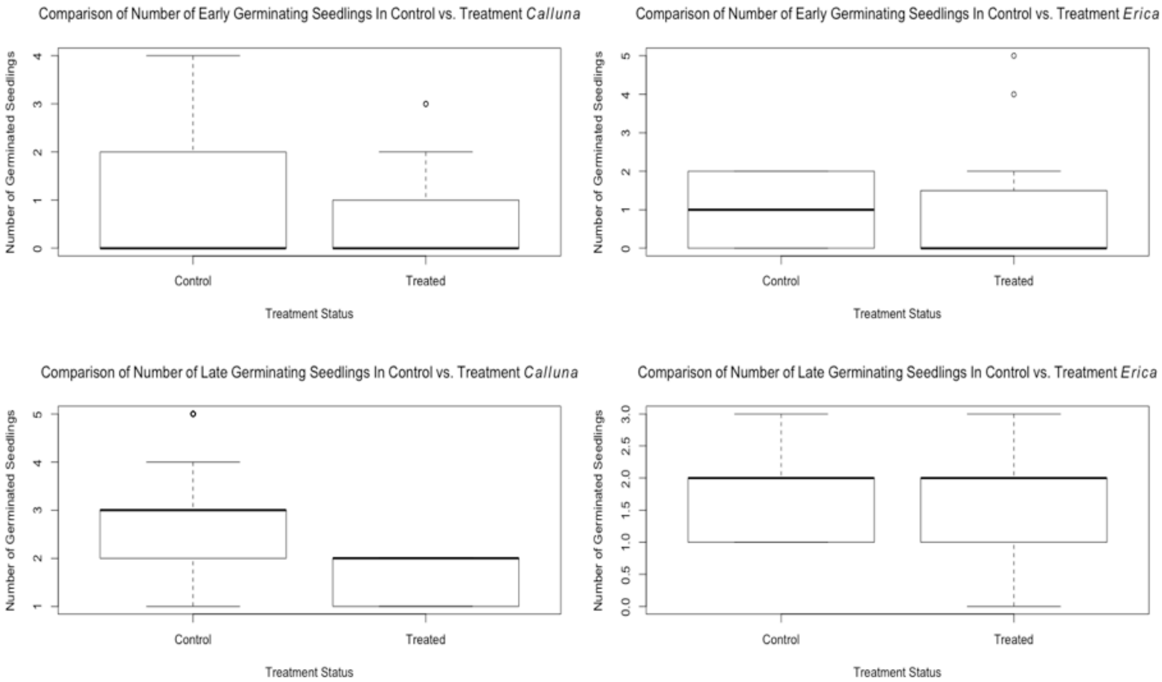
Comparing treatments to controls

par(mfrow=c(2,2))

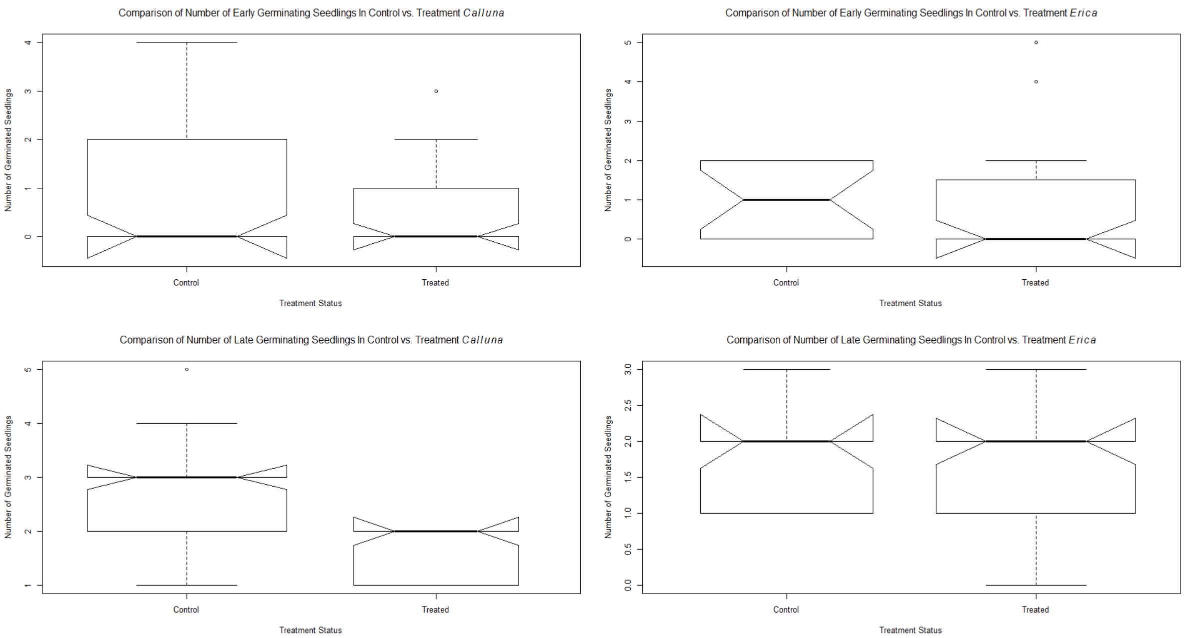
boxplot(cc_germ1,tc_germ1,main=expression(Comparison~of~Number~of~Early~Germinating~Seedlings~In~Control~vs.~Treatment~italic(Calluna)),ylab="Number of Germinated Seedlings",xlab="Treatment Status",names=c("Control","Treated"))

boxplot(ce_germ1,te_germ1,main=expression(Comparison~of~Number~of~Early~Germinating~Seedlings~In~Control~vs.~Treatment~italic(Erica)),ylab="Number of Germinated Seedlings",xlab="Treatment Status",names=c("Control","Treated"))

boxplot(cc_germ2,tc_germ2,main=expression(Comparison~of~Number~of~Late~Germinating~Seedlings~In~Control~vs.~Treatment~italic(Calluna)),ylab="Number of Germinated Seedlings",xlab="Treatment Status",names=c("Control","Treated")) boxplot(ce_germ2,te_germ2,main=expression(Comparison~of~Number~of~Late~Germinating~Seedlings ~In~Control~vs.~Treatment~italic(Erica)),ylab="Number of Germinated Seedlings",xlab="Treatment Status",names=c("Control","Treated"))



When adding notch=TRUE,varwidth=TRUE you get the following plots:



Looking at late germinating seeds of *Calluna* – the notches don't overlap indicating that there is a significant difference between the control and treatment groups.

Comparing the means of the two groups using t-tests/wilcoxon (a non-parametric alternative)

There is only a significant difference when comparing treatment and control *Calluna* at the second germination, whilst it is pretty close to significant when comparing treatment and control *Calluna* at the first germination date.

```
> var.test(cc_germ1,tc_germ1)
            F test to compare two variances
data:  cc_germ1 and tc_germ1
```

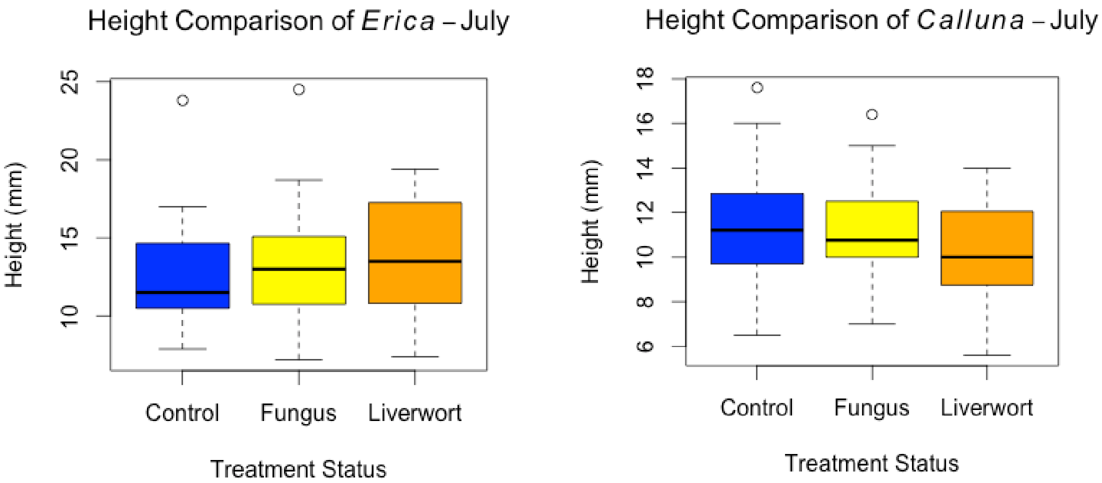
```
F = 2.085, num df = 50, denom df = 34, P-value = 0.02587*
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 1.095143 3.823446
sample estimates:
ratio of variances
        2.085043
> var.test(ce_germ1,te_germ1)
                    F test to compare two variances
data:  ce_germ1 and te_germ1
F = 0.3984, num df = 17, denom df = 23, P-value = 0.05597
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.1649252 1.0247446
sample estimates:
ratio of variances
       0.3984016
> var.test(cc_germ2,tc_germ2)
                    F test to compare two variances
data:  cc_germ2 and tc_germ2
F = 5.7838, num df = 50, denom df = 34, P-value = 5.891e-07***
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
  3.037888 10.606110
sample estimates:
ratio of variances
        5.783838
> var.test(ce_germ2,te_germ2)
                    F test to compare two variances
data:  ce_germ2 and te_germ2
F = 0.7061, num df = 17, denom df = 23, P-value = 0.4663
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.2923114 1.8162449
sample estimates:
ratio of variances
       0.7061222
> wilcox.test(cc_germ1,tc_germ1)
                    Wilcoxon rank sum test with continuity correction
data:  cc_germ1 and tc_germ1
W = 1075, P-value = 0.06644
alternative hypothesis: true location shift is not equal to 0
> t.test(ce_germ1,te_germ1)
                    Welch Two Sample t-test
data:  ce_germ1 and te_germ1
t = 0.4375, df = 39.026, P-value = 0.6641
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.5535194  0.8590750
sample estimates:
mean of x mean of y
0.9444444 0.7916667
> wilcox.test(ce_germ2,te_germ2)
                    Wilcoxon rank sum test with continuity correction data:
```

Appendix 13 - Rstudio transcript, field data, July 2014

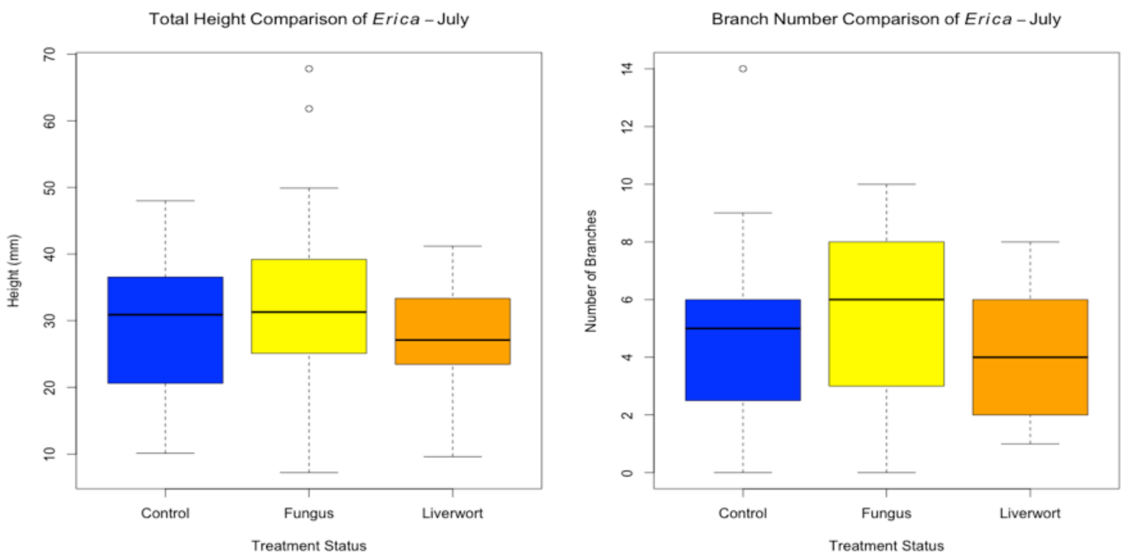
<u>Max height data</u> Use: field_data.txt

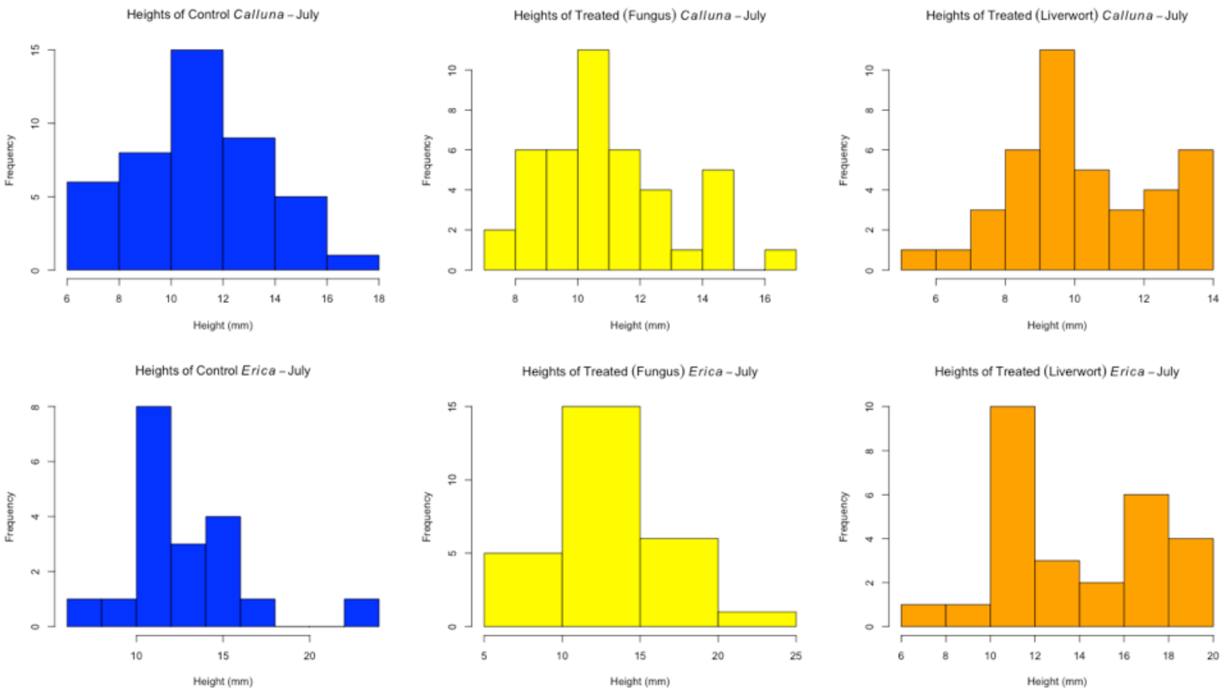
<u>Boxplot</u>

```
boxplot(ccal_height,fcal_height,lcal_height,main=expression(Height~Comparison~of~italic(Calluna)~-July),ylab="Height(mm)",xlab="Treatment Status",col=c("blue","yellow","orange"),names=c("Control","Fungus","Liverwort"))
```




```
boxplot(ceri_height,feri_height,leri_height,main=expression(Height~Comparison~of~italic(Erica)~-July),ylab="Height (mm)",xlab="Treatment Status",col=c("blue","yellow","orange"),names=c("Control","Fungus","Liverwort"))

par(mfrow=c(1,2))

boxplot(ceri_total,feri_total,leri_total,main=expression(Total~Height~Comparison~of~italic(Erica)~-July),ylab="Height (mm)",xlab="Treatment Status",col=c("blue","yellow","orange"),names=c("Control","Fungus","Liverwort"))

boxplot(ceri_branch,feri_branch,leri_branch,main="Branch~Number~Comparison~of~italic(Erica)~-July),ylab="Number of Branches",xlab="Individual Status",col=c("blue","yellow","orange"),names=c("Control","Fungus","Liverwort"))
```



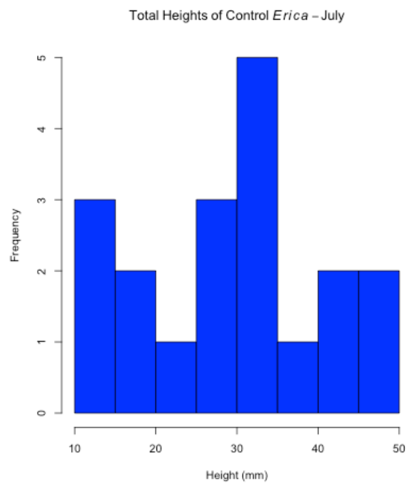


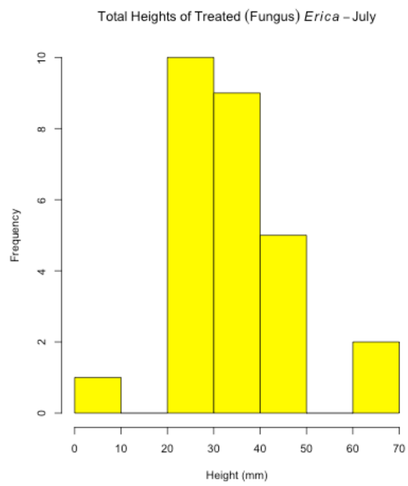
<u>Histograms</u>

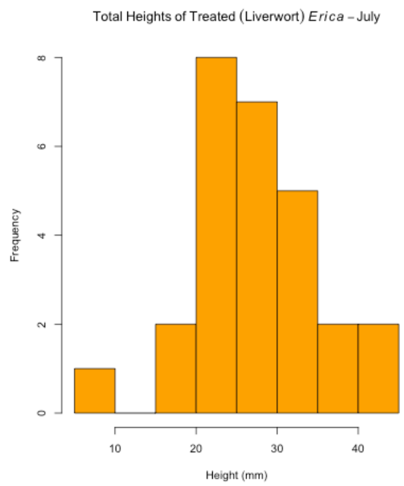
```
par(mfrow=c(2,3))

hist(ccal_height,main=expression(Heights~of~Control~italic(Calluna)~-July),ylab="Frequency",xlab="Height (mm)",col=c("blue"))

hist(fcal_height,main=expression(Heights~of~Treated~(Fungus)~italic(Calluna)~-July),ylab="Frequency",xlab="Height (mm)",col=c("yellow"))

hist(lcal_height,main=expression(Heights~of~Treated~(Liverwort)~italic(Calluna)~-July),ylab="Frequency",xlab="Height (mm)",col=c("orange"))

hist(ceri_height,main=expression(Heights~of~Control~italic(Erica)~-July),ylab="Frequency",xlab="Height (mm)",col=c("blue"))

hist(feri_height,main=expression(Heights~of~Treated~(Fungus)~italic(Erica)~-July),ylab="Frequency",xlab="Height (mm)",col=c("yellow"))

hist(leri_height,main=expression(Heights~of~Treated~(Liverwort)~italic(Erica)~-July),ylab="Frequency",xlab="Height (mm)",col=c("orange"))
```

<u>*Erica* Total Height Data</u>

```
par(mfrow=c(1,3))

hist(ceri_total,main=expression(Total~Heights~of~Control~italic(Erica)~-July),ylab="Frequency",xlab="Height (mm)",col=c("blue"))

hist(feri_total,main=expression(Total~Heights~of~Treated~(Fungus)~italic(Erica)~-July),ylab="Frequency",xlab="Height (mm)",col=c("yellow"))

hist(leri_total,main=expression(Total~Heights~of~Treated~(Liverwort)~italic(Erica)~-July),ylab="Frequency",xlab="Height (mm)",col=c("orange"))
```





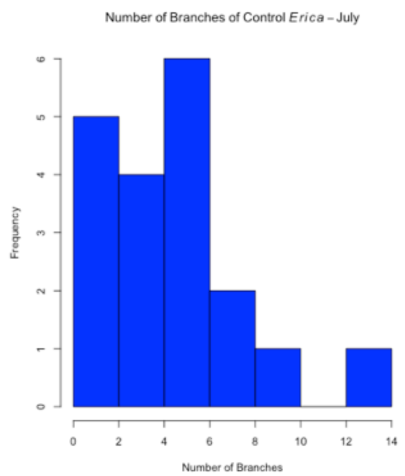


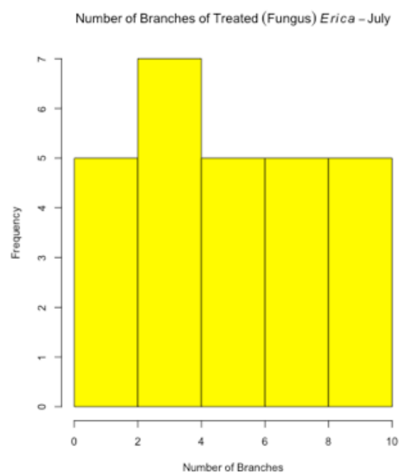
<u>*Erica* Branching Data</u>

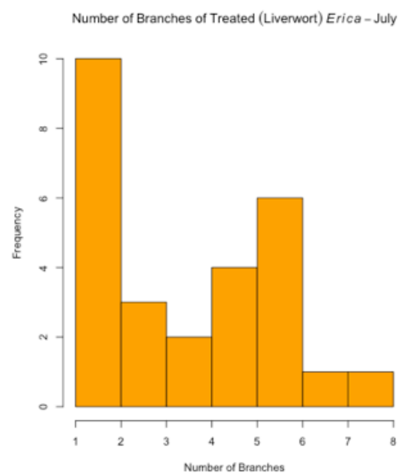
hist(ceri_branch,main=expression(Number~of~Branches~of~Control~italic(Erica)~-July),ylab="Frequency",xlab="Number of Branches",col=c("blue"))

hist(feri_branch,main=expression(Number~of~Branches~of~Treated~(Fungus)~italic(Erica)~-July),ylab="Frequency",xlab="Number of Branches",col=c("yellow"))

hist(leri_branch,main=expression(Number~of~Branches~of~Treated~(Liverwort)~italic(Erica)~-July),ylab="Frequency",xlab="Number of Branches",col=c("orange"))







Data Comparison of Field_data: use field_data, comparing the two treatments to each other (i.e. Fungus to Liverwort)

The only significant result is from the last t-test indicates that there is a difference between the effect of fungus and liverwort on *Erica* branch number.

var.test(fcal_height,lcal_height)

F test to compare two variances

F = 0.9769, num df = 41, denom df = 39, *P*-value = 0.9394

alternative hypothesis: true ratio of variances is not equal to 1

t.test(fcal_height,lcal_height)

Welch Two Sample t-test

t = 1.9696, df = 79.703, *P*-value = 0.05236

alternative hypothesis: true difference in means is not equal to 0

var.test(feri_height,leri_height)

F test to compare two variances

F = 1.0657, num df = 26, denom df = 26, *P*-value = 0.8723

alternative hypothesis: true ratio of variances is not equal to 1

t.test(feri_height,leri_height)

Welch Two Sample t-test

t = -0.505, df = 51.947, *P*-value = 0.6157

alternative hypothesis: true difference in means is not equal to 0

var.test(feri_total,leri_total)

F test to compare two variances

F = 2.9743, num df = 26, denom df = 26, *P*-value = 0.007164**

alternative hypothesis: true ratio of variances is not equal to 1

wilcox.test(feri_total,leri_total)

Wilcoxon rank sum test with continuity correction

W = 462, *P*-value = 0.09331

alternative hypothesis: true location shift is not equal to 0

var.test(feri_branch,leri_branch)

F test to compare two variances

F = 2.1467, num df = 26, denom df = 26, *P*-value = 0.05658

alternative hypothesis: true ratio of variances is not equal to 1

t.test(feri_branch,leri_branch)

Welch Two Sample t-test

t = 2.2572, df = 45.904, *P*-value = 0.0288*

alternative hypothesis: true difference in means is not equal to 0

Comparing control to treated plants

Using field_data_consolidated

No significant results

var.test(ccal_height,tcal_height)

F test to compare two variances

F = 1.3193, num df = 43, denom df = 81, *P*-value = 0.2825

alternative hypothesis: true ratio of variances is not equal to 1

t.test(ccal_height,tcal_height)

Welch Two Sample t-test

t = 1.4878, df = 78.222, P-value = 0.1408

alternative hypothesis: true difference in means is not equal to 0

var.test(ceri_height,teri_height)

F test to compare two variances

F = 0.9826, num df = 18, denom df = 53, *P*-value = 0.9852

alternative hypothesis: true ratio of variances is not equal to 1

t.test(ceri_height,teri_height)

Welch Two Sample t-test

t = -0.8114, df = 31.814, *P*-value = 0.4232

alternative hypothesis: true difference in means is not equal to 0 var.test(ceri_total,teri_total)

F test to compare two variances

F = 1.1688, num df = 18, denom df = 53, *P*-value = 0.6385

alternative hypothesis: true ratio of variances is not equal to 1

t.test(ceri_total,teri_total)

Welch Two Sample t-test

t = -0.4407, df = 29.558, *P*-value = 0.6626

alternative hypothesis: true difference in means is not equal to 0

var.test(ceri_branch,teri_branch)

F test to compare two variances

F = 1.8037, num df = 18, denom df = 53, *P*-value = 0.09946

alternative hypothesis: true ratio of variances is not equal to 1

t.test(ceri_branch,teri_branch)

Welch Two Sample t-test

t = 0.0169, df = 25.38, *P*-value = 0.9866

alternative hypothesis: true difference in means is not equal to 0

end of Rscript

Summary of proportion data analysis (collected July 28th, 2014)

Health

Alive

	Calluna	Erica
Control	43	18
Fungus	40	25
Liverwort	40	26

Poor health

	Calluna	Erica
Control	1	1
Fungus	2	2
Liverwort	0	1

Dead

	Calluna	Erica
Control	2	1
Fungus	0	2
Liverwort	1	2

Total

	Calluna	Erica
Control	46	20
Fungus	42	29
Liverwort	41	29

Prop.test on calluna treated vs not treated (poor health=alive)	Not significant	p-value = 0.7418	prop.test(c(43,81),c(46,84))
Prop.test on Erica treated vs not treated (poor health=alive)	Not significant	p-value = 1	prop.test(c(18,51),c(20,58))
Prop.test on Calluna different treatments (poor health=alive)	Not significant	p-value = 1	prop.test(c(40,40),c(42,41))
Prop.test on Erica different treatments (poor health=alive)	Not significant	p-value = 1	prop.test(c(25,26),c(29,29))

*AND one living treated Calluna not on table as treatment type is unknown

Stress Response

Stressed

	Calluna	Erica
Control	44	7
Fungus	42	9
Liverwort	40	6

Not Stressed

	Calluna	Erica
Control	0	12
Fungus	0	18
Liverwort	0	21

Total

	Calluna	Erica
Control	44	19
Fungus	42	27
Liverwort	40	27

Prop.test on Calluna treated vs. non-treated	Not significant	p-value = NA	prop.test(c(44,83),c(44,83))
Prop.test on Erica treated vs. non-treated	Not significant	p-value = 0.6528	prop.test(c(7,15),c(19,54))
Prop.test on Calluna different treatments	Not significant	p-value = NA	prop.test(c(42,40),c(42,40))
Prop.test on Erica different treatments	Not significant	p-value = 0.5434	prop.test(c(9,6),c(27,27))

*AND one stressed treated Calluna not on table as treatment type is unknown

Flowering

Flowering

	Calluna	Erica
Control	10	2
Fungus	13	8
Liverwort	6	5

Not flowering

	Calluna	Erica
Control	34	17
Fungus	29	19
Liverwort	34	22

Total

	Calluna	Erica
Control	44	19
Fungus	42	27
Liverwort	40	27

Appendix 14 - The Delft, plant survival by plot

ACTUAL								
Plot 1		*Erica*				*Calluna*		
blue:	orig	control	orig	inoculated	orig	control	orig	inoculated
alive	13	7	13	11	11	10	18	18
dead		3		1		1		0
mia		1		0		0		0
nf		2		1		0		0
peach:	orig		orig		orig		orig	
alive	12	10	12	12	11	10	14	12
dead		2		0		0		0
mia		0		0		1		0
NF		0		0		0		2
white:	orig		orig		orig			
alive	11	6	11	5	15	10	24	19
dead		0		2		0		3
mia		0		0		0		0
nf		5		4		5		2
Plot 2		*erica*				*calluna*		
blue:	orig	control	orig	inoculated	orig	control	orig	inoculated
alive	0	0	17	13	10	7	15	15
dead		0		0		3		0
mia		0		2		0		0
nf		0		2		0		0
peach:								
alive	14	11	22	22	11	10	7	7
dead		0		0		1		0
mia		0		0		0		0
NF		3		0		0		0
white:								
alive	21	12	26	16	14	9	17	9
dead		0		0		0		2
mia		0		0		1		3
nf		9		10		4		3
Plot 3		*erica*				*calluna*		
blue:	orig	control	orig	inoculated	orig	control	orig	inoculated
alive	0	0		0	1	0	2	1
dead		0		0		1		1
mia		0		0		0		0
nf		0		0		0		0
peach:								
alive	0	0	1	0	0	0	0	0
dead		0		1		0		0
mia		0		0		0		0
NF		0		0		0		0

white:									
alive	16	8	17	11	14	13	15	12	
dead		7		6		1		3	
mia		1		0		0		0	
nf		0		0		0		0	
Totals	87	87	119	119	87	87	112	112	**405**
alive		54	62%	90	76%	69	79%	93	83%
dead		12	14%	10	8%	7	8%	9	8%
mia		2	2%	2	2%	2	2%	3	3%
nf		19	22%	17	14%	9	10%	7	6%

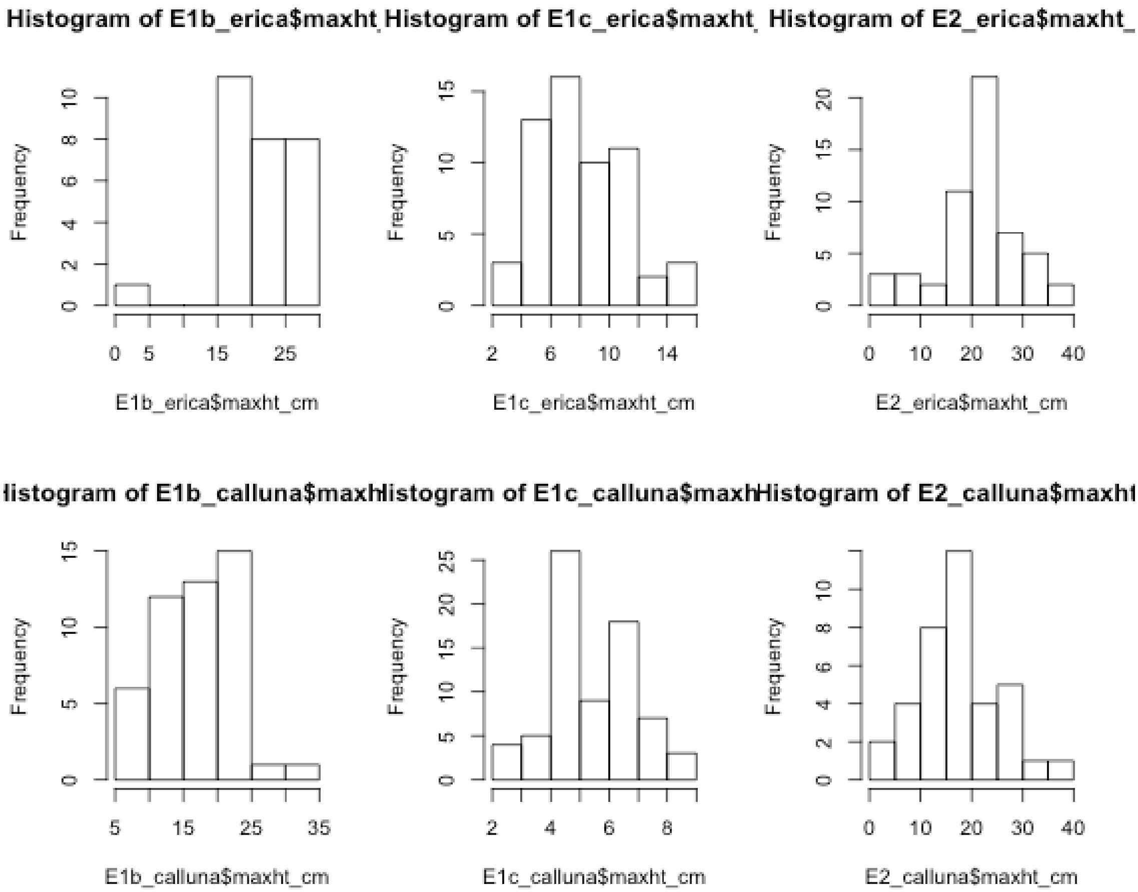
Note: peach (2), blue (1B) and white (1C) shading represent the three different nursery experiments.

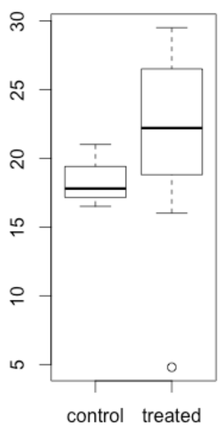
Appendix 15 – Rstudio script from Norfolk and Thursley field experiments

####Norfolk analysis

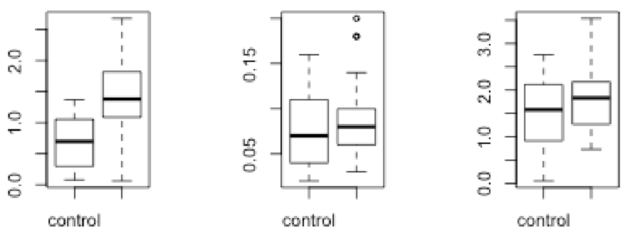
```
###Analysis 1 - all plots with survival, height and weight data
library(lattice) #need lattice package

##import data
norfolk <- read.csv("norfolk.csv")
head(norfolk)

##remove peach and blue plants from block 3
norfolk <- norfolk[-c(22,56,57,189),]
pairs(norfolk) #correlation plot
##change factor levels
norfolk$experiment <- factor(norfolk$experiment)
norfolk$treatment <- factor(norfolk$treatment)
norfolk$taxa <- factor(norfolk$taxa)
norfolk$D.or.A. <- factor(norfolk$D.or.A.)
norfolk$alive <- norfolk$D.or.A.
levels(norfolk$alive) <- c(1,0)
##Split data frame by group and species
E1b_erica <- norfolk[norfolk$experiment == "blue" & norfolk$taxa == "erica",]
E1c_erica <- norfolk[norfolk$experiment == "white" & norfolk$taxa == "erica",]
E2_erica <- norfolk[norfolk$experiment == "peach" & norfolk$taxa == "erica",]
E1b_calluna <- norfolk[norfolk$experiment == "blue" & norfolk$taxa == "calluna",]
E1c_calluna <- norfolk[norfolk$experiment == "white" & norfolk$taxa == "calluna",]
E2_calluna <- norfolk[norfolk$experiment == "peach" & norfolk$taxa == "calluna",]

##simple linear model
##Max height
par(mfrow=c(2,3))
hist(E1b_erica$maxht_cm)
hist(E1c_erica$maxht_cm)
hist(E2_erica$maxht_cm)
hist(E1b_calluna$maxht_cm)
hist(E1c_calluna$maxht_cm)
hist(E2_calluna$maxht_cm)
par(mfrow=c(1,2))
lm_ht_1b_er <- lm(maxht_cm ~ treatment + block, data = E1b_erica)
boxplot(maxht_cm ~ treatment, data = E1b_erica)
lm_ht_1c_er <- lm(maxht_cm ~ treatment + block, data = E1c_erica)
boxplot(maxht_cm ~ treatment, data = E1c_erica)
lm_ht_2_er <- lm(maxht_cm ~ treatment + block, data = E2_erica)
boxplot(maxht_cm ~ treatment, data = E2_erica)
lm_ht_1b_ca <- lm(maxht_cm ~ treatment + block, data = E1b_calluna)
boxplot(maxht_cm ~ treatment, data = E1b_calluna)
lm_ht_1c_ca <- lm(maxht_cm ~ treatment + block, data = E1c_calluna)
boxplot(maxht_cm ~ treatment, data = E1c_calluna)
summary(lm_ht_1b_er)
summary(lm_ht_1c_er)
summary(lm_ht_2_er)
summary(lm_ht_1b_ca)
summary(lm_ht_1c_ca)
summary(lm_ht_2_ca)

# without block effect
par(mfrow=c(1,2))

lm_ht_1b_er <- lm(maxht_cm ~ treatment, data = E1b_erica)
boxplot(maxht_cm ~ treatment, data = E1b_erica)
lm_ht_1b_ca <- lm(maxht_cm ~ treatment, data = E1b_calluna)
boxplot(maxht_cm ~ treatment, data = E1b_calluna)
```

```
###Dead and alive

glm_alive_1b_er <- glm(alive ~ treatment + block, data = E1b_erica, family = "binomial")
summary(glm_alive_1b_er)
tapply(as.numeric(as.character(E1b_erica$alive)), E1b_erica$treatment, function(x) mean(x, na.rm=T))
glm_alive_1c_er <- glm(alive ~ treatment + block, data = E1c_erica, family = "binomial")
summary(glm_alive_1c_er)
tapply(as.numeric(as.character(E1c_erica$alive)), E1c_erica$treatment, function(x) mean(x, na.rm=T))
glm_alive_2_er <- glm(alive ~ treatment + block, data = E2_erica, family = "binomial")
summary(glm_alive_2_er)
tapply(as.numeric(as.character(E2_erica$alive)), E2_erica$treatment, function(x) mean(x, na.rm=T))

glm_alive_1b_ca <- glm(alive ~ treatment + block, data = E1b_calluna, family = "binomial")
summary(glm_alive_1b_ca)
tapply(as.numeric(as.character(E1b_calluna$alive)), E1b_calluna$treatment, function(x) mean(x, na.rm=T))
glm_alive_1c_ca <- glm(alive ~ treatment + block, data = E1c_calluna, family = "binomial")
summary(glm_alive_1c_ca)
tapply(as.numeric(as.character(E1c_calluna$alive)), E1c_calluna$treatment, function(x) mean(x, na.rm=T))
glm_alive_2_ca <- glm(alive ~ treatment + block, data = E2_calluna, family = "binomial")
summary(glm_alive_2_ca)
tapply(as.numeric(as.character(E2_calluna$alive)), E2_calluna$treatment, function(x) mean(x, na.rm=T))
##Dry weight
par(mfrow=c(2,3))
hist(E1b_erica$wt_gr)
hist(E1c_erica$wt_gr)
hist(E2_erica$wt_gr)
hist(E1b_calluna$wt_gr)
hist(E1c_calluna$wt_gr)
hist(E2_calluna$wt_gr)
par(mfrow=c(2,3))
lm_wt_1b_er <- lm(wt_gr ~ treatment + block, data = E1b_erica)
boxplot(wt_gr ~ treatment, data = E1b_erica)
lm_wt_1c_er <- lm(wt_gr ~ treatment + block, data = E1c_erica)
boxplot(wt_gr ~ treatment, data = E1c_erica)
lm_wt_2_er <- lm(wt_gr ~ treatment + block, data = E2_erica)
boxplot(wt_gr ~ treatment, data = E2_erica)
lm_wt_1b_ca <- lm(wt_gr ~ treatment + block, data = E1b_calluna)
boxplot(wt_gr ~ treatment, data = E1b_calluna)
lm_wt_1c_ca <- lm(wt_gr ~ treatment + block, data = E1c_calluna)
boxplot(wt_gr ~ treatment, data = E1c_calluna)
lm_wt_2_ca <- lm(wt_gr ~ treatment + block, data = E2_calluna)
boxplot(wt_gr~ treatment, data = E2_calluna)
summary(lm_wt_1b_ca)
summary(lm_wt_1c_ca)
summary(lm_wt_2_ca)
summary(lm_wt_1b_er)
summary(lm_wt_1c_er)
summary(lm_wt_2_er)
##Height weight ratio
par(mfrow=c(2,3))
hist(E1b_erica$ht.wt)
hist(E1c_erica$ht.wt)
hist(E2_erica$ht.wt)
hist(E1b_calluna$ht.wt)
hist(E1c_calluna$ht.wt)
hist(E2_calluna$ht.wt)
hist(log(E1b_erica$ht.wt))
hist(log(E1c_erica$ht.wt))
hist(log(E2_erica$ht.wt))
hist(log(E1b_calluna$ht.wt))
hist(log(E1c_calluna$ht.wt))
hist(log(E2_calluna$ht.wt))
```





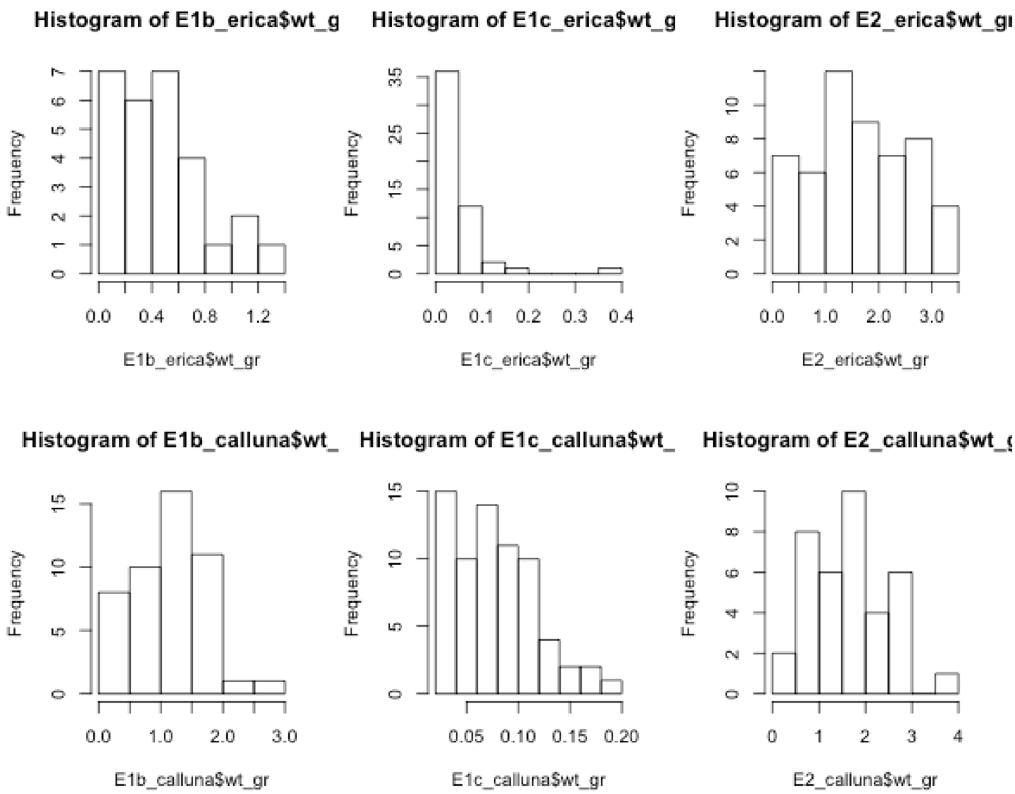
Experiment 1B *Erica* height

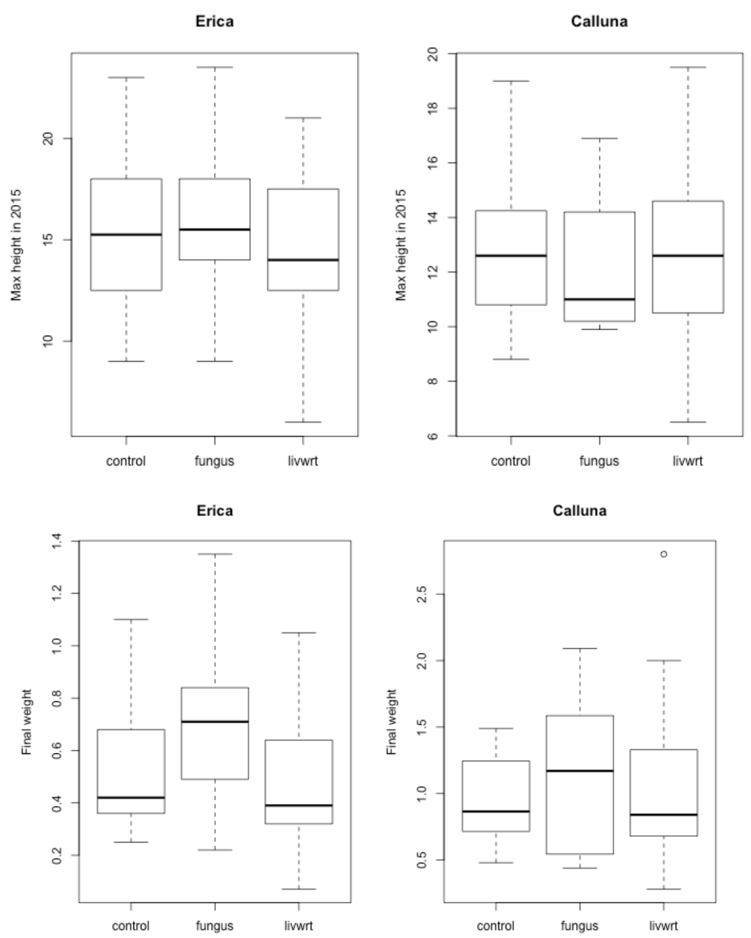


Experiment 1B, 1C, 2, *Calluna* biomass (gr)

```
####Thursley analysis
###Analysis 1 - all plots with survival, height and weight data
library(lattice) #need lattice package
##import data
setwd("N:/CEH/Kew analysis")
thursley <- read.csv("thursley.csv")
head(thursley)
summary(thursley)
#add block numbers
thursley$block[thursley$plot %in% c(1,2,3)] <- "A"
thursley$block[thursley$plot %in% c(4,5,6)] <- "B"
thursley$block[thursley$plot %in% c(7,8,9,10,11)] <- "C"
#convert block to factor
thursley$block <- factor(thursley$block)
#split by species
thurs_erica <- thursley[thursley$taxa == "er",]
thurs_calluna <- thursley[thursley$taxa == "cal",]
###Max Height (2015)
#look at data for each species and produce plot
#top line writes to png file
png("Thursley max height boxplots.png", height = 480, width = 700)
par(mfrow=c(1,2))
boxplot(maxht_cm_15 ~ treatment, data = thurs_erica, main = "Erica", ylab = "Max height in 2015")
boxplot(maxht_cm_15 ~ treatment, data = thurs_calluna, main = "Calluna", ylab = "Max height in 2015")
#last line needed to close plotting device (only need if writing to a file)
dev.off()
#look at distribution of height data
hist(thurs_erica$maxht_cm_15)
hist(thurs_calluna$maxht_cm_15)
#both look normal so use normal model
##run model and return anova style results for each species
#use lm function
lm1 <- lm(maxht_cm_15 ~ treatment + block, data = thurs_erica)
anova(lm1)
##Don't need block effect for calluna as all in one block
lm2 <- lm(maxht_cm_15 ~ treatment, data = thurs_calluna)
anova(lm2)
# no block effect for erica
###Weight
#look at data for each species and produce plot
#top line writes to png file
png("Thursley weight boxplots.png", height = 480, width = 700)
par(mfrow=c(1,2))
boxplot(wt_gr ~ treatment, data = thurs_erica, main = "Erica", ylab = "Final weight")
boxplot(wt_gr ~ treatment, data = thurs_calluna, main = "Calluna", ylab = "Final weight")
#last line needed to close plotting device (only need if writing to a file)
dev.off()
#look at distribution of weight data
hist(thurs_erica$wt_gr)
hist(thurs_calluna$wt_gr)
#both look pretty normal so use normal model
##run model and return anova style results for each species
#use lm function
lm1 <- lm(wt_gr ~ treatment + block, data = thurs_erica)
anova(lm1)
#Evidence of a block effect here
##Don't need block effect for calluna as all in one block
lm2 <- lm(wt_gr ~ treatment, data = thurs_calluna)
anova(lm2)
###Height change 2014-2015
#look at data for each species and produce plot
#top line writes to png file
png("Thursley height change boxplots.png", height = 480, width = 700)
par(mfrow=c(1,2))
boxplot(ht_change ~ treatment, data = thurs_erica, main = "Erica", ylab = "Height change 2014-2015")
boxplot(ht_change ~ treatment, data = thurs_calluna, main = "Calluna", ylab = "Height change 2014-2015")
```

```
#last line needed to close plotting device (only need if writing to a file)
dev.off()
#look at distribution of height change data
hist(thurs_erica$ht_change)
hist(thurs_calluna$ht_change)
#both look pretty normal so use normal model
##run model and return anova style results for each species
#use lm function
lm1 <- lm(ht_change ~ treatment + block, data = thurs_erica)
anova(lm1)
##Don't need block effect for calluna as all in one block
lm2 <- lm(ht_change ~ treatment, data = thurs_calluna)
anova(lm2)
###Survival
#create column of alive/dead as 1/0
thurs_erica$alive[thurs_erica$D_or_A == "A"] <- 1
thurs_erica$alive[thurs_erica$D_or_A == "D"] <- 0
thurs_calluna$alive[thurs_calluna$D_or_A == "A"] <- 1
thurs_calluna$alive[thurs_calluna$D_or_A == "D"] <- 0
##Need to use a binomial model here, not possible to evaluate graphically
#Look at proportions dead/alive in each treatment
tapply(thurs_erica$alive, thurs_erica$treatment, mean)
tapply(thurs_calluna$alive, thurs_calluna$treatment, mean)
##run model and return anova style results for each species
#use lm function
glm1 <- glm(alive ~ treatment + block, data = thurs_erica, family = "binomial")
anova(glm1)
#look at summary to see if any of the differences from baseline are significant
summary(glm1)
##Don't need block effect for calluna as all in one block
glm2 <- glm(alive  ~ treatment, data = thurs_calluna, family = "binomial")
anova(glm2)
summary(glm2)
#indicates significant difference between control and liverwort treatment
```





Norfolk raw data

norfolk plots: planted nov 5, 2014, harvest October 15th

nil=no number tag but plant and or experiment stick in situ
NF - cant find number indicating plant; MIA- found sticks lying about not secured, not near a plant

num	experiment	treatment	taxa	block	D or A*	maxht_cm	wt_gr	ht:wt
515	blue	control	calluna	1	A	18.8	1.13	17
524	blue	control	calluna	1	A	6.4	0.18	36
545	blue	control	calluna	1	A	11.0	0.28	39
573	blue	control	calluna	1	A	5.0	0.08	67
687	blue	control	calluna	1	A	12.5	0.23	53
688	blue	control	calluna	1	A	21.5	1.37	16
699	blue	control	calluna	1	A	11.6	0.35	33
692	blue	control	calluna	1	A	12.5	0.85	15
881	blue	control	calluna	1	A	23.0	1.06	22
nil	blue	control	calluna	1	A	22.3	0.31	72
508	blue	control	calluna	2	A	22.5	0.79	29
568	blue	control	calluna	2	A	20.0	1.05	19
572	blue	control	calluna	2	A	23.0		

679	blue	control	calluna	2	A	8.5	0.57	15
818	blue	control	calluna	2	A	15.0	1.31	11
850	blue	control	calluna	2	A	12.5	0.60	21
913	blue	control	calluna	2	A	12.0	0.93	13
608	blue	control	calluna	1	D	[redacted]		
532	blue	control	calluna	2	D			
868	blue	control	calluna	2	D			
660	blue	control	calluna	2	D			
547	blue	control	calluna	3	D			
690	blue	control	calluna	1	NF	remove from NF		
649	blue	treated	calluna	1	A	8.0	0.16	49
990	blue	treated	calluna	1	A	17.0	0.94	18
564	blue	treated	calluna	1	A	22.2	2.68	8
693	blue	treated	calluna	1	A	20.1	1.15	17
704	blue	treated	calluna	1	A	16.0	1.19	13
705	blue	treated	calluna	1	A	16.0	1.08	15
727	blue	treated	calluna	1	A	6.2	0.06	109
732	blue	treated	calluna	1	A	22.8	1.20	19
763	blue	treated	calluna	1	A	23.5	1.39	17
929	blue	treated	calluna	1	A	13.0	1.09	12
930	blue	treated	calluna	1	A	22.0	1.16	19
933	blue	treated	calluna	1	A	10.2	0.59	17
946	blue	treated	calluna	1	A	25.2	1.56	16
950	blue	treated	calluna	1	A	25.0	1.90	13
969	blue	treated	calluna	1	A	18.0	1.13	16
970	blue	treated	calluna	1	A	19.1	2.17	9
981	blue	treated	calluna	1	A	20.0	2.00	10
983	blue	treated	calluna	1	A	16.6	1.24	13
712	blue	treated	calluna	2	A	16.5	1.47	11
716	blue	treated	calluna	2	A	15.4	0.85	18
718	blue	treated	calluna	2	A	31.0	1.52	20
722	blue	treated	calluna	2	A	13.0	1.51	9
737	blue	treated	calluna	2	A	10.0	0.86	12
768	blue	treated	calluna	2	A	8.2	0.41	20
776	blue	treated	calluna	2	A	20.0	1.79	11
888	blue	treated	calluna	2	A	24.5	1.89	13
937	blue	treated	calluna	2	A	24.0	2.00	12
956	blue	treated	calluna	2	A	11.0	0.60	18
979	blue	treated	calluna	2	A	20.0	1.38	14
989	blue	treated	calluna	2	A	13.0	1.79	7
991	blue	treated	calluna	2	A	16.0	0.83	19
nil	blue	treated	calluna	2	A	22.0	1.85	12
920	blue	treated	calluna	2	A	22.0	1.85	12
nil	blue	treated	calluna	3	A	22.0		

982	blue	treated	calluna	3	D			
784	blue	treated	calluna	2	NF	remove from NF		
899	blue	control	erica	1	A	16.5	0.53	31
594	blue	control	erica	1	A	4.5	0.04	107
603	blue	control	erica	1	A	19.0	0.24	79
613	blue	control	erica	1	A	17.8	0.21	86
863	blue	control	erica	1	A	16.0	0.25	65
880	blue	control	erica	1	A	24.5	0.73	33
856	blue	control	erica	1	A	21.0	0.20	107
633	blue	control	erica	1	D			
691	blue	control	erica	1	D			
839	blue	control	erica	1	D			
674	blue	control	erica	1	MIA			
611	blue	control	erica	1	NF			
908	blue	control	erica	1	NF			
664	blue	treated	erica	1	A	29.0	1.01	29
550	blue	treated	erica	1	A	17.8	0.28	63
606	blue	treated	erica	1	A	19.5	0.35	56
611	blue	treated	erica	1	A	22.8	0.17	138
628	blue	treated	erica	1	A	29.5	1.21	24
681	blue	treated	erica	1	A	21.5	0.59	36
803	blue	treated	erica	1	A	19.5	0.52	38
819	blue	treated	erica	1	A	19.8	0.62	32
846	blue	treated	erica	1	A	25.0	1.07	23
848	blue	treated	erica	1	A	17.0	0.37	46
851	blue	treated	erica	1	A	4.8	0.05	91
671	blue	treated	erica	2	A	25.5	0.81	31
548	blue	treated	erica	2	A	23.0	0.53	44
598	blue	treated	erica	2	A	16.0	0.13	126
623	blue	treated	erica	2	A	29.5	0.12	257
672	blue	treated	erica	2	A	18.5	0.28	66
744	blue	treated	erica	2	A	18.0	0.51	35
796	blue	treated	erica	2	A	22.2	0.49	45
808	blue	treated	erica	2	A	26.5	0.22	120
823	blue	treated	erica	2	A	28.4	0.69	41
842	blue	treated	erica	2	A	21.0	0.19	113
852	blue	treated	erica	2	A	18.8	0.20	93
855	blue	treated	erica	2	A	27.5	0.59	46
865	blue	treated	erica	2	A	29.0	0.61	47
904	blue	treated	erica	2	A	24.5	0.62	39
901	blue	treated	erica	1	D			
371	blue	treated	erica	2	MIA			
530	blue	treated	erica	2	MIA			
657	blue	treated	erica	1	NF			

593	blue	treated	erica	2	NF			
690	blue	treated	erica	2	NF			
nil	blue	treated	not sure	3	D		left out of count	
1036	peach	control	calluna	1	A	8.0	0.99	8
1037	peach	control	calluna	1	A	18.0	2.60	7
1040	peach	control	calluna	1	A	13.2	1.17	11
1048	peach	control	calluna	1	A	26.5	1.67	16
1052	peach	control	calluna	1	A	13.7	2.37	6
1054	peach	control	calluna	1	A	18.0	1.81	10
1056	peach	control	calluna	1	A	14.5	1.87	8
nil	peach	control	calluna	1	A	18.5	1.59	12
nil	peach	control	calluna	1	A	14.5	2.53	6
1021	peach	control	calluna	2	A	18.8	0.73	26
1034	peach	control	calluna	2	A	12.5	1.50	8
1035	peach	control	calluna	2	A	27.5	1.24	22
1038	peach	control	calluna	2	A	4.0	0.21	19
1039	peach	control	calluna	2	A	11.0	0.79	14
1041	peach	control	calluna	2	A	16.0	0.83	19
1041	peach	control	calluna	2	A	23.0	1.57	15
1046	peach	control	calluna	2	A	27.5	2.76	10
1055	peach	control	calluna	2	A	31.5	2.61	12
nil	peach	control	calluna	2	A	39.0	1.86	21
1019	peach	control	calluna	2	D			
1047	peach	control	calluna	1	MIA			
1043	peach	control	calluna	1	NF	remove from NF		
1050	peach	control	calluna	1	NF	remove from NF		
1044	peach	control	calluna	2	NF	remove from NF		
1024	peach	control	calluna	1	A	1.5	0.05	33
643	peach	treated	calluna	1	A	21.5	2.68	8
507	peach	treated	calluna	1	A	7.5	0.79	10
509	peach	treated	calluna	1	A	19.0	2.25	8
517	peach	treated	calluna	1	A	22.5	2.18	10
820	peach	treated	calluna	1	A	14.2	0.77	18
843	peach	treated	calluna	1	A	8.0	0.95	8
858	peach	treated	calluna	1	A	9.5	0.73	13
879	peach	treated	calluna	1	A	13.0	1.67	8
879	peach	treated	calluna	1	A	17.0	1.27	13
883	peach	treated	calluna	1	A	18.5	3.54	5
nil	peach	treated	calluna	1	A	23.5	2.18	11
627	peach	treated	calluna	2	A	28.2	1.28	22
817	peach	treated	calluna	2	A	28.0	1.87	15
854	peach	treated	calluna	2	A	19.5	2.56	8

861	peach	treated	calluna	2	A	19.0	1.30	15
867	peach	treated	calluna	2	A			
886	peach	treated	calluna	2	A	19.0	1.83	10
nil	peach	treated	calluna	2	A	15.5	1.94	8
598	peach	treated	calluna	1	NF	remove from NF		
698	peach	treated	calluna	1	NF	remove from NF		
880	peach	treated	calluna	1	NF			
882	peach	treated	calluna	1	NF			
879A	peach	treated	calluna	1	NF			
1001	peach	control	erica	1	A	23.3	1.42	16
1003	peach	control	erica	1	A	25.0	1.66	15
1011	peach	control	erica	1	A	7.0	0.03	212
1012	peach	control	erica	1	A	25.0	2.79	9
1017	peach	control	erica	1	A	17.8	0.40	45
1025	peach	control	erica	1	A	15.0	0.60	25
1030	peach	control	erica	1	A	32.6	2.68	12
1033	peach	control	erica	1	A	38.0	2.56	15
nil	peach	control	erica	1	A	25.8	1.61	16
nil	peach	control	erica	1	A	3.0	0.10	31
1006	peach	control	erica	2	A	26.5	1.11	24
1009	peach	control	erica	2	A	19.5	0.85	23
1010	peach	control	erica	2	A	9.0	0.46	20
1013	peach	control	erica	2	A	20.0	1.27	16
1018	peach	control	erica	2	A	22.0	1.61	14
1028	peach	control	erica	2	A	29.0		
1029	peach	control	erica	2	A	24.0	1.55	15
1031	peach	control	erica	2	A	24.0	0.95	25
1032	peach	control	erica	2	A	19.5	1.94	10
nil	peach	control	erica	2	A	25.0	1.43	17
1026	peach	control	erica	2	A	29.0	2.48	12
1007	peach	control	erica	1	D			
1015	peach	control	erica	1	D			
1016	peach	control	erica	1	NF	remove from NF		
1002	peach	control	erica	2	NF			
1005	peach	control	erica	2	NF			
1014	peach	control	erica	2	NF			
1020	peach	control	erica	2	NF			
nil	peach	treated	erica	1	A	30.5	1.43	21
518	peach	treated	erica	1	A	21.0	3.12	7
520	peach	treated	erica	1	A	20.5	2.54	8
543	peach	treated	erica	1	A	4.8	0.17	29
578	peach	treated	erica	1	A	21.5	3.37	6
600	peach	treated	erica	1	A	33.5	2.85	12

869	peach	treated	erica	1	A	9.5	0.19	51
886	peach	treated	erica	1	A	19.0	0.70	27
898	peach	treated	erica	1	A	32.0	2.03	16
917	peach	treated	erica	1	A	21.5	1.94	11
334	peach	treated	erica	2	A	19.0	2.14	9
503	peach	treated	erica	2	A	22.0	2.68	8
504	peach	treated	erica	2	A	28.5	1.38	21
505	peach	treated	erica	2	A	17.0	0.68	25
528	peach	treated	erica	2	A	22.8	1.44	16
531	peach	treated	erica	2	A	22.0	1.62	14
577	peach	treated	erica	2	A	20.0	2.07	10
582	peach	treated	erica	2	A	20.0	3.31	6
596	peach	treated	erica	2	A	23.5	1.51	16
599	peach	treated	erica	2	A	37.0	2.61	14
609	peach	treated	erica	2	A	20.0	1.35	15
614	peach	treated	erica	2	A	24.0	3.30	7
617	peach	treated	erica	2	A	22.2	2.05	11
624	peach	treated	erica	2	A	23.0	2.67	9
634	peach	treated	erica	2	A	24.0	2.03	12
806	peach	treated	erica	2	A	34.0	1.77	19
837	peach	treated	erica	2	A	22.0		
841	peach	treated	erica	2	A	25.0	1.43	17
875	peach	treated	erica	2	A	17.5	1.49	12
877	peach	treated	erica	2	A	14.0	0.88	16
888	peach	treated	erica	2	A	27.5	2.04	14
912	peach	treated	erica	2	A	21.0	1.37	15
nil	peach	treated	erica	2	A	5.0	0.08	60
898	peach	treated	erica	3	D	[redacted]		
576	peach	treated	erica	1	NF	26.8	1.49	18
815	peach	treated	erica	1	NF	maybe the nil in 2		
nil	white	control	calluna	1	A	6.0	0.05	115
nil	white	control	calluna	1	A	7.1	0.15	48
nil	white	control	calluna	1	A	6.5	0.12	53
nil	white	control	calluna	1	A	6.5	0.06	103
nil	white	control	calluna	1	A	6.8	0.04	170
nil	white	control	calluna	1	A	4.5		
nil	white	control	calluna	1	A	8.0	0.21	38
nil	white	control	calluna	1	A	6.0	0.11	55
nil	white	control	calluna	1	A	3.5	0.03	140
nil	white	control	calluna	1	A	6.0	0.14	43
nil	white	control	calluna	2	A	9.0	0.16	57
nil	white	control	calluna	2	A	6.5	0.14	46
nil	white	control	calluna	2	A	5.0	0.07	71
nil	white	control	calluna	2	A	2.0	0.03	69
nil	white	control	calluna	2	A	4.0		

nil	white	control	calluna	2	A	5.0	0.11	45
nil	white	control	calluna	2	A	7.5	0.12	61
nil	white	control	calluna	2	A	3.0	0.03	88
nil	white	control	calluna	2	A	7.5	0.11	68
nil	white	control	calluna	3	A	4.7	0.04	124
nil	white	control	calluna	3	A	7.0	0.06	113
nil	white	control	calluna	3	A	2.0	[redacted]	
nil	white	control	calluna	3	A	5.0	0.09	54
nil	white	control	calluna	3	A	6.2	0.07	91
nil	white	control	calluna	3	A	4.6	0.05	87
nil	white	control	calluna	3	A	3.0	0.02	150
nil	white	control	calluna	3	A	8.2	0.11	78
nil	white	control	calluna	3	A	4.2	0.03	140
nil	white	control	calluna	3	A	6.8	0.11	60
nil	white	control	calluna	3	A	6.5	0.07	90
nil	white	control	calluna	3	A	6.5	0.03	191
304	white	control	calluna	3	A	3.6	0.04	84
232	white	control	calluna	2	MIA			
230	white	control	calluna	3	MIA			
249	white	control	calluna	1	NF	remove from NF		
250	white	control	calluna	1	NF	remove from NF		
251	white	control	calluna	1	NF	remove from NF		
252	white	control	calluna	1	NF	remove from NF		
253	white	control	calluna	1	NF	remove from NF		
254	white	control	calluna	1	NF	remove from NF		
256	white	control	calluna	1	NF	remove from NF		
257	white	control	calluna	1	NF	remove from NF		
260	white	control	calluna	1	NF	remove from NF		
261	white	control	calluna	1	NF	remove from NF		
264	white	control	calluna	1	NF			
267	white	control	calluna	1	NF			
271	white	control	calluna	1	NF			
273	white	control	calluna	1	NF			
279	white	control	calluna	1	NF			
238	white	control	calluna	2	NF	removed from NF		
269	white	control	calluna	2	NF	removed from NF		
276	white	control	calluna	2	NF	removed from NF		

277	white	control	calluna	2	NF	removed from NF		
278	white	control	calluna	2	NF	removed from NF		
280	white	control	calluna	2	NF	removed from NF		
281	white	control	calluna	2	NF	removed from NF		
282	white	control	calluna	2	NF	removed from NF		
283	white	control	calluna	2	NF	removed from NF		
284	white	control	calluna	2	NF			
301	white	control	calluna	2	NF			
302	white	control	calluna	2	NF			
305	white	control	calluna	2	NF			
231	white	control	calluna	3	NF	remove from NF		
242	white	control	calluna	3	NF	remove from NF		
246	white	control	calluna	3	NF	remove from NF		
265	white	control	calluna	3	NF	remove from NF		
287	white	control	calluna	3	NF	remove from NF		
289	white	control	calluna	3	NF	remove from NF		
290	white	control	calluna	3	NF	remove from NF		
292	white	control	calluna	3	NF	remove from NF		
293	white	control	calluna	3	NF	remove from NF		
294	white	control	calluna	3	NF	remove from NF		
296	white	control	calluna	3	NF	remove from NF		
300	white	control	calluna	3	NF	remove from NF		
23	white	treated	calluna	1	A	4.5	0.05	90
31	white	treated	calluna	1	A	5.0	0.05	93
nil	white	treated	calluna	1	A	4.6	0.04	128
nil	white	treated	calluna	1	A	6.5	0.08	81
nil	white	treated	calluna	1	A	5.0	0.07	69
nil	white	treated	calluna	1	A	3.8	0.03	131
nil	white	treated	calluna	1	A	5.0	0.07	69
36	white	treated	calluna	1	A	7.2	0.18	41
nil	white	treated	calluna	1	A	4.5	0.10	47
nil	white	treated	calluna	1	A	5.5	0.04	149
nil	white	treated	calluna	1	A	7.5	0.12	61
nil	white	treated	calluna	1	A	6.5	0.07	98

nil	white	treated	calluna	1	A	4.5	0.07	62
nil	white	treated	calluna	1	A	4.5	0.08	58
nil	white	treated	calluna	1	A	5.5	0.03	190
nil	white	treated	calluna	1	A	6.1	0.08	73
nil	white	treated	calluna	1	A	4.2	0.06	76
nil	white	treated	calluna	1	A	6.0	0.09	65
nil	white	treated	calluna	1	A	5.0	0.09	59
nil	white	treated	calluna	1	A	6.0	0.10	58
nil	white	treated	calluna	1	A	4.0	0.09	47
50	white	treated	calluna	2	A	4.5	0.09	48
51	white	treated	calluna	2	A	4.5	0.08	59
58	white	treated	calluna	2	A	4.8	0.12	41
63	white	treated	calluna	2	A	7.0	0.14	49
65	white	treated	calluna	2	A	6.5	0.08	86
76	white	treated	calluna	2	A	7.0	0.07	99
89	white	treated	calluna	2	A	5.5	0.12	46
nil	white	treated	calluna	2	A	4.5	0.05	88
nil	white	treated	calluna	2	A	6.5	0.09	69
45	white	treated	calluna	3	A	4.5	0.09	50
46	white	treated	calluna	3	A	7.2	0.11	68
55	white	treated	calluna	3	A	4.5	0.06	80
64	white	treated	calluna	3	A	6.6	0.20	33
nil	white	treated	calluna	3	A	8.5	0.10	89
nil	white	treated	calluna	3	A	6.0	0.09	67
nil	white	treated	calluna	3	A	4.5	0.06	75
nil	white	treated	calluna	3	A	6.8	0.08	83
nil	white	treated	calluna	3	A	6.8	0.13	52
nil	white	treated	calluna	3	A	4.8	0.04	120
nil	white	treated	calluna	3	A	8.0	0.18	45
nil	white	treated	calluna	3	A	4.5	0.03	145
16	white	treated	calluna	1	D			
22	white	treated	calluna	1	D			
48	white	treated	calluna	1	D			
54	white	treated	calluna	2	D			
73	white	treated	calluna	2	D			
71	white	treated	calluna	3	D			
72	white	treated	calluna	3	D			
nil	white	treated	calluna	3	D			
49	white	treated	calluna	2	MIA			
53	white	treated	calluna	2	MIA			
62	white	treated	calluna	2	MIA			
1	white	treated	calluna	1	NF	remove from NF		
4	white	treated	calluna	1	NF	remove from NF		

7	white	treated	calluna	1	NF	remove from NF
8	white	treated	calluna	1	NF	remove from NF
9	white	treated	calluna	1	NF	remove from NF
10	white	treated	calluna	1	NF	remove from NF
12	white	treated	calluna	1	NF	remove from NF
14	white	treated	calluna	1	NF	remove from NF
17	white	treated	calluna	1	NF	remove from NF
18	white	treated	calluna	1	NF	remove from NF
19	white	treated	calluna	1	NF	remove from NF
21	white	treated	calluna	1	NF	remove from NF
24	white	treated	calluna	1	NF	remove from NF
25	white	treated	calluna	1	NF	remove from NF
26	white	treated	calluna	1	NF	remove from NF
27	white	treated	calluna	1	NF	remove from NF
33	white	treated	calluna	1	NF	remove from NF
34	white	treated	calluna	1	NF	remove from NF
35	white	treated	calluna	1	NF	
37	white	treated	calluna	1	NF	
40	white	treated	calluna	2	NF	removed from NF
41	white	treated	calluna	2	NF	removed from NF
43	white	treated	calluna	2	NF	
74	white	treated	calluna	2	NF	
89a	white	treated	calluna	2	NF	
20	white	treated	calluna	3	NF	removed from NF
32	white	treated	calluna	3	NF	removed from NF
42	white	treated	calluna	3	NF	removed from NF
47	white	treated	calluna	3	NF	removed from NF
52	white	treated	calluna	3	NF	removed from NF
57	white	treated	calluna	3	NF	removed from NF
66	white	treated	calluna	3	NF	removed

						from NF		
nil	white	control	erica	1	A	6.0	0.06	102
nil	white	control	erica	1	A	7.1	0.04	182
nil	white	control	erica	1	A	10.0	0.05	208
nil	white	control	erica	1	A	3.5	0.03	113
nil	white	control	erica	1	A	11.5	0.09	131
nil	white	control	erica	1	A	7.5		
207	white	control	erica	2	A	14.0	0.09	165
nil	white	control	erica	2	A	4.0	0.04	93
nil	white	control	erica	2	A	7.8	0.05	144
nil	white	control	erica	2	A	6.5	0.17	38
nil	white	control	erica	2	A	7.5	0.03	234
nil	white	control	erica	2	A	9.0	0.06	155
nil	white	control	erica	2	A	10.0	0.09	115
nil	white	control	erica	2	A	15.5	0.08	207
nil	white	control	erica	2	A	16.0	0.11	145
nil	white	control	erica	2	A	9.0	0.05	180
nil	white	control	erica	2	A	12.0	0.02	600
nil	white	control	erica	2	A	12.0	0.06	211
nil	white	control	erica	3	A	8.7	0.05	171
nil	white	control	erica	3	A	8.0	0.04	229
nil	white	control	erica	3	A	14.5	0.07	220
nil	white	control	erica	3	A	11.6	0.03	363
nil	white	control	erica	3	A	5.0	0.04	139
nil	white	control	erica	3	A	5.0	0.04	125
nil	white	control	erica	3	A	5.0	0.02	217
nil	white	control	erica	3	A	9.8	0.05	209
160	white	control	erica	3	D			
223	white	control	erica	3	D			
210	white	control	erica	3	D			
220	white	control	erica	3	D			
221	white	control	erica	3	D			
221	white	control	erica	3	D			
222	white	control	erica	3	D			
162	white	control	erica	3	MIA			
182	white	control	erica	1	NF	remove from NF		
194	white	control	erica	1	NF	remove from NF		
197	white	control	erica	1	NF	remove from NF		
198	white	control	erica	1	NF	remove from NF		
201	white	control	erica	1	NF	remove from NF		
202	white	control	erica	1	NF	remove from NF		

203	white	control	erica	1	NF	
205	white	control	erica	1	NF	
215	white	control	erica	1	NF	
216	white	control	erica	1	NF	
218	white	control	erica	1	NF	
158	white	control	erica	2	NF	removed from NF
159	white	control	erica	2	NF	removed from NF
164	white	control	erica	2	NF	removed from NF
165	white	control	erica	2	NF	removed from NF
166	white	control	erica	2	NF	removed from NF
170	white	control	erica	2	NF	removed from NF
171	white	control	erica	2	NF	removed from NF
199	white	control	erica	2	NF	removed from NF
200	white	control	erica	2	NF	removed from NF
204	white	control	erica	2	NF	removed from NF
206	white	control	erica	2	NF	removed from NF
208	white	control	erica	2	NF	
209	white	control	erica	2	NF	
214	white	control	erica	2	NF	
217	white	control	erica	2	NF	
219	white	control	erica	2	NF	
224	white	control	erica	2	NF	
225	white	control	erica	2	NF	
226	white	control	erica	2	NF	
228	white	control	erica	2	NF	
153	white	control	erica	3	NF	removed from NF
154	white	control	erica	3	NF	removed from NF
155	white	control	erica	3	NF	removed from NF
156	white	control	erica	3	NF	removed from NF
157	white	control	erica	3	NF	removed from NF
161	white	control	erica	3	NF	removed from NF
163	white	control	erica	3	NF	removed from NF
167	white	control	erica	3	NF	removed from NF

82	white	treated	erica	1	A	10.6	0.03	312
84	white	treated	erica	1	A	11.0	0.06	183
85	white	treated	erica	1	A	10.5	0.04	250
77	white	treated	erica	1	A	5.0	0.05	104
91	white	treated	erica	1	A	7.8	0.13	61
78	white	treated	erica	2	A	8.0	0.38	21
89	white	treated	erica	2	A	12.0	0.06	211
90	white	treated	erica	2	A	4.5	0.04	107
95	white	treated	erica	2	A	7.0	0.05	130
108	white	treated	erica	2	A	8.0	0.04	222
112	white	treated	erica	2	A	6.8	0.04	179
114	white	treated	erica	2	A	4.5	0.04	115
122	white	treated	erica	2	A	10.0	0.06	164
122	white	treated	erica	2	A	9.5	0.04	232
123	white	treated	erica	2	A	4.3	0.05	90
124	white	treated	erica	2	A	12.4	0.04	282
126	white	treated	erica	2	A	11.5	0.05	225
129	white	treated	erica	2	A	4.5		
89a	white	treated	erica	2	A	6.0	0.04	162
nil	white	treated	erica	2	A	5.0		
103	white	treated	erica	2	A	12.0	0.05	240
101	white	treated	erica	3	A	10.2	0.05	200
109	white	treated	erica	3	A	8.0	0.03	267
110	white	treated	erica	3	A	7.7	0.03	248
111	white	treated	erica	3	A	7.0	0.03	250
115	white	treated	erica	3	A	9.6	0.04	246
119	white	treated	erica	3	A	6.2	0.03	248
130	white	treated	erica	3	A	5.5	0.02	344
nil	white	treated	erica	3	A	9.0	0.06	150
nil	white	treated	erica	3	A	5.5		
nil	white	treated	erica	3	A	3.0		
nil	white	treated	erica	3	A	7.8		
79	white	treated	erica	1	D			
80	white	treated	erica	1	D			
105	white	treated	erica	3	D			
120	white	treated	erica	3	D			
121	white	treated	erica	3	D			
127	white	treated	erica	3	D			
81	white	treated	erica	3	D			
777	white	treated	erica	3	D			
86	white	treated	erica	1	NF			
94	white	treated	erica	1	NF			
95	white	treated	erica	1	NF			
112	white	treated	erica	1	NF			
81	white	treated	erica	2	NF	removed		

						from NF	
83	white	treated	erica	2	NF		
94	white	treated	erica	2	NF		
98	white	treated	erica	2	NF		
100	white	treated	erica	2	NF		
102	white	treated	erica	2	NF		
104	white	treated	erica	2	NF		
128	white	treated	erica	2	NF		
131	white	treated	erica	2	NF		
132	white	treated	erica	2	NF		
133	white	treated	erica	2	NF		
107	white	treated	erica	3	NF	removed from NF	
113	white	treated	erica	3	NF	removed from NF	
116	white	treated	erica	3	NF	removed from NF	
117	white	treated	erica	3	NF	removed from NF	
nil	white	control	not sure	2	D		left out of count
nil	white	control	not sure	2	D		left out of count
nil	white	control	not sure	3	D	removed from NF	
nil	white	control	not sure	3	D	removed from NF	
nil	white	control	not sure	3	D	removed from NF	
nil	white	control	not sure	3	D	removed from NF	
nil	white	control	not sure	3	D	removed from NF	
nil	white	control	not sure	3	D	not in above summary yet. Need to look at unaccounted to deduce	
nil	white	control	not sure	3	D	not in above summary yet. Need to look at unaccounted to deduce	
nil	white	control	not sure	3	D	not in above summary yet. Need to look at unaccounte	

						d to deduce	
nil	white	control	not sure	3	D	not in above summary yet. Need to look at unaccounted to deduce	
nil	white	control	not sure	3	D	not in above summary yet. Need to look at unaccounted to deduce	
nil	white	control	not sure	3	D	not in above summary yet. Need to look at unaccounted to deduce	
nil	white	treated	not sure	2	D		left out of count
nil	white	treated	not sure	3	D	not in above summary yet. Need to look at unaccounted to deduce	

Thursley raw data

num	taxa	treatment	plot	D_or_A	maxht_cm_15	totht_cm_15	wt_gr	maxht_cm_14	totht_cm_14
724	cal	control	7	A	11.5	n/a	0.48	8	8
922	cal	control	9	A	9.9	n/a	0.56	8	8
966	cal	control	7	A	8.8	n/a	0.64	7.5	7.5
673	cal	control	8	A	14.6	n/a	0.67	14.5	14.5
938	cal	control	8	A	10.2	n/a	0.76	9.6	9.6
976	cal	control	9	A	13.1	n/a	0.78	12.2	12.2
643	cal	control	11	A	9.8	n/a	0.82	10	10
658	cal	control	7	A	14.0	n/a	0.82	14	14
607	cal	control	7	A	13.5	n/a	0.91	12	12

936	cal	control	7	A	13.5	n/a	1.12	10.5	10.5
960	cal	control	9	A	11.4	n/a	1.21	11.2	11.2
619	cal	control	7	A	19.0	n/a	1.21	16	16
615	cal	control	11	A	11.7	n/a	1.30	10.9	10.9
685	cal	control	7	A	12.1	n/a	1.36	11.5	11.5
672	cal	control	9	A	15.0	n/a	1.49	11.9	11.9
980	cal	control	8	A	14.5	n/a	1.28	14	14
897	cal	fungus	10	A	10.0	n/a	0.44	8.6	8.6
623	cal	fungus	10	A	13.1	n/a	0.51	11.4	11.4
923	cal	fungus	10	A	11.5	n/a	0.58	10.6	10.6
836	cal	fungus	7	A	15.6	n/a	1.10	14.8	14.8
822	cal	fungus	8	A	11.0	n/a	1.14	10.2	10.2
862	cal	fungus	10	A	10.5	n/a	0.48	8.1	8.1
734	cal	fungus	7	A	14.8	n/a	1.20	10.5	10.5
682	cal	fungus	7	A	14.2	n/a	1.30	6.5	41.6
998	cal	fungus	11	A	16.9	n/a	1.44	15	15
647	cal	fungus	11	A	11.0	n/a	1.73	9.5	9.5
869	cal	fungus	7	A	10.2	n/a	1.75	9.5	9.5
839	cal	fungus	11	A	9.9	n/a	2.09	9.4	9.4
617	cal	fungus	10	A	10.0	n/a	NF	8.9	8.9
698	cal	fungus	8	A	n/a	n/a	NF	12.5	12.5
831	cal	fungus	11	A	n/a	n/a	NF	14.5	14.5
885	cal	fungus	10	A	n/a	n/a	NF	16.4	16.4
675	cal	livwrt	11	A	6.5	n/a	0.28	5.6	5.6
664	cal	livwrt	10	A	12.8	n/a	0.46	13	13
632	cal	livwrt	8	A	15.6	n/a	0.48	11.5	11.5
678	cal	livwrt	9	A	10.0	n/a	0.63	9.4	9.4
653	cal	livwrt	7	A	13.0	n/a	0.67	10	10
696	cal	livwrt	7	A	11.5	n/a	0.68	7.5	7.5
616	cal	livwrt	7	A	12.1	n/a	0.70	9.1	9.1
624	cal	livwrt	11	A	12.4	n/a	0.73	12.4	12.4
688	cal	livwrt	7	A	10.5	n/a	0.79	10	10
602	cal	livwrt	8	A	10.5	n/a	0.83	10	10
640	cal	livwrt	8	A	15.0	n/a	0.84	12	12
630	cal	livwrt	11	A	11.3	n/a	0.85	8.4	8.4
659	cal	livwrt	9	A	19.5	n/a	0.87	13.5	13.5
674	cal	livwrt	8	A	18.0	n/a	0.91	12.2	12.2
668	cal	livwrt	8	A	10.1	n/a	1.12	8.9	8.9
662	cal	livwrt	11	A	14.2	n/a	1.33	10.1	10.1
735	cal	livwrt	11	A	14.0	n/a	1.35	10.6	10.6
694	cal	livwrt	11	A	14.5	n/a	1.42	12.1	12.1
670	cal	livwrt	11	A	14.9	n/a	1.98	13.2	13.2
614	cal	livwrt	11	A	10.5	n/a	2.00	10.5	10.5
679	cal	livwrt	11	A	11.2	n/a	2.80	9	9
684	cal	livwrt	11	A	14.6	n/a	NF	13.7	13.7
601	cal	livwrt	10	A	n/a	n/a	NF	8.4	8.4
650	cal	livwrt	9	A	n/a	n/a	NF	14	14
668	cal	livwrt	11	A	n/a	n/a	NF	8.5	8.5

931	er	control	2	A	13.0	37	0.25	10.5	32.8
935	er	control	3	A	9.0	21	0.32	7.9	12.1
957	er	control	1	A	15.5	35.5	0.36	13	28.7
961	er	control	6	A	15.5	37.5	0.36	14.8	41.9
977	er	control	2	A	9.5	19.5	0.36	10	16.5
978	er	control	6	A	23.0	37.5	0.40	23.8	45.8
945	er	control	1	A	19.0	44.5	0.42	15.8	27.5
752	er	control	4	A	20.0	48.3	0.43	6.9	29.8
782	er	control	2	A	17.5	38.5	0.47	16	41.6
941	er	control	4	A	12.0	41	0.68	10.5	32.6
954	er	control	1	A	18.5	51.0	0.69	17	48
962	er	control	2	A	17.5	51.5	0.94	14.5	31.8
921	er	control	1	A	15.0	51.0	1.10	11.5	38.3
721	er	control	3	A	13.5	57	NF	12.4	30.9
753	er	control	6	A	13.0	29	NF	10.9	23.9
951	er	control	5	A	11.0	31	NF	11	34.8
990	er	control	9	A	na	na	NF	8	10.1
788	er	fungus	2	A	15.0	25.5	0.22	14.2	29.2
764	er	fungus	2	A	14.0	20.0	0.25	9.8	31.3
772	er	fungus	4	A	23.5	37.8	0.48	15.6	21.7
791	er	fungus	6	A	16.5	43.5	0.49	15.2	44.8
783	er	fungus	5	A	13.5	54.0	0.50	12.2	67.8
794	er	fungus	4	A	18.0	39.0	0.52	15	28.5
754	er	fungus	3	A	20.0	44.0	0.71	18.7	32.9
799	er	fungus	4	A	15.0	49.0	0.71	10.9	40.3
723	er	fungus	3	A	16.0	48.5	0.75	13	32
715	er	fungus	4	A	18.6	66.5	0.84	10	23.3
757	er	fungus	4	A	13.0	48.5	0.86	10.6	26.9
720	er	fungus	3	A	15.0	67.5	1.10	14.6	49.9
733	er	fungus	11	A	9.0	44.5	1.35	7.2	20.1
708	er	fungus	5	A	13.0	25.5	NF	17	36
710	er	fungus	1	A	18.5	70.0	NF	16.5	61.8
739	er	fungus	4	A	15.5	30.5	NF	12.2	31.1
747	er	fungus	1	A	18.0	38.5	NF	14	38.1
701	er	livwrt	2	A	9.0	11.5	0.07	8.5	25
934	er	livwrt	1	A	11.5	22.5	0.22	10.2	29
725	er	livwrt	3	A	8.0	28.5	0.25	datana	datana
797	er	livwrt	4	A	16.0	24.0	0.28	15.6	23.1
995	er	livwrt	2	A	13.0	31.5	0.32	11	27.3
709	er	livwrt	5	A	12.5	26.5	0.33	12	27
759	er	livwrt	3	A	18.0	26.0	0.35	16.1	18.1
787	er	livwrt	5	A	15.0	43.5	0.36	13.1	41.1
761	er	livwrt	4	A	14.5	39.0	0.39	11.6	27.1
770	er	livwrt	5	A	20.0	40.5	0.49	17.8	36.9
703	er	livwrt	3	A	14.0	37.5	0.62	10.5	26
713	er	livwrt	3	A	21.0	34.0	0.64	18.4	21.1
728	er	livwrt	4	A	13.0	34.5	0.64	10.4	29.7

745	er	livwrt	4	A	12.5	43.0	0.71		12.2	31.1
790	er	livwrt	4	A	17.3	61.5	0.85		17	20.1
762	er	livwrt	4	A	14.0	48.0	0.93		10.6	33.3
798	er	livwrt	3	A	17.5	62.0	1.05		16.7	23.8
965	er	livwrt	5	D	19.0	26.0	dead		19	33.8
948	er	livwrt	6	A	19.0	33.0	inundated		17.5	31.8
1000	er	livwrt	3	A	6.0	7.0	NF		13.5	24.5
992	er	livwrt	6	A	12.0	38.5	NF		11.1	38.8
890	cal	control	9	D	n/a	n/a				
610	cal	control	11	D	n/a	n/a				
612	cal	control	7	D	n/a	n/a				
618	cal	control	11	D	n/a	n/a				
633	cal	control	8	D	n/a	n/a				
634	cal	control	7	D	n/a	n/a				
635	cal	control	10	D	n/a	n/a				
637	cal	control	8	D	n/a	n/a				
641	cal	control	10	D	n/a	n/a				
645	cal	control	11	D	n/a	n/a				
652	cal	control	8	D	n/a	n/a				
655	cal	control	10	D	n/a	n/a				
665	cal	control	9	D	n/a	n/a				
666	cal	control	8	D	n/a	n/a				
667	cal	control	10	D	n/a	n/a				
697	cal	control	11	D	n/a	n/a				
707	cal	control	7	D	n/a	n/a				
742	cal	control	7	D	n/a	n/a				
777	cal	control	10	D	n/a	n/a				
927	cal	control	9	D	n/a	n/a				
932	cal	control	9	D	n/a	n/a				
939	cal	control	11	D	n/a	n/a				
943	cal	control	10	D	n/a	n/a				
944	cal	control	7	D	n/a	n/a				
953	cal	control	9	D	n/a	n/a				
967	cal	control	11	D	n/a	n/a				
968	cal	control	10	D	n/a	n/a				
587	cal	fungus	11	D	n/a	n/a				
603	cal	fungus	7	D	n/a	n/a				
621	cal	fungus	9	D	n/a	n/a				
622	cal	fungus	9	D	n/a	n/a				
625	cal	fungus	9	D	n/a	n/a				
631	cal	fungus	9	D	n/a	n/a				
644	cal	fungus	7	D	n/a	n/a				
646	cal	fungus	7	D	n/a	n/a				
648	cal	fungus	10	D	n/a	n/a				
651	cal	fungus	7	D	n/a	n/a				
656	cal	fungus	7	D	n/a	n/a				
657	cal	fungus	11	D	n/a	n/a				

676	cal	fungus	9	D	n/a	n/a	
691	cal	fungus	8	D	n/a	n/a	
719	cal	fungus	11	D	n/a	n/a	
827	cal	fungus	10	D	n/a	n/a	
834	cal	fungus	8	D	n/a	n/a	
853	cal	fungus	10	D	n/a	n/a	
857	cal	fungus	11	D	n/a	n/a	
881	cal	fungus	8	D	n/a	n/a	
958	cal	fungus	8	D	n/a	n/a	
986	cal	fungus	9	D	n/a	n/a	
993	cal	fungus	7	D	n/a	n/a	
604	cal	livwrt	10	D	n/a	n/a	
606	cal	livwrt	11	D	n/a	n/a	
609	cal	livwrt	10	D	n/a	n/a	
626	cal	livwrt	7	D	n/a	n/a	
628	cal	livwrt	10	D	n/a	n/a	
629	cal	livwrt	9	D	n/a	n/a	
639	cal	livwrt	11	D	n/a	n/a	
654	cal	livwrt	9	D	n/a	n/a	
661	cal	livwrt	7	D	n/a	n/a	
663	cal	livwrt	11	D	n/a	n/a	
671	cal	livwrt	10	D	n/a	n/a	
683	cal	livwrt	7	D	n/a	n/a	
689	cal	livwrt	10	D	n/a	n/a	
695	cal	livwrt	9	D	n/a	n/a	
699	cal	livwrt	11	D	n/a	n/a	
700	cal	livwrt	8	D	n/a	n/a	
959	er	control	7	D	n/a	n/a	
736	er	fungus	6	D	n/a	n/a	
758	er	fungus	5	D	n/a	n/a	
767	er	fungus	5	D	n/a	n/a	
786	er	fungus	6	D	n/a	n/a	
730	er	livwrt	1	D	n/a	n/a	inundated
746	er	livwrt	5	D	n/a	n/a	
755	er	livwrt	6	D	n/a	n/a	
773	er	livwrt	1	D	n/a	n/a	
955	er	livwrt	1	D	n/a	n/a	
973	er	livwrt	6	D	n/a	n/a	
677	cal	control	8	NF	n/a	n/a	NF
701	cal	control	8	NF	n/a	n/a	NF
826	cal	fungus	8	NF	n/a	n/a	NF
828	cal	fungus	8	NF	n/a	n/a	NF
889	cal	fungus	8	NF	n/a	n/a	NF
985	cal	fungus	10	NF	n/a	n/a	NF
642	cal	livwrt	7	NF	n/a	n/a	NF
924	er	control	5	NF	n/a	n/a	NF
731	er	fungus	6	NF	n/a	n/a	NF

738	er	fungus	6	NF	n/a	n/a	NF
750	er	fungus	5	NF	n/a	n/a	NF
751	er	fungus	5	NF	n/a	n/a	NF
756	er	fungus	5	NF	n/a	n/a	NF
780	er	fungus	6	NF	n/a	n/a	NF
792	er	fungus	6	NF	n/a	n/a	NF
795	er	fungus	5	NF	n/a	n/a	NF
718	er	livwrt	4	NF	n/a	n/a	NF
Plant	spe cies	treatment	plot				

Branching – Nursery Experiment 2a

No.	Species	treatment	Health	Number of branches	Stem' height (cm)	Mean Branch Length (cm)	Median	Total branch and stem
1048	Calluna	Control	Healthy	8	12.5	1.9	1.1	27.6
1050	Calluna	Control	Healthy	15	9.9	2.7	2	51
1037	Calluna	Control	Healthy	11	7.3	1.8	1.4	26.6
1043	Calluna	Control	Healthy	14	9.1	2.4	2.35	42.9
1040	Calluna	Control	Healthy	14	10.5	3.5	3.6	59.5
1036	Calluna	Control	Healthy	10	8.5	2.0	2.15	28.2
1039	Calluna	Control	Healthy	1	3.6	1.5	1.5	5.1
1054	Calluna	Control	Healthy	9	12.2	2.3	2.1	33.1
1056	Calluna	Control	Healthy	3	5.2	1.0	0.9	8.3
1053	Calluna	Control	Healthy	22	4.9	2.2	1.75	52.5
1047	Calluna	Control	Healthy	12	12.3	2.3	1.95	39.4
1052	Calluna	Control	Healthy	14	4.8	2.2	2.1	35.7
1049	Calluna	Control	Healthy	20	12	2.8	2.2	68.2
1034	Calluna	Control	Healthy	7	9	1.9	1.4	22.3
1035	Calluna	Control	Healthy	13	12.4	1.9	1.1	37.6
1021	Calluna	Control	Healthy	4	7.2	1.2	1.1	12.1
1046	Calluna	Control	Healthy	14	10.6	1.3	1.05	29.1
1038	Calluna	Control	Healthy	0	1.2	NA	NA	1.2
1041	Calluna	Control	Healthy	20	9.1	1.8	1.5	45.6
1055	Calluna	Control	Healthy	27	15	2.2	1.7	74.9
1044	Calluna	Control	Healthy	20	18.6	2.7	2.5	73.3
886	Calluna	Treatment	Healthy	2	5.1	1.9	1.85	8.8
869	Calluna	Treatment	Healthy	0	2.7	NA	NA	2.7
898	Calluna	Treatment	Healthy	6	12.7	2.2	2.5	25.8
578	Calluna	Treatment	Healthy	11	11	4.1	1.8	55.6
518	Calluna	Treatment	Healthy	12	9	2.8	2.7	42.7
520	Calluna	Treatment	Healthy	6	13.5	4.1	3.4	38
886	Calluna	Treatment	Healthy	14	9.1	2.2	1.9	40.3
854	Calluna	Treatment	Healthy	25	10.6	1.7	1.2	52.6
867	Calluna	Treatment	Healthy	19	8.7	2.2	2.1	51.3
817	Calluna	Treatment	Healthy	22	12.2	1.3	1.2	41.4

861	Calluna	Treatment	Healthy	30	8.9	1.8	1.2	62.2
899	Calluna	Treatment	Healthy	12	13.7	1.6	1.3	33
849	Calluna	Treatment	Healthy	15	18.2	2.1	1.8	50.3
507	Calluna	Treatment	Healthy	1	3.5	0.8	0.8	4.3
509	Calluna	Treatment	Healthy	21	6.5	2.2	2.2	53.3
858	Calluna	Treatment	Healthy	24	11	2.2	1.75	64.1
517	Calluna	Treatment	Healthy	11	11.6	1.2	1.1	24.7
698	Calluna	Treatment	Healthy	49	19.5	1.8	1.4	109.2
883	Calluna	Treatment	Healthy	11	8.1	1.4	1.1	23.2
820	Calluna	Treatment	Healthy	2	4	1.1	1.1	6.2
882	Calluna	Treatment	Healthy	42	10.5	1.8	1.5	87.5
880	Calluna	Treatment	Healthy	12	8	1.6	1.4	27.5
643	Calluna	Treatment	Healthy	6	4.6	2.2	1.55	17.8
879	Calluna	Treatment	Healthy	6	8.1	1.0	0.9	13.8
531	Calluna	Treatment	Healthy	4	13.1	3.7	3.75	28
841	Calluna	Treatment	Healthy	4	16.1	2.8	2.4	27.3
879	Calluna	Treatment	Healthy	4	8.2	4.4	4.15	25.6
627	Calluna	Treatment	Healthy	2	6.1	0.9	0.9	7.9
843	Calluna	Treatment	Healthy	6	4	1.0	1.05	10.1
1029	Erica	Control	Healthy	2	6.5	1.4	1.35	9.2
1026	Erica	Control	Healthy	4	12	3.2	3.4	24.6
1002	Erica	Control	Healthy	3	9.3	3.2	3.6	18.8
1025	Erica	Control	Healthy	1	4.5	1.0	1	5.5
1023	Erica	Control	Healthy	4	14.5	4.5	5.05	32.6
1027	Erica	Control	Healthy	9	17.6	3.7	2.6	50.6
1028	Erica	Control	Healthy	2	10	4.7	4.65	19.3
1030	Erica	Control	Healthy	7	17.7	4.4	3.1	48.2
1031	Erica	Control	Healthy	13	15	4.4	2.5	71.7
1032	Erica	Control	Healthy	6	13.9	3.9	3.55	37.5
1008	Erica	Control	Healthy	5	6	3.6	3.7	23.9
1010	Erica	Control	Healthy	2	7.7	2.3	2.3	12.3
1001	Erica	Control	Healthy	3	13.2	4.7	3.6	27.4
1020	Erica	Control	Healthy	7	17.7	3.8	2.6	44
1018	Erica	Control	Healthy	8	7.2	3.2	2.9	33
1033	Erica	Control	Healthy	9	14.6	4.9	2.9	58.3
1003	Erica	Control	Healthy	4	13	3.5	2.65	27.1
1006	Erica	Control	Healthy	2	14.1	5.5	5.5	25.1
1009	Erica	Control	Healthy	3	12	1.4	1.6	16.3
1011	Erica	Control	Healthy	1	9.5	4.2	4.2	13.7
1012	Erica	Control	Healthy	6	14.1	3.3	3.4	34.1
1014	Erica	Control	Healthy	6	17.7	5.1	4.4	48.2
1005	Erica	Control	Healthy	10	17.2	3.7	4.1	54.4
1016	Erica	Control	Healthy	4	15.2	3.5	2.3	29
1015	Erica	Control	Healthy	0	4.9	NA	NA	4.9
334	Erica	Treatment	Healthy	2	9.6	2.2	2.15	13.9
535	Erica	Treatment	Healthy	4	6.5	2.5	1.9	16.5

917	Erica	Treatment	Healthy	4	7.3	2.2	1.9	16
579	Erica	Treatment	Healthy	1	4.8	2.1	2.1	6.9
600	Erica	Treatment	Healthy	6	17.1	3.1	2.3	35.4
576	Erica	Treatment	Healthy	5	10.4	2.7	2.4	24
614	Erica	Treatment	Healthy	3	9.4	4.5	2	22.9
806	Erica	Treatment	Healthy	4	18	4.9	3.75	37.5
504	Erica	Treatment	Healthy	3	14.5	4.8	5	29
877	Erica	Treatment	Healthy	2	14.2	3.5	3.5	21.2
582	Erica	Treatment	Healthy	10	9.2	3.4	2.35	43.2
599	Erica	Treatment	Healthy	3	18.6	4.8	4.4	33.1
503	Erica	Treatment	Healthy	4	14.5	1.6	1.45	20.8
624	Erica	Treatment	Healthy	4	13.1	4.1	4.2	29.4
596	Erica	Treatment	Healthy	7	15.5	5.8	6.2	56.4
528	Erica	Treatment	Healthy	3	12.2	1.6	1.6	17
888	Erica	Treatment	Healthy	6	16.7	5.0	3.65	46.9
617	Erica	Treatment	Healthy	7	14.4	4.0	3.1	42.7
912	Erica	Treatment	Healthy	4	10.5	2.3	1.35	19.8
634	Erica	Treatment	Healthy	3	5.8	1.4	1.2	9.9
875	Erica	Treatment	Healthy	6	13.9	3.2	2.05	32.9
837	Erica	Treatment	Healthy	6	6.5	2.0	2	18.7
505	Erica	Treatment	Healthy	1	6.3	2.6	2.6	8.9
609	Erica	Treatment	Healthy	1	9.4	3.0	3	12.4
577	Erica	Treatment	Healthy	9	16.7	3.4	3.3	47.4
1051	Calluna	Control	Dead	0		NA	NA	0
1045	Calluna	Control	Dead	0		NA	NA	0
824	Calluna	Treatment	Dead	0		NA	NA	0
884	Calluna	Treatment	Dead	1	2.5	0.9	0.9	3.4
1024	Erica	Control	Dead	0		NA	NA	0
1022	Erica	Control	Dead	0		NA	NA	0
1042	Erica	Control	Dead	0		NA	NA	0
1019	Erica	Control	Dead	0		NA	NA	0
1017	Erica	Control	Dead	2	5.8	2.6	2.55	10.9
1013	Erica	Control	Dead	0	3	NA	NA	3
1007	Erica	Control	Dead	0	4.2	NA	NA	4.2
906	Erica	Treatment	Dead	1	3.4	1.2	1.2	4.6