

FINAL REPORT: Effects of Chihuahuan Desert soil microbial communities on early lettuce establishment in lunar regolith simulant.

PLANT THE MOON EPCC TEAM VOYAGER: 25324

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El Paso Community College

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Introduction

Lunar regolith presents a significant challenge for plant growth due to the lack of biological and chemical properties necessary to support life. Unlike terrestrial soils, regolith forms in the absence of a biosphere and is therefore composed entirely of inorganic materials such as silicates, metals, and fragmented rock particles (Noble, 2019). Regolith use in agriculture remains highly limited. The limitations of lunar regolith are both chemical and physical. Chemically, it lacks nutrients such as nitrogen, phosphorus, and potassium, and contains high levels of metals, including aluminum and iron, which can inhibit plant growth, especially when pH falls into the acidic range. Physically, its irregular particle size and structure lead to compaction, poor aeration, and low water retention, further restricting root development and microbial colonization (Fackrell et al., 2024). Together, these conditions create an environment that is highly unfavorable for agriculture, making microbial colonization challenging, even if introduced artificially.

On Earth, plant growth is strongly supported by interactions with soil microbial communities. These microbes enhance nutrient availability, improve water retention, and increase plant tolerance to environmental stress. In particular, soil microbes can play a key role in facilitating nutrient uptake and maintaining soil structure (Montoel-Gonzalez et al., 2017). Because lunar regolith lacks these biological components, introducing microbial communities has been proposed in this study as a potential strategy to improve its agricultural viability. Microorganism symbioses are significant in helping plants regulate water, tolerate stress, and aggregate soil in the normal ecosystems they grow in, the fertility of lunar regolith poses a major barrier to its functionality in extraterrestrial agriculture. A promising strategy to limit these issues is the introduction of microbes and AMF (Mei et al., 2026, Atkin, 2025, Fackrell et al., 2024).

Microbe relationships are vital, helping plants take up nutrients by breaking down organic matter, taking up carbon dioxide, and releasing it as an acid to release ions for the plant to absorb, increasing the amount of nutrients the plant takes up compared to what it could do on its own, transforming nutrients to consumable forms for the plant to absorb, with varying degrees of helpfulness (Katznelson, H., et al 1948).

Most existing research has focused on the role of AMF in improving plant growth in regolith while others examine the relationships with specific bacteria. However, less attention has been given to the broader microbial communities that exist in extreme terrestrial environments. Desert ecosystems, such as the Chihuahuan Desert, contain microbial populations that are adapted to high stress conditions, including low water availability, high radiation, and nutrient limitations. These characteristics make desert microbes a promising candidate for introduction into regolith-like environments.

Recent research has demonstrated that microbial communities in the Chihuahuan Desert are structured by landscape-level characteristics rather than a single dominant factor. Variables such as soil texture, moisture, pH, salinity, vegetation type, and landform interact to shape microbial composition and diversity (Hansen et al., 2023). This indicates that desert microbiomes are adapted to complex and interacting environmental stressors rather than isolated conditions. Because these communities function as integrated systems shaped by multiple environmental pressures, examining them as whole communities may be more informative than isolating individual microbial traits. This perspective is particularly relevant when applying terrestrial microbiomes to novel environments, where community-level interactions may play a critical role in determining crop success. Microbial communities in these arid regions are also

well known for helping sustain vegetation and biodiversity through complex interactions, including symbioses and biocrust formation (Hansen et al., 2023, Flores-Margez et al., 2020, Bowker et al., 2018, Chamizo et al., 2016).

Theory

This study investigates whether Chihuahuan Desert soil and its associated microbial communities can improve plant growth in lunar regolith simulant. Specifically, it aims to determine whether plant establishment is driven by microbial activity or by the abiotic factors in the soil.

The following research questions guide this study:

1. Does the introduction of desert microbes improve plant growth in regolith?
2. Is plant establishment driven by microbial communities or by other characteristics in desert soil?

Hypotheses

Microbial communities

H_{a1}: Microbes positively influence the biomass of lettuce seedlings when present.

H₀₁: Microbes do not affect the biomass of lettuce seedlings when present.

Soil

H_{a2}: Abiotic Chihuahuan desert soil features positively influence lettuce seedling biomass.

H₀₂: Abiotic Chihuahuan desert soil features do not influence lettuce seedling biomass.

Measurement and Methods

Experimental Design

This experiment investigates whether Chihuahuan desert soil could improve plant growth in lunar regolith simulant. Differences in soil microbial activity and pH were evaluated for which type of soil conditions may best support plants. Five experimental groups were established, with each pot containing 120 mL of unpacked substrate. Each treatment consisted of six replicates, although some did not germinate. Pots were lined with coffee filters to prevent soil loss and filled with 120 mL of the designated substrate.

Table 1. Descriptions of each treatment group and their composition.

Role	Group Name	Composition
Negative Control	Regolith	100% Regolith
Positive Control	Potting Soil	100% Potting Soil
Environmental Control	Desert Soil	100% Desert Soil
Experimental Treatment	Live Mix	50% Regolith/50% Desert Soil
Experimental Treatment	Sterile Mix	50% Regolith/50% HTPT Desert Soil

This experiment investigated whether Chihuahuan Desert soil could improve plant growth in lunar regolith simulant by comparing differences in soil composition and microbial presence across treatments.

Substrate Preparation

Desert soil was collected from shrubland-type sites located on campus and private property. Dominant vegetation at these sites included Honey Mesquite, Creosote, and Agave Lechuguilla. Collected soils were combined and homogenized to create a composite sample prior to use in experimental treatments.

The desert soil used in the sterile mix treatment was processed using an autoclave at 121°C and 18 psi for 30 minutes. This treatment was intended to sterilize the soil; however, as observed during the experiment, microbial growth still occurred. Therefore, this soil is more accurately described as high temperature and pressure treated (HTPT) rather than fully sterile. All other substrates were combined based on proportions in Table 1, totaling 120 mL per pot.

Growth Conditions

All pots were placed under red and blue grow lights to simulate sunlight and maintained under a 12/12-hour light/dark cycle. To reduce excessive drying, pots were enclosed within a chamber to maintain more stable moisture conditions. Plants were watered with 30 mL of filtered water as needed throughout the experiment. To supplement nutrient availability, each plant received 3 mL of a liquid fertilizer (75–20–5 ppm, NPK) solution halfway through the experiment.

Soil conditions were monitored regularly, including pH, moisture, temperature, light, and humidity. Soil pH was measured weekly using a soil pH tester, with additional measurements taken during the first and final weeks of plant growth to track changes over time.

Plants were grown for 28 days following germination. At the end of the growth period, plants were harvested and measured for growth metrics. Plant height and leaf number were

recorded prior to harvest. Plants were then separated into shoots and roots, and wet biomass was measured using a scale. Samples were stored in labeled bags according to treatment group for further analysis.

Statistical Analysis

All statistical analyses were performed in R using the ggplot2 package. Separate one-way ANOVAs were conducted to evaluate differences in plant height, shoot biomass, and root biomass among soil treatments. Tukey's HSD test was used for pairwise comparisons with a significance level of $\alpha = 0.05$.

Results

Growth Metrics

Plant growth was evaluated by measuring height and biomass, as these directly relate to overall plant size. At the end of the experiment, plants were harvested and separated into shoots and roots, and biomass was measured using a digital scale. Plant height and roots data were recorded at the end of the experiment. These measurements were used to assess growth across all different soils and are summarized in Table 2. The environmental control and sterile mix showed greater variation in biomass and height compared to the live mix and regolith treatments, which exhibited consistently low growth across replicates. Table 3 summarizes pairwise comparisons among the treatment.

Table 2. Biomass and plant height summary statistics.

Treatment	Mean	SD	Variance	SE
Root Mass (g)				
<i>Env. Cont.</i>	0.0789	0.1162	0.0135	0.0291
<i>Live Mix</i>	0.0234	0.0158	0.0002	0.0041
<i>Potting Soil</i>	0.0850	0.0495	0.0025	0.0350
<i>Regolith</i>	0.0300	0.0141	0.0002	0.0038
<i>Sterile Mix</i>	0.1088	0.0934	0.0087	0.0233
Shoot Mass (g)				
<i>Env. Cont.</i>	0.2613	0.2531	0.0640	0.0633
<i>Live Mix</i>	0.0420	0.0174	0.0003	0.0045
<i>Potting Soil</i>	0.0800	0.0566	0.0032	0.0400
<i>Regolith</i>	0.0421	0.0189	0.0004	0.0050
<i>Sterile Mix</i>	0.2088	0.2718	0.0739	0.0679
Height (mm)				
<i>Env. Cont.</i>	26.2000	16.4682	271.2000	7.3648
<i>Live Mix</i>	7.1667	3.3714	11.3667	1.3764
<i>Potting Soil</i>	1.0000	0.0000	0.0000	0.0000
<i>Regolith</i>	6.6667	2.5820	6.6667	1.0541
<i>Sterile Mix</i>	63.3333	23.0796	532.6667	9.4222

Table 3. P-values reported from ANOVA Tukey HSD pairwise comparisons.

	Height	Shoot Mass	Root Mass
<i>Live Mix - Env. Cont.</i>	0.1960414	0.0172016	0.2731579
<i>Potting Soil - Env. Cont.</i>	0.2295106	0.7067650	0.9999714
<i>Regolith- Env. Cont.</i>	0.1770059	0.0202861	0.4173590
<i>Sterile Mix - Env. Cont.</i>	0.0021529	0.9342340	0.8068073
<i>Potting Soil - Live Mix</i>	0.9812953	0.9988582	0.8232135
<i>Regolith - Live Mix</i>	0.9999962	1.0000000	0.9993470
<i>Sterile Mix - Live Mix</i>	0.0000075	0.1168036	0.0244382
<i>Regolith - Potting Soil</i>	0.9863264	0.9988933	0.8769828
<i>Sterile Mix - Potting Soil</i>	0.0001884	0.8933048	0.9937693
<i>Sterile Mix - Regolith</i>	0.0000066	0.1288646	0.0516586

Bold numbers represent a significant or marginal differences.

Plant Height

Plant height showed the strongest and most consistent differences among treatments. The sterile mix produced the tallest plants (63.33 mm), followed by the environmental control (26.2 mm). In contrast, the live mix (7.17 mm) and regolith (6.67 mm) treatments resulted in substantially shorter plants, while potting soil showed minimal growth (1.0 mm).

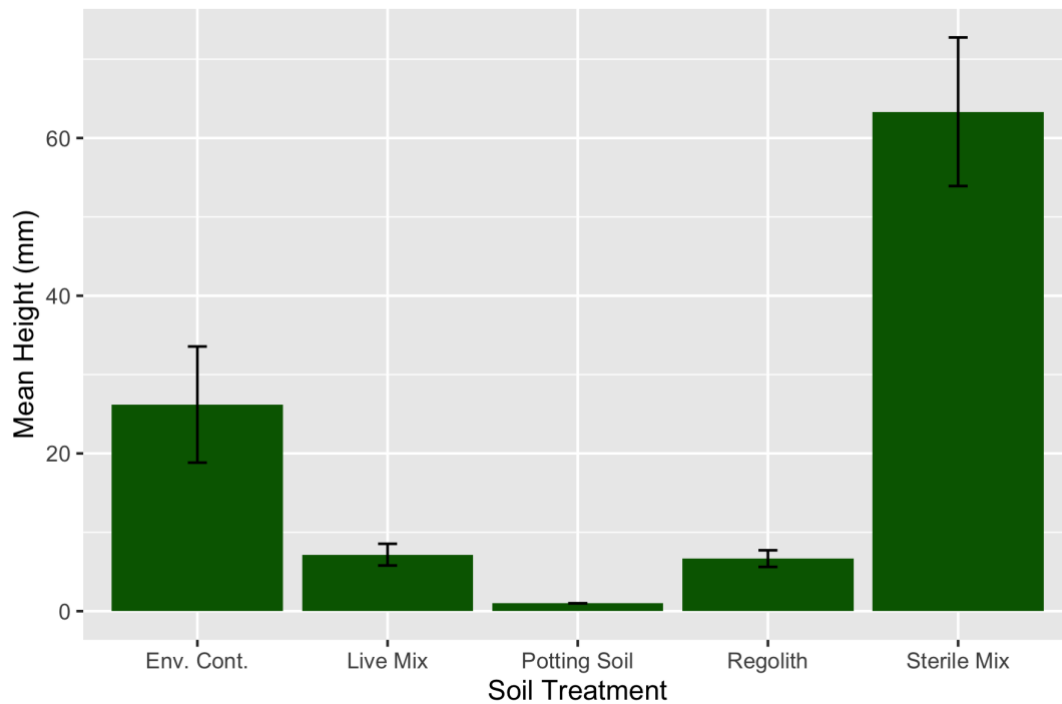


Figure 1. Mean height group comparison. Sterile mix was significantly different to all other groups, $p < 0.01$).

Statistical analysis confirmed that the sterile mix was significantly greater in height than all other treatments ($p < 0.01$ for all comparisons). No other pairwise comparisons showed significant differences. These results indicate that plant height was most strongly influenced by the sterile mix treatment.

Shoot Biomass

Shoot biomass varied across treatments but showed fewer statistically significant differences. The environmental control (0.2613 g) and sterile mix (0.2088 g) produced the highest above-ground biomass, while the live mix (0.042 g) and regolith (0.0421 g) produced the lowest values. Potting soil showed intermediate shoot biomass (0.08 g).

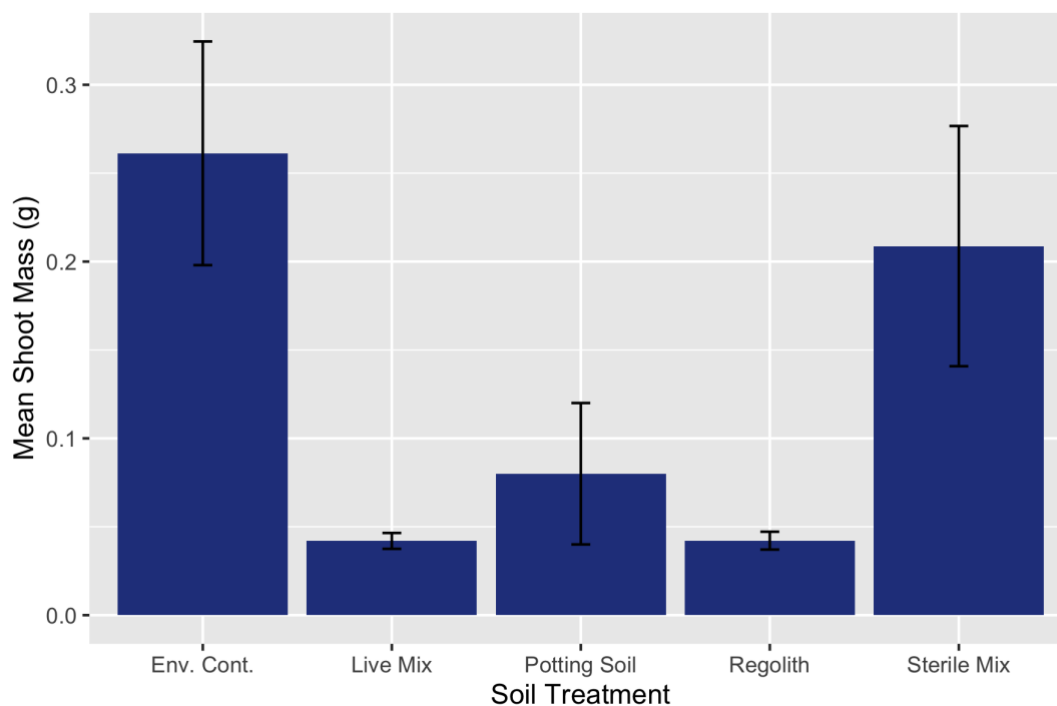


Figure 2. Mean shoot mass comparison. Significant differences were found between environmental control compared to live mix and pure regolith, $p < 0.05$). Marginal significant difference ($p > 0.10$) in live mix and regolith compared to sterile mix.

Significant differences were observed between the environmental control and both the live mix ($p = 0.017$) and regolith ($p = 0.02$). However, no significant differences were detected between the sterile mix and any other treatment. These results suggest that while desert soil supported greater shoot biomass, the effect of the sterile mix was not statistically distinct from

other treatments. This is extremely important as it showed that even when mixed with regolith, this treatment did not significantly differ from the environmental control, indicating that these plants grew similarly to how they would grow in desert soil.

Root Biomass

Root biomass followed a similar trend to shoot biomass, with the sterile mix producing the highest average root mass (0.1088 g), followed by potting soil (0.085 g) and the environmental control (0.0789 g). The live mix (0.0234 g) and regolith (0.03 g) showed substantially lower root biomass.

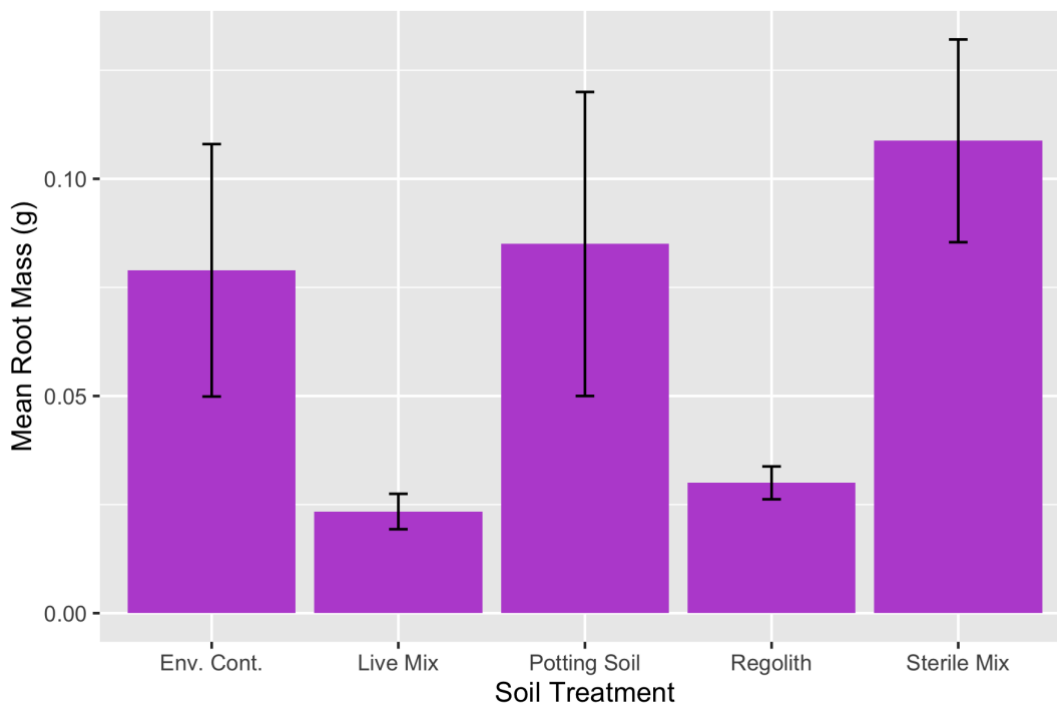


Figure 3. Mean root mass comparison. Significant differences were found between sterile mix compared to live mix and pure regolith, $p < 0.05$). Marginal significant difference ($p = 0.051$) in sterile mix and regolith compared to sterile mix.

A significant difference was observed between the sterile mix and the live mix ($p = 0.024$). The comparison between the sterile mix and regolith approached significance ($p = 0.051$), while all other comparisons were not statistically significant. These findings indicate that the sterile mix improved root development relative to the lowest-performing treatments.

Overall Trends

Across all measured variables, the sterile mix consistently produced the greatest plant growth, particularly in plant height, where it was significantly greater than all other treatments. The environmental control also supported strong growth, especially in shoot biomass. In contrast, the live mix and regolith treatments consistently produced the lowest growth across all metrics. Potting soil showed moderate biomass production but minimal plant height, indicating inconsistent performance across growth measurements.

Experiment Observations

Visible white mycelial growth was observed in all sterile mix (HTPT) samples during the experiment (Figure 4). This growth became apparent during the early stages of plant development. No comparable fungal growth was observed in the environmental control, live mix, potting soil, or regolith treatments.



Figure 4. Photographs of the fungal growth in sterile mix.

It was uncertain what kind of fungi was growing, consequently roots for the sterile mix group were processed, stained using a 5% ink–vinegar using a slightly modified protocol from Vierheilig et al. (1998) after being cleared in 10% Potassium Hydroxide, and micrographs were taken to examine root inoculation by AMF (Figure 5).

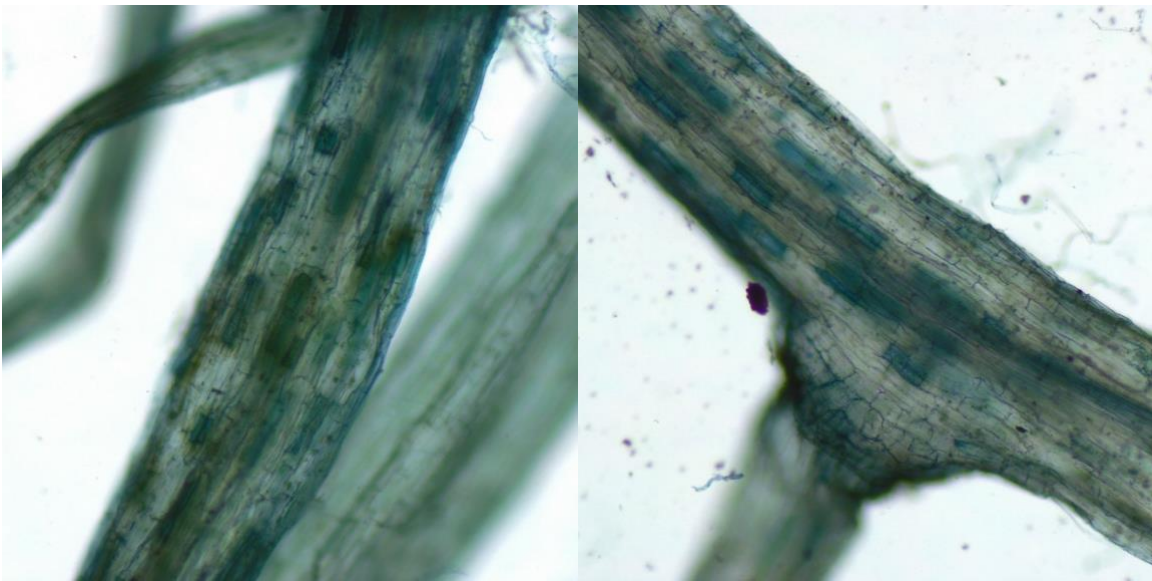


Figure 5. Images showing AMF colonization in lettuce root systems. Arbuscules and hyphae are seen in bright blue.

Discussion

Experiments and limitations

This study evaluated whether Chihuahuan Desert soil and its associated microbial communities could improve plant growth in lunar regolith simulant. Overall, plant growth differed across treatments, with the high temperature and pressure treated (HTPT) soil consistently producing the greatest growth, particularly in plant height. In contrast, the live mix and regolith treatments showed consistently low performance across all growth metrics.

The results did not provide sufficient evidence to reject either null hypothesis. While desert soil supported plant growth, the presence of a full microbial community did not consistently improve plant performance when combined with the lunar regolith. In fact, the live mix, which contained both regolith and untreated desert soil, produced growth comparable to regolith alone. This suggests that the addition of an intact microbial community did not enhance plant establishment under these conditions.

However, a key limitation of this study is that the HTPT treatment was not fully sterile, making it difficult to isolate the effects of microbial presence from soil properties. Future studies should further control microbial composition and directly measure microbial activity to better understand these interactions.

Microbial Communities and Opportunistic Growth

The live mix treatment did not perform as well as the HTPT. This suggests that transplanting the entire microbial community did not support the organism, but rather a subset that remained after the heat and pressure treatment. In contrast, the HTPT treatment produced the

highest growth across most metrics, despite being intended as a sterile control. However, visual observations confirmed that the soil was not fully sterile, as fungal growth was observed in all HTPT samples (Figure 4). This indicates that a subset of microorganisms survived the sterilization process, resulting in a modified microbial community rather than complete sterility. There is no clear explanation as to why it failed to sterilize the soil, but it is suspected that fungal spores may have been protected within the soil or the duration of the cycle.

One possible explanation for these results is that the reduction of microbial diversity in the HTPT treatment decreased competition among microorganisms, allowing certain organisms, such as fungi to dominate. Microbial communities are known to regulate themselves through competition, preventing any single group from becoming dominant. By reducing this competition, the surviving organisms may have been able to more effectively utilize available resources and support plant growth. These findings are consistent with other studies in which soil microorganisms are known to suppress fungal growth (Svenningsen et al., 2018; Wilson et al., 1988). In this case, the fungal growth may have been the result of opportunistic colonization as the high temperature and pressure might have been enough to kill most microbes but not enough for fungi.

The presence of visible fungal growth in the HTPT treatment further supports this explanation. Fungi, particularly arbuscular mycorrhizal fungi (AMF), play a key role in nutrient uptake and plant-soil interactions. The observed fungal colonization (Figure 5) suggests that these organisms may have contributed to the increased growth observed in the HTPT treatment, although this cannot be confirmed without further experimentation and analysis. The examination for the presence of AMF was performed only to this treatment to confirm whether

beneficial fungi were present, as the results were unexpected. It was expected that other treatment groups would develop these relationships but not confirmed via root staining.

The variability observed in the HTPT and environmental control treatments suggests that growth responses were not uniform across replicates for that treatment, potentially reflecting differences in microbial composition or activity. In contrast, the consistently low growth observed in the live mix and regolith treatments indicates that these conditions were uniformly limiting to plant growth. These findings suggest that microbial changes may have influenced soil interactions by enhancing resource efficiency, which supported greater plant biomass. This outcome aligns with findings that microbial communities, when selectively preserved, can adapt to stress and optimize nutrient cycling for vegetation (King et al., 2024).

Future Directions

These findings highlight the importance of considering and experimenting using microbial communities as dynamic systems rather than collections of individual organisms. The results suggest that modifying microbial communities, rather than simply introducing them, may be an important factor in improving plant growth in regolith-like environments. For instance, Hansen and others (2023) found that variation exists in microbial communities as they relate to vegetation and substrate type as they are well adapted to that environment. Within the Chihuahuan Desert, soil composition can vary with plant species and geological features, including regions richer in andesite or basalt, while limestone remains common (Aide and Auken, 1985). This region is not rich in basalt therefore it might explain why the live mix was unsuccessful.

Overall, this study suggests that selective microbial survival and reduced competition may play a role in enhancing plant growth in challenging substrates such as lunar regolith simulant. These findings provide insight into how microbial communities may be manipulated to improve agricultural potential in extraterrestrial environments. From an evolutionary perspective, the establishment of effective symbiotic relationships among microorganisms and plants depends on selective pressures that shape community structure over time. In natural systems, microbial communities are regulated through competition and selection, allowing beneficial interactions to emerge while less effective traits are reduced. In contrast, artificially selecting individual species based solely on performance may overlook these complex interactions and potentially maintain less optimal community dynamics by not allowing deleterious alleles to be removed (Porter and Sachs, 2020).

Lunar regolith represents a largely abiotic and microbially unstructured environment, lacking the ecological context in which these interactions typically develop. In contrast, extreme terrestrial environments such as the Chihuahuan Desert support diverse microbial communities that have adapted to multiple environmental stressors, including nutrient limitation, temperature variability, and water scarcity. The findings of this study suggest that exploring how microbial communities establish and interact under extreme environmental conditions may be important for developing microbiomes suited for lunar agriculture. In particular, environments with characteristics similar to lunar regolith, such as regions with high mineral content or basaltic substrates, may provide useful information for understanding how these interactions develop under extreme conditions.

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TEAM VOYAGER



APPENDIX A



Figure 6. Initial photos of experiment setup.

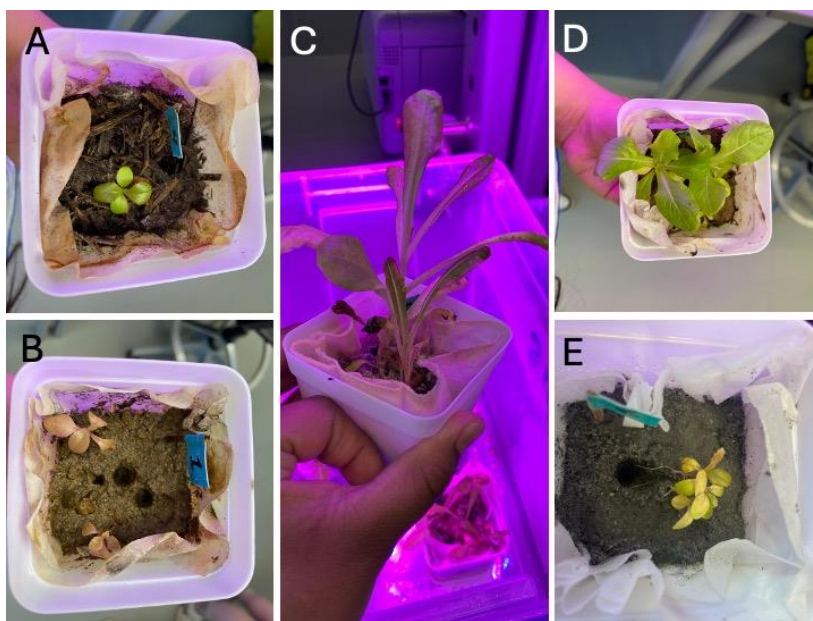


Figure 7. Figure shows final experimental growth before harvesting. Each plant is a representative of each group.

A=Potting soil group, B=Live mix group, C=Sterile mix group (HTPT), D=Environmental control group,
E=Regolith group.



Figure 8. Photographs showing fungal hyphae growth in the HTPT group.



Figure 9. Images of the experimental harvest for biomass processing.

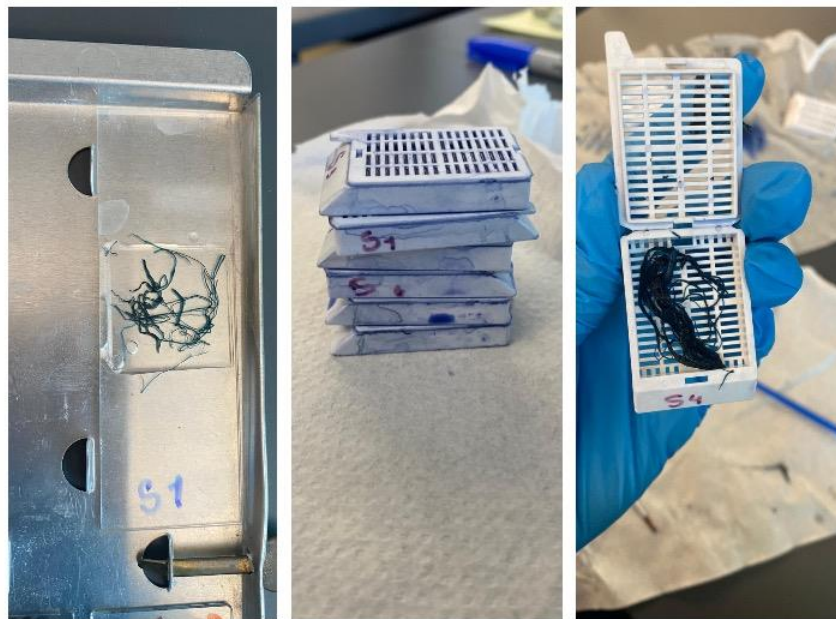


Figure 10. Photographs of root sample processing using the ink-vinegar method.

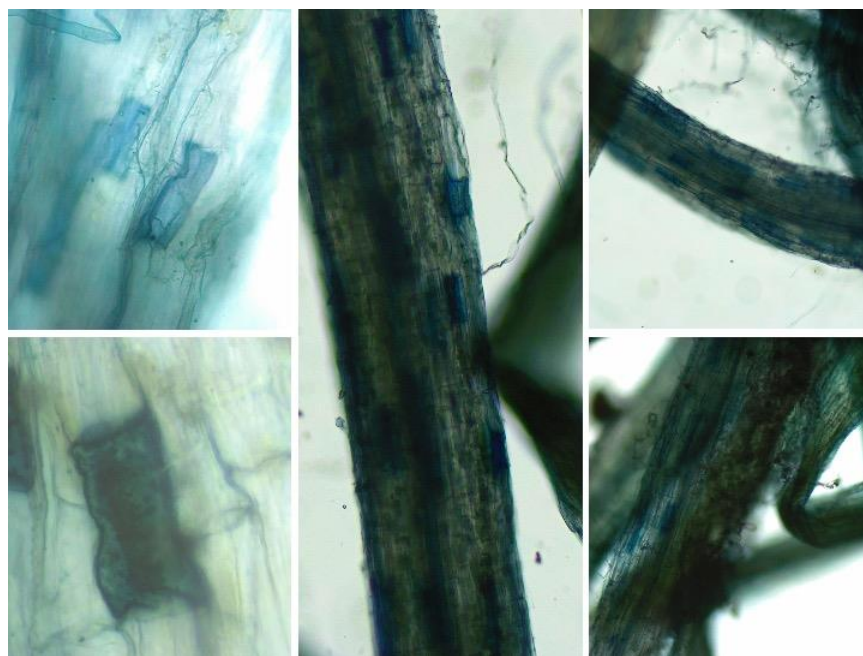


Figure 11. Micrographs of AMF root colonization from the HTPT group.

APPENDIX B

R-Script:

```
data_m <- read.csv("data_m.csv")
data_h <- read.csv("data_h.csv")
num_col_m <- names(data_m)[sapply(data_m, is.numeric)]
sum_stat_m <- function(x){
  c(mean=mean(x, na.rm= TRUE),
    sd=sd(x, na.rm= TRUE),
    var=var(x, na.rm= TRUE),
    se= sd(x, na.rm=TRUE)/sqrt(sum(!is.na(x))))}
summary_vals_m <- aggregate(data_m[,num_col_m], by=list(treatment=data_m$soil),
  FUN=sum_stat_m)
sum_mass <- do.call(data.frame,summary_vals_m)
write.csv(sum_mass, "summary_stats_mass.csv")
num_col_h <- names(data_h)[sapply(data_h, is.numeric)]
sum_stat_h <- function(x){
  c(mean=mean(x, na.rm= TRUE),
    sd=sd(x, na.rm= TRUE),
    var=var(x, na.rm= TRUE),
    se= sd(x, na.rm=TRUE)/sqrt(sum(!is.na(x))))}
summary_vals_h <- aggregate(data_h[,num_col_h], by=list(treatment=data_h$soil), FUN=sum_stat_h)
sum_height <- do.call(data.frame,summary_vals_h)
write.csv(sum_height, "summary_stats_height.csv")
library(ggplot2)
aov_root_m <- aov(root_mass ~ soil, data=data_m)
aov_root_m
aov_root_mass_hsd <- (TukeyHSD(aov_root_m))
aov_root_mass_hsd
aov_shoot_m <- aov(shoot_mass ~ soil, data=data_m)
aov_shoot_m
aov_shoot_mass_hsd <- (TukeyHSD(aov_shoot_m))
aov_shoot_mass_hsd
aov_shoot_h <- aov(stem_height_mm ~ soil, data=data_h)
aov_shoot_h
aov_shoot_height_hsd <- (TukeyHSD(aov_shoot_h))
aov_shoot_height_hsd
plot_sh <- ggplot(data_h, aes(x = soil, y = stem_height_mm)) + stat_summary(fun = "mean", geom =
  "col", fill = "darkgreen") + stat_summary(fun.data = mean_se, geom = "errorbar", width = 0.1) + labs(x =
  "Soil Treatment", y = "Mean Height (mm)") + scale_x_discrete(labels = c(
  "des_c" = "Env. Cont.",
  "des_reg" = "Live Mix",
  "pot" = "Potting Soil",
  "reg" = "Regolith",
  "stl_reg" = "Sterile Mix"))
ggsave("plot_height.png", plot=plot_sh, width=1800, height=1200, units="px")
```


2/11 /26	l2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	l3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	l4	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	l5	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	l6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	dc 1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	dc 2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	dc 3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	dc 4	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	dc 5	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/11 /26	dc 6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A		
2/16 /26	c(+) 1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	
2/16 /26	c(+) 2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	
2/16 /26	c(+) 3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	
2/16 /26	c(+) 4	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	
2/16 /26	c(+) 5	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	
2/16 /26	c(+) 6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	
2/16 /26	s1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starti ng growi ng
2/16 /26	s2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starti ng growi ng
2/16 /26	s3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starti ng growi ng

												growing
2/16/26	l6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starting growing
2/16/26	dc 1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	
2/16/26	dc 2	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starting growing
2/16/26	dc 3	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starting growing
2/16/26	dc 4	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starting growing
2/16/26	dc 5	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starting growing
2/16/26	dc 6	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	starting growing
2/18/26	c(+) 1	2270	43	7.5	72.8	780	31	N/A	N/A	N/A	Y	
2/18/26	c(+) 2	3000	49	7.5	72.8	805	32	N/A	N/A	N/A	Y	
2/18/26	c(+) 3	3000	46	7.5	72.8	780	29	N/A	N/A	N/A	Y	
2/18/26	c(+) 4	3000	37	7.5	74.6	828	25	N/A	N/A	N/A	Y	
2/18/26	c(+) 5	2560	49	7.5	72.8	826	35	N/A	N/A	N/A	Y	
2/18/26	c(+) 6	2573	48	7.5	71	783	41	N/A	N/A	N/A	Y	
2/18/26	s1	2390	13	7.5	69.8	459	32	N/A	N/A	N/A	Y	
2/18/26	s2	3700	28	7.5	66.6	416	25	N/A	N/A	N/A	Y	
2/18/26	s3	3040	13	7.5	69.8	459	32	N/A	N/A	N/A	Y	

3/11/26	c(+) 6	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	7.61	Y	
3/11/26	s1	N/A	N/A	N/A	N/A	N/A	N/A	8	N/A	8.63	Y	
3/11/26	s2	N/A	N/A	N/A	N/A	N/A	N/A	5	N/A	7.94	Y	
3/11/26	s3	N/A	N/A	N/A	N/A	N/A	N/A	6	N/A	8.06	Y	
3/11/26	s4	N/A	N/A	N/A	N/A	N/A	N/A	5	N/A	7.95	Y	
3/11/26	s5	N/A	N/A	N/A	N/A	N/A	N/A	5	N/A	7.89	Y	
3/11/26	s6	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	7.4	Y	
3/11/26	c(-) 1	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	7.13	Y	
3/11/26	c(-) 2	N/A	N/A	N/A	N/A	N/A	N/A	4	N/A	6.73	Y	
3/11/26	c(-) 3	N/A	N/A	N/A	N/A	N/A	N/A	4	N/A	6.6	Y	
3/11/26	c(-) 4	N/A	N/A	N/A	N/A	N/A	N/A	4	N/A	6.54	Y	
3/11/26	c(-) 5	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	7.07	Y	
3/11/26	c(-) 6	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	6.92	Y	
3/11/26	l1	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	6.57	Y	
3/11/26	l2	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	6.81	Y	
3/11/26	l3	N/A	N/A	N/A	N/A	N/A	N/A	3	N/A	7.11	Y	
3/11/26	l4	N/A	N/A	N/A	N/A	N/A	N/A	4	N/A	7.18	Y	
3/11/26	l5	N/A	N/A	N/A	N/A	N/A	N/A	2	N/A	7.05	Y	
3/11/26	l6	N/A	N/A	N/A	N/A	N/A	N/A	2	N/A	7.3	Y	
3/11/26	dc 1	N/A	N/A	N/A	N/A	N/A	N/A	0	N/A	7.89	Y	
3/11/26	dc 2	N/A	N/A	N/A	N/A	N/A	N/A	5	N/A	7.84	Y	
3/11/26	dc 3	N/A	N/A	N/A	N/A	N/A	N/A	5	N/A	7.87	Y	
3/11/26	dc 4	N/A	N/A	N/A	N/A	N/A	N/A	5	N/A	7.88	Y	
3/11/26	dc 5	N/A	N/A	N/A	N/A	N/A	N/A	4	N/A	7.88	Y	
3/11/26	dc 6	N/A	N/A	N/A	N/A	N/A	N/A	6	N/A	7.73	Y	

3/25 /26	c(+) 1	673	50	7.5	72.5	770	18	N/A	N/A	7.68	N/A	
3/25 /26	c(+) 2	326	42	7.5	72.5	795	20	N/A	N/A	7.53	N/A	
3/25 /26	c(+) 3	585	33	7.5	74.3	790	26	N/A	N/A	7.83	N/A	
3/25 /26	c(+) 4	640	25	7.5	74.3	794	31	4	1	7.63	N/A	
3/25 /26	c(+) 5	627	42	7.5	74.3	823	34	N/A	N/A	7.72	N/A	
3/25 /26	c(+) 6	462	32	7.5	74.3	801	36	3	1	7.85	N/A	
3/25 /26	s1	411	52	7.5	72.8	1100	25	3	64	6.68	N/A	
3/25 /26	s2	537	54	7.5	71	710	25	6	96	7.31	N/A	
3/25 /26	s3	403	54	7.5	71	567	25	5	32	7.76	N/A	
3/25 /26	s4	451	54	7.5	71	557	24	4	45	8.16	N/A	
3/25 /26	s5	473	55	7.5	69.2	550	22	6	63	7.75	N/A	
3/25 /26	s6	560	54	7.5	69.2	602	22	6	80	8.57	N/A	
3/25 /26	c(-) 1	154	46	7.5	68.7	724	19	2	10	7.29	N/A	
3/25 /26	c(-) 2	219	49	7.5	70.5	765	21	3	9	7.23	N/A	
3/25 /26	c(-) 3	124	45	7	72.3	747	22	5	6	7.25	N/A	
3/25 /26	c(-) 4	18	12	7.5	74.3	801	25	4	3	6.6	N/A	
3/25 /26	c(-) 5	122	34	7.5	72.5	780	23	3	5	7.32	N/A	
3/25 /26	c(-) 6	230	46	7.5	72.5	822	25	2	7	7.27	N/A	
3/25 /26	l1	378	49	7.5	74.6	796	18	4	8	7.02	N/A	
3/25 /26	l2	442	49	7.5	69.2	544	19	4	10	7.14	N/A	
3/25 /26	l3	497	53	7.5	71	807	20	4	5	7.16	N/A	
3/25 /26	l4	451	54	7.5	69.2	820	23	5	12	7.27	N/A	
3/25 /26	l5	435	53	7.5	69.2	744	22	2	4	7.27	N/A	

3/25 /26	l6	265	43	7.5	69.2	750	22	3	4	7.31	N/A	
3/25 /26	dc 1	464	42	7.5	72.5	820	26	N/A	N/A	7.76	N/A	
3/25 /26	dc 2	544	55	7	72.5	796	32	4	4	7.6	N/A	
3/25 /26	dc 3	431	57	7	72.5	776	34	6	32	7.44	N/A	
3/25 /26	dc 4	555	53	7	72.5	833	37	4	40	6.9	N/A	
3/25 /26	dc 5	534	57	7	72.5	848	40	3	14	7.27	N/A	
3/25 /26	dc 6	574	59	7	72.1	820	36	5	41	7.63	N/A	

BIOMASS

date_mm_dd_yyyy	soil	id	root_mass	shoot_mass
4/1/26	reg	C- 1 (1)	0.03	0.02
4/1/26	reg	C- 1 (2)	0.02	0.02
4/1/26	reg	C- 2 (1)	0.06	0.05
4/1/26	reg	C- 2 (2)	0.04	0.03
4/1/26	reg	C- 3 (1)	0.02	0.02
4/1/26	reg	C- 3 (2)	0.03	0.04
4/1/26	reg	C- 3 (3)	0.02	0.04
4/1/26	reg	C- 4 (1)	0.02	0.08
4/1/26	reg	C- 4 (2)	0.02	0.06
4/1/26	reg	C- 5 (1)	0.04	0.06
4/1/26	reg	C- 6 (1)	0.05	0.06
4/1/26	reg	C- 6 (2)	0.02	0.04
4/1/26	reg	C- 6 (3)	0.04	0.05
4/1/26	reg	C- 6 (4)	0.01	0.02
4/1/26	des_c	DC-2 (1)	0.1	0.14
4/1/26	des_c	DC-3 (1)	0.07	0.25
4/1/26	des_c	DC-3 (2)	0.07	0.23
4/1/26	des_c	DC-3 (3)	0.04	0.18
4/1/26	des_c	DC-3 (4)	0.04	0.19
4/1/26	des_c	DC-3 (5)	0.02	0.12
4/1/26	des_c	DC-3 (6)	0.03	0.11
4/1/26	des_c	DC-4 (1)	0.12	0.63
4/1/26	des_c	DC-4 (2)	0.08	0.43
4/1/26	des_c	DC-4 (3)	0.03	0.12
4/1/26	des_c	DC-4 (4)	0.001	0.05
4/1/26	des_c	DC-5 (1)	0.02	0.08

4/1/26	des_c	DC-5 (2)	0.001	0.05
4/1/26	des_c	DC-5 (3)	0.001	0.05
4/1/26	des_c	DC-6 (1)	0.48	0.85
4/1/26	des_c	DC-6 (2)	0.16	0.7
4/1/26	des_reg	L-1(1)	0.03	0.01
4/1/26	des_reg	L-1(2)	0.01	0.04
4/1/26	des_reg	L-2(1)	0.01	0.07
4/1/26	des_reg	L-2(2)	0.02	0.07
4/1/26	des_reg	L-2(3)	0.01	0.04
4/1/26	des_reg	L-2(4)	0.01	0.04
4/1/26	des_reg	L-3(1)	0.04	0.06
4/1/26	des_reg	L-3(2)	0.02	0.06
4/1/26	des_reg	L-4(1)	0.04	0.04
4/1/26	des_reg	L-4(2)	0.03	0.03
4/1/26	des_reg	L-4(3)	0.05	0.05
4/1/26	des_reg	L-4(4)	0.05	0.04
4/1/26	des_reg	L-4(5)	0.01	0.02
4/1/26	des_reg	L-5	0.001	0.03
4/1/26	des_reg	L-6	0.02	0.03
4/1/26	stl_reg	s1(1)	0.12	0.24
4/1/26	stl_reg	s1(2)	0.14	0.28
4/1/26	stl_reg	s1(3)	0.03	0.06
4/1/26	stl_reg	s2(1)	0.22	1.16
4/1/26	stl_reg	s2(2)	0.1	0.01
4/1/26	stl_reg	s3(1)	0.19	0.26
4/1/26	stl_reg	s3(2)	0.06	0.07
4/1/26	stl_reg	s3(3)	0.04	0.05
4/1/26	stl_reg	s4(1)	0.39	0.05
4/1/26	stl_reg	s4(2)	0.08	0.19
4/1/26	stl_reg	s4(3)	0.08	0.14
4/1/26	stl_reg	s5(1)	0.04	0.04
4/1/26	stl_reg	s5(2)	0.1	0.07
4/1/26	stl_reg	s5(3)	0.08	0.24
4/1/26	stl_reg	s6(1)	0.04	0.3
4/1/26	stl_reg	s6(2)	0.03	0.18
4/1/26	pot	c+(4)	0.05	0.04
4/1/26	pot	c+(6)	0.12	0.12

HEIGHT

date_mm_dd_yyyy	soil	id	stem_height_mm
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3/25/26	pot	c(+)4	1
3/25/26	pot	c(+)6	1
3/25/26	stl_reg	s1	64
3/25/26	stl_reg	s2	96
3/25/26	stl_reg	s3	32
3/25/26	stl_reg	s4	45
3/25/26	stl_reg	s5	63
3/25/26	stl_reg	s6	80
3/25/26	reg	c(-)1	10
3/25/26	reg	c(-)2	9
3/25/26	reg	c(-)3	6
3/25/26	reg	c(-)4	3
3/25/26	reg	c(-)5	5
3/25/26	reg	c(-)6	7
3/25/26	des_reg	l1	8
3/25/26	des_reg	l2	10
3/25/26	des_reg	l3	5
3/25/26	des_reg	l4	12
3/25/26	des_reg	l5	4
3/25/26	des_reg	l6	4
3/25/26	des_c	dc2	4
3/25/26	des_c	dc3	32
3/25/26	des_c	dc4	40
3/25/26	des_c	dc5	14
3/25/26	des_c	dc6	41