

Supplementary Material

Table S1. The ANOVA P-value for total biomass, shoot biomass of *A. sativa*, *F. rubra*, *T. repens*, and shoot:root ratio.

| | Aboveground biomass of | | | Total biomass | Shoot:root ratio |
|--------------------------------------|------------------------|-----------------|------------------|---------------|------------------|
| | <i>A. sativa</i> | <i>F. rubra</i> | <i>T. repens</i> | | |
| Tailings | 0.000 *** | 0.123 | 0.136 | 0.000 *** | 0.112 |
| Amendment | 0.001 ** | 0.001 ** | 0.526 | 0.001 ** | 0.165 |
| Symbiotic | 0.002 ** | 0.175 | 0.003 ** | 0.001 ** | 0.411 |
| HerbMix | 0.000 *** | 0.005 ** | 0.004 ** | 0.000 *** | 0.429 |
| Tailings:Amendment | 0.123 | 0.002 ** | 0.314 | 0.075 | 0.761 |
| Tailings:Symbiotic | 0.649 | 0.089 | 0.269 | 0.664 | 0.511 |
| Amendment:Symbiotic | 0.700 | 0.182 | 0.120 | 0.921 | 0.190 |
| Tailings:HerbMix | 0.421 | 0.738 | 0.228 | 0.000 *** | 0.394 |
| Amendment:HerbMix | 0.008 ** | 0.172 | 0.034 * | 0.001 ** | 0.194 |
| Symbiotic:HerbMix | 0.226 | 0.979 | 0.063 | 0.887 | 0.089 |
| Tailings:Amendment:Symbiotic | 0.419 | 0.365 | 0.806 | 0.481 | 0.280 |
| Tailings:Amendment:HerbMix | 0.142 | 0.383 | 0.300 | 0.381 | 0.881 |
| Tailings:Symbiotic:HerbMix | 0.556 | 0.447 | 0.108 | 0.666 | 0.294 |
| Amendment:Symbiotic:HerbMix | 1.000 | 0.139 | 0.751 | 0.250 | 0.650 |
| Tailings:Amendment:Symbiotic:HerbMix | 0.548 | 0.091 | 0.785 | 0.101 | 0.308 |

Significance codes: $P < 0.001$ '***', $P < 0.01$ '**', $P < 0.05$ '*'

Table S2. The standard deviation of random effect factors on split-split plot design for each dependent variable data group of total biomass, shoot biomass of *A. sativa*, *F. rubra*, *T. repens*, and shoot:root ratio.

| Groups | No. of Obs. | Aboveground biomass of | | | Total biomass | Shoot:root ratio |
|---|-------------|------------------------|-----------------|------------------|---------------|------------------|
| | | <i>A. sativa</i> | <i>F. rubra</i> | <i>T. repens</i> | | |
| Inoculation:(Supplement:(Tailings:Block)) | 36 | 0.000 | 0.000 | 0.627 | 0.000 | 0.000 |
| Supplement:(Tailings:Block) | 18 | 0.058 | 0.069 | 0.000 | 0.013 | 0.000 |
| Tailings:Block | 6 | 0.000 | 0.275 | 0.772 | 0.000 | 0.200 |
| Block | 3 | 0.129 | 0.140 | 0.000 | 0.120 | 0.084 |
| Residual | | 0.260 | 0.243 | 0.775 | 0.208 | 0.277 |

Table S3. Type III Analysis of Variance Table with Satterthwaite's method on diameter growth of tree species on waste rock and fine tailing without spacing factor.

| Source | Sum Sq | DF | F value | Pr(>F) |
|---------------------|--------|----|---------|-----------|
| Species | 5.760 | 3 | 1.030 | 0.378 |
| Biochar | 5.027 | 1 | 2.696 | 0.101 |
| Inoculation | 5.751 | 1 | 3.085 | 0.079 |
| Tailings | 3.100 | 1 | 1.663 | 0.215 |
| HerbMix | 0.270 | 1 | 0.145 | 0.704 |
| InitDiameter | 28.560 | 1 | 15.318 | 0.000 *** |
| Species:Biochar | 4.930 | 3 | 0.882 | 0.450 |
| Species:Inoculation | 35.145 | 3 | 6.284 | 0.000 *** |
| Biochar:Inoculation | 5.386 | 1 | 2.889 | 0.089 |
| Species:Tailings | 3.689 | 3 | 0.660 | 0.577 |
| Biochar:Tailings | 4.276 | 1 | 2.293 | 0.130 |

| | | | | | |
|---|--------|---|-------|-------|----|
| Inoculation:Tailings | 8.169 | 1 | 4.381 | 0.037 | * |
| Species:HerbMix | 1.624 | 3 | 0.290 | 0.832 | |
| Biochar:HerbMix | 0.201 | 1 | 0.108 | 0.743 | |
| Inoculation:HerbMix | 17.020 | 1 | 9.129 | 0.003 | ** |
| Tailings:HerbMix | 1.122 | 1 | 0.602 | 0.438 | |
| Species:InitDiameter | 25.883 | 3 | 4.628 | 0.003 | ** |
| Biochar:InitDiameter | 3.250 | 1 | 1.743 | 0.187 | |
| Inoculation:InitDiameter | 2.403 | 1 | 1.289 | 0.256 | |
| Tailings:InitDiameter | 11.263 | 1 | 6.041 | 0.014 | * |
| HerbMix:InitDiameter | 1.484 | 1 | 0.796 | 0.372 | |
| Species:Biochar:Inoculation | 7.171 | 3 | 1.282 | 0.279 | |
| Species:Biochar:Tailings | 5.221 | 3 | 0.933 | 0.424 | |
| Species:Inoculation:Tailings | 7.982 | 3 | 1.427 | 0.233 | |
| Biochar:Inoculation:Tailings | 8.304 | 1 | 4.454 | 0.035 | * |
| Species:Biochar:HerbMix | 1.737 | 3 | 0.311 | 0.818 | |
| Species:Inoculation:HerbMix | 27.813 | 3 | 4.973 | 0.002 | ** |
| Biochar:Inoculation:HerbMix | 5.302 | 1 | 2.844 | 0.092 | |
| Species:Tailings:HerbMix | 0.975 | 3 | 0.174 | 0.914 | |
| Biochar:Tailings:HerbMix | 1.026 | 1 | 0.550 | 0.458 | |
| Inoculation:Tailings:HerbMix | 8.164 | 1 | 4.379 | 0.037 | * |
| Species:Biochar:InitDiameter | 3.895 | 3 | 0.696 | 0.554 | |
| Species:Inoculation:InitDiameter | 22.732 | 3 | 4.064 | 0.007 | ** |
| Biochar:Inoculation:InitDiameter | 4.528 | 1 | 2.429 | 0.119 | |
| Species:Tailings:InitDiameter | 4.659 | 3 | 0.833 | 0.476 | |
| Biochar:Tailings:InitDiameter | 4.380 | 1 | 2.349 | 0.125 | |
| Inoculation:Tailings:InitDiameter | 13.223 | 1 | 7.092 | 0.008 | ** |
| Species:HerbMix:InitDiameter | 1.438 | 3 | 0.257 | 0.856 | |
| Biochar:HerbMix:InitDiameter | 0.543 | 1 | 0.291 | 0.590 | |
| Inoculation:HerbMix:InitDiameter | 10.533 | 1 | 5.650 | 0.018 | * |
| Tailings:HerbMix:InitDiameter | 3.206 | 1 | 1.720 | 0.190 | |
| Species:Biochar:Inoculation:Tailings | 9.056 | 3 | 1.619 | 0.183 | |
| Species:Biochar:Inoculation:HerbMix | 22.172 | 3 | 3.964 | 0.008 | ** |
| Species:Biochar:Tailings:HerbMix | 1.562 | 3 | 0.279 | 0.840 | |
| Species:Inoculation:Tailings:HerbMix | 11.877 | 3 | 2.124 | 0.095 | |
| Biochar:Inoculation:Tailings:HerbMix | 0.201 | 1 | 0.108 | 0.742 | |
| Species:Biochar:Inoculation:InitDiameter | 4.923 | 3 | 0.880 | 0.451 | |
| Species:Biochar:Tailings:InitDiameter | 5.946 | 3 | 1.063 | 0.364 | |
| Species:Inoculation:Tailings:InitDiameter | 8.433 | 3 | 1.508 | 0.211 | |
| Biochar:Inoculation:Tailings:InitDiameter | 2.546 | 1 | 1.365 | 0.243 | |
| Species:Biochar:HerbMix:InitDiameter | 3.230 | 3 | 0.577 | 0.630 | |
| Species:Inoculation:HerbMix:InitDiameter | 24.610 | 3 | 4.400 | 0.004 | ** |
| Biochar:Inoculation:HerbMix:InitDiameter | 2.582 | 1 | 1.385 | 0.239 | |
| Species:Tailings:HerbMix:InitDiameter | 2.438 | 3 | 0.436 | 0.727 | |
| Biochar:Tailings:HerbMix:InitDiameter | 1.380 | 1 | 0.740 | 0.390 | |
| Inoculation:Tailings:HerbMix:InitDiameter | 8.491 | 1 | 4.554 | 0.033 | * |
| Species:Biochar:Inoculation:Tailings:HerbMix | 6.679 | 3 | 1.194 | 0.310 | |
| Species:Biochar:Inoculation:Tailings:InitDiameter | 4.024 | 3 | 0.720 | 0.540 | |
| Species:Biochar:Inoculation:HerbMix:InitDiameter | 25.259 | 3 | 4.516 | 0.004 | ** |

| | | | | |
|---|--------|---|-------|-------|
| Species:Biochar:Tailings:HerbMix:InitDiameter | 1.716 | 3 | 0.307 | 0.821 |
| Species:Inoculation:Tailings:HerbMix:InitDiameter | 12.417 | 3 | 2.220 | 0.084 |
| Biochar:Inoculation:Tailings:HerbMix:InitDiameter | 0.048 | 1 | 0.026 | 0.873 |
| Species:Biochar:Inoculation:Tailings:HerbMix:InitDiameter | 7.498 | 3 | 1.340 | 0.259 |

Significance codes: $P < 0.001$ '***', $P < 0.01$ '**', $P < 0.05$ '*'

Table S4. The standard deviation of random effect factors on split-split plot design for regression model on data group of fine tailing and waste rock without spacing effect. The total observation data is 2795.

| Groups | No. of Obs. | Variance | Std.Dev. |
|---|-------------|----------|----------|
| HerbMix:(Inoculation:(Biochar:(Block:(Tailings:Location)))) | 122 | 0.051 | 0.226 |
| Inoculation:(Biochar:(Block:(Tailings:Location))) | 63 | 0.052 | 0.228 |
| Biochar:(Block:(Tailings:Location)) | 32 | 0.000 | 0.000 |
| Block:(Tailings:Location) | 16 | 0.001 | 0.030 |
| Tailings:Location | 4 | 0.031 | 0.177 |
| Location | 2 | 0.000 | 0.000 |
| Residual | | 1.864 | 1.365 |

Table S5. Type III Analysis of Variance Table with Satterthwaite's method on diameter growth of tree species on fine tailing only with the inclusion of spacing factor.

| Source | Sum Sq | DF | F value | Pr(>F) | |
|----------------------------------|--------|----|---------|--------|----|
| Species | 21.944 | 3 | 3.946 | 0.008 | ** |
| InitDiameter | 5.209 | 1 | 2.810 | 0.094 | |
| Biochar | 0.694 | 1 | 0.374 | 0.541 | |
| Inoculation | 0.054 | 1 | 0.029 | 0.865 | |
| HerbMix | 0.333 | 1 | 0.180 | 0.672 | |
| Spacing | 2.663 | 2 | 0.718 | 0.488 | |
| Species:InitDiameter | 15.171 | 3 | 2.728 | 0.043 | * |
| Species:Biochar | 2.786 | 3 | 0.501 | 0.682 | |
| InitDiameter:Biochar | 0.186 | 1 | 0.101 | 0.751 | |
| Species:Inoculation | 19.401 | 3 | 3.489 | 0.015 | * |
| InitDiameter:Inoculation | 5.091 | 1 | 2.746 | 0.098 | |
| Biochar:Inoculation | 0.000 | 1 | 0.000 | 0.994 | |
| Species:HerbMix | 3.028 | 3 | 0.544 | 0.652 | |
| InitDiameter:HerbMix | 0.288 | 1 | 0.156 | 0.693 | |
| Biochar:HerbMix | 0.862 | 1 | 0.465 | 0.496 | |
| Inoculation:HerbMix | 1.853 | 1 | 1.000 | 0.318 | |
| Species:Spacing | 8.036 | 6 | 0.722 | 0.632 | |
| InitDiameter:Spacing | 5.002 | 2 | 1.349 | 0.260 | |
| Biochar:Spacing | 2.981 | 2 | 0.804 | 0.448 | |
| Inoculation:Spacing | 3.679 | 2 | 0.992 | 0.371 | |
| HerbMix:Spacing | 17.429 | 2 | 4.701 | 0.009 | ** |
| Species:InitDiameter:Biochar | 6.319 | 3 | 1.136 | 0.333 | |
| Species:InitDiameter:Inoculation | 10.523 | 3 | 1.892 | 0.129 | |
| Species:Biochar:Inoculation | 1.750 | 3 | 0.315 | 0.815 | |
| InitDiameter:Biochar:Inoculation | 1.623 | 1 | 0.876 | 0.350 | |
| Species:InitDiameter:HerbMix | 5.297 | 3 | 0.952 | 0.414 | |
| Species:Biochar:HerbMix | 3.629 | 3 | 0.653 | 0.581 | |
| InitDiameter:Biochar:HerbMix | 0.613 | 1 | 0.331 | 0.565 | |

| | | | | | |
|--|--------|---|-------|-------|----|
| Species:Inoculation:HerbMix | 9.528 | 3 | 1.713 | 0.162 | |
| InitDiameter:Inoculation:HerbMix | 0.147 | 1 | 0.079 | 0.778 | |
| Biochar:Inoculation:HerbMix | 4.057 | 1 | 2.189 | 0.139 | |
| Species:InitDiameter:Spacing | 8.470 | 6 | 0.762 | 0.600 | |
| Species:Biochar:Spacing | 4.014 | 6 | 0.361 | 0.904 | |
| InitDiameter:Biochar:Spacing | 1.813 | 2 | 0.489 | 0.613 | |
| Species:Inoculation:Spacing | 15.594 | 6 | 1.402 | 0.210 | |
| InitDiameter:Inoculation:Spacing | 4.324 | 2 | 1.166 | 0.312 | |
| Biochar:Inoculation:Spacing | 3.091 | 2 | 0.834 | 0.435 | |
| Species:HerbMix:Spacing | 13.021 | 6 | 1.171 | 0.319 | |
| InitDiameter:HerbMix:Spacing | 17.884 | 2 | 4.824 | 0.008 | ** |
| Biochar:HerbMix:Spacing | 0.323 | 2 | 0.087 | 0.917 | |
| Inoculation:HerbMix:Spacing | 0.070 | 2 | 0.019 | 0.981 | |
| Species:InitDiameter:Biochar:Inoculation | 1.829 | 3 | 0.329 | 0.805 | |
| Species:InitDiameter:Biochar:HerbMix | 3.504 | 3 | 0.630 | 0.596 | |
| Species:InitDiameter:Inoculation:HerbMix | 5.815 | 3 | 1.046 | 0.371 | |
| Species:Biochar:Inoculation:HerbMix | 6.229 | 3 | 1.120 | 0.340 | |
| InitDiameter:Biochar:Inoculation:HerbMix | 4.693 | 1 | 2.532 | 0.112 | |
| Species:InitDiameter:Biochar:Spacing | 3.955 | 6 | 0.356 | 0.907 | |
| Species:InitDiameter:Inoculation:Spacing | 12.619 | 6 | 1.135 | 0.340 | |
| Species:Biochar:Inoculation:Spacing | 10.646 | 6 | 0.957 | 0.453 | |
| InitDiameter:Biochar:Inoculation:Spacing | 1.588 | 2 | 0.428 | 0.652 | |
| Species:InitDiameter:HerbMix:Spacing | 13.069 | 6 | 1.175 | 0.317 | |
| Species:Biochar:HerbMix:Spacing | 3.440 | 6 | 0.309 | 0.932 | |
| InitDiameter:Biochar:HerbMix:Spacing | 1.258 | 2 | 0.339 | 0.712 | |
| Species:Inoculation:HerbMix:Spacing | 16.563 | 6 | 1.489 | 0.178 | |
| InitDiameter:Inoculation:HerbMix:Spacing | 0.034 | 2 | 0.009 | 0.991 | |
| Biochar:Inoculation:HerbMix:Spacing | 3.937 | 2 | 1.062 | 0.346 | |
| Species:InitDiameter:Biochar:Inoculation:HerbMix | 6.493 | 3 | 1.167 | 0.321 | |
| Species:InitDiameter:Biochar:Inoculation:Spacing | 9.475 | 6 | 0.852 | 0.530 | |
| Species:InitDiameter:Biochar:HerbMix:Spacing | 7.393 | 6 | 0.665 | 0.678 | |
| Species:InitDiameter:Inoculation:HerbMix:Spacing | 17.857 | 6 | 1.605 | 0.142 | |
| Species:Biochar:Inoculation:HerbMix:Spacing | 19.573 | 6 | 1.760 | 0.104 | |
| InitDiameter:Biochar:Inoculation:HerbMix:Spacing | 4.111 | 2 | 1.109 | 0.330 | |
| Species:InitDiameter:Biochar:Inoculation:HerbMix:Spacing | 20.132 | 6 | 1.810 | 0.093 | |

Significance codes: $P < 0.001$ '***', $P < 0.01$ '**', $P < 0.05$ '*'

Table S6. The standard deviation of random effect factors on split-split plot design for regression model on data group of fine tailing with spacing effect. The total observation data is 2132.

| Groups | No. of Obs. | Variance | Std.Dev. |
|--|-------------|----------|----------|
| HerbMix:(Inoculation:(Biochar:(Block:Location))) | 64 | 0.044 | 0.211 |
| Inoculation:(Biochar:(Block:Location)) | 32 | 0.023 | 0.153 |
| Biochar:(Block:Location) | 16 | 0 | 0 |
| Block:Location | 8 | 0 | 0 |
| Location | 2 | 0.062 | 0.249 |
| Residual | | 1.854 | 1.362 |