Supplementary material

Endophytic bacterial consortia isolated from disease-resistant *Pinus pinea* increase germination and plant quality in a susceptible pine species

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Table S1 – Taxonomic identification, plant growth promoting traits and enzymatic activity of the 68 representative strains isolated from the root of *Pinus pinea.*

(Excel file titled Table S1)

Table S2 – Table of the bacteria selected for *in vivo* trials containing the taxonomic information on the isolates and its respective inhibition percentage values against *Fusarium circinatum*.

(Excel file titled Table S2)

Table S3- Morphological traits of seedling inoculated with consortia and control (no consortia). No asterisks are included since there were no significant differences for each consortia vs control, for a p-value < 0.05 and N = 18. Mean: Average; SD: Standard deviation

	Shoot size (cm)		Root size (cm)		Biomass (mg)	
Consortia ID	Mean	SD	Mean	SD	Mean	SD
C5	4.75	0.57	4.66	2.44	22.79	6.52
C4	4.28	1.19	5.45	3.32	25.67	6.84
C3	4.47	0.79	4.39	2.73	30.75	8.71
C2	4.57	0.80	4.46	2.18	23.38	3.78
C1	4.76	0.77	4.54	2.70	23.98	8.23
Control	4.84	0.99	7.28	6.08	20.50	4.83
P5	4.96	0.99	3.40	0.42	21.22	3.79

P4	5.03	0.96	3.55	0.21	28.66	8.93
P3	4.80	0.65	2.97	0.60	19.77	2.21
P2	4.76	1.09	4.07	2.04	20.88	4.60
P1	4.30	0.74	3.93	3.16	22.92	7.01

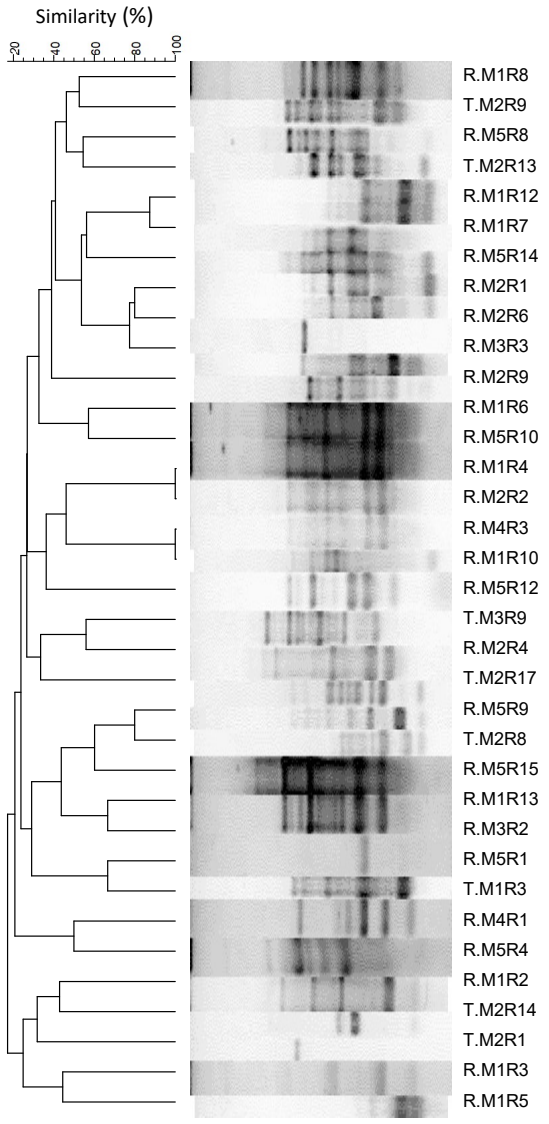


Figure S1 - Dendrogram of BOX-PCR fingerprinting patterns of 35bacterial endophytes isolated from *Pinus pinea* roots. The analysis was performed using GelCompar II software (Applied Maths, Belgium), employing the Dice similarity coefficient and UPGMA clustering method with 1% band position tolerance. Isolate codes indicate the isolation culture media (R-R2A; T-TSA), the tree (M1, M2, etc.), sample type (R: root) followed by the number of the isolate.

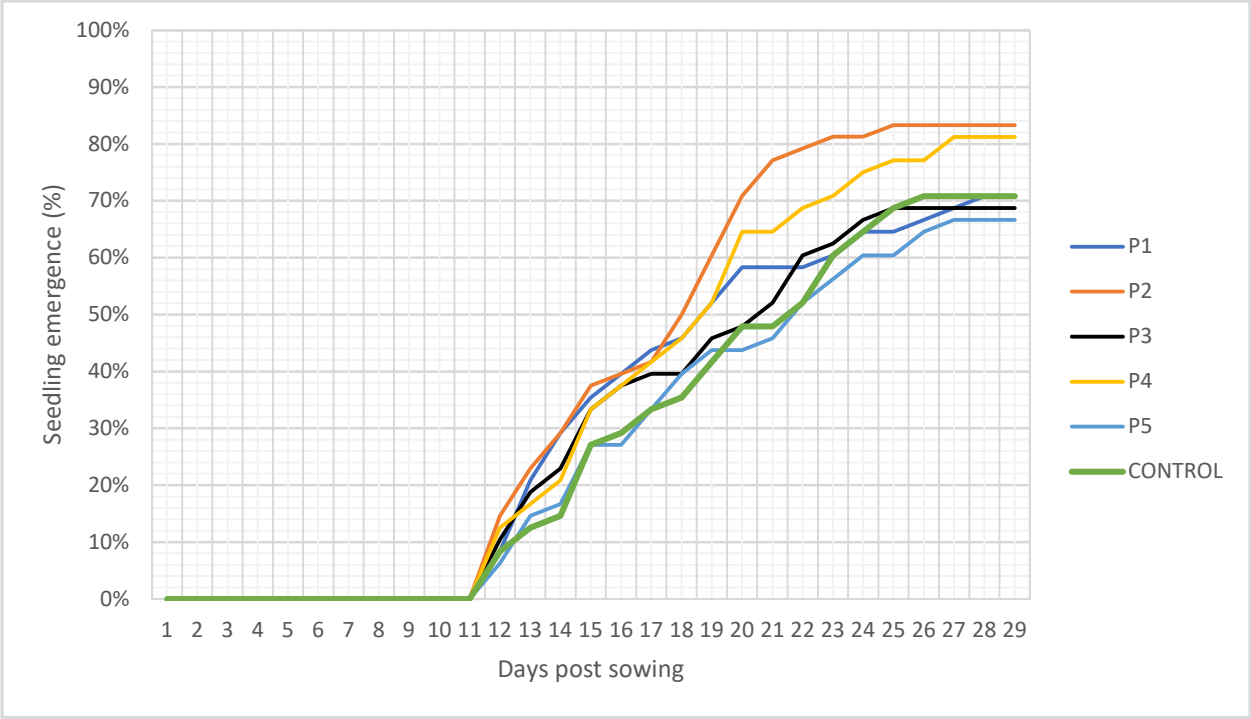


Figure S2 – Seedling emergence percentage of *Pinus radiata* across bacterial formulations P1 to P5 and respective control.

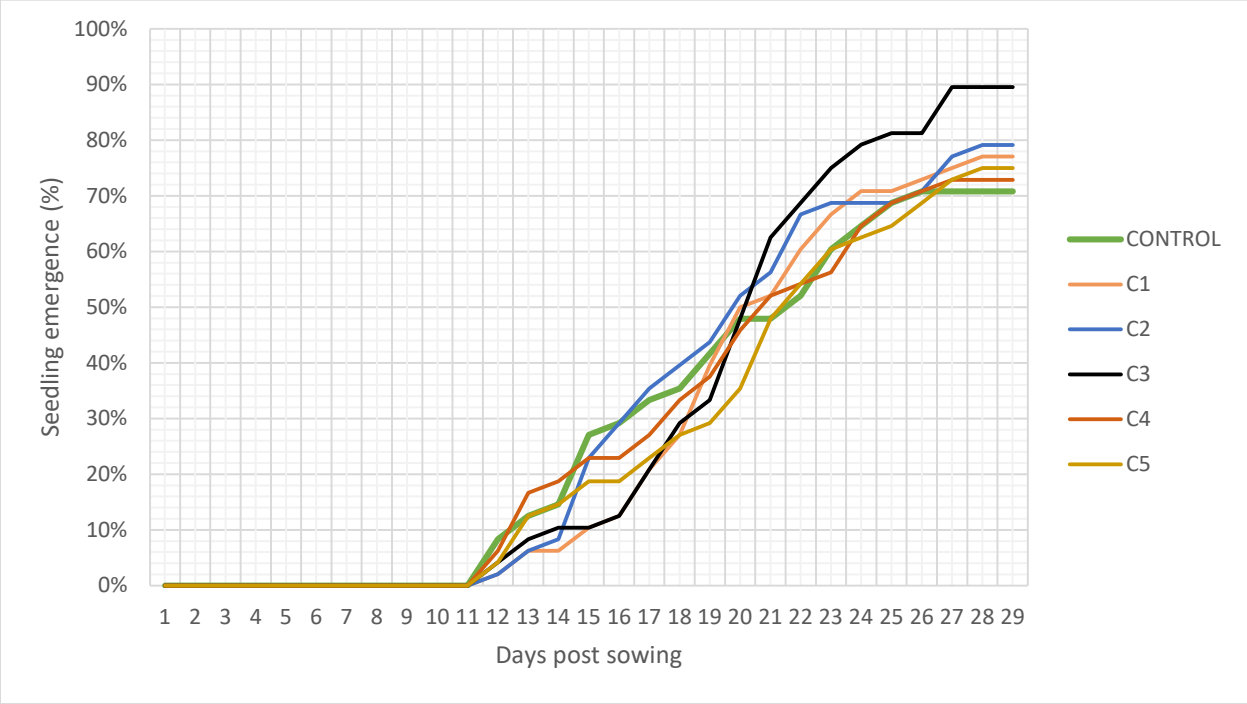


Figure S3 – Seedling emergence percentage of *Pinus radiata* across bacterial formulations C1 to C5 and respective control.

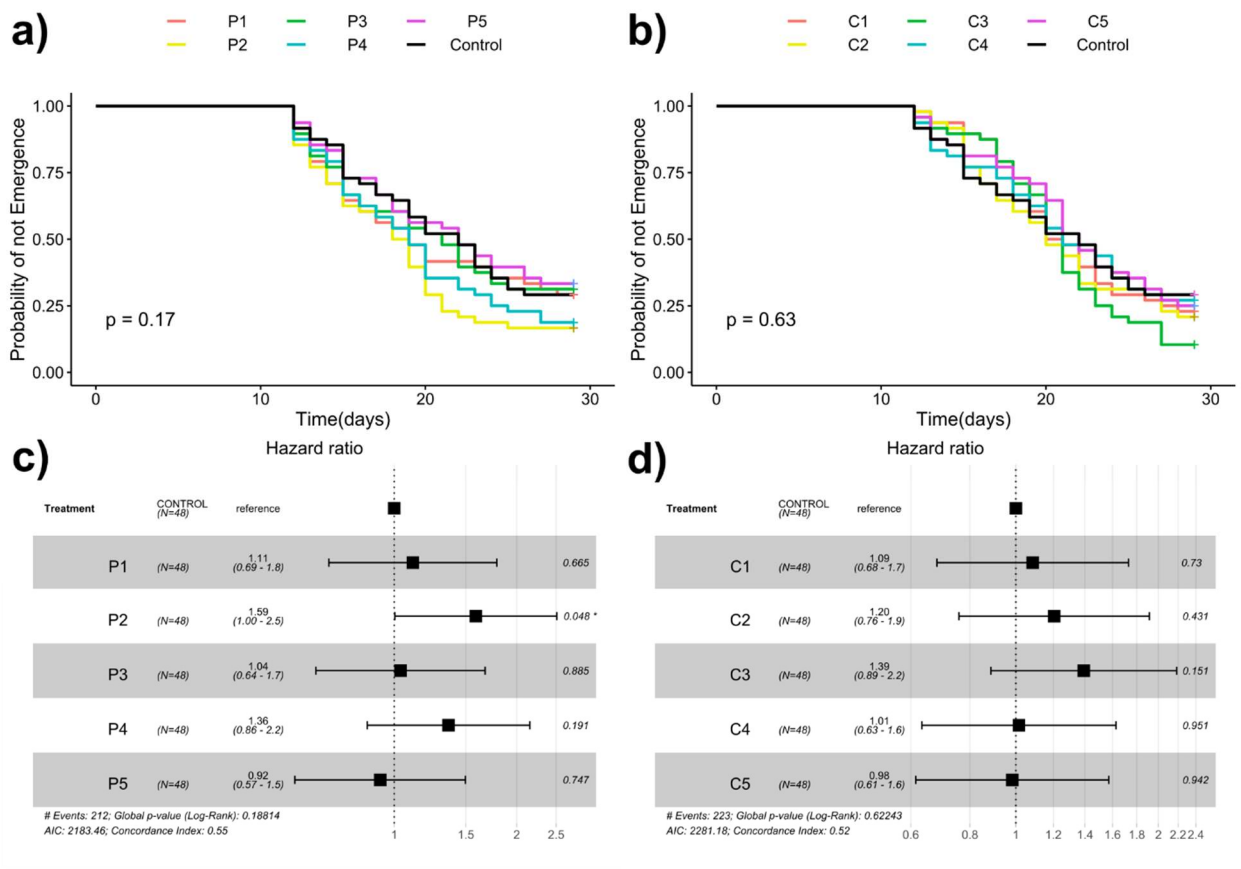


Figure S4- (a, b) Kaplan-Meier curves depicting the cumulative probability of non-emergence over time (days) for seedlings (n=48) under different bacterial formulation application (P1-P5 in a; C1-C5 in b) and a control group. (c, d) Forest plots of Hazard Ratios (HR) from Cox Proportional Hazards models, showing the effect of different bacterial formulation application (P1-P5 in c; C1-C5 in d) on emergence rate relative to Control. Squares represent HR, and horizontal lines denote 95% Confidence Intervals. Asterisks (*) indicate statistical significance ($p<0.05$). Below each plot are the total number of emergence events, the global p-value (Log-Rank) for the model, AIC, and Concordance Index.

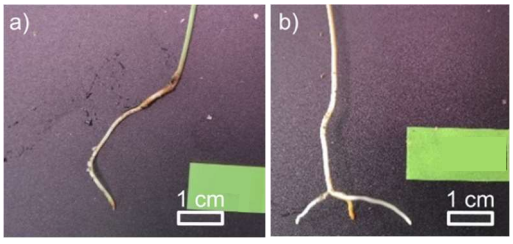


Figure S5- Representative photos of root structure for Control treatment (a) and P4 consortium (b).

Table S4 - Summary of germination metrics for seeds pretreated with bacterial formulation. Formulations correspond to different bacterial formulations (C1–C5, P1–P5) applied prior to sowing; Control indicates untreated seeds. Mean Germination Time and Germination Speed were calculated using seedling emergence data as a proxy for germination.

Formulations	Mean Germination Time	Germination Speed
C1	20.64865	1.853418
C2	19.94737	1.991453
C3	21.02326	2.123211
C4	19.80000	1.870244
C5	20.80556	1.827068
Control	19.32353	1.855223
P1	17.92500	2.327499
P2	17.77500	2.347147
P3	18.18182	1.911935
P4	18.66667	2.200978
P5	19.12500	1.769223