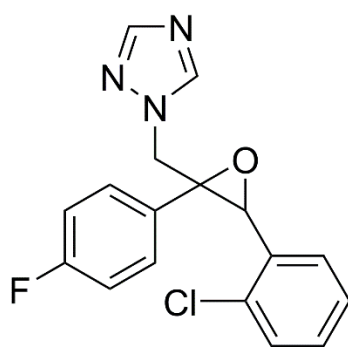
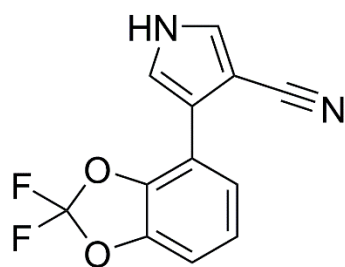


Figure S1. Chemical structure of the target fungicides.



Epoxiconazole



Fludioxonil

Figure S2. Growth of the bacterial isolates retrieved from the EPO and FLU-enriched consortia on 400 mgL⁻¹ of sodium acetate. Results are expressed as the mean of triplicates and error bars represent standard deviation. Lines connecting data points are just for guiding purposes.

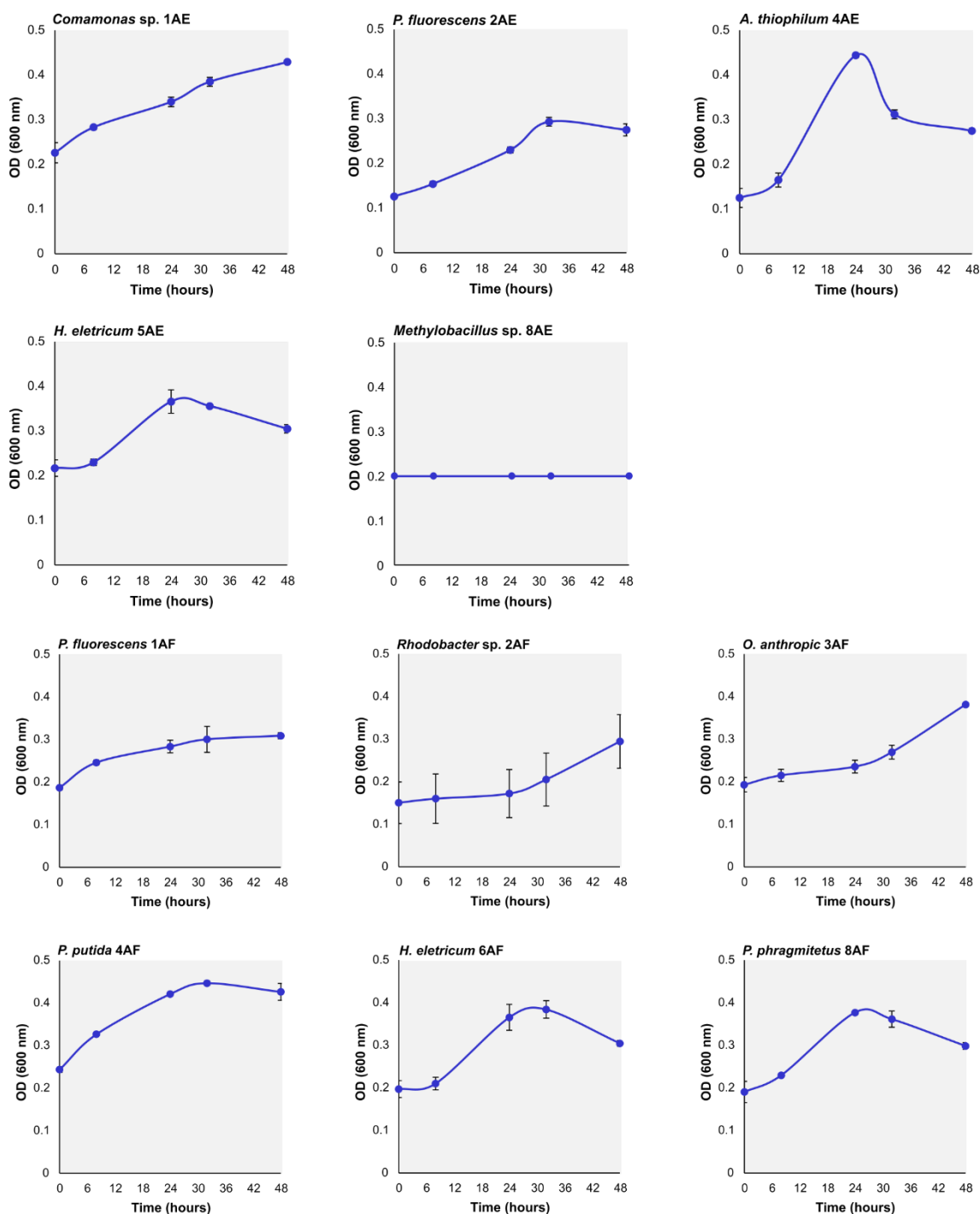


Table S1. Number of reads obtained for each OTU representing $\geq 1\%$ of the relative abundance of the EPO-enriched consortium, either at the beginning (0 days) or at the end of the incubation period (21 days)

OTU taxonomy	Number of reads	
	0 days	21 days
<i>Azospirillum</i>	48358	34953
<i>Methylobacillus</i>	122	3983
<i>Proteiniphilum</i>	2297	2912
<i>Reyranella</i>	1261	2003
<i>Lentimicrobium</i>	1830	1555
<i>Pannonibacter</i>	3961	1452
<i>Arenimonas</i>	1128	1324
<i>Hydrogenophaga</i>	656	1699
<i>Prolixibactereaceae</i>	54	1049
<i>Taonella</i>	1451	1025
<i>Paludibacter</i>	185	1014
<i>Devosia</i>	480	930
<i>Bryobacter</i>	701	915
<i>Taibaiella</i>	844	884
<i>Rikenellaceae</i>	558	614
<i>Persicitalea</i>	1672	414

Table S2. Number of reads obtained for each OTU representing $\geq 1\%$ of the relative abundance of the FLU-enriched consortium, either at the beginning (0 days) or at the end of the incubation period (21 days)

OTU taxonomy	Number of reads	
	0 days	21 days
<i>Azospirillum</i>	22390	20611
<i>Pannonibacter</i>	13626	1627
<i>Spirosomaceae</i>	8524	3692
<i>Chryseobacterium</i>	2921	1056
<i>Proteiniphilum</i>	2531	683
<i>Reyranella</i>	1948	898
<i>Taibaella</i>	1406	825
<i>Desulfovibrio</i>	1005	683
<i>R-7 group</i>	961	942
<i>Hydrogenophaga</i>	745	3
<i>Rikenellaceae</i>	731	132
<i>Petrimonas</i>	559	5041
<i>Stenotrophomonas</i>	417	681
<i>Shinella</i>	132	570
<i>Brevundimonas</i>	392	475
<i>Desulfosporosinus</i>	782	1005
<i>Ruminiclostridium</i>	584	744
<i>Hyphomonas</i>	160	544