



HAL
open science

Engineering multi-degrading bacterial communities to bioremediate soils contaminated with pesticides residues

Sylvia Thieffry, Julie Aubert, Marion Devers-Lamrani, Fabrice Martin-Laurent, Sana Romdhane, Nadine Rouard, Mathieu Siol, Aymé Spor

► To cite this version:

Sylvia Thieffry, Julie Aubert, Marion Devers-Lamrani, Fabrice Martin-Laurent, Sana Romdhane, et al. Engineering multi-degrading bacterial communities to bioremediate soils contaminated with pesticides residues. *Journal of Hazardous Materials*, 2024, 471, pp.134454. 10.1016/j.jhazmat.2024.134454 . hal-04627424

HAL Id: hal-04627424

<https://hal.inrae.fr/hal-04627424>

Submitted on 27 Jun 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License



Engineering multi-degrading bacterial communities to bioremediate soils contaminated with pesticides residues

Sylvia Thieffry^{a,b,*}, Julie Aubert^{b,1}, Marion Devers-Lamrani^{a,1}, Fabrice Martin-Laurent^{a,1}, Sana Romdhane^{a,1}, Nadine Rouard^{a,1}, Mathieu Siol^a, Aymé Spor^{a,*,1}

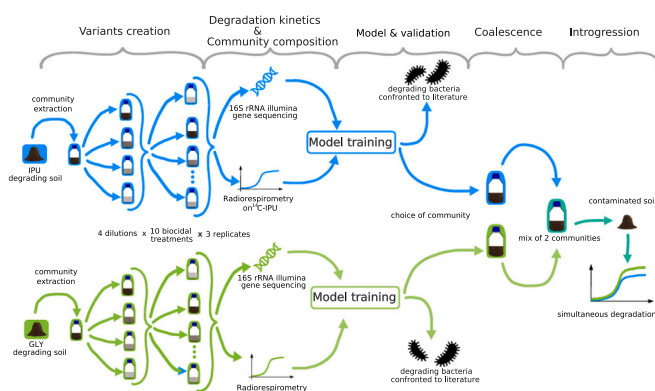
^a INRAE, Institut Agro, Université de Bourgogne, Université de Bourgogne Franche-Comté, Agroécologie, 21000 Dijon, France

^b Université Paris-Saclay, AgroParisTech, INRAE, UMR MIA Paris-Saclay, 91120 Palaiseau, France

HIGHLIGHTS

- Pesticides persist in soil and cause increasingly documented ecological damages.
- We present a bioremediation protocol via modifications of two bacterial communities.
- We transposed statistical tools from genomic selection to microbial ecology.
- Using coalescence, we successfully built multi-degrading bacterial communities.
- We efficiently transferred the degrading capacities towards the receiving soil.

GRAPHICAL ABSTRACT



ARTICLE INFO

Keywords:

Bioremediation
Ecological engineering
Coalescence
Glyphosate
Isoproturon

ABSTRACT

Parallel to the important use of pesticides in conventional agriculture there is a growing interest for green technologies to clear contaminated soil from pesticides and their degradation products. Bioaugmentation *i. e.* the inoculation of degrading micro-organisms in polluted soil, is a promising method still in needs of further developments. Specifically, improvements in the understanding of how degrading microorganisms must overcome abiotic filters and interact with the autochthonous microbial communities are needed in order to efficiently design bioremediation strategies. Here we designed a protocol aiming at studying the degradation of two herbicides, glyphosate (GLY) and isoproturon (IPU), via experimental modifications of two source bacterial communities. We used statistical methods stemming from genomic prediction to link community composition to herbicides degradation potentials. Our approach proved to be efficient with correlation estimates over 0.8 - between model predictions and measured pesticide degradation values. Multi-degrading bacterial communities were obtained by coalescing bacterial communities with high GLY or IPU degradation ability based on their community-level properties. Finally, we evaluated the efficiency of constructed multi-degrading communities to remove pesticide contamination in a different soil. While results are less clear in the case of GLY, we showed an

* Corresponding authors at: INRAE, Institut Agro, Université de Bourgogne, Université de Bourgogne Franche-Comté, Agroécologie, 21000 Dijon, France.

E-mail addresses: sylvia.thieffry@inrae.fr (S. Thieffry), ayme.spor@inrae.fr (A. Spor).

¹ Authors are listed alphabetically.

efficient transfer of degrading capacities towards the receiving soil even at relatively low inoculation levels in the case of IPU. Altogether, we developed an innovative protocol for building multi-degrading simplified bacterial communities with the help of genomic prediction tools and coalescence, and proved their efficiency in a contaminated soil.

1. Introduction

Pesticides are still widely used in conventional agriculture to maintain high yield by controlling pests among which broadleaf weeds competing with the crops [1]. Yet their persistence in soil and their transfer to water resources cause ecological damages that are increasingly documented [2]. Indeed, pesticides or their degradation metabolites can have negative effects on animals and microorganisms which in turn affect ecosystem functions and services [3,4].

Recurrent pesticides exposure can lead to the selection of degrading populations among soil bacterial community that are able to use pesticides as nutrient and energy source for their growth [5]. Pesticide biodegradation by soil microorganisms has been amply documented and represents a precious baseline to develop bioremediation strategies of polluted ecosystems [6,7]. Classically, bioaugmentation strategies relies on the isolation of specific degrading strain(s) by enrichment in a selective medium supplemented with the pesticide as sole carbon or nitrogen source. This process is time consuming and assumes that the degrading bacteria can survive and grow in laboratory conditions, which is known to be the case for only a small fraction of all microorganisms [8]. Besides isolation, multiple studies showed that bioaugmentation with pure degrading strains or simple bacterial consortia turned out to be inefficient in field-scale experiments, due to establishment and survival problems of microbial inocula or to an *in situ* decline of their degrading activities [9,10].

In order to overcome these limitations, we propose to adopt the vision of quantitative geneticists who try to introgress a genomic region into a given genetic background to select a phenotype of interest. By doing so, pesticide-degrading bacteria are seen as the alleles responsible for the phenotype of interest *i. e.* pesticide biodegradation, that need to be introgressed into a contaminated soil microbial community, corresponding to the genetic background to improve. Hence, the microbial community matches the plant or animal individual as the experimental unit. Therefore, we transposed tools from genomic selection used by quantitative geneticists to microbial ecology with a bioremediation perspective.

Statistical methods used in genomic selection result from a mix of two historical approaches: the Best Linear Unbiased Predictor approach (BLUP), blind to genetic trait determinism, uses kinship level between individuals to derive the proportion of expected shared alleles and guides choice for individuals to cross [11,12]. The second approach, akin to the QTL approach is based on genomic markers to identify regions implied in the expression of phenotypes of interest [13]. The emergence of NGS (Next Generation Sequencing) opened the possibility to precisely estimate shared alleles between individuals, allowing the use of BLUP type models based on the realised, instead of expected, kinship matrix. We can then use individual genotype as a proxy to predict the genetic value. Correspondingly, one could develop a prediction model for microbial community "phenotype" (community function) from their "genotype", which consists of its specific composition determined by sequencing of taxonomic markers (*e.g.* 16 S rDNA amplicon). Such an approach, linking community composition to a community function, has not yet been explored in the context of microbial community engineering.

To test the relevance of this original approach, we focused our research on two herbicides: Glyphosate (GLY) and Isoproturon (IPU) and experimentally obtained a cohort of microbial communities degrading these two xenobiotics. After extraction of degrading communities, one for each of the two herbicides, serial dilutions coupled with a range of

biocidal treatments were performed in order to obtain compositional variants. Importantly, they were inoculated in the recipient soil previously sterilized, as a mean to select degrading bacteria able to grow in this specific environmental niche [14]. Indeed, environmental filtering by pH, soil structure, organic matter proportion, is thought to be a major cause for the inefficiency of strain bioaugmentation [15]. For each of the compositional variant, degrading capacity was measured by radiorespirometry and 16 S rDNA sequencing were undertaken, allowing us to explore the links between the pesticide-degrading function and the bacterial community composition at the Operational Taxonomic Unit (OTU) level. We used statistical methods routinely used in genomic prediction, focusing on two models derived from linear regression, Ridge Regression (RR) and LASSO, as well as a nonlinear machine-learning method: Random Forest (RF) [16]. We then investigated the explanatory power of the models and looked at highlighted OTUs. To go further, coalescence of GLY and IPU degrading communities, specifically chosen based on their intrinsic properties such as diversity levels, degrading capacities and relative abundance of OTUs of interest, was performed in order to explore the compatibility of degrading communities. The multi-degrading communities were finally inoculated in a recipient inhabited soil to evaluate the efficiency of the proposed protocol to bioremediate a pesticide contaminated soil.

2. Materials and methods

2.1. Soil sampling

We collected three different soils based on their potential to degrade two herbicides, glyphosate (GLY) and isoproturon (IPU). One soil was collected from Noiron-sous-Gevrey (France, 47°11'36.38"N, 5°4'55.44"E) for its potential to degrade GLY, likely due to recurrent use of this herbicide. It contains 42% silt, 42% clay and 15% sand and shows a pH of 8.04, as well as 25.37 g/kg organic carbon and 2.15 g/kg nitrogen. A second was collected from the Epoisses INRAE experimental farm (Bretenière, France, 47°30'22.18"N, 4°10'26.46"E) for its potential to degrade IPU which is due to long term exposure to this compound. Soil properties were as follows: 51.9% silt, 41% clay, and 6.2% sand, pH 7.2, and organic carbon and nitrogen content 15.5 g/kg and 1.4 g/kg dry soil, respectively. A third soil was collected from the CEREEP Ecotron Research Station (Saint-Pierre-lès-Nemours, France, geographic coordinates: 48°16'58.9"N, 2°40'19"E) and displayed a poor degradation potential for both herbicides. This last soil is a cambisol with moor composed of 19% silt, 6.98% clay, 74.1% sand, and with 14.7 g/kg organic C; 1.19 g/kg N; pH of 5.22. All three soils were sieved at 4 mm, and a sufficient amount of the Ecotron soil was sterilised by γ sterilisation (2 times 35 kGy in Conservatoire, Dagneux, France). The Noiron-sous-Gevrey and Epoisses soils were pre-incubated for 30 days in 300 g microcosms in triplicates with their attributed herbicide (GLY and IPU, respectively at days 1 and 15 according to their agronomical dose, *i. e.* 3 mg/kg equivalent dry mass (edm) for GLY and 2 mg/kg edm for IPU).

2.2. Glyphosate and Isoproturon mineralisation potentials

Mineralisation ability of the two herbicides were measured on 15 g edm soil samples that were adjusted to the same moisture level (70% of water holding capacity (WHC) of the soil). Solutions of ^{14}C -ring labelled IPU and ^{14}C -GLY (on C-P bond) were obtained at a concentration reaching 1 667 Bq radioactivity per dose (400 μl of herbicide solution

added to the samples at agronomical dose). All samples were then placed in closed jars along with 10 ml water in an open container to maintain humidity and 5 ml sodium hydroxide NaOH at 0,2 M to trap emitted $^{14}\text{CO}_2$. The jars were put in the dark at room temperature (20 °C) for 42 days. The NaOH containers were regularly replaced for temporal assessments of emitted $^{14}\text{CO}_2$ with addition of 10 ml scintillation fluid (ACSII, Amersham) and measures on a Beckman scintillation counter. For each herbicide, the mineralisation potential was expressed as the cumulative percentage of $^{14}\text{CO}_2$ evolved from the initially added ^{14}C -pesticide over time.

2.3. Microbial community variants construction

For each herbicide-degrading soil microbial community, compositional variants were obtained by coupling serial dilutions with biocidal treatments, as described in Romdhane et al., 2021 [17]. Each soil community was first extracted by blending 33 g edm of soil with 60 ml sterile distilled water, then diluted 10 times with sterile 0.9% NaCl solution to get the 10^0 dilutions. 10^{-1} , 10^{-2} and 10^{-3} dilutions were retrieved by 10 times serial-dilutions. For each dilution level, we applied 9 different biocidal treatments (see Table 1 for more details) in triplicates and kept untreated samples as controls. This experimental procedure led to a total of 120 community suspensions (= 4 dilutions x 10 treatments x 3 replicates) per herbicide-degrading community. A volume of 10.5 ml from each suspension was inoculated into 50 g dry sterilized Ecotron soil in plasma flasks closed with sterile cotton lids, with addition of 2 ml of the adequate herbicide solution to reach the agronomical dose in order to facilitate the establishment of the degrading community. All microcosms were kept for 43 days in the dark at room temperature (20 °C) and moisture was adjusted to vary between 50% to 70% of WHC by addition of sterile water. After 43 days, 250 mg edm of soil was collected for each microcosm to assess microbial community composition using 16 S rDNA sequencing, 5 g to determine relative humidity and 15 g to assess herbicide mineralisation potentials.

2.4. Assessment of microbial community composition and diversity

DNA was extracted from 250 mg edm for the 246 samples (compositional variants and original soils) using the DNeasy PowerSoil-htp 96 well DNA isolation kit (Qiagen, Hilden, Germany). Generation of amplicons for Illumina MiSeq sequencing was done according to a two steps PCR protocol as follows: i) amplification in duplicates of the V3-V4 hyper-variable region of the bacterial 16 s rRNA with fusing primers U341F (5'-CCTACGGGRRSGCAGCAG-3') and 805 R (5'-GACTACCAGGGTATCTAAT-3'), and, to allow the subsequent addition of multiplexing index-sequences, overhang adapters (forward:TCGTCCGCGCTCAGATGTGTATAAAGAGACAG, adapter: GTCTCGTGGGCTCGGAGATGTGTATAAAGAGACAG). PCR cycles started at 98 °C for 30 s, then 55 °C for 30 s and 72 °C for 30 s and a final extension for 10 min at 72 °C, ii) pooling of duplicates and amplification with unique pairs of tag per sample, at PCR cycles starting with 8 °C for 3 min followed by 98 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s and a final extension for 10 min at 72 °C. 2% agarose gel were prepared to

visually verify amplicon sizes, and we noted two samples (both from the GLY compositional variants) without amplicons that were taken out for downstream analyses. All samples were then cleaned with SequalPrep Normalization plate kit 96-well (Invitrogen, Carlsbad, CA, USA), pooled and sequenced on MiSeq (Illumina, 2 x 250 bp) using the MiSeq reagent kit v2 (500 cycles).

The sequence data were analysed using an in house developed Jupyter Notebook [18] streaming together different bioinformatics tools. Briefly, R1 and R2 sequences were assembled using PEAR [19] with default settings. Further quality checks were conducted using the QIIME pipeline [20] and short sequences were removed (< 400 bp). Reference-based and *de novo* chimera detection, as well as clustering in OTUs were performed using VSEARCH [21] and the adequate reference databases (SILVA's representative set of sequences). The identity thresholds were set at 94% based on replicate sequencing of a bacterial mock community containing 40 bacterial species. Representative sequences for each OTU were aligned using MAFFT [22] and a 16 S phylogenetic tree was constructed using FastTree [23]. Taxonomy was assigned using BLAST [24] and the SILVA reference database v138 [ref 25]. Diversity metrics, that is, Faith's Phylogenetic Diversity (PD) [26], richness (observed species) and evenness (Simpson's reciprocal index), describing the structure of microbial communities were calculated based on rarefied OTU tables (10 000 sequences per sample). UniFrac distance matrices [27] were also computed to detect global variations in the composition of microbial communities. OTUs showing low abundance were discarded with a threshold of 210 counts across the compositional variants, to avoid artefactual association of rare OTUs with degradation potential and to lower the number of parameters (OTUs) to be estimated, from 5145 to 1316. In addition, one GLY compositional variant had a read depth below 5000 and was then removed for downstream analyses (mean of count per community around 16,700).

2.5. Co-occurrence networks and visualisation of OTU predictors

Bacterial co-occurrence networks were constructed based on filtered OTU count data (1316 OTUs) over the 240 samples degrading communities using a sparse multivariate Poisson log-normal (PLN) network model with a latent Gaussian layer and an observed Poisson layer using the R package PLNmodels v0.11.04 [ref. 28,29]. The best model was selected using a Stability Approach to Regularisation Selection [30]. Phylogenetic relationships between OTU predictors were visualized using the Interactive Tree of Life webservice [31].

2.6. Predicting herbicide mineralisation potential from microbial community composition

We derived the principle of predicting herbicide mineralisation potential from the bacterial community composition from the same logic as used in genomic prediction, where a model is trained to predict phenotype on the basis of the genotype of individuals as assessed through numerous molecular markers. Here we trained models to predict herbicide degradation based on the composition of bacterial

Table 1
Biocidal treatments applied on herbicide-degrading communities.

Treatment	Abbreviation	Modality
Ciprofloxacin (antibiotic)	Cipro	5 h incubation at 25 °C with ciprofloxacin at 66 µg/ml
Ramoplanin (antibiotic)	Ramo	5 h incubation at 25 °C with ramoplanin at 70 µg/ml
pH2	pH2	2 h incubation at 25 °C with 730 µl acid malic 1 M then 3 washes
pH11	pH11	2 h incubation at 25 °C with 370 µl ammoniac 20% 1 M then 3 washes
Oxidant 1 – strong	Ox1	1 h incubation at 25 °C with 730 µl H2O2 0,98 M
Oxidant 2 – mild	Ox2	1 h incubation at 25 °C with 295 µl H2O2 0,98 M
Heat shock	HS	0 °C for 5 min; 70 °C for 15 min; 0 °C for 5 min
UV	UV	2 h exposition to UVC light
Freeze-thaw	FT	6 x (-80 °C for 15 min; 30 °C for 15 min)
Control	CT	/

communities. All the following analyses are based on three statistical methods used in genomic prediction: Ridge Regression (RR), LASSO and Random Forest (RF). The first 2 methods build a regression model based on the relative composition in OTUs of the compositional variants over the function performed by their community. This leads to dealing with a high number of parameters to be estimated (the effect of each of the ~ 1316 OTUs, namely) compared to the number of experimental samples (120 compositional variants per herbicide-degrading community). In this so-called large p small n setting, using a regular linear regression (Ordinary Least-Square) would lead to inflated variance of the estimates. To alleviate this problem, penalized regression methods use various penalty functions to shrink all estimates (Ridge Regression) and/or perform variable selection (in the case of LASSO). Here we used a Bayesian implementation of these 2 penalized regression methods with prior distribution of bacterial species or OTU effects chosen as a Gaussian Distribution for Bayesian Ridge Regression (BRR) and a Laplace distribution for Bayesian LASSO (BL). They were run using the R package BGLR v1.1.0 [ref. 32]. The third method, Random Forest, is an ensemble method based on building decision trees to determine the importance of the OTUs by partitioning them depending on their counts in relation with the measured community function [33]. This method uses a combination of tree predictors and has the advantage of not hypothesizing additive effects of the OTUs and can thus be powerful in non-additive situations. The R package RandomForest v4.7-1.1 [ref. 34] was used for the following analysis, with parameters: number of trees of 500, node size of 5 and tested variables at each split of 1000.

Prior to any analysis, OTUs counts were corrected for sequencing depth (data/community sum * max of all community sum) then centered and reduced. Based on the mineralisation curves (see Supp. Fig. 1), we estimated 3 measurable curve parameters that were further considered as our community phenotypes: the total cumulative mineralisation after 42 days (Total), mineralisation value at the time point at which the variance across samples of the cumulative mineralisation potential is maximised (HighVar) and the slope of the linear regression of the cumulative mineralisation potential over the first 10 days (Slope). This last parameter approximates the mineralisation potential rate. Note that for GLY, HighVar is estimated at day 42, and is therefore equivalent to Total. On the opposite, for IPU, HighVar landed on day 13. To assess the

prediction potential of these 3 statistical methods, we used a cross-validation scheme using 4/5 of the data to train the models, and the remaining 1/5 of the data to test its accuracy. The process was repeated 8 times, redrawing the sets each time. The metric we used to assess the accuracy of prediction was the Pearson correlation between predicted and measured herbicide mineralisation potential.

2.7. Mixing herbicide-degrading compositional variants

We created artificial microbial communities by mixing GLY-degrading with IPU-degrading compositional variants. The modalities used to create these communities were driven by different hypotheses leading to six scenarios based on community structure or degrading features (Fig. 1): i) measured mineralisation rate for the herbicide they were selected for, ii) diversity of the compositional variants, iii) predicted mineralisation potential rate of the other herbicide and iv) abundance of OTUs detected as having positive or negative associations with the measured mineralisation rate. For each scenario, 5 IPU-degrading communities and 5 GLY-degrading communities were selected and mixed by random pairing (see Supplementary Materials for scenarios details).

For community mixing, 2.5 g of each parental community was added in 50 g sterilised dry Ecotron soil.

All microcosms were then watered up to 70% of soil water holding capacity and boosted by the addition of an agronomical dose of both IPU and GLY, closed with sterile cotton lids and incubated for 45 days. The resulting 30 microcosms were then sampled, and the GLY and IPU mineralisation potential of the resulting microbial communities were then assessed using radiorespirometry.

2.8. Coalescence of the herbicide multi-degrading communities into the original non-degrading soil

We selected the 5 best communities derived from the mixing of compositional variants based on their efficient IPU mineralisation and their improved GLY mineralisation compared to their parents. 4 levels of inoculations were prepared for each of these communities, reaching 50 g edm of soil in each microcosm. Inoculations were handled by mixing

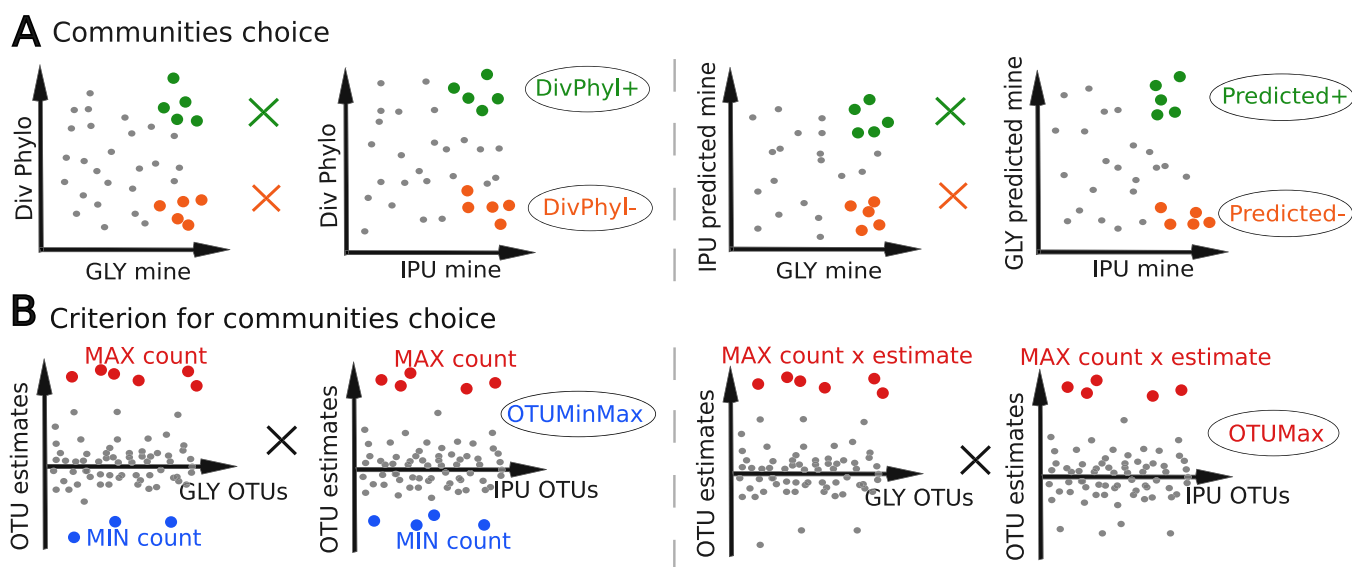


Fig. 1. Graphical representation of criterion for selection of IPU and GLY communities to be mixed, under 6 scenarios. Crosses represent the mixing between IPU and GLY communities. Scenarios in panel A are based on communities' characteristics: measured pesticide mineralisation rate (mine), phylogenetic diversity (Div Phylo) and predicted mineralisation by BL model for Slope (predicted mine). In Panel B, community choice is based on OTUs estimates (BL model for slope phenotype). Coloured dots (red for positive and blue for negative estimates) are the OTUs taken in account for the community choice, Scenario OTUMinMax maximizes the abundance of OTUs with high estimates and minimizes OTUs with low estimates while OTUMax maximizes the product of abundance of high estimates OTUs and their estimates.

0.1 g, 0.5 g, 1 g or 5 g (corresponding respectively to 0.2%, 1%, 2% and 10% mixing-ratio) of soil of the best communities with the original, non-sterilised Ecotron soil, with addition of 2 ml of both herbicide solutions to reach the agronomical dose, in order to facilitate the establishment of the degrading communities and mimic an herbicide contamination. IPU and GLY mineralisation potential of the coalesced communities were then assessed by radiorespirometry.

3. Results

3.1. Evaluation of the GLY and IPU mineralisation potential of the three selected soils

Mineralisation potentials of IPU and GLY differed greatly between soils, with the Ecotron soil showing the lowest potential for both pesticides (Supp. Fig. 2). IPU is far better mineralised in Epoisses (27.3% \pm 1.4) soil as compared to the two other soils (6.5% \pm 0.04 for Ecotron and 14.7% \pm 0.2 for Noiron). The Noiron soil exhibits the highest GLY mineralization (30.0% \pm 0.6), although the difference with the other soils is less striking than it is with IPU (17.9% \pm 0.1 for Ecotron and 21.6% \pm 0.5 for Epoisses).

3.2. GLY and IPU-degrading compositional variants

We coupled serial dilutions with different biocidal treatments to construct compositional variants of GLY-degrading bacterial communities from Noiron soil and IPU-degrading ones from Epoisses soil (Table 1). Principal coordinates analysis of the weighted Unifrac distance matrix revealed a continuous variation in composition across both

IPU and GLY communities (Supp. Fig. 3). Compositional variants are significantly different from the original communities found in IPU and GLY degrading soils. This indicates that community manipulation was successful to construct compositional variants for both GLY and IPU original communities.

We then evaluated mineralisation potential for both GLY and IPU-degrading compositional variants. Concerning GLY communities, the overall temporal dynamics of GLY mineralisation curves were similar between the different treatments with a slow saturation yielding in a cumulative mineralisation after 42 days ranging between 12.3% and 40.4% of ^{14}C -IPU initially added to microcosms. Moreover, we found a strong and significant impact of soil suspension dilution on GLY mineralisation potential, with a marked decreased GLY mineralisation in the more diluted soil suspensions (Fig. 2 A & C). Specific treatments (HS, Ox1, pH11) displayed a stronger reduction of total mineralisation compared to the control microcosms (Fig. 2 C). Furthermore, we noted that none of the compositional variants reached the total mineralisation potential of the original Noiron soil. This points out an overall decline either due to the experimental manipulation of soil suspensions or to differences in physico-chemical properties of the receiving soil (sterilized Ecotron soil), both potentially affecting GLY mineralisation capacities.

Regarding IPU communities, three distinct dynamics can be identified: i) some microcosms displayed IPU mineralisation kinetics with a rapid start reaching a plateau in about 15 days with a high final cumulative mineralisation (around 50% to 60%, even higher than the original Epoisses soil that only reached 36%), ii) some microcosms displayed kinetics with a lag phase of about 10 days followed by an increase of mineralisation rate up to reaching a plateau at the end of the

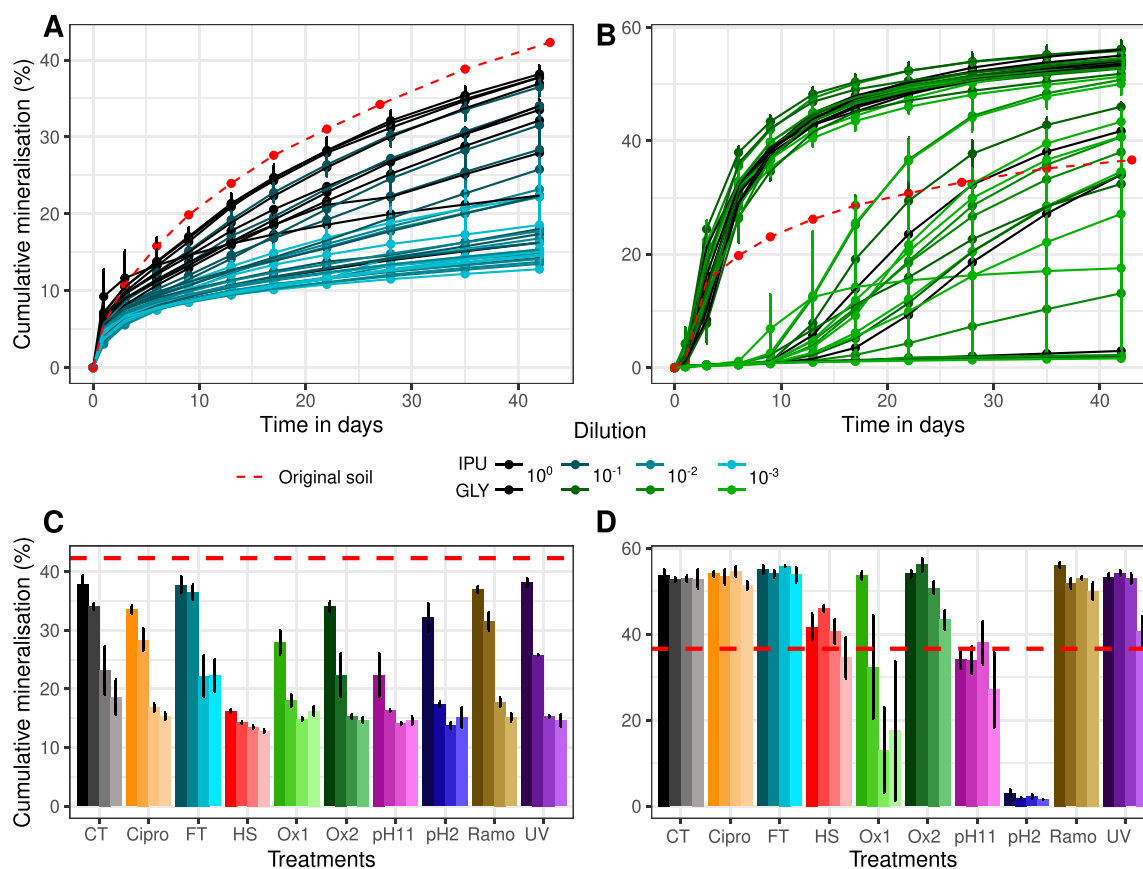


Fig. 2. Kinetics of mineralisation and cumulative mineralisation of GLY and IPU. Potential of GLY mineralization of communities derived from Noiron soil (A & C) and of IPU mineralization from Epoisses soil (B & D). Lines for kinetics (A & B) and bars for cumulative total (C & D) correspond to one condition of treatments and dilutions with error bars as standard error of the mean ($n = 3$). Dashed lines are for original soil community, dotted and dashed for original soil communities after 30 days pesticide incubation. Biocidal treatments are listed in Table 1.

experiment, with a total cumulative mineralisation ranging between 30% to 50% and *iii*) some microcosms displayed nearly no mineralisation with cumulative mineralisation after 42 days below 4% (Fig. 2 B & D). The acidic treatment (pH2) had the strongest negative impact on IPU mineralisation, followed by the basic (pH11) and heat shock (HS) treatments. Interestingly, diluting soil suspensions did not have an effect on IPU mineralisation as observed for GLY communities. However, for some treatments (e.g. for Ox1, Ox2 and pH11 treatments) dilutions increased the variance between triplicates.

3.3. Association between bacterial community composition and herbicide mineralisation potential

The three aforementioned statistical methods (BRR, BL and RF) were applied to our set of community variants. Specifically, we used the normalized OTU table as the set of predictors, for which effects have to be estimated, and three parameters of herbicide mineralisation kinetics as the predicted variables: the Slope on the mineralisation curve over the first 10 days, the cumulative mineralisation (Total) and the percent of pesticides mineralisation at the time point where the variance is the highest (HighVar). Correlations between the actual and predicted variables after cross-validation depicted in Fig. 3 are overall very high, often with correlation coefficient well above 0.75. Unsurprisingly, correlations on training data are close to 1 (higher than 0.95 for IPU communities, and ranging from 0.89 to 0.98 for GLY) with very low variance. Looking at the prediction accuracy on testing sets, the values are also higher for IPU than for GLY, with the exception of the Total for which correlations went down from above 0.9 to 0.8–0.85. Prediction accuracy for GLY communities are comprised between 0.77 and 0.85 with no clear difference between the 3 predicted variables. We also did not detect any clear difference in the prediction accuracy of the different statistical methods. Even if RF yielded the highest correlation on the training set, its results on the testing set were in the same range as the two penalized regression methods.

The capacity of the different methods to accurately predict mineralisation parameters was further investigated by looking at OTUs with a strong effect on mineralisation, *i. e.* having a large estimated effect size, either positive or negative. Interestingly, detected OTUs by RF were overall largely different from the ones detected by BL and BRR for which 28 OTUs were common over the 30 most important detected for Slope variable for both pesticides (Supp. Fig. 4). We therefore looked in more details at the taxonomy and the partial correlation patterns between OTUs detected by both BL and BRR models applied on the Slope and

Total (Fig. 4). Overall, there are less negative than positive estimates, and their amplitudes are lower than positive ones. In addition, for the IPU communities, OTUs that are detected as having an effect on the Slope variable were also detected as important for the Total (19 out of 27), which is not the case for the GLY communities (7 out of 26). Overall, the co-occurrence analysis laid a large majority of positive and weak partial correlations with 2292 positive links against 63 negative ones. Across the OTUs detected as associated to the mineralization potential, Co-occurrence pattern are particularly present between taxonomically close OTUs *e.g.* across *Pseudomonas* genus or Cytophagales. Interestingly, a recurrent pattern of taxonomically-related OTUs showing opposite estimates was detected for both herbicides (e.g. Actinomycetales order in GLY and IPU, *Pseudomonas* genus, Sphingobacteriales and Bacilliales in IPU). Some of the selected OTUs are also important for degradation prediction by the RF method and even if they are not the ones with highest estimates (as determined by BL), they can be seen as robust because detected by all three methods. Moreover, 6 OTUs are shared by GLY and IPU linear prediction models, underlying either multi-degrading strains or more likely strains involved in the downstream part of mineralisation pathways. They could also be facilitators of degrading strains, altering the abiotic conditions favourably (or unfavourably for Rhizobiales *Balneimonas* in the case of IPU).

3.4. Mixing compositional variants and evaluating the GLY and IPU mineralisation potential of the resulting communities

The next step consisted in mixing GLY with IPU compositional variants in order to construct multidegrading communities and inoculate them into the non-degrading sterile Ecotron soil. We tested six different mixing scenarios in order to detect which community characteristics could impact the degrading ability of resulting communities. Interestingly, only slight differences were found between the six tested scenarios when comparing the GLY and IPU mineralisation potential of the resulting communities compared to their parental ones (Fig. 5). These results indicate that no strong antagonism between bacterial populations associated with the degradation of IPU and GLY exists, but also that no overyielding of the mineralisation potential was detected. However, we observed that the choice of the phylogenetic diversity level of the parental communities impacted the mineralisation potential of the resulting communities. On the one hand, choosing parental IPU communities with low phylogenetic diversity led on average to lower IPU mineralisation potential in the resulting communities. On the other hand, choosing parental GLY communities with high phylogenetic

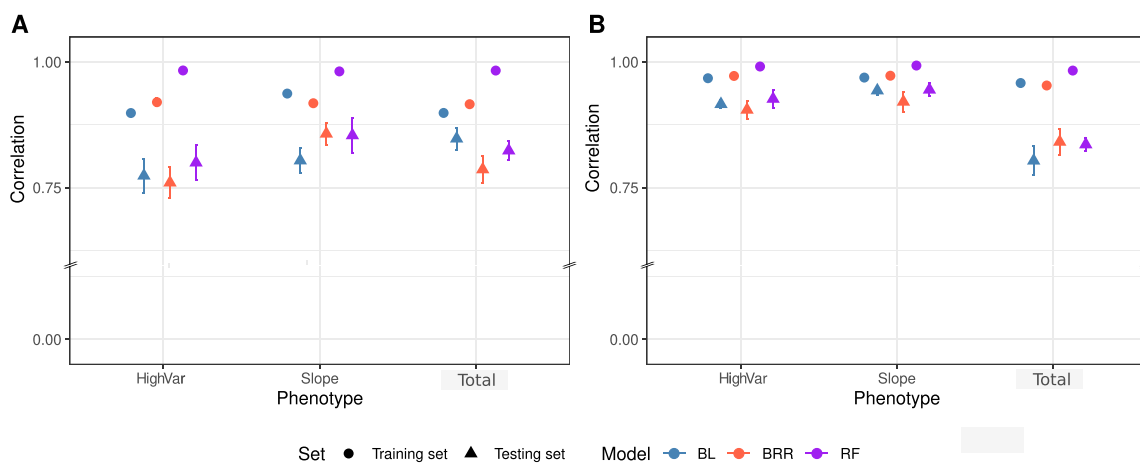


Fig. 3. Prediction accuracy assessed by cross-validation on mineralisation data. 5-Fold CV with shuffling between 8 runs. Errors bars represent standard error of the mean for A) GLY mineralisation and B) IPU mineralisation. Phenotypes are mineralisation kinetic parameters as described in the [Material and Methods](#) section.

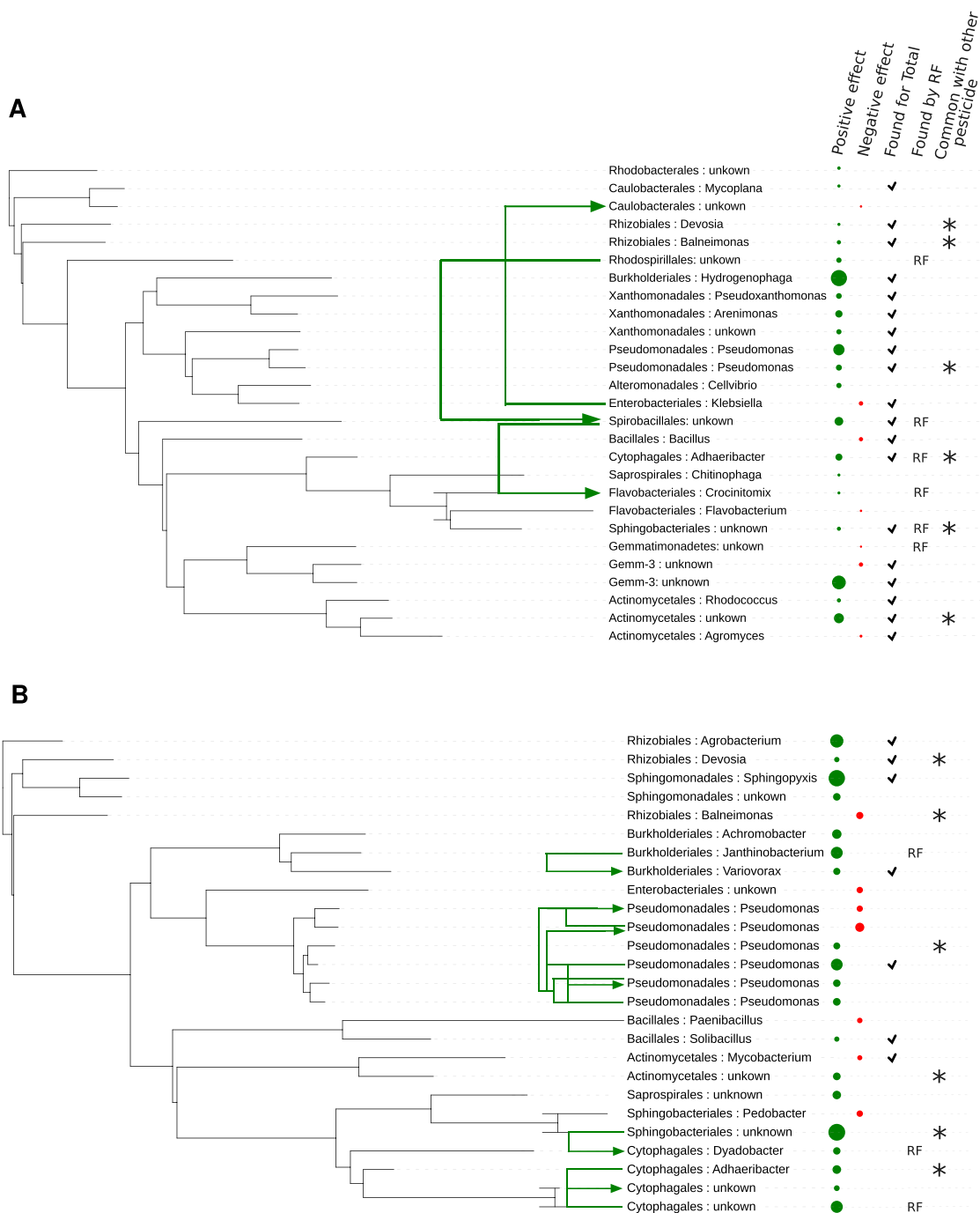


Fig. 4. Taxonomic classification, importance and relationship between OTUs with highest predicted effect. Taxonomic classification ("order: genus" if known (otherwise "unknown")) of OTUs having highest estimators predicted by BL and BRR for the Slope phenotype for A) GLY and B) IPU. Green arrows link OTUs with significant co-occurrence pattern, determined by positive partial correlation. Dot size displays the effect size of positive (green) and negative (red) estimates. Checks indicate OTUs also detected for Total by BL and BRR, then "RF" indicates OTUs detected by RF method on Slope phenotype.

diversity resulted on average in communities with higher GLY mineralisation potential (Fig. 5).

3.5. Coalescence of the herbicide multi-degrading communities into a non-degrading soil

Finally, we tested the efficiency of coalescing the resulting multi-degrading communities into the non-degrading non-sterile Ecotron soil by selecting the five best communities. We evaluated different inoculation ratios and results are contrasted, depending on the herbicide (Fig. 6). For GLY, non-inoculated control showed relatively high

mineralisation ability averaging 21.7% after 42 days of incubation, attesting the mineralisation ability of the indigenous microbial community. Furthermore, low inoculation ratios did not increase this potential and high inoculation ratios (5 g mixed in 50 g) produced only a slight increase in GLY mineralisation ability (mean of 24.9%). On the other hand, IPU mineralisation potential was quite low in the non-inoculated control (mean of 11.1%). It increased significantly and strongly in response to inoculation of even small quantities of multi-degrading communities (mean of 28.4% for 0.1 g, going up to 42% for 1 g).

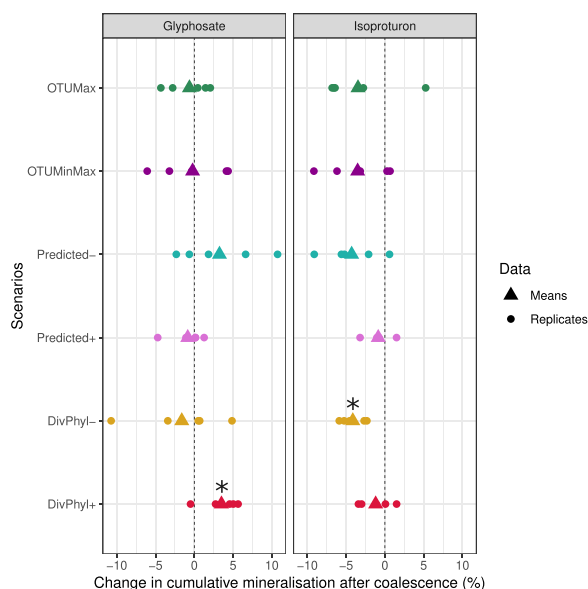


Fig. 5. Cumulative mineralisation differences between original and coalesced communities depending on original communities' properties. Mineralisation difference of total cumulative degradation (42 days, $n = 5$) for the 6 scenarios of community coalescence based on their properties. Stars show distributions with mean significantly different from 0. Mixing Scenarios are described in [Material and Methods](#).

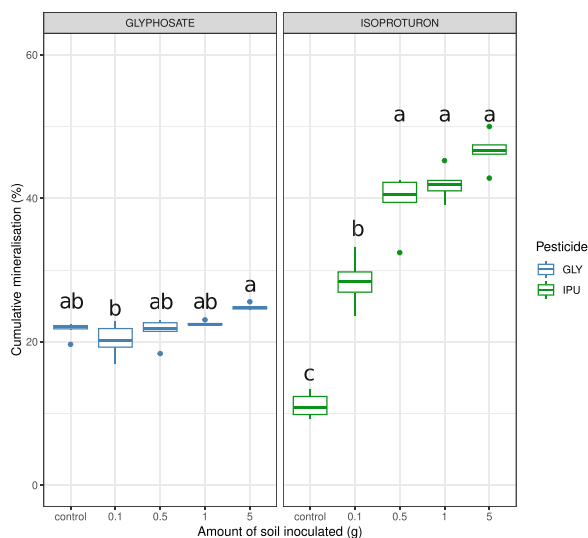


Fig. 6. Cumulative mineralisation of GLY and IPU in pesticide spiked soil microcosms inoculated with multi-degrading community. For each gradual inoculation $n = 5$, from 0 (control) to 5 g of soil in 30 g of non-sterile soil. Cumulative mineralisation is showed after 42 days of incubation.

4. Discussion

4.1. Environmental filtering and impact of diversity loss

Environmental filtering refers to the process by which local abiotic conditions select organisms that are able to cope with the existing physico-chemical properties [14]. It is thought to be one of the main processes causing the inefficiency of *in situ* microbiome engineering [15, 35, 36]. Here, we chose to γ -sterilize the target environment, *i. e.* the environment in which bioremediation of a pollutant is targeted, and use it as a first screening for degrading microbial communities. After community extraction, manipulation and inoculation of the target sterilized

soil, we observed that herbicide mineralisation potential was kept at high levels and even exceeded the original soils mineralisation potential in the case of IPU (Fig. 2). The bacterial community structure of the manipulated GLY and IPU mineralising communities was drastically altered compared to the original soils from which they originated (Supp. Fig. 3), probably in relation with the sandier structure and the more acidic conditions of the target environment. This confirms the strong role of environmental filtering in shaping microbial communities, albeit without impairment of their functioning in our case.

We combined serial dilution to biocidal treatments to create compositional variants of GLY and IPU mineralising bacterial communities. Consistent with theory and previous studies [14, 37], dilution had a strong impact on bacterial richness (Fig. 2), higher levels of dilution resulting in less diverse communities illustrating the loss of rare taxa. In the case of GLY, this decline in bacterial richness was associated with a decrease in the mineralisation capacity, underlining a relatively straightforward link between diversity and functioning often reported in the literature [38–40]. However, in the case of IPU degrading communities, we did not observe such a relationship, suggesting that the IPU mineralisation function might be supported by a specific group of originally common OTUs, which might even have benefited either from the community manipulation or the target environment local conditions we subjected them to. This interpretation is supported by the general knowledge that IPU mineralization abilities is shared only among a small amount of bacteria genus [41], although experimental evidence is needed and could be the matter of further research.

4.2. Predicting herbicides mineralisation potential from bacterial community composition

The successful implementation of our prediction approach relied on our ability to generate a compositional continuum of communities varying in their capacity to degrade the pesticides. A strong level of structure in the composition of the communities following our treatments could be detrimental to the overall ability of the model to yield satisfactory predictions. The same restriction is faced in genomic prediction and regular updates with new data (phenotype-genotype information) are carried out to keep the model adjusted over time [42]. Our success in obtaining a continuous distribution of community variants notwithstanding, the transfer of genomic prediction tools on microbial function is challenged by two main differences in data: presence/absence of alleles are replaced by a more continuous and potentially limitless count of OTUs, and the likely change in community composition over time compared to the fixed genetic information. This last point turned out to be particularly relevant in IPU case, with clearly superior predictions for starting mineralisation rate than final mineralisation potential (Fig. 3). For future consideration, monitoring the change of degrading communities over time seems crucial for our ability to devise prediction models trained on data that are not too divorced from the data they try to predict. Despite all these potential pitfalls, our approach gave very satisfying preliminary results and is supported by promising results from machine learning methods tested on microbial communities to predict community function [43, 44].

There was no clear distinction in prediction accuracy between the three statistical methods that we used (BL, BRR and RF). In parallel, and to get an idea of the intrinsic properties of microbial communities that could influence the statistical power of these methods, we used simulations of degrading capacities of an existing OTUs table postulating various "trait architecture" (*i. e.* various ways for OTUs to contribute or not to the simulated phenotype). The results showed that predictions were better when the simulated phenotype was underlain by a few abundant OTUs (Supp. Informations). This type of architecture matches well what we observe for IPU degradation, which seems to be performed by a few specific OTUs [45], and consistent with the fact that our model gives a very high prediction accuracy. The case of GLY is different, with the degrading potential seemingly more spread out across OTUs, yet we

obtained reasonably accurate predictions there too.

4.3. Identification of specific OTUs associated with herbicide mineralisation potential

To validate the model predictions, we looked at OTUs with the highest and lowest predicted effect sizes and checked whether they were already identified in previous literature. Two *Pseudomonas spp.* strains are identified for their GLY degrading capacities, which matches 2 OTUs with positive estimates in our analysis [46,47]. On the opposite, two OTUs with negative estimate, *Bacillus cereus* and *Flavobacterium sp.*, show isolated strains for their GLY degrading capacities [46,47]. These last apparently mixed results could be explained by a competition pattern related to phylogeny, pattern well known in microbial ecology [48]. Indeed, we noticed that phylogenetically close OTUs often turned out to have opposite effect on degradation function, suggesting that they might be in competition, with one bearing the degrading capacity and the other occupying a similar ecological niche. These non-degrading competitors would expand in absence of degrading OTUs, and therefore be negatively correlated with pesticide mineralisation. This appealing hypothesis has yet to be tested for each pesticide.

Concerning IPU, degrading strains are mostly found within the *Shingomonas* genus [49,50], which matches our model prediction with two OTUs with positive estimates belonging to this taxon. The other OTUs with high prediction power have not yet been described as IPU degraders but are good candidates either directly involved in the degradation or facilitated by degrading OTUs.

4.4. Evaluating the herbicide mineralisation potential of the mixed communities

Increasing interest for community coalescence as a widespread microbial ecological event and recent studies [51,52] prompted us to establish coalescence scenarios based on community-level properties. By doing so, our initial objective of building multi-degrading communities turned out to be a great success. All coalesced communities proved to be efficient at degrading both pesticides. However, among all tested community properties, only the phylogenetic diversity was revealed as an important community feature to maintain high degradation capacities for both pesticides after coalescence.

Moreover, we can hypothesize from our results that no strong antagonisms exist between IPU and GLY degrading community members, which is consistent with the chemical structure discrepancy between the two pesticides and their degrading pathways [45,46]. This suggests a modular coalescence in which input communities are preserved and only limited new interactions between communities are established, as opposed to chimeric coalescence showing numerous new interactions [51].

4.5. Coalescence of the herbicide multi-degrading communities into a non-degrading soil

Introgession of the multi-degrading communities in an inhabited polluted soil resulted in contrasted outputs between the 2 pesticides. A clear transfer of IPU degradation capacity was observed, even at low inoculation levels. This success can be explained by the establishment of cohesive unit of co-selected taxa along the experiments for their use of IPU as substrate, a hypothesis supported by previous theoretical work [53]. Conversely, introgession of GLY degrading capacities gave mixed results, consistent with an already present degrading potential. Indigenous community benefits of the priority effect [54], making it difficult for new taxa to establish. At high inoculation level though, degradation is enhanced, either demonstrating the importance of invasive pressure [15,55], or the additive relationship between species richness and community phenotype [40,52].

5. Conclusion

Microbiome engineering is a promising approach for bioremediation purposes based on the bacterial capacities to degrade pollutants. We propose here an innovative and efficient strategy for building multi-degrading bacterial communities. Our approach is based on predictions of the degradation potential of pesticides from microbial community composition (with more than 80% efficiency).

Using the coalescence framework, we succeeded in building multi-degrading communities that *i)* established efficiently in a contaminated soil, *ii)* brought its IPU mineralisation potential up to 40%, while *iii)* at least, stabilizing its GLY mineralisation potential. We advocate for applying this approach to a vast range of pesticides which would allow identifying microbial key players involved in their degradation in soils. This would be the first step towards a rapid selection of pesticide multi-degrading microbial communities.

Environmental implication

Pesticides are still widely used in conventional agriculture yet their persistence in soil and their transfer to water cause increasingly documented ecological damages. Bioremediation via the inoculation of degrading micro-organisms is a promising method still in needs of further developments. Here we designed a protocol aiming at studying the degradation of two herbicides, glyphosate (GLY) and isoproturon (IPU), via modifications of two source bacterial communities. Specifically, we transposed tools from genomic selection to microbial ecology with a bioremediation perspective. We built multi-degrading bacterial communities and evaluated their efficiency to remove pesticide contamination from a soil.

CRedit authorship contribution statement

Mathieu SIOL: Writing – review & editing, Writing – original draft, Supervision, Investigation, Funding acquisition, Formal analysis, Conceptualization. **Nadine ROUARD:** Methodology, Formal analysis, Data curation. **Sana ROMDHANE:** Writing – review & editing, Methodology, Investigation, Formal analysis. **Fabrice MARTIN-LAURENT:** Writing – review & editing, Investigation. **Marion DEVERS-LAMRANI:** Writing – review & editing, Methodology, Investigation, Conceptualization. **Julie AUBERT:** Writing – review & editing, Visualization, Supervision, Resources, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Sylvia THIEFFRY:** Writing – original draft, Visualization, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Aymé SPOR:** Writing – review & editing, Writing – original draft, Supervision, Methodology, Investigation, Funding acquisition, Formal analysis, Conceptualization.

Declaration of Competing Interest

The authors have declared no conflict of interests.

Data availability

Data will be made available on request.

Acknowledgements

We thank members of the EMFEED team for their help and support, and specifically Laurent Philippot for his inputs. This work was partially supported by grants from the INRAE HoloFlux Metaprogramme (INT-BXL project).

Appendix A. Supporting information

Supplementary data associated with this article can be found in the

online version at [doi:10.1016/j.jhazmat.2024.134454](https://doi.org/10.1016/j.jhazmat.2024.134454).

References

- [1] Sharma, Kumar, A., Shahzad, V., Tanveer, B., Sidhu GPS, M., Handa, N., et al., 2019. Worldwide pesticide usage and its impacts on ecosystem (Available from: <https://doi.org/10.1007/s42452-019-1485-1>).
- [2] Jacobsen, C.S., Hjelmsø, M.H., 2014. Agricultural soils, pesticides and microbial diversity (Available from: <https://doi.org/10.1016/j.copbio.2013.09.003>).
- [3] Rumschlag, S.L., Mahon, M.B., Hoverman, J.T., Raffel, T.R., Carrick, H.J., Hudson, P.J., et al., 2020. Consistent effects of pesticides on community structure and ecosystem function in freshwater systems (Available from: <https://doi.org/10.1038/s41467-020-20192-2>).
- [4] Lushchak, V.I., Matviishyn, T.M., Husak, V.V., Storey, J.M., Storey, K.B., 2018. Pesticide toxicity: a mechanistic approach. *Doc1101; ISSN 1611-2156 EXCLI J 17*.
- [5] Haney, R.L., Senseman, S.A., Hons, F.M., Zuberer, D.A., 2000. Effect of glyphosate on soil microbial activity and biomass (Available from: [https://doi.org/10.1614/0043-1745\(2000\)048\[0089:eogom\]2.0.co;2](https://doi.org/10.1614/0043-1745(2000)048[0089:eogom]2.0.co;2)).
- [6] Fenner, K., Canonica, S., Wackett, L.P., Elsner, M., 2013. Evaluating pesticide degradation in the environment: blind spots and emerging opportunities (Available from: <https://doi.org/10.1126/science.1236281>).
- [7] Lopes, P.R.M., Cruz, V.H., de Menezes, A.B., Gadanhoto, B.P., de Almeida Moreira, B.R., Mendes, C.R., et al., 2022. Microbial bioremediation of pesticides in agricultural soils: an integrative review on natural attenuation, bioaugmentation and biostimulation (Available from: <https://doi.org/10.1007/s11577-022-09637-w>).
- [8] Alain, K., Querellou, J., 2009. Cultivating the uncultured: limits, advances and future challenges (Available from: <https://doi.org/10.1007/s00792-009-0261-3>).
- [9] Vogel, T.M., 1996. Bioaugmentation as a soil bioremediation approach (Available from: [https://doi.org/10.1016/s0958-1669\(96\)80036-x](https://doi.org/10.1016/s0958-1669(96)80036-x)).
- [10] Thompson, I.P., van der Gast, C.J., Ciric, L., Singer, A.C., 2005. Bioaugmentation for bioremediation: the challenge of strain selection (Available from: <https://doi.org/10.1111/j.1462-2920.2005.00804.x>).
- [11] Habier, D., Fernando, R.L., Garrick, D.J., 2013. Genomic BLUP decoded: a look into the black box of genomic prediction (Available from: <https://doi.org/10.1534/genetics.113.152207>).
- [12] VanRaden, P.M., 2008. Efficient methods to compute genomic predictions (Available from: <https://doi.org/10.3168/jds.2007-0980>).
- [13] Georges, M., 2007. Mapping, fine mapping, and molecular dissection of quantitative trait loci in domestic animals (Available from: <https://doi.org/10.1146/annurev.genom.8.080706.092408>).
- [14] Yan, Y., Klinkhamer, P.G.L., van Veen, J.A., Kuramae, E.E., 2019. Environmental filtering: a case of bacterial community assembly in soil (Available from: <https://doi.org/10.1016/j.soilbio.2019.107531>).
- [15] Albright, M.B.N., Louca, S., Winkler, D.E., Feeser, K.L., Haig, S.J., Whiteson, K.L., et al., 2021. Solutions in microbiome engineering: prioritizing barriers to organism establishment (Available from: <https://doi.org/10.1038/s41396-021-01088-5>).
- [16] de los Campos, G., Hickey, J.M., Pong-Wong, R., Daetwyler, H.D., Calus, M.P.L., 2013. Whole-genome regression and prediction methods applied to plant and animal breeding (Available from: <https://doi.org/10.1534/genetics.112.143313>).
- [17] Romdhane, S., Spor, A., Aubert, J., Bru, D., Breuil, M.C., Hallin, S., et al., 2021. Unraveling negative biotic interactions determining soil microbial community assembly and functioning (Available from: <https://doi.org/10.1038/s41396-021-01076-9>).
- [18] Kluyver, T., Ragan-Kelley, B., Pérez, F., Granger, B., Bussonnier, M., Frederic, J., et al., 2016. Jupyter Notebooks – A Publishing Format for Reproducible Computational Workflows. *IOS Press*.
- [19] Zhang, J., Kobert, K., Flouri, T., Stamatakis, A., 2013. PEAR: a fast and accurate Illumina paired-end reAd mergeR (Available from: <https://doi.org/10.1093/bioinformatics/btt593>).
- [20] Caporaso, J.G., Bittinger, K., Bushman, F.D., DeSantis, T.Z., Andersen, G.L., Knight, R., 2009. PyNAST: a flexible tool for aligning sequences to a template alignment (Available from: <https://doi.org/10.1093/bioinformatics/btp636>).
- [21] Rognes, T., Flouri, T., Nichols, B., Quince, C., Mahé, F., 2016. VSEARCH: a versatile open source tool for metagenomics (Available from: <https://doi.org/10.7717/peerj.2584>).
- [22] Katoh, K., Standley, D.M., 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability (Available from: <https://doi.org/10.1093/molbev/mst010>).
- [23] Price, M.N., Dehal, P.S., Arkin, A.P., 2009. FastTree: computing large minimum evolution trees with profiles instead of a distance matrix (Available from: <https://doi.org/10.1093/molbev/msp077>).
- [24] Altschul, S.F., Gish, W., Miller, W., Myers, E.W., Lipman, D.J., 1990. Basic local alignment search tool (Available from: [https://doi.org/10.1016/s0022-2836\(05\)80360-2](https://doi.org/10.1016/s0022-2836(05)80360-2)).
- [25] Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., et al., 2012. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools (Available from: <https://doi.org/10.1093/nar/gks1219>).
- [26] Faith, D.P., 1992. Conservation evaluation and phylogenetic diversity (Available from: [https://doi.org/10.1016/0006-3207\(92\)91201-3](https://doi.org/10.1016/0006-3207(92)91201-3)).
- [27] Lozupone, C., Knight, R., 2005. UniFrac: a new phylogenetic method for comparing microbial communities (Available from: <https://doi.org/10.1128/aem.71.12.8228-8235.2005>).
- [28] Chiquet, J., Robin, S., Mariadassou, M., 2019. Variational Inference for sparse network reconstruction from count data. In: Chaudhuri, K., Salakhutdinov, R. (Eds.), Proceedings of the 36th International Conference on Machine Learning. vol. 97 of Proceedings of Machine Learning Research. PMLR, pp. 1162–1171. Available from: <https://proceedings.mlr.press/v97/chiquet19a.html>).
- [29] Chiquet, J., Mariadassou, M., Robin, S., 2021. The poisson-lognormal model as a versatile framework for the joint analysis of species abundances (Available from: <https://doi.org/10.3389/fevo.2021.588292>).
- [30] Liu, H., Roeder, K., Wasserman, L., 2010. Stability Approach to Regularization Selection (StARS) for High Dimensional Graphical Models. In: Lafferty, J., Williams, C., Shawe-Taylor, J., Zemel, R., Culotta, A. (Eds.), Advances in Neural Information Processing Systems, vol. 23. Curran Associates, Inc. Available from: <https://proceedings.neurips.cc/paper/2010/file/301ad0e3bd5cb1627a2044908a42fd2-Paper.pdf>).
- [31] Letunic, I., Bork, P., 2021. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation (Available from: <https://doi.org/10.1093/nar/gkab301>).
- [32] Pérez, P., de los Campos, G., 2014. Genome-wide regression and prediction with the BGLR statistical package (Available from: <https://doi.org/10.1534/genetics.114.164442>).
- [33] Breiman L. Machine Learning. 2001;45(1):5–32. Available from: <https://doi.org/10.1023/a:1010933404324>.
- [34] Liaw A., Wiener M. Classification and Regression by randomForest. *R News*. 2002;2(3):18–22. Available from: <https://CRAN.R-project.org/doc/Rnews/>.
- [35] Wainwright, C.E., Staples, T.L., Charles, L.S., Flanagan, T.C., Lai, H.R., Loy, X., et al., 2017 Aug. Links between community ecology theory and ecological restoration are on the rise (Available from: <https://doi.org/10.1111/1365-2664.12975>).
- [36] Silverstein, M.R., Segre, D., Bhatnagar, J.M., 2023. Environmental microbiome engineering for the mitigation of climate change (Available from: <https://doi.org/10.1111/gcb.16609>).
- [37] Calderón, K., Spor, A., Breuil, M.C., Bru, D., Bizouard, F., Violle, C., et al., 2016. Effectiveness of ecological rescue for altered soil microbial communities and functions (Available from: <https://doi.org/10.1038/ismej.2016.86>).
- [38] Yu, X., Polz, M.F., Alm, E.J., 2019. Interactions in self-assembled microbial communities saturate with diversity (Available from: <https://doi.org/10.1038/s41396-019-0356-5>).
- [39] Langenheder, S., Bulling, M.T., Solan, M., Prosser, J.I., 2010. Bacterial biodiversity-ecosystem functioning relations are modified by environmental complexity (Available from: <https://doi.org/10.1371/journal.pone.0010834>).
- [40] Bell, T., Newman, J.A., Silverman, B.W., Turner, S.L., Lilley, A.K., 2005. The contribution of species richness and composition to bacterial services (Available from: <https://doi.org/10.1038/nature03891>).
- [41] Sorensen, S.R., Ronen, Z., Aamand, J., 2001. Isolation from agricultural soil and characterization of a iSphingomonas/i sp. able to mineralize the phenylurea herbicide isoproturon (Available from: <https://doi.org/10.1038/5409.2001>).
- [42] Rincin, R., Laloë, D., Nicolas, S., Altmann, T., Brunel, D., Revilla, P., et al., 2012. Maximizing the reliability of genomic selection by optimizing the calibration set of reference individuals: comparison of methods in two diverse groups of maize inbreds (iZea mays/i L.) (Available from: <https://doi.org/10.1534/genetics.112.141473>).
- [43] Thompson, J., Johansen, R., Dunbar, J., Munsky, B., 2019. Machine learning to predict microbial community functions: an analysis of dissolved organic carbon from litter decomposition (Available from: <https://doi.org/10.1371/journal.pone.0215502>).
- [44] Bokulich, N., Dillon, M., Bolyen, E., Kaehler, B., Huttlely, G., Caporaso, J., 2018. q2-sample-classifier: machinelearning tools for microbiome classification and regression (Available from: <https://doi.org/10.21105/joss.00934>).
- [45] Hussain, S., Arshad, M., Springael, D., SoRensen, S.R., Bending, G.D., Devers-Lamrani, M., et al., 2015 Jan. Abiotic and biotic processes governing the fate of phenylurea herbicides in soils: a review (Available from: <https://doi.org/10.1080/10643389.2014.1001141>).
- [46] Sviridov, A.V., Shushkova, T.V., Ermakova, I.T., Ivanova, E.V., Epiktetov, D.O., Leontievsky, A.A., 2015 Mar. Microbial degradation of glyphosate herbicides (Review) (Available from: <https://doi.org/10.1134/s0003683815020209>).
- [47] Zhan, H., Feng, Y., Fan, X., Chen, S., 2018. Recent advances in glyphosate biodegradation (Available from: <https://doi.org/10.1007/s00253-018-9035-0>).
- [48] Russel, J., Røder, H.L., Madsen, J.S., Burmølle, M., Sørensen, S.J., 2017. Antagonism correlates with metabolic similarity in diverse bacteria (Available from: <https://doi.org/10.1073/pnas.1706016114>).

- [49] Sørensen, S.R., Bending, G.D., Jacobsen, C.S., Walker, A., Aamand, J., 2003. Microbial degradation of isoproturon and related phenylurea herbicides in and below agricultural fields (Available from:). *FEMS Microbiol Ecol* 45 (1), 1–11. [https://doi.org/10.1016/s0168-6496\(03\)00127-2](https://doi.org/10.1016/s0168-6496(03)00127-2).
- [50] Bending, G., Shaw, E., Walker, A., 2001. Spatial heterogeneity in the metabolism and dynamics of isoproturon degrading microbial communities in soil (Available from:). *Biol Fertil Soils* 33 (6), 4849. <https://doi.org/10.1007/s003740100356>.
- [51] Castledine, M., Sierocinski, P., Padfield, D., Buckling, A., 2020. Community coalescence: an eco-evolutionary perspective (Available from:). *Philos Trans R Soc B: Biol Sci* 375 (1798), 20190252. <https://doi.org/10.1098/rstb.2019.0252>.
- [52] Sierocinski, P., Milferstedt, K., Bayer, F., Großkopf, T., Alston, M., Bastkowski, S., et al., 2017. A single community dominates structure and function of a mixture of multiple methanogenic communities, 3390-3395.e4. Available from: *Curr Biol* 27 (21) <https://doi.org/10.1016/j.cub.2017.09.056>.
- [53] Lechón-Alonso, P., Clegg, T., Cook, J., Smith, T.P., Pawar, S., 2021. The role of competition versus cooperation in microbial community coalescence (Available from:). *PLOS Comput Biol* 17 (11), e1009584. <https://doi.org/10.1371/journal.pcbi.1009584>.
- [54] Debray, R., Herbert, R.A., Jaffe, A.L., Crits-Christoph, A., Power, M.E., Koskella, B., 2021. Priority effects in microbiome assembly (Available from:). *Nat Rev Microbiol* 20 (2), 109–121. <https://doi.org/10.1038/s41579-021-00604-w>.
- [55] Vila, J.C.C., Jones, M.L., Patel, M., Bell, T., Rosindell, J., 2019. Uncovering the rules of microbial community invasions (Available from: <https://doi.org/>). *Nat Ecol Evol* 3 (8), 1162–1171. <https://doi.org/10.1038/s41559-019-0952-9>.