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Assessing the effects of β -triketone herbicides on HPPD from environmental bacteria using a combination of in silico and microbiological approaches

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36 **Abstract:**

37 4-hydroxyphenylpyruvate dioxygenase (HPPD) is the molecular target of β -triketone herbicides in
38 plants. This enzyme, involved in the tyrosine pathway, is also present in a wide range of living
39 organisms, including microorganisms. Previous studies, focusing on a few strains and using high
40 herbicide concentrations, showed that β -triketones are able to inhibit microbial HPPD. Here, we
41 measured the effect of agronomical doses of β -triketone herbicides on soil bacterial strains. The HPPD
42 activity of six bacterial strains was tested with $1\times$ or $10\times$ the recommended field dose of the herbicide
43 sulcotrione. The selected strains were tested with $0.01\times$ to $15\times$ the recommended field dose of
44 sulcotrione, mesotrione and tembotrione. Molecular docking was also used to measure and model the
45 binding mode of the three herbicides with the different bacterial HPPD. Our results show that responses
46 to herbicides are strain-dependent with *Pseudomonas fluorescens* F113 HPPD activity not inhibited by
47 any of the herbicide tested; when all three β -triketone herbicides inhibited HPPD in *Bacillus cereus*
48 ATCC14579 and *Shewanella oneidensis* MR-1. These responses are also molecule-dependent with
49 tembotrione harboring the strongest inhibitory effect. Molecular docking also reveals different binding
50 potentials. This is the first time that the inhibitory effect of β -triketone herbicides is tested on
51 environmental strains at agronomical doses, showing a potential effect of these molecules on the HPPD
52 enzymatic activity of non-target microorganisms.

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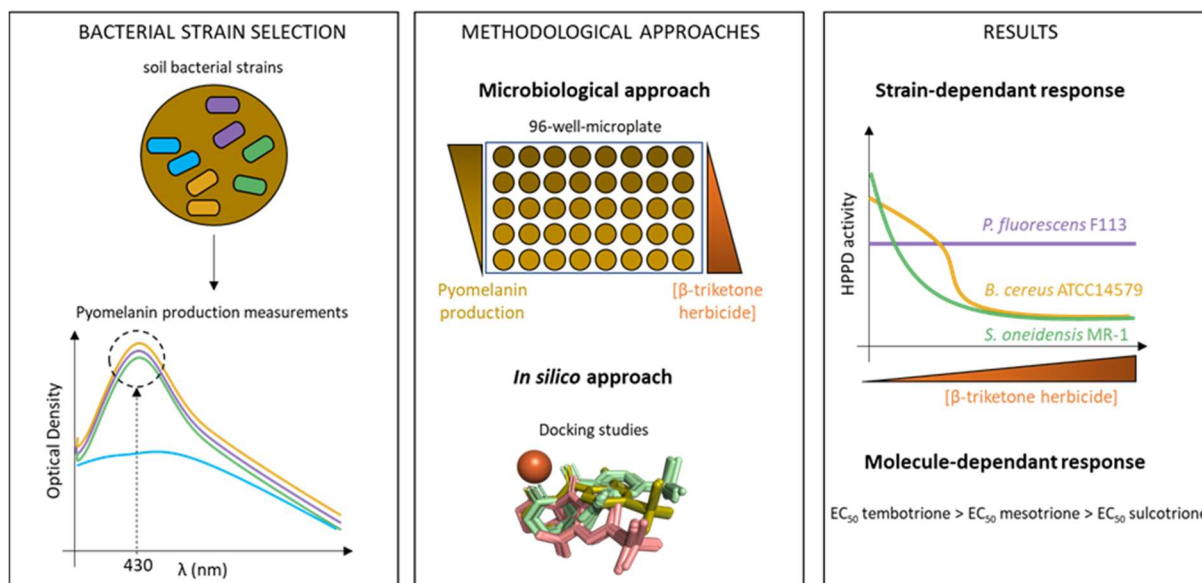
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66 **Graphical abstract:**



67

68 **Keywords:** pyomelanin; 4-hydroxyphenylpyruvate dioxygenase; soil bacteria; β-triketone herbicides;
 69 tembotrione; molecular docking.

70 **Introduction**

71 Herbicides account for 60% of the volume of all plant protection products applied worldwide [1], and
 72 for 30% in the European Union Member States (EU Eurostats). Following atrazine ban in Europe in
 73 2003, β-triketones herbicides have been commonly used as pre- and post-emergent selective compounds
 74 and are among the top five most used herbicides on maize crops. β-triketones herbicides are synthesized
 75 based on the structure of leptospermone, a natural phytotoxin produced by the Californian bottlebrush
 76 plant, *Callistemon citrinus* [2]. Sulcotrione (2-(2-chloro-4-methylsulfonylbenzoyl)cyclohexane-1,3-
 77 dione) was the first β-triketone herbicide commercialized [3], followed by mesotrione (2-[4-
 78 (methylsulfonyl)-2-nitrobenzoyl]cyclohexane-1,3-dione) and, more recently, by tembotrione (2-[2-
 79 chloro-4-methylsulfonyl-3-(2,2,2-trifluoroethoxymethyl)benzoyl]cyclohexane-1,3-dione) [4] (**Table**
 80 **1**).

81 Plant 4-hydroxyphenylpyruvate dioxygenase (HPPD, EC 1.13.11.27) is the biochemical target of β-
 82 triketones herbicides. This enzyme is a non-heme iron enzyme involved in the second reaction of the
 83 tyrosine catabolism pathway by converting 4-hydroxyphenylpyruvate (HPP) in homogentisate (HGA)
 84 *via* oxidative decarboxylation, aromatic ring hydroxylation and carboxymethyl group rearrangement [5].
 85 HGA is a key precursor of α-tocopherol and plastoquinone, that acts as an essential cofactor for phytoene
 86 desaturase, allowing plants to produce carotenoids required to protect them from light and free radicals
 87 [6].

88 HPPD is ubiquitous in almost all living organisms [7]. In non-photosynthetic organisms, including
89 humans, HPPD is also involved in tyrosine degradation, leading to HGA synthesis, the latter is involved
90 in the synthesis pathway of fumarate, one of the intermediates of the Krebs cycle, and acetoacetate,
91 involved in lipid biosynthesis [8].

92 In some microorganisms, HPPD activity is linked to pyomelanin production, a pigment accumulating
93 following oxidation and polymerization of HGA. This brown pigment is easily observable on culture
94 media supplemented with L-tyrosine, and its production has been described in various microbial species
95 such as fungi and yeasts [9–12] and in numerous bacterial species such as *Legionella pneumophila*,
96 *Shewanella oneidensis*, *Streptomyces avermitilis*, *Burkholderia cenocepacia*, *Bacillus thuringiensis*,
97 *Alteromonas stellipolaris*, *Rubrivivax benzoatilyticus*, *Klebsiella pneumoniae*, *Alcaligenes faecalis*,
98 *Enterobacter* sp. and *Vibrio angillarum* [13–21]. Some of these studies report either a protective role
99 of pyomelanin against environmental stresses, such as reactive oxygen species for the soil-borne plant
100 pathogen *Ralstonia solanacearum* [22], light for *L. pneumophila* [23], ultraviolet irradiation for the
101 marine bacteria *Vibrio splendidus* [24], or a modification in virulence for pathogenic bacteria [19],
102 highlighting the importance of deciphering HPPD function in microbes.

103 Nonetheless, microbial HPPD structure and β -triketone herbicide binding mode are only described in
104 two microorganisms : *Pseudomonas fluorescens* F113 (also called *Pseudomonas kilonensis* F113 [25])
105 and *Streptomyces avermitilis* [14,26]. Studies on binding modes of β -triketones were mainly performed
106 on HPPD plant models such as *Arabidopsis thaliana* [5,27,28]. Most inhibition studies are performed
107 on recombinant plants or bacterial HPPD cloned and expressed in *Escherichia coli* strains [29–31]. Only
108 a few studies take an interest in deciphering the potential inhibition of soil microbial HPPD by β -
109 triketone herbicides under agronomical conditions [32]. Also, the effect of β -triketone herbicides on
110 microbial pigmentation production has been tested only with few pure strains and always using high
111 herbicide concentration (from 12 to 200 \times the recommended field dose (RfD)) [16,21,33].

112 As the use of β -triketone herbicides on crops continues to expand, it is important to assess their effect
113 on “non-target organisms” [34], and especially on the HPPD activity of soil microbiota. We could
114 wonder if the protective role of pyomelanin production against environmental stresses observed in some
115 bacterial species, could be modified by the application of β -triketone herbicides on crops. Such an effect
116 could affect the balance of soil microbiota and alter, for example, microbial populations playing a key
117 role in plant growth, such as Plant Growth Promoting Rhizobacteria (PGPR), and consequently could
118 have an impact on soil ecosystem services.

119 The aim of this study is to decipher the possible impacts of three triketone molecules on the HPPD
120 enzymatic activities of different bacterial strains belonging to various genera. Six environmental
121 bacterial strains were selected and tested for their pyomelanin production. Strains were exposed to 1 \times

122 or 10× RfD of sulcotrione. Three strains, selected according to their different sensitivities to sulcotrione,
123 were then exposed, in a whole-cell assay, to increasing doses of three β-triketone herbicides, namely
124 sulcotrione, mesotrione and tembotrione. As the calculated EC₅₀ (half-maximum Effective
125 Concentration) varied depending the strain and the molecule considered, *in silico* molecular docking
126 was performed to document the binding mode of β-triketones with bacterial HPPD and to explain, at a
127 molecular level, the differences observed in the whole-cell assay when working at a population level.

128 **Material and methods**

129 **Bacterial strains and culture conditions**

130 *B. cereus* ATCC14579, *P. fluorescens* F113, *P. fluorescens* CTR1015 and *P. fluorescens* NEM419 were
131 cultured in a Lysogenic Broth (LB: 10 g/l tryptone; 5 g/l yeast extract; 10 g/l NaCl). *S. oneidensis* MR-
132 1 was grown in a Tryptic Soy Broth (TSB: 17 g/l tryptone; 3 g/l soy; 5 g/l NaCl; 2.5 g/l K₂HPO₄; 2.5 g/l
133 glucose) and *R. etli* CFN42 in Tryptone Yeast extract media supplemented with CaCl₂ (TY+CaCl₂: 5
134 g/l tryptone; 3 g/l yeast extract; 0.9 g/l CaCl₂×2H₂O; pH=6.8).

135 **Pyomelanin production**

136 In order to test their ability to produce pyomelanin, each of the six bacterial strains were grown in their
137 appropriate culture medium supplemented with 0.9 g/l of tyrosine at 24 °C with constant shaking at 120
138 rpm. Samples of each culture were collected at T0, 48 h, 72 h, and a last point between 6 to 10 days
139 depending of the strain, and centrifugated at 5,000 rpm for 10 min. The absorbance spectra of cell-free
140 supernatant were recorded in a UV-Vis spectrophotometer in the range of 250 to 600 nm, as soluble
141 pyomelanin can be quantified at different wavelengths, ranging from 400 to 430 nm [18,21,22,29,35].
142 The *E. coli* BL21 strain, known as a non-producing pyomelanin strain, was added to this experiment as
143 negative control, and the *E. coli* BL21 HPPD, modified to produce pyomelanin, as the positive control
144 [29].

145 **Bacterial resting cells preparation**

146 Resting cells were prepared for each of the six strains in Phosphate Buffer (PB) in order to work at
147 constant biomass, in a unique solution, whatever the strain. Each bacterial strain was grown overnight
148 at 28°C and 110 rpm in its appropriate culture medium. Overnight cultures were diluted and incubated
149 in a new fresh appropriate medium during three to eight-hour according to its growth capacity, to reach
150 the exponential phase of growth. Then, cells were harvested by centrifugation for 5 min at 5,000 rpm,

151 washed twice in 20 mM PB, and then resuspended in a volume of PB calculated to have an OD₆₀₀ of 3.
152 In this way, biomass was similar in all the resting cells.

153 **Colorimetric method for HPPD activity monitoring using whole-cell assay in a 96-well multiplate**
154 **format**

155 To assess the HPPD activity of the six selected strains, a colorimetric test in a 96-well multiplate format
156 was developed. 96-well-microplates were all filled with 50 µL of resting cells, and completed with 125
157 µL of L-Tyrosine 1.8 g/l (pH 9), and with 75 µL of herbicide solutions diluted in PB for the assays (A)
158 or with 75 µL of PB for the positive control (PC). For the negative control (NC), only 200 µL of PB
159 were added to the resting cells. Herbicide concentrations ranged from 0.05 to 15 times of the RfD for
160 each molecule tested; corresponding to: 0.23 to 67.5 µM for sulcotrione; 0.22 to 66 µM for mesotrione
161 and 0.17 to 52.5 µM for tembotrione. All herbicides solutions were prepared in PB. All controls and
162 assays were performed in triplicate. Microplates were covered with a Breathseal sealer (Greiner Bio-
163 One™, Germany) and incubated at 28°C and 110 rpm. After 48 hours of incubation, OD₄₃₀, and OD₆₀₀
164 were measured using an Epoch 2 Microplate Spectrophotometer (Greiner Bio-One™, Germany).
165 Pyomelanin detection was measured at OD₄₃₀ rather than OD₄₀₀ because of a better signal observed at
166 this wavelength due to the resting cell mode done in PB. PB solely had the same absorbance as empty
167 wells and was not included to our controls. In the second experiment, microplates were first centrifuged
168 at 6000 rpm for 6 minutes and OD₄₃₀ of the supernatant was measured.

169 For each triplicate, normalized OD₄₃₀ (OD_{430N}) was calculated according to:

$$170 \text{OD}_{430N} = \text{OD}_{430A} \text{ (or } \text{OD}_{430PC}) - \text{OD}_{430NC}$$

171 where OD_{430A} is the mean OD₄₃₀ measured at various concentrations of herbicide, OD_{430PC} is the mean
172 OD₄₃₀ measured at 0 µM of herbicide (i.e. PC) and OD_{430NC} is the mean OD₄₃₀ measured for the NC.

173 The enzymatic activity percentage, Act. %, was calculated according to the equation:

$$174 \text{Act. \%} = \left(\frac{\text{OD}_{430A}}{\text{OD}_{430PC}} \right) \times 100$$

175 **Dose-response curves**

176 For each herbicide tested, EC₅₀ was calculated using the “*drc*” package in R [36]. A three-parameter
177 log-logistic function with lower limit 0 was applied to our datasets, corresponding to this equation:

178
$$f(x) = 0 + \frac{d - 0}{1 + \exp(b(\log(x) - \log(e)))}$$

179 where b, d and e are estimated by the model with a p<0.05.

180 **In silico analysis**

181 Protein sequences were retrieved from GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) with
182 WP_000810922.1 corresponding to the accession number of *B. cereus* ATCC14579 HPPD sequence
183 and WP_011072057.1, WP_011425038.1 and WP_014347821.1 corresponding to the HPPD sequences
184 of *S. oneidensis* MR-1, *R. etli* CFN42 and *P. fluorescens* F113 respectfully. The protein sequences of
185 both *P. fluorescens* CTR1015 and *P. fluorescens* NEM419 are not available yet. Protein sequences of
186 *L. pneumophila* (WP_011216180.1), *P. aeruginosa* (PWU35210.1), *A. salmonicida*
187 (WP_059112190.1), *V. parahaemolyticus* (WP_057619320.1) and *V. anguillarum* (QEH62709.1) were
188 also added to the analysis. Sequences were aligned using ClustalW [37].

189 *Homology modelling*

190 Homology models of each of the HPPDs were obtained using the multiple alignment function of
191 Modeller version 9.22 [38,39], including the crystal structures of HPPD from *Streptomyces avermitilis*
192 and from *Arabidopsis thaliana* (1t47 and 5yy6, respectively) [14,40]. The crystal structure of *A. thaliana*
193 was included because it incorporates the conformational change known to occur upon binding of the
194 inhibitors. Preliminary models with the lowest DOPE scores were selected for further refinement using
195 GROMACS (version 2018.3) [41,42]. The structures were relaxed to correct for steric clashes or
196 inappropriate geometries prior to molecular dynamics simulation. The final topology of the homology
197 models were evaluated using MolProbity [43,44].

198 *Docking of herbicides*

199 The structures of mesotrione and tembotrione were downloaded as sdf files from PubChem
200 (pubchem.ncbi.nlm.nih.gov), edited with Spartan18 (Wavefunction Inc., Irvine CA 92612) to include
201 delocalized -1 charges over two of the three keto groups, and saved as saved as pdb files. The structures
202 were converted to Autodock compatible pdbqt format using AutoDockTools (version 1.5.6). These
203 herbicides were docked to the catalytic domain of HPPD using Autodock4 [45,46], using the iron metal
204 dication (with a +0.6 partial charge) as an anchor [44] and the following conserved residues (T164,
205 S202, P215, N217, Q240, L295, F312, F321, L341, F333, N337, F338). The binding energy of the
206 herbicides on the bacterial HPPD models were obtained from the dock.dlg file. Proteins and ligand

207 interactions were visualized using PyMOL (The PyMOL Molecular Graphics System, Version 2.0
208 Schrödinger, LLC) [47].

209 **Results and discussion**

210 **Pyomelanin production in the six bacterial strains**

211 In order to study the potential effect of β -triketones on microbial HPPD activity, six environmental
212 bacterial strains were selected: *Pseudomonas fluorescens* F113, as the HPPD study model [26], two *P.*
213 *fluorescens* strains CTR1015 and NEM419 as PGPR bacteria models isolated from soil [48,49],
214 *Rhizobium etli* strain CFN42 as a symbiotic bacteria model [50], the well-studied pyomelanin producer
215 *Shewanella oneidensis* MR-1 [22] and *Bacillus cereus* ATCC14579 the only Gram-positive bacterium
216 of this study [51].

217 A first experiment was performed to validate that these six bacterial strains produce pyomelanin. As
218 previously described, soluble pyomelanin can be quantified measuring absorbance at different
219 wavelengths, ranging from 400 to 430 nm [16,18,21,22,29]. Spectrophotometric analysis of cell-free
220 supernatants of the six strains showed a significant increase of OD₄₀₀ between the different sampling
221 time, similar to what observed for *P. fluorescens* F113 (**Supplementary Information 1a**). Final OD₄₀₀
222 were reported for the six tested strains, and for the two controls, validating the pyomelanin production
223 for the studied bacterial strains (**Supplementary Information 1b**).

224 **Development of a multiplate colorimetric whole-cell assay for HPPD activity analysis**

225 To assess the HPPD activity of the six selected strains, a colorimetric test in a 96-well multiplate format
226 was developed. Resting cells were prepared for each of the six strains in PB and added to the assay in
227 order to work at constant biomass, in a unique solution whatever the strain. Then, OD₄₃₀, characterizing
228 the melanin-like pigment, and thus, reflecting the HPPD activity [18,29] was, for each strain, directly
229 measured in each well containing bacterial resting cells, PB and tyrosine. *P. fluorescens* F113 HPPD
230 expressed the highest production of pyomelanin pigment with an OD_{430N} of 1.43 ± 0.11 , followed by *P.*
231 *fluorescens* CTR1015 and NEM419 with OD_{430N} of 0.86 ± 0.01 and 0.74 ± 0.02 respectively, and then
232 *S. oneidensis* MR-1, *B. cereus* ATCC14579 and *R. etli* CFN42 with OD_{430N} of 0.70 ± 0.12 ; 0.66 ± 0.07
233 and 0.55 ± 0.03 respectively (**Supplementary Information 2**). These results were similar to those
234 obtained in the first experiment, validating the miniaturization of the assay, and the pigmentation
235 measurement in PB.

236 **Studying the effect of β -triketones on HPPD activity using the colorimetric whole-cell assay**

237 The resting cells of the six bacterial strains of our study were exposed or not to 1×RfD or 10×RfD of
238 sulcotrione. The HPPD enzymatic activity percentage (Act. %) was calculated for each strain and is
239 depicted in **Figure 1**. In *B. cereus* ATCC14579, *S. oneidensis* MR-1 and *P. fluorescens* CTR1015,
240 HPPD activity clearly decreased with increasing doses of sulcotrione, with a decrease of, at least, 31 %
241 at 1×RfD, and of, at least, 74 % at 10×RfD. In *R. etli* CFN42, HPPD activity decreased of 15% at
242 1×RfD and 12% at 10×RfD. In *Pseudomonas* NEM 419 enzymatic activity remained unchanged at
243 1×RfD but decreased of 50% at 10×RfD. On the contrary, HPPD activity of *P. fluorescens* F113
244 slightly decreased in response to sulcotrione exposure but not significantly compared to the control.
245 There is indeed a strain-dependant response to sulcotrione, even within strains belonging to the same
246 genus. To characterize more accurately the inhibition of bacterial HPPD activity in response to
247 sulcotrione, two bacterial strains were exposed to increasing doses of this herbicide, more finely between
248 0 and 10×RfD. *P. fluorescens* F113, in which the HPPD is well described and which is known to have
249 an ecological role in rhizosphere, was considered in these experiments [25,26]. As *P. fluorescens* F113
250 HPPD activity does not seem to be affected by sulcotrione, we also exposed *S. oneidensis* MR-1 to this
251 herbicide, a strain in which the HPPD activity was well-documented [16]. The obtained results
252 confirmed our previous observations: *P. fluorescens* F113 OD_{430N} appeared constant even with 10×RfD
253 of sulcotrione (**Figure 2.A**) whereas the one of *S. oneidensis* MR-1 was drastically decreasing
254 proportionally to the RfD of sulcotrione, losing around 50% of HPPD activity from 2×RfD of
255 sulcotrione (**Figure 2.B**). This first assay informed us about the existence of tolerant HPPD activities,
256 such as the one of *P. fluorescens* F113, and sensitive one, such as the one of *S. oneidensis* MR-1. This
257 phenomenon has already been reported for bacterial strains carrying acetohydroxyacid synthase
258 (AHAS), the target enzyme of the sulfonylurea herbicides (SN). Enterobacteriaceae, carrying AHAS
259 isoform 1 are tolerant to SN, whereas other bacteria carrying isoform 2 or 3 are sensitive to those
260 herbicides [32,52]. Concerning *P. fluorescens* F113, one may hypothesize either such a difference
261 between several bacterial HPPD isoforms, or a possible detoxification phenomenon supporting
262 resistance to β-triketones specific to this bacterial strain. In this latter case, detoxification could be
263 achieved by the transformation of the active compound. Although *P. putida* 1OP is known to degrade
264 sulcotrione and used it as a source of carbon [53], the transformation of β-triketones by *P. fluorescens*
265 F113 has not yet been described. Detoxification can also be achieved by efflux pumps that are pumping
266 herbicides out of the cell. As an example, a putative major facilitator superfamily (MFS) transporter
267 encoded by the *yhhS* gene conferred resistance in an *E. coli* strain to glyphosate [54]. Efflux pumps are
268 commonly described in Gram-negative and especially in *P. aeruginosa* where they impart resistance to
269 antibiotics [55,56]. Other studies have tested the HPPD activity of *P. aeruginosa* strains in presence of
270 NTBC, a β-triketone used in human medicine, and inhibitory effects are observed at high doses of the
271 inhibitor. For the DKN343 and 1111 isolates, NTBC (up to 900 μM) showed no inhibitory effects on
272 HPPD activity and in the PAO1 mutant, *P. aeruginosa* *hmga::tn*, 300 μM of NTBC are required to
273 inhibit the enzyme activity [57]. The same authors showed that the expression of the *MexAB-OprM*

274 efflux pump is required for resistance to NTBC in DKN343 [58]. This efflux pump is known to pump
275 out a broad range of antibiotics, detergents or organic solvents [59]. We can then hypothesize that a
276 similar efflux pump can allow β -triketone such as sulcotrione, to be pumped out by *P. fluorescens* F113.
277 Anyhow, further studies reporting a possible expression of genes encoding efflux pumps in parallel with
278 an exposition to sulcotrione could be needed to reinforce this hypothesis.

279 Designing dose-response curves on three bacterial models

280 In order to refine our results, we decided to expose to other β -triketone herbicides three of the six
281 bacterial strains: a Gram-negative harbouring a sensitive HPPD activity (*S. oneidensis* MR-1), a tolerant
282 one (*P. fluorescens* F113), and the only Gram-positive (*B. cereus* ATCC14579). Using the colorimetric
283 whole-cell assay, resting cells of *S. oneidensis* MR-1, *B. cereus* ATCC14579 and *P. fluorescens* F113
284 were exposed to increasing doses of sulcotrione, mesotrione and tembotrione. The pre-screening at high
285 doses of herbicides allowed us to select specific inhibitory concentrations ranging from $0\times$ to $10\times$ RfD
286 for sulcotrione (**Figure 3.A**), $0\times$ to $0.5\times$ RfD for mesotrione (**Figure 3.B**) and $0\times$ to $0.07\times$ RfD for
287 tembotrione (**Figure 3.C**). As previously showed with sulcotrione, the HPPD activity of *P. fluorescens*
288 F113 is not inhibited by any of the three β -triketones tested (**Figure 3.A, 3.B and 3.C**) even at high
289 doses, up to $15\times$ RfD (data not shown). At these concentrations, a clear dose-dependent response was
290 observed in *B. cereus* ATCC14579 and *S. oneidensis* MR-1 which allowed us to calculate EC_{50} for the
291 different herbicides. Tembotrione appears to have the strongest inhibiting effect on the HPPD activity
292 of both bacteria. Indeed, EC_{50} are not even calculable due to a too rapid decrease of HPPD activity.
293 However, we can assume that, for both *B. cereus* ATCC14579 and *S. oneidensis* MR-1, EC_{50} is below
294 $0.02\times$ RfD of tembotrione, corresponding to $0.07\ \mu\text{M}$, and that tembotrione has a slightly higher effect
295 on the HPPD activity of *S. oneidensis* MR-1. Similarly, mesotrione has a lower effect on the HPPD
296 activity of *B. cereus* ATCC14579 with an EC_{50} of $2.2 \pm 0.3\ \mu\text{M}$ than on the one of *S. oneidensis* MR-1
297 for which the EC_{50} cannot be calculated because a too rapid decrease of its HPPD activity but can be
298 easily graphically estimated below $0.2\times$ RfD of mesotrione, being $0.88\ \mu\text{M}$. Sulcotrione appears to be
299 the active compound with the lowest effect whatever the strain considered with an EC_{50} of $8.5 \pm 3.3\ \mu\text{M}$
300 in *B. cereus* ATCC14579 and $8.8 \pm 2.8\ \mu\text{M}$ in *S. oneidensis* MR-1. This experiment confirmed our
301 previous results with a strain-dependant response but also highlights a molecule-dependant response.
302 Indeed, β -triketones were ranked as follows from the highest to the lowest inhibitory effect: tembotrione,
303 mesotrione and sulcotrione. Tembotrione appears then to have the lowest EC_{50} in both *B. cereus*
304 ATCC14579 and *S. oneidensis* MR-1. This molecule was shown to be more toxic on the earthworm
305 *Dendrobaena veneta* than glyphosate and nicosulfuron [60]. Even though the cited study did not
306 compare tembotrione to other β -triketones, it provides insights in its potential toxicity. When cloned in
307 *E. coli*, the topramezone-resistant HPPD of the bacterium *Sphingobium* sp. TPM-19 exhibits a higher
308 resistance to mesotrione (EC_{50} of $4.2\ \mu\text{M}$) compared to tembotrione (EC_{50} of $2.5\ \mu\text{M}$) [31] suggesting

309 that, as observed in our study, tembotrione is more active than mesotrione on HPPD activity even for
310 resistant HPPDs. This higher activity might be due to the fluorinated tail (-O-CH₂-CF₃) which increases
311 its lipophilicity and favors the passage of hydrophilic and lipophilic barriers [61]. However, tembotrione
312 physico-chemical properties such as solubility or pKa do not explain its little or no effect on the HPPD
313 enzymatic activity of *P. fluorescens* F113. One can notice that the *MexAB-OprM* efflux pump previously
314 cited is not yet described neither in *B. cereus* ATCC14579 nor in *S. oneidensis* MR-1, suggesting that
315 these bacteria cannot extrude tembotrione once it has entered the cell. Regarding a possible
316 biodegradation mechanism of tembotrione, the trifluoromethyl group added to this compound could
317 make difficult its biodegradation. Moreover, it is known that, in soils, half-life time (DT₅₀) of
318 sulcotrione, mesotrione and tembotrione are comprised between 3.2 and 144 days depending on the soil
319 tested [61]. A possible abiotic or biotic degradation in our culture conditions is, then, quite unlikely.
320 Taken together, these hypotheses can explain the fact that tembotrione harbors a higher inhibitory effect
321 on the HPPD activities of certain bacteria than sulcotrione does.

322 Beyond the cellular level, one can imagine that such strain- and molecule-dependent responses may also
323 be due to molecular changes in the studied HPPD. As it is the case in plants where maize harbors a
324 resistant HPPD [62], bacteria could also harbor HPPD with different sensitivities to β -triketones.

325 **In silico HPPD sequences analysis**

326 We then conducted *in silico* analysis in order to identify possible differences in the HPPD sequences of
327 the tested strains and, following that, molecular docking was led to identify different binding responses.
328 HPPD protein sequences of the three bacteria previously studied were aligned (**Supplementary**
329 **Information 3**), together with the HPPD of *R. etli* CFN42, which was available online and was part of
330 our first experiment, and five others HPPD sequences from different bacteria strains, whose pyomelanin
331 production has been described [13,19,63,64]. Even though these nine sequences have relatively low
332 similarity, ranging from 35.26 to 87.39%, they retain some highly conserved regions. Firstly, the
333 catalytic domain, located in the C-terminus involves a triad consisting of one glutamate (E) and two
334 histidine (H) residues. This triad is highly conserved in bacteria, plant and mammalian forms of HPPD,
335 because these three residues coordinate the binding of a metal dication (either Fe or Co) involved in the
336 catalytic function of HPPD [26,62] (**Figure 4A**), thus playing an essential role in enzyme function.
337 Always in the C-terminal region, the motifs H-I/V/L/L-A and F-F/I/V/L-E, common across HPPD from
338 different bacterium phyla are identified. They are typical from the active site of the enzyme and are
339 conserved among 2506 bacterial protein sequences [65]. Additionally, the binding domain of the
340 substrate HPP is a highly conserved area formed by mostly hydrophobic residues (T164, S202, P215,
341 N217, Q240, L295, F312, F321, F333, N337, F338, L341 based on sequence of *P. fluorescens* HPPD)
342 (**Figure 4C and Supplementary Information 3 and 4**). These 12 amino acids present almost 100% of

343 identity with just one exception for the HPPD sequence of *B. cereus* in the position 164, where a Valine
344 replace Tyrosine. This binding domain plays an important role in positioning HPP in the proper position
345 for the region specific hydroxylation reaction catalyzed by HPPD [66]. β -triketone herbicides are known
346 to interact at this interphase by forming a stable complex between two of their keto groups towards a
347 bidentate association with the active-site metal ion by coordinate as well as this hydrophobic domain
348 [14]. Amino acid sequence comparison of the bacterial HPPD revealed a highly conserved active site
349 and could not explain the differences of inhibition previously observed between the different strains of
350 our study when working on the whole-cell assay. Similar observations were done when HPPD sequence
351 of maize, whose HPPD is naturally tolerant to β -triketone, was compared with other HPPD sequences
352 from β -triketone sensible plants as *A. thaliana* [62].

353 To go further, molecular docking was then carried out with the HPPD from bacterial strains either
354 sensitive or tolerant to β -triketone to explore the complex formed between bacterial enzyme and
355 inhibitors.

356 **Docking of sulcotrione, mesotrione and tembotrione to microbial HPPD**

357 The capacity of the three β -triketone compounds to fit within the substrate binding pocket of the
358 microbial HPPD of *S. oneidensis* MR-1, *B. cereus* ATCC14579 and *P. fluorescens* F113 was estimated
359 by the binding energy. This parameter was determined for each docking experiments as the average of
360 the energy of the correct orientations between the herbicide and the ligand based on homology model of
361 *P. fluorescens* F113. For example, the docking results obtained with mesotrione coordinated on the
362 metal dication on homology model of *P. fluorescens* F113 generated 25 different poses. On these 25
363 poses generated by the docking algorithm, 18 were in an orientation most similar to that observed with
364 inhibitors co-crystalized with HPPD, 3 were in the less favourable pose and 4 in the least desirable
365 orientation (**Supplementary Information 5**). Regardless of the poses, all docking resulted in proper
366 interaction with the iron metal dication (**Supplementary Information 6**).

367 As we can observed, molecular docking revealed that sulcotrione, mesotrione and tembotrione are able
368 to bind with HPPD of *B. cereus* ATCC14579, *S. oneidensis* MR-1 and *P. fluorescens* F113. Whatever
369 the strain, docking results suggest that tembotrione and sulcotrione binds more tightly to the bacterial
370 HPPDs tested than mesotrione. Regarding the number of docking achieving the preferred binding pose
371 (similar to green pose in **Supplementary Information 6**), both sulcotrione and mesotrione docked
372 correctly and more frequently than tembotrione. These latter observations do not correspond to the one
373 obtained with whole-cell assay experiments where tembotrione had a higher inhibitory potential than
374 sulcotrione and mesotrione whatever the strains. Interestingly, Moran *et al.*, suggest that HPPD inhibitor
375 selectivity is based more on bioavailability of the molecule than on direct affinity for HPPD from a

376 specific organism [5]. This observation could explain the apparent discrepancy observed in the results
377 between docking and whole-cell experiments.

378 Our results also showed that the binding force of the three tested β -triketones with the HPPD of *P.*
379 *fluorescens* F113 is lower than the one of the two others strains, suggesting that these three compounds
380 are less able to fit the substrate binding pocket of the HPPD of *P. fluorescens* F113 than that of the two
381 others microbial HPPD. It is noteworthy that these docking predictions agree with the measurement
382 done with our colorimetric whole-cell assay.

383 In fact, *P. fluorescens* F113, was tolerant to the tested β -triketones despite the fact that docking predicted
384 that these active compounds can interact with the active site of its HPPD, even if this HPPD presents
385 the lowest binding force of interaction. Therefore, this poor interaction with the HPPD enzyme of *P.*
386 *fluorescens* F113 cannot only explained the β -triketone tolerance of this strain. Thus, *in silico* analysis
387 is useful to understand and describe molecular interaction between the active compound and the target.
388 However, it is not enough to fully predict the tolerance or the sensitivity of the bacterial HPPD to β -
389 triketones because there are a range of other abiotic and biotic processes involved in the response
390 bacterial cells to β -triketones. A new screening of bacterial strains having either tolerant or sensitive
391 HPPD activity have to be done to gain more information and validate the docking results obtained with
392 the three HPPD sequences of this study. Furthermore, additional experiments analysing the inhibitor
393 binding kinetics on purified HPPDs from these microorganisms would yield important information
394 regarding their affinity. Our docking provides insight on the K_{on} values of the herbicides, but it is well
395 known that HPPD inhibitors bind very tightly to the target site [67]. Consequently, measuring the K_{off}
396 values might be even more insightful. Indeed, compounds with high K_{off} values (binding for a very
397 short time) may not be very active. On the other hand, compounds with low K_{off} values (tight binding
398 or irreversible inhibition) would potentially be more active [68]. However, this is beyond the scope of
399 this paper.

400 **Conclusion**

401 At a molecular level, molecular docking reveals that tembotrione and sulcotrione appear to have a
402 stronger binding force to the bacterial HPPD enzymes than mesotrione. However, *in silico* study shows
403 that tembotrione binds less frequently than the two other molecules. At a cellular level, whole-cell assays
404 show that inhibitory potential is also molecule dependent but with tembotrione on the top step of the
405 podium. Such differences allow us to think that *in silico* and *in vivo* approaches complement each other.
406 HPPD enzymatic activity inhibition also appears strain-dependent. At a molecular level, *P. fluorescens*
407 F113 shows a lower binding force to herbicides than *B. cereus* ATCC14579 and *S. oneidensis* MR-1,
408 confirming the observations made at the cellular level. By combining approaches at both cellular and

409 molecular levels, this is the first study that assesses the effect of agronomical doses of three β -triketone
410 active compounds on the HPPD enzymatic activities of six environmental bacterial strains.

411 At the community level, a recent lab-to-field study demonstrates that, neither sulcotrione nor its
412 formulated product, Decano[®], has an effect on the abundance and the diversity of both total and *hppd*
413 bacterial communities [32]. As we measure that tembotrione has a lower EC₅₀ than sulcotrione in some
414 bacteria, conducting a lab-to-field experiment with tembotrione and one of its formulated products could
415 be interesting. Actually, working at a lower biological level (*i.e.* whole-cell assay coupled with
416 molecular docking) should be of interest, prior to conducting microcosm or field experiments, which
417 are more difficult to set up.

418 Whole-cell assay developed in this study could be applied to other herbicides and pesticides that also
419 target an enzyme harbored by non-target organisms and, more precisely, by microorganisms, like
420 EPSPSynthase, targeted by Glyphosate or ALSynthase targeted by sulfonylurea herbicides [69], as there
421 is a need to develop new tools for pesticide risk assessment on soil microorganisms [70,71].

422 **References**

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607 Lamrani and Christophe Calvayrac conceived and designed research. Franck E. Dayan conducted *in*
608 *silico* analysis and docking experiments. Clémence Thiour-Mauprivez conducted the resting cells
609 experiments. Hugo Terol conducted the pyomelanin production measurements. All authors read and
610 approved the manuscript.

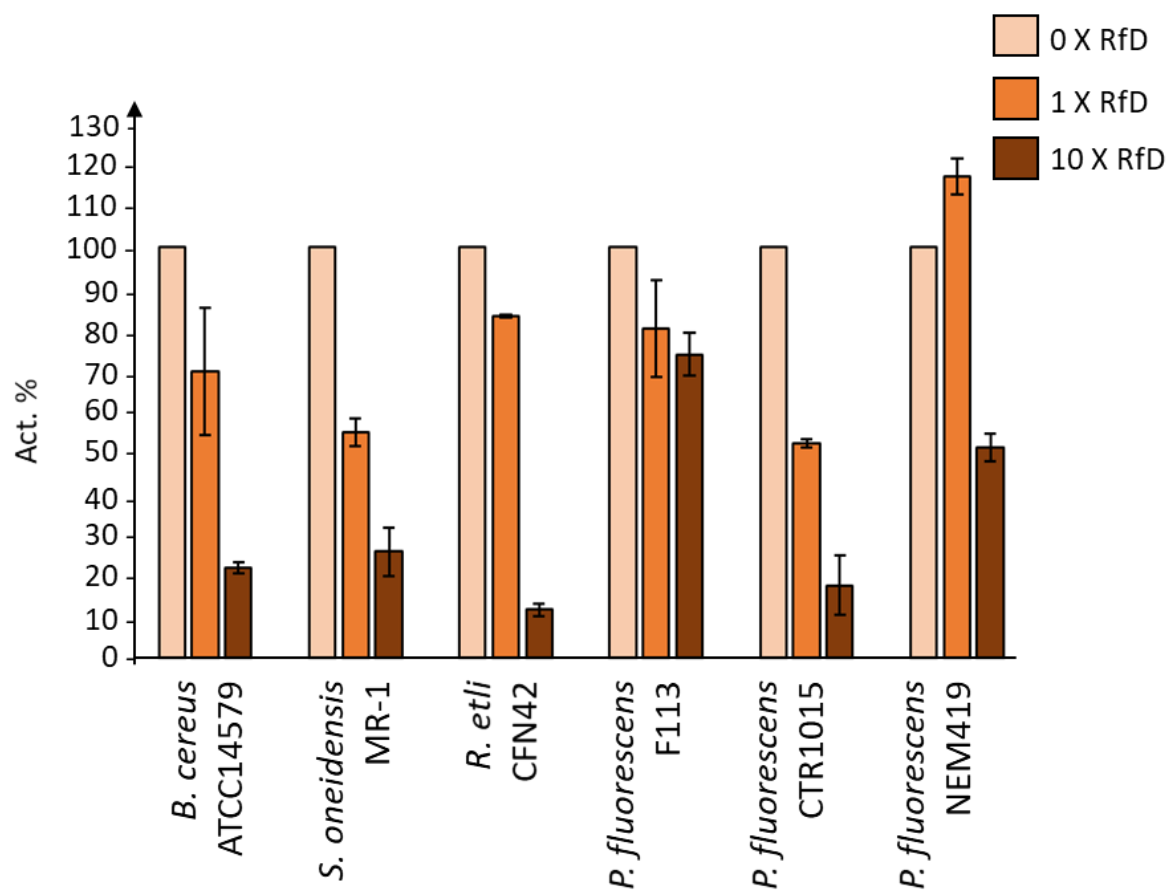


Figure 1. HPPD relative activity (Act. %) measured in the six different strains (*P. fluorescens* F113, *P. fluorescens* CTR1015 and NEM419, *S. oneidensis* MR-1, *B. cereus* ATCC14579 and *R. etli* CFN42) exposed to 0×, 1× or 10× RfD of sulcotrione. 0× RfD represents the positive control of our experiment. Error bars are calculated from the standard deviation for each series.

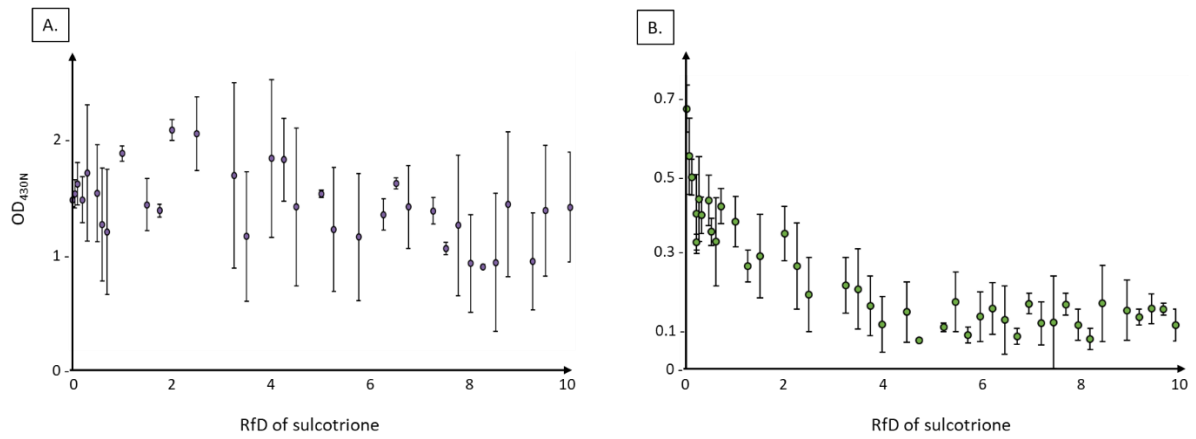


Figure 2. OD_{430N} in *P. fluorescens* F113 (A) and *S. oneidensis* MR-1 (B) in regard to increasing RfD of sulcotrione. Each value is obtained by subtracting the mean OD_{430} obtained at various concentrations of sulcotrione (i.e. OD_{430A}) from the mean OD_{430} obtained in negative controls (i.e. OD_{430NC}) and is depicted on this figure as “ OD_{430N} ”. Error bars are calculated from the standard deviation for each series.

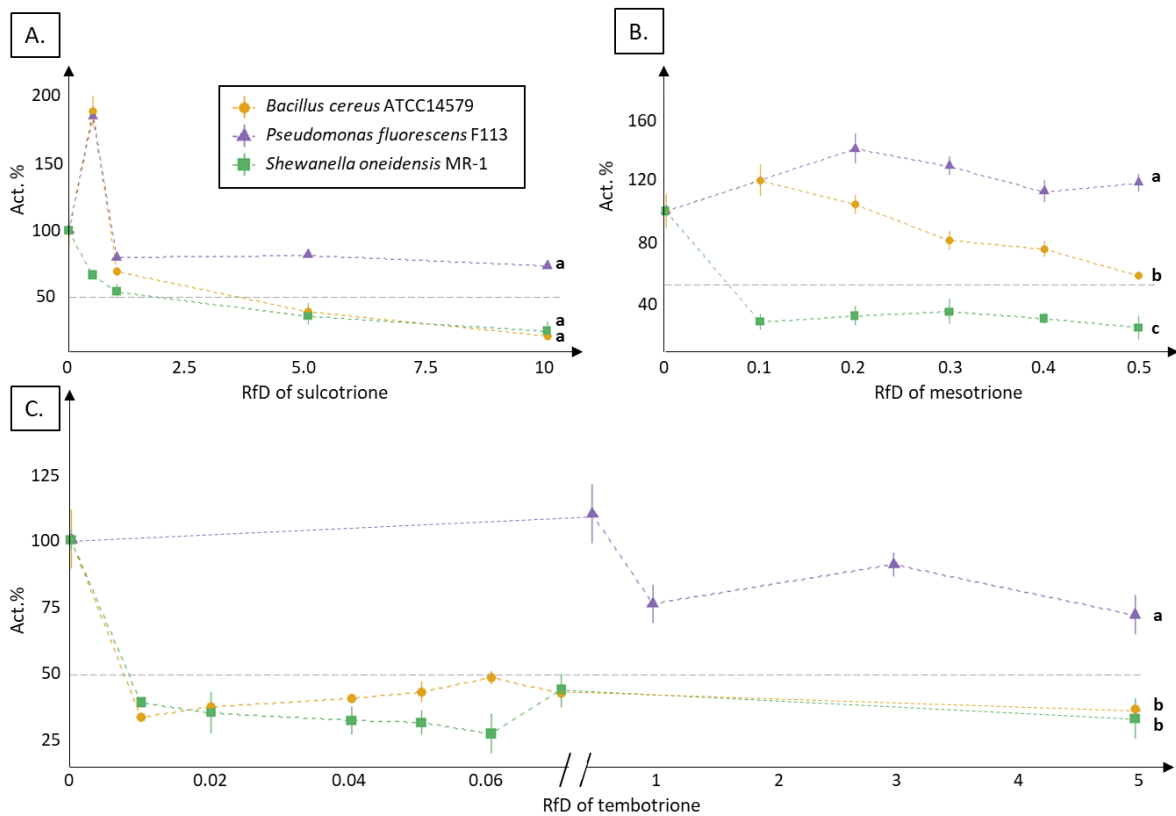


Figure 3. HPPD relative activity (Act. %) in *B. cereus* ATCC14579, *S. oneidensis* MR-1 and *P. fluorescens* F113 exposed to sulcotrione (A), mesotrione (B) and tembotrione (C). Act. % represents the percentage obtained by dividing the mean OD₄₃₀ obtained at various concentrations of sulcotrione, mesotrione or tembotrione (i.e. OD_{430A}) from the mean OD₄₃₀ obtained in the positive control (i.e. OD_{430PC}). The grey dotted line corresponds to 50% of activity. Error bars are calculated from the standard deviation for each series. **Significant differences between means are indicated by different letters (Kruskal–Wallis tests, $p < 0.05$).**

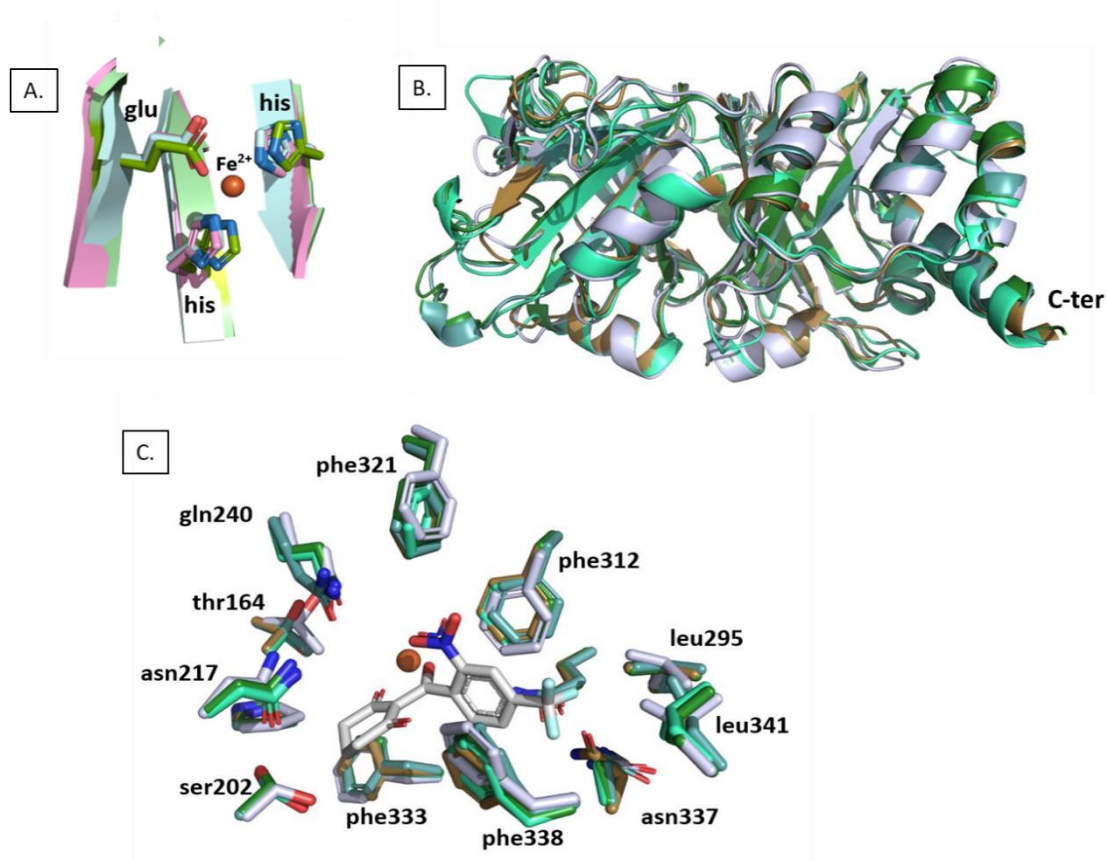
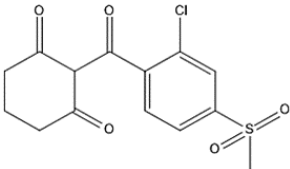
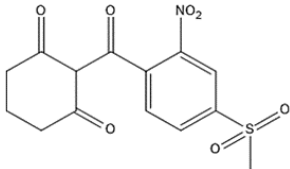
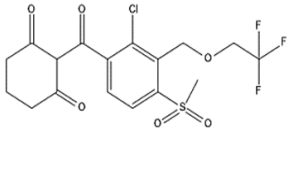


Figure 4. A) Residues involved in stabilizing the metal dication (Fe^{2+}) within the HPPD catalytic domain of *P. fluorescens* in pink (1cxj), *A. thaliana* in green (6isd) and *H. sapiens* in blue (3isq). B) Alignment of the 4 bacterial models derived from the HPPD sequences of *P. fluorescens* F113, *B. cereus* ATCC14579, *S. oneidensis* MR-1 and *R. etli* CFN42. C) Amino acid residues lining the substrate binding pocket of HPPD are highly conserved of the 4 bacterial homology models. Numbering is based on sequence of *P. fluorescens* HPPD.

Table 1. β -triketone molecules used as herbicides. CMBA: 2-chloro-4-methyl sulfonyl benzoic acid; CHD: 1,3-cyclohexanedione MNBA: 4-methylsulfonyl-2-nitro benzoic acid; AMBA: 2-amino-4-methylsulfonylbenzoic acid TCMBA: 2-(2-chloro-4-mesyl-3-(2,2,2-trifluoroethoxy) methyl) benzoic acid.

Molecule	Sulcotrione	Mesotrione	Tembotrione
Chemical structure			
IUPAC name	2-(2-Chloro-4-(methylsulfonyl)benzoyl)cyclohexane-1,3-dione	2-(4-mesyl-2-nitrobenzoyl)cyclohexane-1,3-dione	2-(2-Chloro-4-((2,2,2-trifluoroethoxy)methyl)benzoyl)cyclohexane-1,3-dione
MW (g/mol)	324.8	339.3	440.8
pKa	3.13	3.12	3.18
Solubility in water at pH 7 (g/L)	0.17	15	28.3
Log Kow	0.55	-0.17	1.8
Main degradation product	CMBA; CHD	MNBA; AMBA	TCMBA