
Article:
Moir, James orcid.org/0000-0003-2972-5235 (2017) Microbial changes linked to the accelerated degradation of the herbicide atrazine in a range of temperate soils. Environmental Science and Pollution Research (ESPR). pp. 7359-7374. ISSN 1614-7499

https://doi.org/10.1007/s11356-017-8377-y

Title of article: Microbial changes linked to the accelerated degradation of the herbicide atrazine in a range of temperate soils

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Abstract

Accelerated degradation is the increased breakdown of a pesticide upon its repeated application, which has consequences for the environmental fate of pesticides. The herbicide atrazine was repeatedly applied to soils previously untreated with *s*-triazines for >5 years. A single application of atrazine, at an agriculturally relevant concentration, was sufficient to induce its rapid dissipation. Soils with a range of physico-chemical properties and agricultural histories, showed similar degradation kinetics, with the half-life of atrazine decreasing from an average of 25 days after the first application to <2 days after the second. A mathematical model was developed to fit the atrazine degrading kinetics, which incorporated the exponential growth of atrazine-degrading organisms. Despite the similar rates of degradation, the repertoire of atrazine degrading genes varied between soils. Only a small portion of the bacterial community had the capacity for atrazine degradation. Overall the microbial community was not significantly affected by atrazine treatment. One soil, characterised by low pH, did not exhibit accelerated degradation and atrazine degrading genes were not detected. Neutralisation of this soil restored accelerated degradation and the atrazine-degrading genes became detectable. This illustrates the potential for accelerated degradation to manifest when conditions become favourable. Additionally, the occurrence of accelerated degradation under agriculturally relevant concentrations supports the consideration of the phenomena in environmental risk assessments.

Keywords: microbial communities, atrazine, risk assessment, fate modelling, soil pH, adaptation

Introduction

In the EU registration of a new plant protection product requires a risk assessment which includes evaluation of its environmental fate (EC, 2009). This is strongly affected by degradation processes (Katayama et al. 2010) which are often mediated by microorganisms (Dodge et al. 2012; Howell et al. 2014). Upon the repeated application of a pesticide or its analogue microbial communities are able to adapt and degrade the pesticide a faster rate, referred to as accelerated degradation (Racke 1990). Accelerated degradation has been shown to occur for a broad range of pesticides classes (Arbeli and Fuetes 2007), although it is not currently considered in the EU registration studies. For example to determine the transformation of a chemical in soil, such studies specify that the soils used for the test must not been treated with the substance or its analogues for four years (OECD, 2002), however it has been shown that the capacity for pesticide degradation can be maintained for up to 10 years (Cheyns et al. 2012).

Accelerated degradation has the potential to reduce pesticide persistence in the environment (Shaner et al. 2007), but also to deplete the efficacy of a pesticide (Krutz et al. 2008). This may contribute to pressure on pesticide use in the light of the limited number of active substances (Chapman, 2014) and increased pest resistance (Heap 2016). The phenomenon is dependent on the microbial community, however the specific changes that occur in the microbial community between pesticide applications and lead to the faster rate of degradation, are poorly understood (Arbeli and Fuetes 2007; Itoh et al. 2014).

The herbicide atrazine (1-Chloro-3-etylamino-5-isohpropylamino-2, 4, 6-triazine) was selected as a model pesticide to determine the changes that occurred in the microbial community during accelerated degradation. Atrazine was selected as it is highly effective and extensively used around the world (Syngenta 2016), although banned in the EU since 2003 (EC 2015). Additionally, its microbial degrading pathway is well characterised (Udikovic-Kolic et al. 2012), see Online Resource 1, which enabled the microbial capacity for the degradation of atrazine to be tracked.

Previous studies that have examined the accelerated degradation of atrazine used high concentrations of atrazine to isolate highly tolerant microorganisms for bioremediation (Cai et al. 2003; Wang et al. 2014), often around agrochemical factories, (Udikovic-Kolic 2008; Udikovic-Kolic 2010) or atrazine treated agricultural fields (Zablotowicz et al. 2007). This may have biased microbial changes in favour of the fastest growing and most

72 readily culturable members of the community (Dunbar et al. 1997). We used soils with no documented history
73 of *s*-triazine application and applied atrazine at an agriculturally relevant rate to gain an insight into the potential
74 for accelerated degradation in soils that have previously been un-treated, or at least have not recently had
75 concerted exposure to atrazine. We then tracked the microbial changes linked to accelerated degradation as it
76 manifested. Pyrosequencing of the 16S rRNA bacterial gene was adopted to enable the community to be
77 analysed more comprehensively compared to fingerprinting techniques such as fatty acid methyl ester (FAME)
78 which had been done previously (Zablotowicz et al. 2007), and which have been shown to lack resolution (Bent
79 et al. 2007). We concentrated on the bacterial portion of the community, as they have been shown to be mainly
80 responsible for accelerated degradation (Walker 1993).
81
82 A broad range of soil properties have been associated with influencing accelerated degradation from plant
83 exudates (Piutti et al. 2002) to moisture content (Schroll et al. 2006) and carbon availability in the soil (Popov et
84 al. 2005, Ngigi et al. 2013). Specifically for atrazine soil pH has shown to affect degradation (Houot et al. 2000).
85 The effect of pH has been examined previously, but not linked to detection of the atrazine degrading genes or
86 the manifestation of accelerated degradation.

87
88 Currently there is no attempt to account for accelerated degradation in the models used for pesticide dissipation
89 for regulatory purposes, despite the potentially enormous influence of adaptive, biological pesticide degradation
90 on both product effectiveness and residual concentration in soils. To address this, we developed a growth-linked
91 model based on the accumulation of pesticide degrading microorganisms to fit the kinetics of atrazine
92 disappearance and to facilitate incorporation of accelerated degradation into environmental risk assessments.
93

94 **2. Materials and methods**

95 Three major groups of experiments were conducted in this study; the first to examine the microbial changes
96 associated with accelerated degradation, the second to determine the effect of soil properties on accelerated
97 degradation and the third to explore the effect of pH on accelerated degradation. All three groups of experiments
98 monitored atrazine dissipation to determine the capacity of the soils for accelerated degradation and the presence
99 of the atrazine degrading genes to track accelerated degradation. The soils used for each experiment are detailed
100 in Table 1 and the sampling regime is detailed in online resource 2.

2.1. Soil collection

Nine soils which had no documented history of being treated with *s*-triazines were collected from 4 UK farms, with different physical and chemical properties; Cotril (C): 54° 8' 2.832" N, 0° 58' 36.098" W; Mount (M): 54° 5' 36.218" N, 1° 1' 38.770" W; Grange (GR): 54° 6' 10.703" N, 0° 50' 9.082" W and Ganthorpe (G): 54° 7' 27.026" N, 0° 56' 48.793" W. The latitude and longitude for each farm were determined from postcodes inputted into http://www.latlong.net/ (LatLong, 2012-2014) and converted into coordinates using http://www.sunearthtools.com (SunEarthTools.com, 2009-2016).

From each farm two soils with different management histories were removed. One soil had been out of agricultural practice for over 5 years, and was referred to as set-aside (S) while the other soil, that had been under continuous agricultural practice, including pesticide treatment for over 5 years (Online Resource 3), was referred to as the agricultural (A) soil. The set aside soils had slightly different management histories as follows; CS and GRS were grassland, whilst MS was a buffer strip and GS was fallow.

All soils were collected in 2013 apart from the Ganthorpe soils, which were first collected in 2012, and soil from the agricultural site was resampled in 2013, to see if the repertoire of pesticide degrading genes had changed. In addition the soil for the pH study was collected from Grange in 2014 (Table 1). At each field site, the debris was removed from the soil surface and then ~ 10 kg of soil, from the top 10 cm was transferred into bags and kept at 4 °C for up to 12 hours prior to processing.

2.2. Soil characterisation

Soil pH was measured in H_2O in 1:2.5 w/v suspensions (Avery and Bascomb 1974) using a pH probe. The pH probe was calibrated and 10 g of soil added into a 50 mL polyethene beaker with 25 mL of distilled water, stirred and left to stand for 10 min. The pH probe was then introduced, and recorded when stable. The moisture content of each soil upon sampling was determined in grams water per gram of oven dried soil (105 °C), shown in Table 1, while the maximum water holding capacity was determined using the Avery and Bascomb method (Avery and Bascomb 1974).

Total organic carbon was measured using the Walkley and Black method (Walkley and Black 1934), total nitrogen using the AOAC method (AOAC 1990) and the soil textural class USDA using the Black method (Black 1965), conducted by Natural Resource Management (NRM) Ltd., Berkshire, UK.

2.3. Microcosm construction

Soils were processed in accordance with OECD 307 guidelines for analysis of chemical transformation in soils (OECD 2002) as follows: soils were air-dried then sieved to 2 mm, moisture adjusted to 40 – 60 % of the MWHC and were maintained at 20 °C ± 2 °C in the dark. The soils GA_2012 and GS_2012 consisted of 12 treated subsamples and 4 control samples -the extra treated samples enabled an assessment of the variation in atrazine recoveries between replicates to be made. For the soils collected in 2013 and 2014, 8 subsamples of 400 g (on a dry weight basis) were transferred into glass amber jars secured with foam bungs. For each soil 4 jars were treated with atrazine and 4 jars were untreated controls.

As a sterile control, 4 x 10 g of GRA soil replicates were autoclaved at 121 °C for 15 min., treated with atrazine as above, and sampled in quadruplicate at day 0, 1, 3, 7 and 14 days.

2.4. pH adjustment

The soils GRA_pH and GRS_pH had their pH altered according to the method applied by Nicol et al. (2008). GRS (pH 5.4) had 2 mg g^{-1} of lime ($Ca(OH)_2$) added to maintain ~ pH 7 (Online Resource 4), and was referred to as GRS amended (GRSa). The GRA_pH soil (pH 6.2) had 8 mg g^{-1} of aluminium sulphate ($Al_2(SO_4)_3$) added and was maintained at ~ pH 4 throughout the study (Online Resource 4), and was referred to as GRA amended (GRAa). Soil pH was monitored in a non-atrazine treated control pot weekly for each soil and each amendment added as required, followed by moisture adjustments.

2.5. Atrazine application

Atrazine (PESTANAL, Sigma Aldrich) was applied to 4 amber jars per soil type (12 for the GA_2012 and GS_2012). Due to its low water solubility atrazine was dissolved in methanol and added to 5 g of 1 mm silica sand. The methanol was left to evaporate and the sand mixed into the soil samples. Atrazine was applied at a final agriculturally relevant concentration of 6 µg g^{-1} of dry soil (Tomlin 2009). The four control samples per soil, had silica sand with evaporated methanol added. Atrazine was applied in this way three times (twice for the

154 pH study) over an interval of 60 days for the first application and 28 days between the second and third
155 application.

156 ***2.6. Atrazine extraction & detection***

157 Samples were removed for analysis 0, 1, 3, 7, 14, 28, 45 and 60 days (day 45 samples were not removed for the
158 GA_2012 and GS_2012) after the first atrazine application and 0, 1, 3, 7, 14, 28 days after the second and third
159 application.
160
161 Atrazine was extracted from 1 g (dry weight basis) soil sub-samples by homogenisation with 20 mL of methanol
162 and shaken on a side-side shaker at 230 rpm for 30 min. Following centrifugation (2500 rpm for 5 min), 10 mL
163 of the supernatant was filtered (cellulose acetate 0.45 µm) and 2 mL of the filtrate concentrated to dryness under
164 a flow of nitrogen at 35 °C. The residue was then re-suspended in 200 µL of methanol:water (50:50) using a
165 vortex mixer. Extracts were transferred to HPLC vials and stored at -20 °C prior to analysis.
166
167 The concentration of atrazine was determined on the Agilent 1100 series and 1200 series UV module HPLC
168 using a methanol:water mobile phase (50:50) at 1 mL min^{-1}, injection volume of 20 µL, separated on a C18
169 column with UV detection of atrazine at 222 nm after ~ 8.3 min. The estimated limit of detection (LOD) based
170 on the lowest calibration standard was 0.02 µg mL^{-1}. The chromatograms were manually integrated using the
171 Chemstation software in order to estimate peak areas, which were then converted into concentrations from
172 calibration curves. Calibration curves were prepared by producing atrazine standards in methanol:water (50:50)
173 at six concentrations from 0.02 µg mL^{-1} to 5.0 µg mL^{-1}. Plots of atrazine concentration vs. peak area were
174 constructed and linear regression used for determining the atrazine concentration in the samples.

175 ***2.7. Modelling of atrazine dissipation***

176 Modelling of atrazine dissipation over the three applications and in the pH and sterile control samples, was
177 conducted according to the recommendations of the forum for the co-ordination of pesticide fate models and
178 their use (FOCUS 2006) to obtain estimated values of the dissipation time 50 (DT_{50}). The percentage recoveries
179 of atrazine from the theoretical amount applied were modelled using the KinGUii software v2. Initially the data
180 was optimised to fit the single first order (SFO) model. The visual fit of the data, χ^2 value and spread of the
181 residuals were used to determine if a biphasic model would be a better suited to the data, dependent on whether
182 10 % of the initial measured concentration had been reached (FOCUS 2006). A biphasic model was only fitted

to the data if compared to SFO the biphasic model resulted in an improved visual fit, low Chi squared (χ^2) estimate (< 15 %) and the model parameters passed the t-test (FOCUS 2006).

To take into account the impact of accelerated degradation on atrazine removal, an alternative approach to modelling the atrazine degradation data was developed, referred to as the 'growth linked model'. This involved accounting for the increase in a community of biological atrazine degraders over time during the incubation of soils, as accelerated degradation has been associated with an increase in degrader abundance (Bending et al. 2001). The model consisted of two rates of degradation: (i) a first order exponential decay rate (chemical), and (ii) a biological decay rate, dependent hyperbolically on atrazine concentration. The difference in atrazine concentration [Atr] between two time points (time t, and time t+n) was calculated computationally as follows;

$$[Atr](t+n) = [Atr]t - \left(Y \times n \times k_1 \times e^{-k1t}\right) - \left(N \times n \times V \times [Atr] \div ([Atr] + K_s)\right)$$

For the exponential term, Y is the percentage of atrazine that is available for degradation, n is the length of the time-step (typically set at 0.01 days) used in the modelling, k_1 is the exponential atrazine decay rate. For the hyperbolic term, N is the size of the atrazine degrader community, V is the maximum rate of atrazine removal, K_s is the Michaelis constant representing the concentration of atrazine that gives half the maximum rate of hyperbolic atrazine degradation. The size of the atrazine degrader community (N) changes over time as the community of atrazine degrading organisms grows (as the soil community adapts to atrazine being available). N is calculated as a number between 0 and 100, by the following equation:

$$N = N_0{}^{e\mu t}$$

where μ is the exponential growth rate of atrazine degraders and N_0 is the initial size of the atrazine degrading community capable of growth. N is limited to a maximum arbitrary size of 100.

The model was implemented using a custom-made script written in Python, and the parameters determined based on qualitative fit to the data.

2.8. Sorption

To investigate the effect of soil pH on sorption of atrazine, batch sorption experiments were conducted as described in OECD 106 (OECD 2000). Prior to the batch sorption experiment atrazine was determined to be stable in 0.01 M $CaCl_2$ for at least 24 hours. Sorption of the atrazine was estimated for the GRS_pH and

212 GRA_pH soils and following alteration of their pH GRSa and GRAa, using the standard batch sorption method
213 detailed in OECD 106 (OECD 2000).
214
215 Five grams of each soil, in duplicate tubes were pre-equilibrated with 22.5 mL of 0.01M $CaCl_2$ by shaking at
216 200 rpm on a side to side shaker overnight. Atrazine stock solutions of 0.2 µg mL^{-1}, 5.0 µg mL^{-1} and 20.0 µg
217 mL^{-1} were added in either 2.5 mL or 1 mL volumes to obtain theoretical concentrations of 0.02 µg mL^{-1}, 0.08 µg
218 mL^{-1}, 0.20 µg mL^{-1}, 0.80 µg mL^{-1} and 2.0 µg mL^{-1}. Additional 0.01 M $CaCl_2$ was added to ensure all tubes had
219 25 mL of 0.01 M $CaCl_2$, to achieve a 1:5 soil to solution ratio. After atrazine addition soil suspensions were
220 returned to the shaker for 24 hrs to reach pseudo-equilibrium. The samples were then centrifuged at 3000 rpm
221 for 5 min and the supernatants then filtered (0.2 µm PTFE membrane filters) into 2 mL HPLC vials which were
222 stored at 4 °C prior to analysis.
223
224 The final solute concentration of atrazine in solution after adsorption (C_{aq}) was determined from the HPLC of
225 the supernatant, assuming that all atrazine removed from solution, has been adsorbed. The concentration sorbed
226 to soil (C_s) was calculated as below;
227 $$C_S = K_f \times C_e^{1/n}$$
228 Values for the Freundlich adsorption coefficient (K_f) and the regression constant (n) for the Freundlich
229 adsorption equation were obtained using a solver in Excel by selecting values that minimised the sum of the
230 least squares between measured and modelled values. C_{aq} values were then plotted against C_s to examine the
231 change in sorption as a function of concentration.

232 ***2.9. Measuring ATP***

233 Total Adenosine Triphosphate (ATP) was extracted from 7 days after each application in triplicate from
234 GA_2012 and GS_2012 to monitor the total microbial activity. The Celsis Beverage Kit™ (Brussels, Belgium)
235 was used to measure ATP and the positive control kit (Celsis) used to check the functioning of the Celsis
236 Cellscan M201B luminometer. For the positive control sample 1 g of sterilised soil was mixed with 10 mL of
237 nuclease-free water (Severn biotech Ltd, Worcestershire, UK) and 100 µL of *E. coli* (NCTC 9703) cell
238 suspension, while a blank cuvette was used as a negative control. The ATP content of 1 g (dry weight) of soil
239 was used for all reactions and 10 mL of nuclease-free water (Severn biotech Ltd, Worcestershire, UK) was
240 added and samples were shaken and processed using the Celsis Beverage Kit. Initially the variability of ATP

241 (measured in relative light units) was measured in 3 subsamples of the same atrazine un-treated soil sample, two
242 aliquots of the soil sludge were then recorded, the variation between the subsamples was determined not to be
243 significant, using a Student's t-test; all $p>0.20$, (Online Resource 5). One gram sub-samples from atrazine
244 treated pots were monitored in triplicate 7 days after each application.

245 ***2.10. DNA extraction & PCR***

246 Total community DNA was isolated from the atrazine treated and control soils across the three applications of
247 atrazine (two applications for the pH study). Approximately 5 g of soil per sample were homogenised in an
248 automatic shaker (Merris Engineering Ltd, Galway, UK) for 2 min., with 10 mL of CTAB (Cetyl Trimethyl
249 Ammonium Bromide) buffer (120mM sodium phosphate buffer pH 8, 2 % CTAB, 1.5 M NaCl), 0.3 mL of
250 antifoam B (Sigma-Aldrich, Dorset, UK) and 10 metal ball bearings (10 mm diameter). The supernatant was
251 removed and centrifuged at 2000 g for 2 min., and vortexed with 250 µL of Food Buffer B (Promega, Madison,
252 USA) until it appeared milky. This was followed by addition of 750 µL of Precipitation Buffer (Promega) which
253 was vortexed and centrifuged at 13000 g for 10 min. The extracted DNA was then purified using the Promega
254 wizard food kit, in conjunction with the Kingfisher™ mL system (Thermo Fisher Scientific Inc., Massachusetts,
255 USA) with a magnetic particle processor using the "gDNAnew" programme. The programme was as follows:
256 750µL of the cleared sample was mixed with 600 µL of isopropanol with 50 µL of the magnesil beads
257 (Promega) for 10 min and the genomic DNA bound to the magnetic particles, transferred to 1 mL of lysis buffer
258 B (Promega) for 2 min, followed by 4 washes in 1 mL of 70 % ethanol for 2 minutes each, followed by 5 min.,
259 of heating at 65 °C and final elution in 200 µl of TE buffer (pH 8). The purity of extracted DNA was determined
260 using the nanodrop (ND 1000 3.3) system (Thermo Fisher Scientific Inc), and frozen at -20 °C in TE buffer (10
261 mM Tris, 1 mM EDTA, pH 8).

262 ***2.11. Detection & sequencing of atrazine degrading genes***

263 Samples from different time points across the three applications of atrazine (2 applications for the pH study)
264 were checked for atrazine degrading genes (Online Resource 1). The PCR mix consisted of 1x KAPA HiFi
265 fidelity buffer (Kapa Biosystems, Woburn, MA, USA), 0.3 µM of dNTPs, 0.3 µM of each primer (Table 2), 1 U
266 μL^{-1} KAPA HiFi polymerase and nuclease-free water (Severn biotech Ltd, Worcestershire, UK) to reach 25 µL
267 final volume. The PCR followed these thermal cycling conditions: initial denaturation at 95 °C for 5 min, and 30
268 cycles of denaturation at 98 °C for 30 sec, annealing for 15 sec (at the specified temperature in Table 2) and 15
269 sec elongation at 72 °C, followed by a final extension of 5 min at 72 °C (Bio-Rad Laboratories, Inc, USA).

Products were visualised on a 2 % agarose gel, containing 0.5 µg mL^{-1} ethidium bromide for DNA binding. Bands of the expected size were gel extracted using the Qiagen gel purification kit (Qiagen, Hilden, Germany) and quantified using nanodrop v3.3. Amplicons at concentrations of 4-10 ng μl^{-1} were re-suspended in nuclease-free water (Severn Biotech Ltd, Worcestershire, UK) and 0.3 µM of the forward primer added and directly sequenced using the Applied Biosystems instrument 3130XL (CA, USA). DNA sequences were analysed using the Sequence Scanner 1.0 software and similarity to previously sequenced genes was determined from the NCBI using the nucleotide BLAST tool (Altschul et al. 1990).

Genomic DNA that did not produce a detectable atrazine degrading gene product was tested for the effect of inhibitors by adding 2 µL aliquots of the potentially "inhibitory" genomic DNA to a working PCR using undiluted, and diluted DNA extracts (1:10 and 1:100), failure to produce a PCR product in an initially working PCR following addition of the "inhibitory" genomic DNA would indicate that the gene may not be absent in that gDNA sample, but its amplification may have been prevented by inhibition. However in this study no inhibition of the PCR was evident.

2.12. Real Time PCR

Relative quantification of *trzN* was performed by Q-PCR to estimate the proportion of the community in the soils GA_2012 and GS_2012 containing the atrazine degrading gene. The *trzN* gene was selected as the gene of interest it was the most commonly identified atrazine degrading gene in this study, in-line with previous studies (Arbeli and Fuetes 2010).

The 16S ribosomal RNA gene was selected as a normalisation gene, due to its presence in all bacteria, although different copy numbers are found in some species (Acinas et al. 2004). Quantification of *trzN* could then be compared between different samples, despite differences in the number of bacteria and or concentration of gDNA template. Primers for the gene targets (TrzN_Q_F & R,. 16S_Q_F & R, the latter from Yang et al. (2002) were selected using the Primer Express® Software for Real-Time PCR version 3.0 (Applied Biosystems) and synthesised by Eurofins MWG Operon. Primers are listed in Table 2. The Q-PCR method was adapted from Udikovic-Kolic et al. (2010) and was performed on an Applied Biosystems StepOne™ instrument using SYBR Green® for detection in 20 µL reactions. Each reaction consisted of 10 µL of Power SYBR® Green Mix 2 x (Applied Biosystems), 6.2 µL Nuclease-free dH_2O (Ambion®), 0.4 µL of each primer (5 µM each) and 3 µL of

gDNA. Reactions were run in 96-Well Optical Reaction Plates (Applied Biosystems) for relative quantification, according to the manufacturer's instructions.

Thermal cycling conditions were as follows; hold at 95 °C for 10 min, 40 cycles at 95 °C for 15 seconds and 60 °C for 1 min. The final step was added initially to produce a melt curve, starting from 60 °C to 95 °C to ensure that a single product was produced. Each sample was run in triplicate per target, to obtain average Ct (cycle threshold) values.

Standard curves of *trzN* and *16S rRNA* were constructed using purified PCR products for these genes amplified from a soil sample that had been treated with atrazine three times. The PCR amplicons were purified using the Qiagen gel purification kit and quantified based on absorbance at 260 nm using Nanodrop v3.3. Amplicons were required to have a 260/280 ratio between 1.8 and 2.0. For relative quantification standard curves were produced by serially diluting the amplicons tenfold, four times for *trzN* and five times for *16S rRNA*. The standard curves *16S rRNA* and *trzN* are shown in Online Resource 6 and 7, respectively. Plots of log DNA concentration vs. Ct value were constructed and the linear regression line used for determining the gene concentration in the sample. The percentage of the bacterial community containing *trzN* was then calculated using the following formula;

$$\frac{trzN\ gene concentration}{16S rRNA\ gene concentration} \times \frac{length\ of\ 16S\ gene product\ (bp)}{length of\ trzN\ gene product\ (bp)} \times 100$$

Significant differences in the portion of the community containing *trzN* between treated and control samples, for each soil was determined by unpaired t-tests.

2.13. Community analysis

To determine the bacteria present in the GA_2012 and GS_2012 soils, the V3-V5 fragment of the 16S rRNA gene was amplified by the polymerase chain reaction (PCR) and pyrosequenced using primers previously tested by Klindworth et al. (2013). PCR primers were adapted to 454 amplicon sequencing, for which a M13 adapter (bold and underlined) was attached to the target forward primer Bakt_341F (5'-**CACGACGTTGTAAAACGAC**CCTACGGGNGGCWGCAG -3'). To aid multiplexing different samples, different barcodes were included using the M13 adapter. Sequence adapter A (bold) was followed by the 454 amplicon sequencing specific 4-mer amplification key (italics) followed by a 10-mer sequence (NNNN) barcode and M13 (bold and underlined) (5'-

CCATCTCATCCCTGCGTGTCTCCGAC*TCAG*NNNN**CACGACGTTGTAAAACGAC** -3'). An overview of barcode sequences used can be found in Online Resource 8. The 25-mer Lib-L specific sequence adapter B was followed by the reverse template specific primer sequence Bakt_805R (italics) (5' CCTATCCCCTGTGTGCCTTGGCAGTC*GACTACHVGGGTATCTAATCC* -3').

The PCR mix consisted of 1x KAPA HiFi fidelity buffer (Kapa Biosystems, Woburn, MA, USA), 0.3 µM of dNTPs, 0.3 µM of each primer, 1 U μL^{-1} KAPA HiFi polymerase, 0.3 µM M13 adapter and nuclease-free water (Severn Biotech Ltd, Worcestershire, UK) to reach 25 µL final volume. The PCR followed these thermal cycling conditions: initial denaturation at 95 °C for 5 min, and 30 cycles of denaturation at 98 °C for 30 sec, annealing for 15 sec at 55.3 °C and 15 sec elongation at 72 °C, followed by a final extension of 5 min at 72 °C using the Bio-Rad C1000 (Bio-Rad Laboratories, Inc, USA). Products were visualised on a 1 % agarose gel, containing 0.5 µg mL^{-1} ethidium bromide for DNA binding. Band intensity of 16S rRNA gene amplicons of the correct size (469 bp) was used to estimate quantity for pooling. Subsequently, pooled amplicons were run on a 3.5 % gel to separate out small fragments, which were excised and extracted using the Qiagen Gel purification kit according to the manufacturer's instructions. This concentrated pooled sample was heated for 5 min at 95 °C and snap cooled on ice for 2 min. This was followed by a second gel electrophoresis on a 2 % gel of the concentrated pooled amplicons. The excised band of correct size was extracted using the Qiagen kit. The purity and concentration was determined using Nanodrop (ND-1000 3.3) and DNA fragment pattern assessed using a DNA 1000 Chip on the Agilent Bioanalyser, 2100 series (Agilent Technologies Inc, CA, USA).

The sequences of partial 16S rRNA genes were obtained using a Roche GS-FLX 454 pyrosequencer (Roche, Mannheim, Germany) using picotiter sequencing plates and sequenced as advised by the manufacturer for amplicon sequencing. Samples were processed through the QIIME (quantitative insights into microbial ecology) pipeline (Caporaso et al. 2010b). Initially samples were filtered by quality (-M4; maximum number of primer mismatches, -s 30; minimum average quality score allowed in read) and were split by their barcode sequence. The number of sequences present before and after quality filtering is shown in Online Resource 9. Clustering into operational taxonomic units (OTUs) was then performed using UCLUST at the 97 % similarity level, indicative of species level (Edgar 2010). The most abundant sequences were chosen as being representative of a cluster and aligned with the PYNAST method (Caporaso et al. 2010a). The OTU table generated was then rarefied to 2910 sequences per sample, to avoid bias. OTUs present in 1 or 2 samples were removed from the

358 rarefied OTU table (L6) and this table was then transformed by square root and a Bray Curtis resemblance
359 matrix was constructed in PRIMER6 (Primer-E Ltd, Lutton, UK).
360
361 The Bray-Curtis matrix was clustered using hierarchical-clustering with group-average linkage to produce a
362 dendrogram representing the scaled similarity between samples. Nonmetric multidimensional scaling (nMDS)
363 plots were used to provide a visual representation of the similarities between bacterial communities, based on
364 the Bray Curtis similarity index. On the nMDS plots the clustering of data points was highlighted by overlaying
365 ellipses based on the clustering. The significance of bacterial community clustering was quantified using
366 analysis of similarity (ANOSIM) which is an analogue to the standard univariate one-way ANOVA (analysis of
367 variance) designed for ecological data. ANOSIM generates an R statistic that indicates the separation between
368 groups where an R of 1 indicates complete separation and R of 0 indicates there is no separation (Clarke et al.
369 2006).
370
371 To test the variation in the bacterial community explained by each variable PERMANOVA was calculated using
372 the Adonis function in the R package vegan (Oksannen et al. 2013). A matrix of variables (atrazine, soil and
373 incubation time) versus samples was constructed that corresponded to the relative abundance of each OTU in
374 each sample. The test statistic and associated *p* value was calculated using 999 random permutations on the
375 basis of Bray Curtis distances. A *p* value was calculated using the classical F distribution approximation. The
376 significance level to reject the null hypothesis was set a priori to 0.05. Results were visualised using R (version
377 3.2.1) R Core Team, 2015.

378 ***2.14. Principal Component Analysis***

379 To explore the variation between the 9 soils, principal component analysis (PCA) was conducted in PRIMER v6
380 (Clarke et al. 2006), based on different soil properties. A draftsman plot showed the data points were equally
381 spread, therefore multivariate normality was assumed. Each variable was normalised (subtraction of the mean
382 and dividing by the standard deviation) to provide comparable, dimensionless scales for a correlation based
383 PCA. The PCA was composed of five principal components and the eigenvalues, eigenvectors and principal
384 component scores were used to determine the soil properties that best explained the variation between sites.

385 ***2.15. Accession numbers***

386 The 16 S rRNA amplicons have been deposited in the SRA with the accession number; SRP066748
387 (PRJNA304340).
388

389 **3. Results**

390 ***3.1. Soils of different physico-chemical properties exhibited a similar pattern of accelerated degradation.***

391 Eight out of the nine soils untreated by *s*-triazines for at least 5 years and banned since 2003 (EC, 2015)
392 demonstrated accelerated degradation, evident by their faster rate of dissipation following a second application
393 of atrazine (Fig.1).
394
395 Using the European regulatory FOCUS guidance (FOCUS, 2006), data from the first application of atrazine
396 fitted single first order (SFO) kinetics adequately for all soils, with good visual fits and X^2 error values of < 15
397 % (Table 3). After the second and third applications several soils had poor SFO visual fits missing several
398 points, and this was not improved by fitting the data to biphasic kinetics. Initially four soils; CS, CA, GA and
399 GRS, had estimated DT_{50} values of greater than 30 days and the remaining soils had DT_{50} values of greater than
400 19 days. By the second application all soils, apart from GRS, had DT_{50} values of 3 days or less (Table 3). After
401 the third atrazine application all soils apart from GRS had DT_{50} values of less than 2 days (Table 3). The
402 parameters used for the SFO fits are in the Online Resource 10.
403
404 All eight soils exhibiting accelerated degradation showed a 7 – 32 fold reduction in their DT_{50} values from the
405 first to the second application of atrazine, whereas the DT_{50} of GRS was 48.6 days after the third application
406 (Table 3), with the amount of atrazine appearing to accumulate after each application (Fig. 1).
407
408 It is evident that the vast majority of these soils are exhibiting an accelerated rate of atrazine degradation within
409 60 days of applying atrazine. Using a sterile control, it was shown that sterile soil displayed a DT_{50} of 107.7
410 days compared to 20.4 days in a matched non-sterile soil (Online Resource 11). This confirmed in-line with
411 previous studies, that accelerated degradation of atrazine is microbially driven (Zablotowicz et al. 2007).
412 However, the modelling approaches applied above do not take into account the kinetics of microbial growth or
413 microbial adaptation over multiple applications. In fact, the SFO kinetics applied to the first application of
414 atrazine fails to capture the rate of atrazine decay, which clearly begins to accelerate between 28 and 45 days or

45 and 60 days for most soils. This is illustrated in the GRA soil in which time points at 28 days and 60 days deviate significantly from the exponential fit (Fig. 2). Similar poor fits are also observed during the degradation of the first atrazine application in the other soils (Online Resource 12 - 18).

Therefore we addressed this by developing a model that included an initial rate of exponential atrazine degradation and an activity following hyperbolic, Monod-type kinetics, consistent with a microbially mediated biodegradation. This latter activity was dependent on the size of a microbial community, capable of atrazine utilization. This community was modelled to increase exponentially up to a limit, as would be expected for a microbial community *in vivo*. This more sophisticated approach was able to capture the change in atrazine degradation for each of the degrading soils and accounted for the variation in rate of degradation between atrazine additions. For example the GRA data fitted using the microbial-growth model fits the data much better than the individual exponential fits for each atrazine application (Fig. 2). The growth-linked model enabled a single set of parameters to be used to fit all the atrazine degradation kinetics, rather than using separate parameters for each atrazine addition.

Overall, the growth-linked model gave a superior fit for the data from all 8 soils exhibiting accelerated degradation (Fig. 2 and Online Resource 12 - 18). The parameter that varied the most widely was the initial number of atrazine degraders in the community (Online Resource 19), which varied by 3 orders of magnitude (from 0.00005 to 0.03). The other fitted variables had values in the ranges: k_1 from 0.06 – 0.18, Y from 30 – 65 %, μ from 0.155 to 0.225 day^{-1}, V from 0.6 – 0.7, K_s = 75 in all cases. The K_s value of 75 is a percentage of the initial applied atrazine concentration (6 $\mu g.L^{-1}$), i.e K_s = 20.9 μM. This result from modelling is remarkable given the atrazine degrading enzyme TrzN has been measured to have K_m = 20 μM (Shapir et al. 2005) and 25 μM (Topp et al. 2000).

3.2. The atrazine degrading genes were detectable in soils exhibiting accelerated degradation

To determine if the soils exhibiting accelerated degradation carried the atrazine degrading genes and the extent to which the repertoire of genes varied between soils, DNA from 3, 14 and 28 days after each application of atrazine was tested. All soils that exhibited accelerated degradation contained at least *trzN* while none of the atrazine degrading genes were detectable in GRS (Table 4) which did not exhibit accelerated degradation (Fig. 1).

444 The presence of the atrazine degrading genes (Online Resource 1) was determined for all nine soils. Soil MS
445 exhibited accelerated degradation (Fig. 1), but only *trzN* could be detected (Table 4) and was characterised by its
446 high clay content of 22 % and a low C:N ratio of 9.6 (Table 1).
447
448 In five of the soils that exhibited accelerated degradation (GA_2012, MA, CA, CS and GRA) three atrazine
449 degrading genes were detected (Table 4). All these soils had a pH of greater than 6.3 (Table 1). *AtzA* and *atzB*
450 were detected in six of the eight soils showing accelerated degradation (Table 4), while *atzC* was only detected
451 in GA. The gene *trzD* of the lower atrazine degrading pathway, which is more tightly regulated and less
452 commonly identified (Udikovic-Kolic et al. 2012), was only detected in GA_2012 and GS_2012 (Table 4). It is
453 also notable that resampling of the GA_2012 soil in 2013 (GA) led to a different repertoire of atrazine degrading
454 genes being detectable, with the detection of *atzA* and *atzC* which were below the limit of detection in 2012,
455 while *trzD* was below the limit of detection in 2013. All of the atrazine degrading genes detected had sequences
456 which were 100 % identical to those characterised previously (Online Resource 20).
457 ***3.3. Atrazine treatment does not have a gross impact on the overall microbial community***

458 To determine whether the increase in atrazine degradation was due to an overall increase in microbial activity in
459 soils, soil ATP content was measured following repeated applications of atrazine. There was no significant
460 change in ATP concentration in soils over time (Online Resource 21) indicating that a significant increase in the
461 microbial community is unlikely to explain the increased degradation of atrazine, and that a more likely reason
462 would be proliferation of specific microorganisms containing the atrazine degrading genes.
463
464 It is clear that there is a significantly greater proportion of the bacterial community containing *trzN* after the
465 second and third application of atrazine in the agricultural soil, and after the second application in the set aside
466 soil ($p < 0.05$) (Fig. 3). It is also evident that only a small proportion (< 0.5 %) of the bacterial community
467 contained *trzN*.
468
469 Non-metric multidimensional scaling was conducted using ANOSIM to observe clustering of soil samples
470 according to various variables (Fig. 4). The low abundance of *trzN* relative to the overall number of bacteria
471 present is consistent with the absence of significant clustering between samples based on atrazine treatment
472 (ANOSIM; R: 0.08, p: 0.25). This is also consistent with analysis by PERMANOVA showing that the variation

473 in the bacterial communities was most affiliated with their duration of incubation ($R^2 = 0.23$, p 0.0001) and soil
474 type ($R^2 = 0.17$, p 0.0002) rather than atrazine treatment ($R^2 = 0.08$, p 0.09).

475 ***3.4 GRS was most strongly associated with pH***

476 Atrazine was found to be at least 19 times more persistent in GRS compared to any other soil, following the
477 second and third application of atrazine (Table 3). The soil properties that distinguished this soil from the others
478 that exhibited accelerated degradation were investigated. The 9 soils used in this study had been naïve to *s*-
479 triazines for 5 or more years (Online Resource 3) and the DT_{50} values in the set aside soils, that had not had
480 pesticides applied were very similar to those seen in the agricultural soils (Table 3). Therefore it was unlikely
481 that exposure to pesticides other than *s*-triazines affected accelerated degradation.
482
483 PCA was used to determine the soil physical and chemical properties (Table 1) that explained the variation
484 between soils and those most correlated with the GRS soil, which may have affected its ability to mediate
485 accelerated degradation.
486
487 It is clear that the 7 soils are scattered and do not cluster dependent on the farm they originated from or whether
488 they were collected from set aside or agricultural sites (Fig. 5). PC1 explained 68 % of the variation and PC2, 20
489 %, with most of the remainder explained by PC3 (8.4 %), together explaining 96.3 % of the variation in soil
490 properties (Online Resource 22). It can be inferred that PC1 is roughly an equal weighted combination of most
491 of the soil properties including texture (sand, silt and clay), nutrients (Organic Carbon and Total Nitrogen) and
492 moisture parameters (moisture content (MC) and maximum water holding capacity (MWHC)) with the greatest
493 contribution from sand and organic carbon contents (Online Resource 23).
494
495 PC2 is mainly explained by pH, although there is some contribution from carbon to nitrogen ratio (C:N) and
496 moisture content too, while PC3 is mainly explained by C:N ratio (Online Resource 23). Based on the principal
497 component scores, it was clear that the variation between the agricultural soils; CA, GA and MA were mainly
498 dependent on PC1 (Online Resource 24). Specifically, CA had the highest sand content, while GA and MA had
499 the lowest and highest organic carbon contents, respectively (Table 1). GRA was an outlier from the other soils
500 mainly affiliated with PC3 (Online Resource 24) and explained by having the highest C:N ratio (Table 1),
501 whereas MS and GRS were strongly affiliated with PC2, due to them having the highest and lowest pH
502 respectively.

3.5. Soil pH affected the capacity of the soils to mediate accelerated degradation of atrazine

The GRS soil was the only one not to exhibit accelerated degradation, and was notably the soil with the lowest pH. To determine whether the lack of accelerated degradation was linked to the low pH, and whether the genetic potential for atrazine degradation is retained in this low pH soil, the pH of the GR soils was experimentally altered. GRA which had a pH of 6.2 and had exhibited accelerated degradation (Fig. 1) was acidified and maintained at ~ pH 4 to suppress accelerated degradation, while GRS which had a pH of 5.4 and did not exhibit accelerated degradation (Fig. 1) was neutralised and maintained at ~ pH 7, to determine whether accelerated degradation could be induced.

After the second application of atrazine, the concentration of atrazine was below the limit of detection at day 14 and day 28 in GRSa and at day 28 in GRA, showing how rapid accelerated degradation of atrazine had occurred in the amended GRS sample. Accelerated degradation was only observed in GRSa and GRA (Fig. 6) which both had a pH greater than pH 6.2. The DT_{50} values of these soils were less than 1.6 days after the second application of atrazine although the soils with pH < 5.4.; GRS and GRAa, exhibited DT_{50} values that were longer than 21 days (Table 3), indicating that atrazine will be more persistent in these soils. In addition to its low pH GRS is also affiliated with high contents of clay, moisture and organic carbon (Table 1).

Sorption was shown to increase with atrazine concentration (Online Resource 25) and was slightly higher in the acidic soils GRAa and GRS than the neutral soils GRA and GRSa but these differences were small, and insufficient to explain the >7 fold difference in atrazine dissipation rates between these treatments (Table 3 and Fig. 6).

To see if the change in soil pH modified detection of the atrazine degrading genes in the treated soil PCRs of the atrazine chlorohydrolase genes; *atzA* and *trzN* were conducted. Neither *atzA* nor *trzN* could be detected after multiple applications of atrazine in the acidic soils GRS and GRAa. Contrastingly, both *atzA* and *trzN* were detectable in soils at pH > 6.2 (GRA and GRSa) after 2 applications of atrazine, indicating that the genes are present in both GRA and GRS, but only proliferate to become detectable at near neutral pH.

4. Discussion

4.1. Accelerated degradation manifested in soils with no history of s-triazine use after one application

Eight soils transitioned to an accelerated rate of dissipation within 60 days (Fig. 1) demonstrating that most soils tested had the capacity for the accelerated degradation of atrazine. The soils had no *s*-triazine history documented and atrazine has been banned since 2003 (EC 2015). Previous studies have shown that accelerated degradation was evident in soils that had received two annual applications of atrazine in the field and the rates of mineralisation in these soils were much lower (Zablotowicz et al. 2007; Houot et al. 2000), compared to the very rapid rate of atrazine degradation seen in this study, which could be explained by the shorter interval between applications. In addition most previous studies that have demonstrated accelerated degradation have used soils with long histories of atrazine applications (Zablotowicz et al. 2007). Although spray drift of simazine, which has been applied more widely in the UK (D. Garthwaite: pesticide usage survey; personal communication), cannot be ruled out as a source of low level *s*-triazine availability stimulating these soils, this does not detract from the finding that accelerated degradation of atrazine occurs in soils that have no recorded history of deliberate *s*-triazine application. Such high potential for the accelerated degradation of atrazine could mean that soils with history of *s*-triazine use over 4 years ago may be ineffective, although this will need to be investigated in a field and the extent to which this applies to other pesticides explored. Additionally Orlikowska et al. (2015) detected atrazine in marine waters which they presumed to have reached the sea by run off from agricultural land. An interesting extension to this project would be to investigate the movement of atrazine residues and potentially atrazine degrading organisms, via artificial drainage or run-off.

4.2. Accelerated degradation was associated with the atrazine degrading genes

To examine the microbial changes linked to accelerated degradation, general activity, microbial community structure and the capacity for degradation were monitored. No increase in general biological activity was linked to accelerated degradation (Online Resource 21) in agreement with other studies De Andrea et al. (2013) saw no correlation between dehydrogenase activity and glyphosate mineralisation, whilst Udikovic-Kolic et al. (2011) demonstrated major shifts in microbial communities treated with atrazine. In this study we found there was no significant change in the microbial community in response to atrazine treatment (Fig. 4). This probably relates to the levels of atrazine employed. In the current study, atrazine was used at the recommended agricultural level, whereas the previous analysis concerned a highly contaminated pesticide site (Udikovic-Kolic et al. 2011).

560 Accelerated degradation was associated with detection of the atrazine degrading genes of the hydrolytic
561 pathway, which were detected upon the increased rate of dissipation of atrazine. There is an alternative atrazine
562 degrading pathway; the oxidative-hydrolytic pathway for atrazine dissipation which degrades atrazine via the
563 production of deethylatrazine (DEA) and deisopropylatrazine (DIA) (Giardina et al. 1982). However the
564 oxidative-hydrolytic pathway has mainly been associated with non-adapted soils that have a slow rate of
565 degradation (Fournier et al. 1997). In addition hydroxyatrazine has been shown to be the dominant metabolite in
566 atrazine adapted soils (Krutz et al. 2010) and in atrazine-mineralising cultures (Yanze-Kontchou and Gschwind
567 1994; Mandelbaum et al. 1995; De Souza et al. 1998). PCR was used in an attempt to identify the *thcBCD* genes
568 involved in the oxidative-hydrolytic pathway (Shao and Behki 1996), but were not detected in this study.
569

570 ***4.3. Accelerated degradation of atrazine was associated with a small portion of the microbial community***

571 The repertoire of atrazine degrading genes was variable between soils, and was shown to vary after one year
572 between subsequent samples of the GA soil, possibly due to changes in the exact location the soil was removed
573 (Bending et al. 2001). The high degree of variability in apparent gene content between soils (Table 4), yet the
574 similar atrazine degradation rate following adaptation (Fig. 1), suggests that limitations in the method may also
575 have been an issue. This is also reflected in the relatively low percentage of the microbial community composed
576 of atrazine degraders (estimated to be 0.5 %), (Fig. 3). However the low proportion of atrazine degraders may
577 also have been affected by the low concentration of atrazine available for them to degrade. As Baelum et al.
578 (2006) saw that microbial growth was more pronounced when the bacterial community was supplied with high
579 pesticide concentrations compared to low concentrations. However Udikovic-Kolic et al. (2010) found that only
580 1 - 4 % of their atrazine community contained the atrazine degrading genes, even when the atrazine
581 concentrations were 100 x greater than applied in this study and Sneigowski et al. (2012) showed that only 0.5
582 % v/v of a pesticide degradation inoculum was required for maximum pesticide degradation.
583

584 ***4.4. A new microbial growth linked model enables accelerated degradation to be considered in environmental***
585 ***risk assessments***

586 To enable accelerated degradation to be considered in the risk assessment we modelled our data in-line with the
587 current regulatory approach for modelling pesticide dissipation to a microbial based approach. Fitting the
588 disappearance of atrazine using the standard FOCUS Guidance (FOCUS 2006) used in EU pesticide regulation,

showed a drastic reduction in DT_{50} between the first and second application of atrazine (Table 3). However, SFO kinetics that are the preferred option to derive regulatory degradation endpoints, failed to capture the change in atrazine concentration during the incubation with the first application of atrazine (Fig. 2, Online Resource 12 - 18). To remedy this, we generated a model that took into account the exponential growth of atrazine degraders. This microbial growth model gave better fits to all data sets with much tighter residuals (Fig. 2, Online Resource 12 - 18) than existing accepted methods, which do not consider microbial growth and adaptation between applications as only one application is modelled at a time. Models that build in growth of bacteria during an adaptation phase may have widespread applicability in studies of adaptation to pesticides, but also other microbially catalysed processes in natural and agricultural environments, such as monitoring the numbers of degraders involved in bioremediation (Fuetes et al. 2016).

The parameters obtained from these fits indicated that a key variable between soils is the initial number of atrazine degraders prior to atrazine addition. This varied by up to 3 orders of magnitude between the soils (Online Resource 19), but the final rates of atrazine degradation after adaptation were remarkably stable. It is worth noting that the highest initial numbers of atrazine degrading organisms used to fit the data were over 3000 times less than after adaptation, which may help explain why atrazine degrading genes were initially undetectable in this study.

4.5. The repertoire of the atrazine degrading genes differed between the soils exhibiting accelerated degradation

The final objective of this study was to examine the impact of soil properties on atrazine degradation and its genetic potential. It was shown that all soils that exhibited accelerated degradation contained *trzN*. TrzN has been identified as being more prevalent than the alternative atrazine chlorohyrolase; AtzA (Arbeli and Fuetes 2010) attributed to its catalytic superiority and wider substrate against a range of triazine herbicides (Shapir et al. 2007; Shapir et al. 2005). In addition *atzA* and *atzB* were detected in six of the eight soils showing accelerated degradation. AtzB enables nitrogen to be obtained from atrazine (Seffernick et al. 2007). Although AtzA is a homologue of TrzN and having both enzymes is not required to degrade atrazine, it has been suggested that communities with both may be more tolerant to new environmental conditions (Udikovic-Kolic et al. 2012). *AtzC* could only be detected in GA, which provides isopropylamine released from the s-triazine ring

618 which can be used as carbon, nitrogen and/or energy sources for bacterial growth (Strong et al. 2002). In
619 agreement with other studies few genes of the lower atrazine degrading pathway were detected (Udikovic-Kolic,
620 et al. 2012) possibly due to atrazine not being the primary substrate for bacteria in most soils that are not
621 contaminated with high concentrations of atrazine or alternatively that other unidentified pathways can catalyse
622 these metabolic reactions.

623 The atrazine degrading genes have been identified to be highly conserved in pure cultures and the environment
624 (De Souza et al. 1998a; Sagarkar et al. 2013) and were identical in this study to those identified previously (De
625 Souza et al. 1998a; Sagarkar et al. 2013; Mulbry et al. 2002).
626

627 ***4.6. The capacity for accelerated degradation in an acidic soil was restored upon neutralisation***
628 GRS was the only soil not to exhibit accelerated degradation. Instead, atrazine accumulated after each
629 application and the atrazine degrading genes were not detected in this soil. This soil had the highest carbon
630 content, which has previously been associated with reducing atrazine mineralisation by providing an alternative
631 carbon source to atrazine and / or increasing sorption (Popov et al. 2005; Ngigi et al. 2013). Although the carbon
632 content may have contributed to the accelerated degradation of GRS the PCA analysis showed that a low pH
633 was the defining feature of GRS (Figure 5). A low pH (<6) has previously been associated with inhibiting
634 accelerated degradation of atrazine (Houot et al. 2000; Mueller et al. 2010) and a similar observation was made
635 by Singh et al. (2003) who saw for the insecticide Chloropyrifos that upon transfer of a pesticide degrader to an
636 acidic soil the identified degrader was no longer detectable. Here we showed that the biological potential for
637 atrazine degradation was present in low pH, non-degrading soils (GRS) and was expressed following
638 amendment of these soils to neutral conditions, which allowed recovery of accelerated degradation, an activity
639 that was correlated with the detection of known atrazine degrading genes. This is the first study to demonstrate
640 that the low pH soils retain the genetic potential for atrazine biodegradation. The vast majority of European
641 agricultural soils have a soil pH of 5-7, therefore the abundance of the atz/trz genes could mean a broad range of
642 soils have the potential for accelerated degradation.
643

644 **Conclusions**
645 The accelerated degradation of atrazine occurred in soils that had not been treated with the pesticide or its
646 homologues, at agriculturally relevant levels, and was related to the detection of the atrazine degrading genes.

The atrazine degrading genes were found in all of the soils tested, but were shown to vary dependent on soil properties, demonstrating that the ability to degrade a pesticide is widespread and can be retained for many years. We suggest that accelerated degradation should be explicitly considered in the risk assessment process to gain a more realistic view of pesticide efficacy and fate.

Acknowledgements

FERA for funding this FERA seedcorn project, the landowners for their cooperation, Gareth Bryning for support in developing the analytical chemistry techniques, Toby Stamper for support with bioinformatics and Ummey Hany for help with pyrosequencing.

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Figures

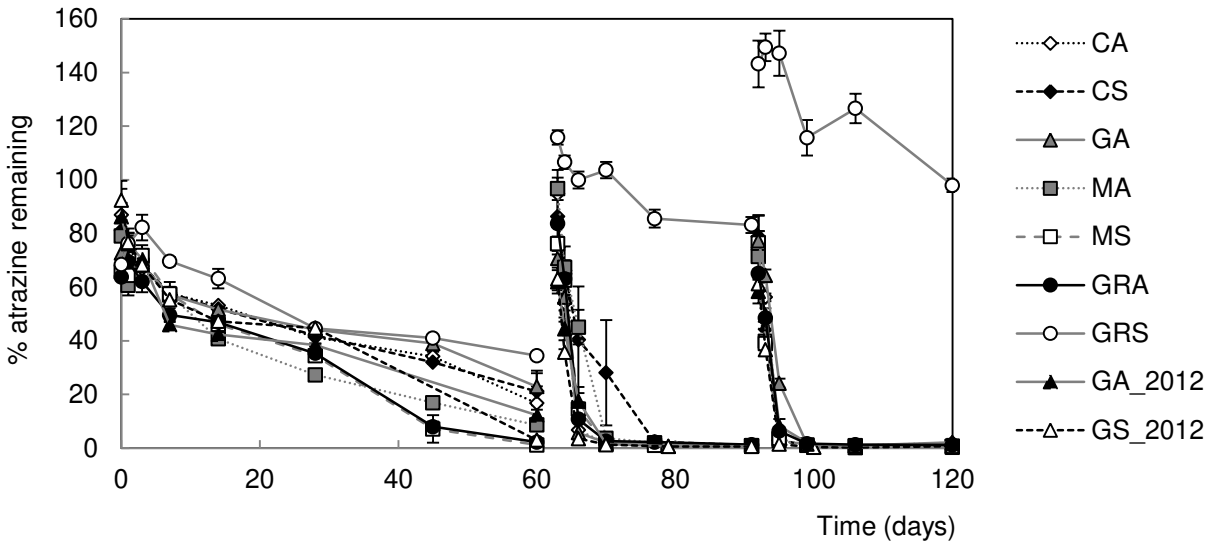

Fig. 1: Dissipation of atrazine over three applications to nine temperate soils. Atrazine concentration in soil subsamples was monitored at regular intervals by HPLC-UV. Error bars show the standard error between replicates, n = 12 for GA_2012 & GS_2012 applications 1 and 2, n = 6 for application 3, n = 4 for all other soils. Soil identifier; CA: Cotril agricultural CS: Cotril set aside, GA: Ganthorpe agricultural MA: Mount agricultural, MS: Mount set aside, GRA: Grange agricultural, GRS: Grange set aside, GA_2012: Ganthorpe agricultural collected in 2012 and GS_2012: Ganthorpe set aside collected in 2012

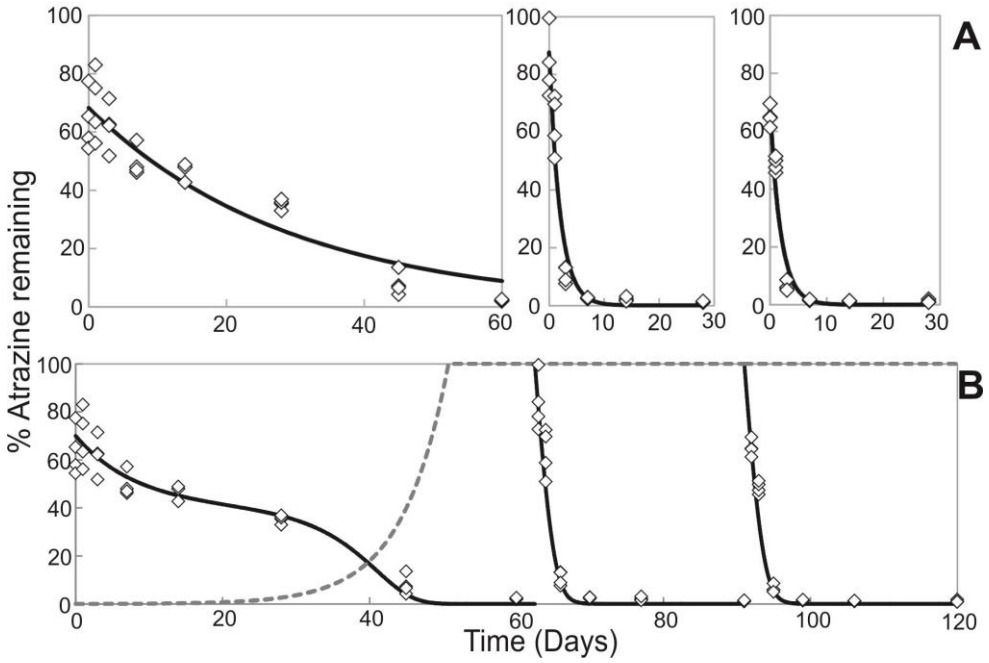

Fig. 2: Comparison of modelling approaches for the dissipation of atrazine in GRA over three applications. Using the regulatory single first order (SFO) approach (A), with each application modelled separately and the 'growth-linked model' described in this study (B). The growth-linked model enabled all applications to be modelled simultaneously. In both modelling approaches the model fit of % atrazine remaining is shown as a solid black line and individual soil sub-samples as diamonds (n = 4). For the growth-linked model (B) the grey dashed line represents the number of atrazine degraders

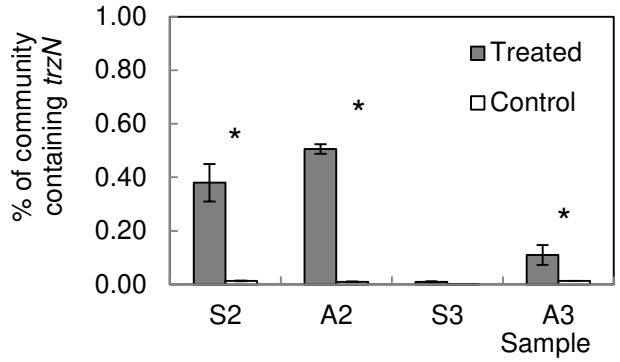

Fig. 3: Percentage of the bacterial community that contain the atrazine degrading gene *trzN* in the GA_2012 and GS_2012 soils. The *trzN* gene was monitored in the Ganthorpe agricultural soil; GA_2012 (A) and Ganthorpe set aside soil; GS_2012 (S) soils fourteen days after the second (2) or third application (3) of atrazine to each soil. *TrzN* was measured in atrazine treated and control sub-samples. The proportions of the community carrying *trzN* was normalised against the *16S rRNA* gene for each sample. Error bars show the standard error between experimental replicates, n = 6. The significant differences between the proportion of the community containing *trzN* between treated and control soils are indicated by * ($p < 0.05$)

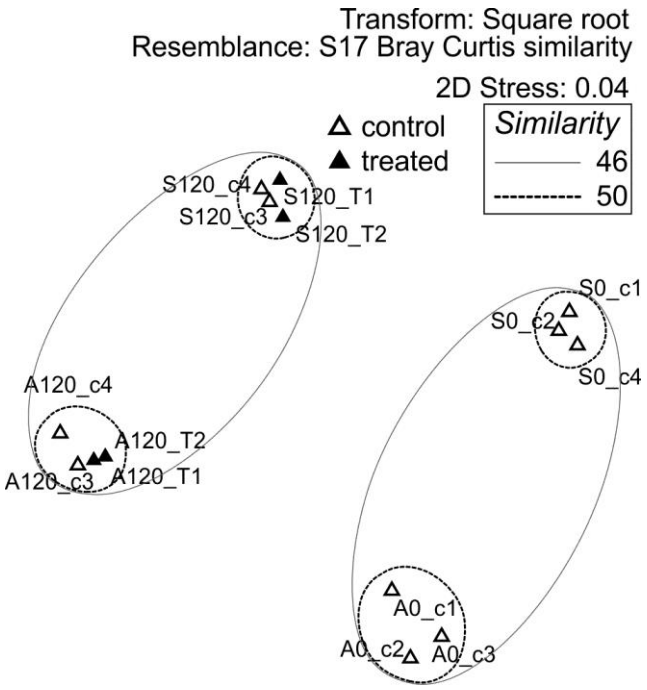

Fig. 4: Non-metric multidimensional scaling plot of the association of bacterial communities with atrazine treatment in the GA_2012 and GS_2012 soils. Each bacterial community is represented by a triangle, originating from the Ganthorpe agricultural soil; GA_2012 (A) and Ganthorpe set aside soil; GS_2012 (S). The bacterial communities are based on OTU clustering of the pyrosequencing of *16S rRNA* genes. The variables included in the analysis were soil history: set aside (S) or agricultural (A), duration in days under incubation conditions (0 or 120 days) and atrazine treatment: treated (T) or control (C). The similarity ellipses are based on hierarchical clustering shown in the Online Resource 26

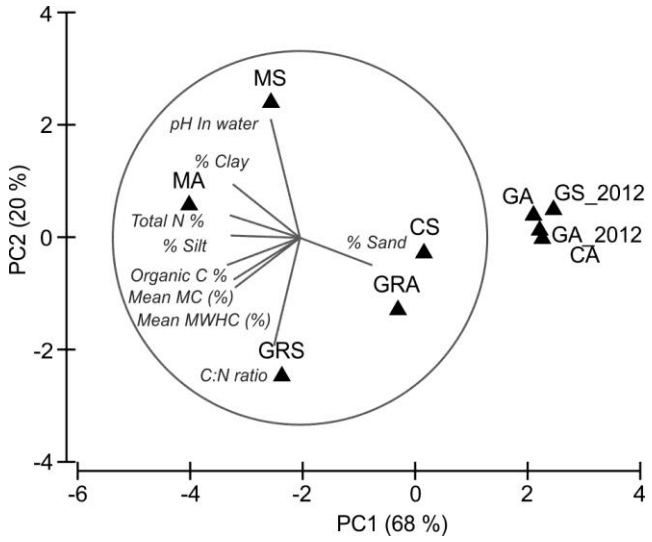

Fig. 5: Principal Component Analysis (PCA) of the association of nine temperate soils with various physio-chemical properties. Measured soil properties were normalised and the corresponding data matrix was subject to PCA. Each triangle represents an individual soil. The association between different soils is plotted along the first two principal components, which represent 68 % and 20 % of the variation between the soils. Soil properties; MWHC; maximum water holding capacity, MC; moisture content, C:N ratio; carbon : nitrogen ratio and total N; total nitrogen. Soil identifier; CA: Cotril agricultural CS: Cotril set aside, GA: Ganthorpe agricultural MA: Mount agricultural, MS: Mount set aside, GRA: Grange agricultural, GRS: Grange set aside, GA_2012: Ganthorpe agricultural collected in 2012 and GS_2012: Ganthorpe set aside collected in 2012

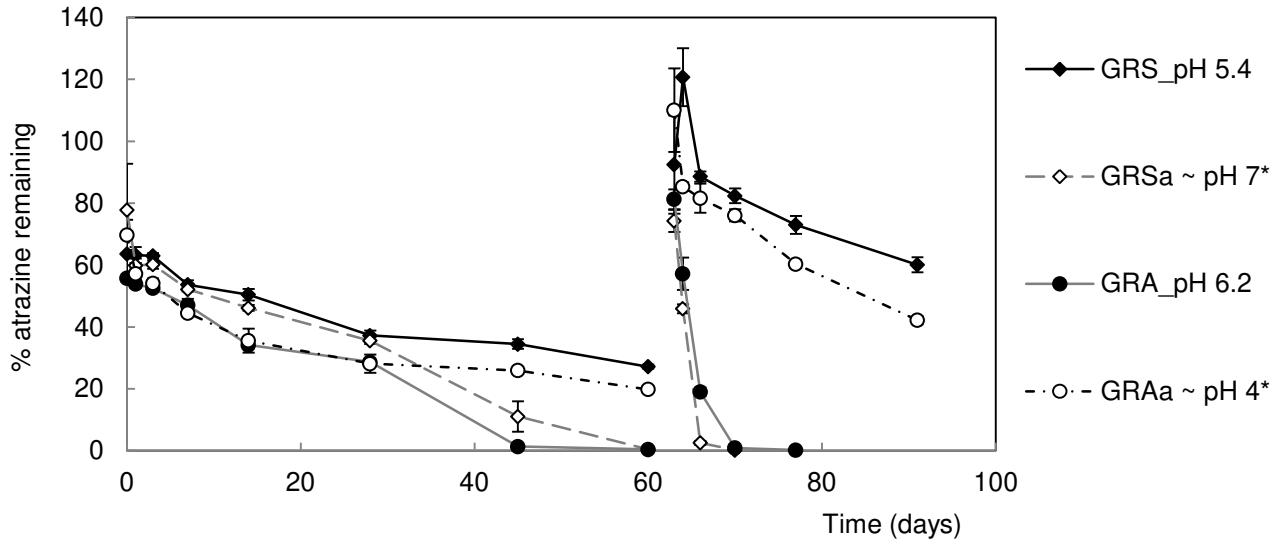

Fig. 6: Effect of soil pH on atrazine dissipation over two applications in the GRA_pH and GRS_pH soils. Atrazine was applied to the Grange set aside soil (GRS_pH) and Grange agricultural soil (GRA_pH) which were collected in 2014 and their pH was amended (-a) to approximately pH 7 (GRSa) and pH 4 (GRAa), respectively. Error bars represent the standard error between replicates (n = 4). Parameters used for the SFO model fits are provided in the Online Resource 10, * shows that the pH of the amended soils (GRSa and GRAa) are only approximate as there was minor variation in their soil pH throughout the experiment (Online Resource 4)

Tables

Table 1. Identification and properties of the soils used in this study.

Soil#	*Farm*	*Year collected*	*Soil history*[$]	*Textural class (USDA)*	*Sand (%)*	*Silt (%)*	*Clay (%)*	*Total N (%)*	*OC (%)*	*C:N ratio*	*pH (In H_2O)*	*Moisture content (g water)*^
GA_2012*	Ganthorpe	2012	A	SL	79	12	9	0.14	1.4	10	6.39	0.12
GS_2012*			S	SL	81	8	11	0.14	1.4	10	6.26	0.07
GA	Ganthorpe		A	SL	79	10	11	0.11	1.2	10.9	6.55	0.15
CS	Cotril		S	SL	77	12	11	0.19	1.9	10	6.32	0.22
CA	Cotril		A	LS	83	8	9	0.12	1.3	10.8	6.64	0.16
MS	Mount	2013	S	SCL	54	24	22	0.23	2.2	9.6	8.14	0.22
MA	Mount		A	SCL	51	24	25	0.24	2.8	11.7	7.43	0.25
GRS	Grange		S	SL	65	20	15	0.21	2.7	12.9	5.43	0.29
GRA	Grange		A	SL	67	22	11	0.14	1.9	13.6	6.53	0.20
GRA_pH**	Grange	2014	A	SL	62	24	14	0.16	1.4	8.8	6.23	0.18
GRS_pH**	Grange		S	SCL	55	26	19	0.33	3.7	11.2	5.39	0.23

Atrazine degradation and the presence of the atrazine degrading genes was monitored in all soils

*soils used to monitor microbial community changes (ATP, Q-PCR and Pyrosequencing)

**soils used to monitor the effect of pH on accelerated degradation

[$]S; set aside soil, A; agricultural soil

^ per g of dry soil (105 °C)

Table 2. Primers used for amplification of the atrazine degrading genes in PCR and Q-PCR. The hydrolytic enzymes that are encoded by each gene are; AtzA/TrzN: atrazine chlorohydrolase; AtzB: hydroxyatrazine hydrolase; AtzC: N-isopropylammelide hydrolase; AtzD/TrzD: cyanuric acid hydrolase; AtzE: biuret hydrolase and AtzF: Allophanate hydrolase.

Gene	*Amplicon Length (bp)*	*Primer name*	*Primer sequence*	*Annealing Temp. (°c)*	*Reference*
atzA	500	atzA_F	CCATGTGAACCAGATCCT	55.7	De Souza et al. 1998
		atzA_R	TGAAGCGTCCACATTACC		
trzN	400	Trz_Nf, C190-10	CACCAGCACCTGTACGAAGG	59	Mulbry et al. 2002
		Trz_Nr, C190-11	GATTCGAACCATTCCAAACG		
atzB	500	atzB_F	TCACCGGGGATGTCGCGGGC	62.4	De Souza et al. 1998
		atzB_R	CTCTCCCGCATGGCATCGGG		
atzC	600	atzC_F	GCTCACATGCAGGTACTCCA	62.4	De Souza et al. 1998
		atzC_R	GTACCATATCACCGTTTGCCA		
atzD	202	atzD_F	TCCCACCTGACATCACAAAC	62.4	Devers et al. 2004
		atzD_R	GGGTCTCGAGGTTTGATTG		
trzD	663	TrzD_F	CACTGCACCATCTTCACC	55	Fruchey et al. 2003
		TrzD_R	GTTACGAAC CTCACCGTC		
atzE	203	atzE_F	GAGCCTCTGTCCGTAGATCG	60	Devers et al. 2004

		atzE_R	GATGGCGTGTACCGTTTACC		
atzF	233	atzF_F	ACCAGCCCTTGAATCATCAG	57	Devers et al. 2004
		atzF_R	TATTGTCCCGATACCCAACG		
16_Q rRNA	161	16S_qPCR_F	TGGAGCATGTGGTTTAATTCGA	-	Yang et al. 2002
		16S_qPCR_R	TGCGGGACTTAACCCAACA		
TrzN_Q	70	TrzN_Q_F	GCTTCTGCGACGACCTGTTC	-	In this study
		TrzN_Q_R	TGGTCGATGAGACCCAG		

Table 3. Estimated time for 50% of atrazine to degrade in days (DT_{50}) and corresponding Chi squared value (χ^2) for single first order (SFO) fits for atrazine dissipation in soils that received two or three successive applications of atrazine. Refer to Table 1 for soil origin.

	First application		*Second application*		*Third application*	
Soil	DT_{50}	X_2	DT_{50}	X_2	DT_{50}	X_2
GS_2012	21.49	10.26	1.76	9.16	1.53	22.24
GA_2012	20.18	11.85	1.08	6. 73	1.01	16.37
CS	32.34	5.72	2.93	12.42	0.98	12.8
CA	30.23	8.2	1.03	10.08	1.3	26.9
MS	19.81	11.09	1.59	17.15	0.91	8.8
MA	19.58	7.84	2.72	5.57	0.97	12.13
GRS	48.14	6.58	57.88	5.66	48.62	5.06
GRA	20.38	10.39	1.39	16.73	1.32	18.61
GA	37.1	10.94	1.13	15.04	1.89	12.26
GRS_pH*	46.08	3.81	32.61	9.45	-	-
GRSa**	18.25	9.78	1.05	13.94	-	-
GRA_pH*	18.04	11.77	1.54	6.64	-	-
GRAa**	30.02	10.83	21.29	7.36	-	-

*soils collect from Grange farm in 2014 for the pH experiment

**GRSa and GRAa soils originated from GRA_pH and GRS_pH after their pH was amended

Table 4. Summary of the atrazine degrading genes detected in nine temperate soils, 14 days after the third application of atrazine. Refer to Table 1 for soil origin. Refer to Table 2 for a description of the hydrolytic enzymes that are encoded by each gene.

Soil	*Number of genes detected* *	*atzA (100 %)*	*trzN (100 %)*	*atzB (100 %)*	*atzC (100 %)*	*atzD*	*trzD (100 %)*	*atzE*	*atzF*
GA_2012	3		+	+			+		
GS_2012	4	+	+	+			+		
CS	3	+	+	+					
CA	3	+	+	+					
MS	1		+						
MA	3	+	+	+					
GRS	0								
GRA	3	+	+	+					
GA	4	+	+	+	+				

*The closest relative for each of the atrazine degrading genes detected are shown in online resource 20