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Executive Summary

IWMPRAISE is not being used to develop new simulation models of the dynamics of weeds either within a single species or across communities but, rather, is using established and well-validated models to predict the long term behaviour of contrasting cropping systems trialled in the field experiments. However, some work needed to be done to adapt and optimise the models for European cropping systems particularly where they had been developed to model different environments. In the case of the model of herbicide resistance evolution, the functions had been parameterised for weeds and cropping systems in Australia and the USA. In the proposal, we said we would optimise the model for European environments focussing on four grass weed species for which there is a specific risk of resistance evolving: *Alopecurus myosuroides*, *Echinocloa crus-galli*, *Apera spica-venti* and *Lolium sp.*

Within the lifetime of the project, we will parameterise the model for all four species but an initial assessment of the species lists from the field trials completed in 2018 revealed that *A.myosuroides* and *E. crus-galli* were the most frequently observed weeds in narrow and wider row crops respectively. As the resistance model has previously been optimised for *E. crus-galli*, efforts in the first 12 months were focussed on *A. myosuroides.* The model was successfully modified to simulate the genetics of *A. myosuroides* and initial runs completed for a business as usual scenario. The data necessary for running the model using case study experiments where *A. myosuroides* was observed are currently being compiled to allow predictions of the relative risk of resistance evolving in the contrasting weed management treatments.

Abbreviations

D   Deliverable

EC   European Commission

WP   Work Package

WT   Work Task

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1 Modified simulation models for evolution of herbicide resistance in EU cropping systems

1.1 Model overview

Neve and colleagues have previously developed a generic modelling framework for simulating the evolution of resistance to herbicides in weed populations. These models have been parameterised for *Lolium rigidum* in Australian wheat production systems (Diggle et al., 2003; Neve et al., 2003 a,b), *Amaranthus spp.* in USA cotton, corn and soybean systems (Neve et al., 2011 a,b) and *Echinochloa crus-galli* in USA rice production systems (Bagavathiannan et al., 2013). These models have been implemented in the STELLA (isee systems, version 10) programming language. Here, the objective was to implement a version of this modelling framework to explore risks of herbicide resistance evolution in agroecosystems in EU countries participating in the IWMPRAISE project.

Recognising that the grass weed, *Alopecurus myosuroides* (blackgrass) is a major, herbicide resistance prone species that is established or emerging as a major weed in five participating countries (UK, FR, DK, IT, NL), the default iteration of this model is based on the annual life cycle and associated parameter estimates for this weed. However, the model is structured in such a way that it can be easily adapted for major annual grass weeds in other countries, should the need arise (note that a previous version has been developed for *Lolium rigidum*, a major resistance prone weed in IT and ES).

The generic, demo-genetic modelling framework is based on a simple annual weed life cycle were plants can exist as seeds (including as a persistent seed bank), seedling, vegetative and reproductive adult plants (life history states). Transitions between states are governed by a series of sub-models, or in simple cases by transition probabilities. For example, the transition from seed to seedling depends on seed depth in the soil profile and simple sub-models that determine the timing of weed germination, giving rise to discrete emergence cohorts. Seedlings transition to adult vegetative plants according to weed control practices (with different cohorts being exposed to different management or being differentially impacted by that management), and density-dependent mortality. Surviving adult plants transition to reproductive maturity, and seed set per surviving plant is determined by density- and size- (cohort) dependent fecundity. Newly produced seeds are dispersed to the soil surface, where they may be predated or may become incorporated into the seed bank through soil tillage practices. Seeds in the seed bank persist according to parameters that describe the probability of seed survival from year to year.

Crucially, the models also incorporate parameters that describe the genetics and inheritance of herbicide resistance traits and the breeding system of the focal weed species. In this implementation of the model, the potential to simulate the simultaneous evolution of resistance to two herbicide modes of action (user-defined) was included, under the simplifying assumption of single gene, Mendelian inheritance and two alleles (resistant and susceptible). The models include parameters that describe the initial frequency of resistance, de novo mutation rates, dominance and inheritance of resistance traits. As such, for each resistance trait, we simulate and track the frequency of SS, RS and RR genotypes through populations accounting for differential impacts of weed management strategies on survival and life state transitions (most notably, the differential survival of RS and RR genotypes following herbicide treatment). Additionally, it is possible to assign different parameters for different genotypes for germination and fecundity, etc. to account for fitness costs of resistance. However, in most cases, the conservative assumption of no costs is made.

Several model parameters are stochastic (Table 1) to account for population and year by environment differences in life history and genetic parameters. As such, for any cropping scenario in which the evolution of resistance is simulated, a Monte Carlo type analysis with multiple model runs is undertaken. Results are presented as the risk of a weed population evolving resistance over the course of the simulation (Probability of resistance at year *x*, based on *y* [usually thousands] model

runs), or as the risk of a population exceeding a pre-defined seed bank density or population size of surviving adult plants.

Table 1. Example parameter estimates for blackgrass iteration of the herbicide resistance model. Note that other parameters are determined by crop grown and weed management strategy. All parameters can be modified to reflect other weed species and/or cropping system characteristics.

| PARAMETER	ESTIMATE (*mean, distribution, standard deviation*)
Field size	15ha
Initial seed bank density (per m^2)	500, lognormal, 500
Annual germination proportion	0.2, normal, 0.075
Annual seed bank mortality (top 5cm)	0.5, normal, 0.075
Annual seed bank mortality (sub 5cm)	0.7, normal, 0.075
Viability of new seed	0.55
Seed losses from surface	0.5, normal, 0.05
Seeds produced per seed head	100, normal, 12.5
Initial frequency of resistance, A	1×10^{-7}
Mutation rate, resistance A	1×10^{-8}
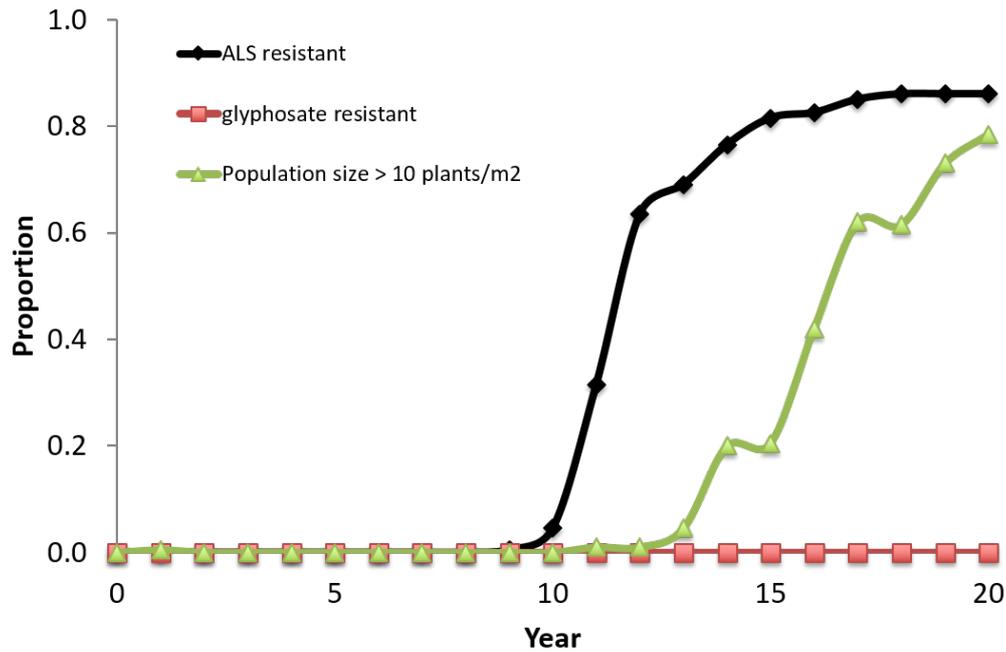
Figure 1. Example model output from a 'business-as-usual' winter wheat: winter wheat: oilseed rape crop rotation in the UK with use of an ALS herbicide for post-emergence weed control in wheat, an alternative mode of action in oilseed rape (resistance not simulated) and annual use of glyphosate for pre-sowing weed control. After 12 years (= 8 ALS applications), ALS resistance is predicted in <60% of blackgrass populations. Density of surviving weeds at harvest exceeds 10m^{-2} in circa 20% of model runs at year 15 of the simulation. Glyphosate resistance does not evolve.

References

1. Bagavathiannan MV, Norsworthy JK, Smith KL, **Neve** P (2013). Modelling the evolution of glyphosate resistance in barnyardgrass (*Echinochloa crus-galli*) in cotton-based production systems of the midsouthern United States. *Weed Technology* **27(3)**: 475-487.

2. Diggle AJ, **Neve P**, Smith FP (2003) Herbicides used in combination can reduce the probability of herbicide resistance. *Weed Research* **43** 371-382.

3. **Neve P**, Smith K, Norsworthy J, Zelaya I (2011). Modelling glyphosate resistance management strategies for Palmer amaranth (*Amaranthus palmeri*) in cotton. *Weed Technology* **25**, 335-343.

4. **Neve P**, Smith K, Norsworthy J, Zelaya I (2011). Modelling evolution and management of glyphosate resistance in *Amaranthus palmeri*. *Weed Research* **51** (2), 99-112.

5. **Neve P**, Diggle AJ, Smith FP, Powles SB (2003). Simulating evolution of glyphosate resistance in *Lolium rigidum* I: Population biology of a rare resistance trait. *Weed Research* **43** (6), 404 – 417.

6. **Neve P**, Diggle AJ, Smith FP, Powles SB (2003) Simulating evolution of glyphosate resistance in *Lolium rigidum* II: past, present and future glyphosate use in Australian cropping. *Weed Research* **43** 418 – 427.