



Alopecurus myosuroides transcriptome database (ALOMYBase): unravelling the genetic bases of non-target-site-based resistance to herbicides

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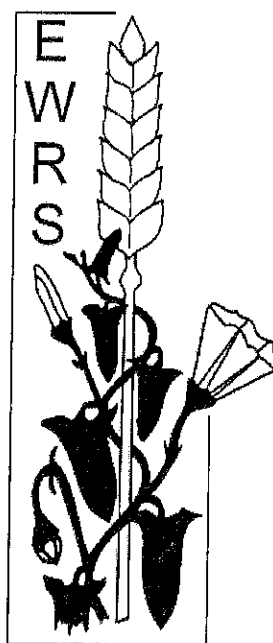
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Individual-based simulation as a tool to help understand how ecology, management and genetics affect the evolution of herbicide resistance

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Herbicide resistance is a growing problem threatening world food production. The way weeds evolve resistance to herbicides depends on a complex interaction between the underlying genetics, the weed management used by the farmer, and the biology of the weed species. Evaluating different management options for delaying or avoiding resistance evolution is a challenge because it depends on this complex interaction of multiple factors at different scales, and because it is a long-term large-scale process that is difficult to investigate properly with small-scale short-term experiments. Simulation modelling provides a means of integrating the various factors involved in resistance, including physiological mechanisms, molecular and population genetics, ecology, evolutionary dynamics, and practical management. To help better understand, predict and manage evolution of herbicide resistance, we developed a model, known as PERTH (Polygenic Evolution of Resistance To Herbicides), to predict the rates and patterns of resistance evolution in a wide range of different conditions. PERTH is based on an individual-based simulation methodology, which allows it to represent a wide range of details of the real biological system. PERTH has been used to help evaluate the efficacy of management options such as herbicide rotation, maintaining robust herbicide rates at high efficacy, avoiding or introducing refuges, and using non-chemical methods of control, and how the efficacy of these options depends on the genetics underlying the resistance. For example, modelling results showed that maintaining robust herbicide rates at high efficacy is an important strategy for avoiding polygenic resistance, but has a negligible effect on the evolution of monogenic resistance. PERTH has also been used to show that the evolution of resistance can affect be affected by ecological functional traits of different weed species, such as seed bank longevity and dormancy, fecundity, seed dispersal, and rates of self-fertilisation versus out-crossing. Recently PERTH has been adapted to account for spatial heterogeneity, which has let us predict that factors such as seed and pollen dispersal can strongly affect the evolution of resistance. We conclude that the strength of simulation models, and of individual-based approaches in particular, is that they provide a means of integrating knowledge from multiple scientific disciplines at a wide range of temporal and spatial scales. Thus they provide a valuable tool to help understand how ecology, management and genetics affect the evolution of herbicide resistance, and ultimately help safeguard the sustainability of world food production.

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Herbicides are the most effective weed control tools, but their efficacy is jeopardized by the evolution of resistances in weeds. Non-target-site-based resistance (NTSR) is the most challenging aspect of herbicide resistance. NTSR is complex, widespread and unpredictable. It can confer resistance to a range of herbicides with different modes of action. Thus, understanding the genetic bases and the evolution of NTSR is crucial to sustain herbicide efficacy. Therefore, the objective of this study is to identify genes involved in NTSR.

NTSR is part of the weed response to the herbicide stress. Accordingly, differences in gene expression between resistant and sensitive plants are considered to be at the root of NTSR. Thus, a transcriptomics-based approach is expected to identify NTSR candidate genes. Such an approach is now feasible with the tremendous progresses achieved by the sequencing technologies (next-generation sequencing). This study focuses on blackgrass (*Alopecurus myosuroides*), a major weed in winter crops in Western Europe that evolved NTSR to the most effective herbicides used to control it (i.e., acetolactate synthase and acetyl-CoA carboxylase inhibitors).

Using the Illumina sequencing technology, an exhaustive transcriptome database was established for *A. myosuroides*. This database was used as a reference to compare the transcriptomes of herbicide-sensitive and herbicide-resistant *A. myosuroides* individuals before and after herbicide treatment along a time-course experiment, using a RNA-Seq approach. Genes showing a constitutive or an herbicide-induced increased expression in resistant plants were sought as candidate NTSR genes. 42 genes fulfilling this criterion were identified. These genes encoded enzymes potentially involved in herbicide degradation or compartmenting, regulator proteins, and putative proteins with unknown functions.

The differences in expression observed were confirmed by quantitative real time PCR, yielding a set of candidate NTSR genes of interest. Further investigation on the role of these genes in NTSR must now be conducted.