A spatial life-cycle model of transgene dynamics in the field



A plant population dynamics model is described for predicting and managing the presence of GM traits in the environment

Why a spatial model?

Arable plants, including volunteer weeds, are distributed irregularly in space.

This spatial heterogeneity has to be accounted for when predicting the population dynamics and spread of transgenes.

To address this we have developed a model of the fate of individuals carrying inserted genes as they undergo their life-cycle, influenced by each other, the farmer and the environment.



Example of the measured patchy distribution of GM oilseed rape volunteers (black dots) amongst other vegetation (grey shading) in a area of field in set-aside.

25m

How the modelled plants interact in space

The model represents a population of individuals that compete for resource, shed seed and cross pollinate.

Individuals progress through of life-history processes influenced by management events and environmental drivers

Innovative features allow virtual plants to interact in space and time through a 'zone of influence'.



Plant A with biomass relative to the area of its circle has zones of influence for competition (dotted circle 1) and for a stated probability of cross pollination (dotted circle 2). It competes and cross-pollinates with plant B, crosses with plant C, but has no interaction (or a very low probability of nteraction) with plant D.



A snapshot of non-GM (open circles) and GM plants (closed red circles) at a stage in the evolution of a mixed population in a simulated field. Each plant interacts with others in their respective zones of influence, which can be genotype-specific. The area shown represents about 5 x 5 m.

Genotypes interacting over space and time

For realism, the model is simulating the life cycle biology and genetic exchanges in the type of GM oilseed rape that has been trialled most widely in the UK - the event Ms8xRf3 conferring herbicide tolerance through the bar gene in the Farm Scale Evaluations.

The events were represented as two independent alleles, H1 - bar/barstar and H2 - bar/barnase which are either present or absent. Individuals with at least one allele, H1 or H2, are glufosinate-ammonium resistant, and those with the H1 allele but not the H2 allele are male sterile. Seed shed by the transgenic crop at harvest contains nine possible genotypes.

The output from the model, e.g. proportions of genotypes and other compatible plants, can be validated against measurements at GM release sites to see whether theory departs from reality.

Stochastic life cycle transitions

Persistence of plants with GM traits depends mostly on two transitions: seed entering the seedbank and emergence of that seed in a future crop.

The model is used to explore the probability of these transitions occurring in various combinations of physiology, weather and agronomy.

Mechanisms for best practice can be identified in relation to varietal physiology, variability in the weather and farmer's options.



The figure shows how (modelled) shed GM seed declines with time as it germinates or is predated on the soil surface. Cultivating soil too early buries seed causing it to become dormant and persist. Current recommendations are for no cultivation before 21 days, but many circumstances (e.g. cold early autumn, dry late summer) will arise when cultivation after 21 days will lead to large GM seedbanks

Uses

Since the basic 'engine' of the model is the life cycle of plants, it can be modified for any forms of oilseed rape, and adapted for any plant species. Present uses are -

- To guide GM growers to enable them to assess a likely GM impurity
- To assess the economics of measures that would allow farmers to switch between different types of oilseed rape (e.g. GM and non-GM)
- To contribute to GM coexistence policy through a European project (EU FP6: SIGMEA).

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