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Simulation study of the impact of changed cropping practices in conventional and GM maize on weeds and associated biodiversity

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ABSTRACT

The introduction of genetically-modified (GM) crops is often accompanied by other changes in cultural practices. The objective of the present study was to evaluate these changes with the simulation model FLORSYS which quantifies the effects of cropping systems and pedoclimate on weed dynamics as well as indicators of weed-related biodiversity (species richness and equitability, trophic resources for birds, insects and pollinators) and crop production loss (yield loss, harvest contamination, harvesting problems, field infestation). The study focused on two GM maize variety types, i.e. expressing Bacillus thuringiensis toxins against insects (Bt) and tolerating the non-selective herbicide glyphosate (HT). Two contrasting maizegrowing sites were studied: Aquitaine, a region in South-Western France, and Catalonia in North-Eastern Spain. Typical regional cropping systems containing maize were identified for each site from expert knowledge and the Biovigilance database recording French agricultural practices. GM scenarios were based on expert knowledge, literature and current Spanish practices. A total of 11 most probable scenarios (1 conventional, 3 Bt and 8 HT) were simulated over 28 years for each region, and repeated with 10 different regional random weather series. An additional series of 5-7 scenarios per region was run to decorrelate factors, and make it easier to identify the cultural practices responsible for changes in weed flora, biodiversity and production. The simulations showed that the changes accompanying the introduction of GM maize varieties affected weed flora as well as weed-related biodiversity and crop production loss, but that the consequences depended on local conditions. Most of these consequences were caused by simplifications in the cropping systems made possible by the GM varieties, rather than by the glyphosate associated to GM varieties. Simplified tillage or no-till increased weed harmfulness, particularly in Aquitaine where the weed flora was poorer and dominated by larger and more persistent species. Conversely, no-till cancelled part or all of the nefarious effects on biodiversity of simplified rotations (maize/wheat and maize monoculture), particularly by improving trophic resources offered by weeds to birds, insects and pollinators. Overall, biodiversity was less affected by simplified rotations in Catalonia where the initial weed flora was richer and more equitable. Delayed maize sowing reduced weed harmfulness and biodiversity, except food offer for insects and pollinators whose pertinent feeding period covered spring and summer (vs. winter for birds). Based on the two most affected weed-based biodiversity indicators, ex post monitoring after GM introduction should focus on birds in Aquitaine and on pollinators in Catalonia. © 2015 Elsevier Ltd. All rights reserved.

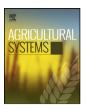
1. Introduction

Major traits of genetically-modified (GM) crops used in agriculture today are herbicide tolerance (HT) and expression of *Bacillus thuringiensis* (Bt) toxins against insects. Whereas in some regions of the world a large proportion of certain crops (soybean, maize, cotton) is cultivated with these traits (James, 2013), in the European Union the area with GM crops is still relatively small. So far, only four events have been approved for cultivation but only one is currently grown (Bt maize MON810).

Benefits and risks are a controversial issue. The technologies have proven profitable and easy to handle in the first years after their introduction in Northern America and other parts of the world. Benefits for users are the simplification of weed and insect management, saving costs for pesticides and associated work chores, preventing yield loss caused by insect damage and crop:weed competition







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(Bradley et al., 2000; Brookes and Barfoot, 2009; Richard-Molard et al., 1996; Shaner, 2000). The use of HT and Bt traits is even seen as a possible component of IPM as one of several weed and insect management options to lower pesticide use in Europe (Meissle et al., 2010). But in several regions overreliance on the singular strategy has led to the development of resistant weed (Powles, 2008) (www.weedscience.com) and insect populations (Albajes et al., 2011), which in turn leads to rising herbicide and insecticide use again (Service, 2013). Other possible risks often associated to GM cropping include toxic effects (of Bt) on non-target organisms (Albajes et al., 2009), gene flow to wild relatives (Ellstrand et al., 1999), admixture of GM seeds in non-GM harvest (Paul et al., 2012) as well as difficulties in managing GM crop volunteers in succeeding crops (Gruber et al., 2008).

Shifts in weed floras are also reported (Heard et al., 2003a, 2003b) due to the changes in herbicide programmes but also due to induced changes in the rotations and cropping systems that the GM crop is introduced into. For instance, rotations are often reported to become less diverse (Fausti et al., 2014). In many countries tillage is often simplified or even abandoned after introducing HT crops to reduce erosion and work load (Cerdeira and Duke, 2006; Costa et al., 2001; Frisvold et al., 2009; Trigo and Cap, 2003). The latter makes possible earlier sowing times (Davies and Finney, 2002). From Spain, it was reported that Bt varieties give the possibility to delay sowing as these varieties are less sensitive to corn borer which is a larger problem in late sown maize (Joan Serra, pers. communication).

All these management factors have been shown to influence weed communities in conventional crops both in abundance and composition (Baessler and Klotz, 2006; Colbach et al., 2014d; Fried et al., 2009). Also, the change from selective herbicides towards the broad spectrum glyphosate causes weed shifts (Gulden et al., 2010; Squire et al., 2009; Wilson et al., 2011).

Weeds are among the most harmful pests, reducing crop yields, impairing the quality of crop production and causing technical problems during harvests (e.g. Oerke, 2006). They can also host other pests such as crop pathogens (ex. of take-all disease of cereals, Gutteridge et al., 2006). However, weed flora is also a major part of arable biodiversity and provides habitat and food resources to a range of animals in agricultural landscapes, notably bees and other insects as well as birds (Evans et al., 2011; Marshall et al., 2003; Petit et al., 2011; Taylor et al., 2006). Weed species greatly differ in their value for animal feeding, due to the content of proteins, sugars and oils as well as flowering times. Any shifts in weed floras may thus adversely affect not only agricultural production but also many other biodiversity components, and these effects still need to be analysed (Squire et al., 2009).

Separating the effects of general changes in agricultural practices from GM cropping effects is an issue. The EFSA framework for environmental risk assessment (EFSA, 2010) proposed a threestep strategy to assess possible effects and rank them in terms of their importance consisting of 1) quantification of background changes in agriculture, 2) identification of most likely GM cropping effects from experimentation, modelling and monitoring, 3) comparison of size and direction of these predicted effect (Sweet and Bartsch, 2011). Because weed seeds can survive for several years in the soil (Gardarin et al., 2010; Thompson et al., 2003), effects of management practices on weed populations are difficult to detect in experimental settings that often last only for a few years. Models predicting the dynamics of biotic components as a function of cropping practices and pedoclimate are therefore a useful alternative to field trials or surveys for evaluating the impact of cropping system changes (Colbach et al., 2014a; Petit et al., 2011). When attempting to evaluate the impact of future events, they are indeed the only possibility.

Consequently, the objective of the present study was to evaluate, with a simulation model, the impact of modifications in

agricultural practices resulting from introducing GM maize into cropping systems on weeds as well as the resulting impacts on crop production and biodiversity. The study will focus on the two main GM maize variety types, i.e. Bt and glyphosate-tolerant. Current and probable future agricultural practices in maize cropping systems were identified from surveys and expert opinion in two large maizegrowing European regions, Aquitaine in South-Western France and Catalonia in North-Eastern Spain. The weed dynamics model used in the study was FLORSYS (Colbach et al., 2014c; Gardarin et al., 2012; Munier-Jolain et al., 2013) which is to date the only multispecies model that predicts the effects of most cropping system components and pedoclimate (Colbach, 2010; Freckleton and Stephens, 2009; Holst et al., 2007). The simulated weed occurrences and densities were translated into a set of indicators reflecting weed impacts on biodiversity (e.g. contribution to vegetal biodiversity and trophic ressources for fauna) and on agricultural production (e.g. yield loss, harvest contamination, Mézière et al., 2014).

2. Materials and methods

2.1. FLORSYS

The structure of FLORSYs is described in detail in previous papers (Colbach et al., 2014b, 2014c; Gardarin et al., 2012; Munier-Jolain et al., 2013, 2014). Only the main aspects are described here. The input variables of FLORSYs consist of:

- the above-ground weather (evapotranspiration on bare-soil, radiation, temperature, rainfall and radiation) measured for each simulated day by standard weather stations;
- a description of the simulated location: soil texture and depth as well as latitude;
- the initial weed seed bank (i.e. seed density for each weed species and for each cm soil down to 30 cm);
- the cropping system during the whole simulated period, comprising the crop sequence including cover and undersown crops, the date of all operations (e.g. sowing, harvest) and their characteristics (e.g. sowing density, depth, pattern and crop variety for a sowing operation).

The heart of FLORSYS is a generic life-cycle consisting of a succession of life-stages chosen for their interaction with cropping system components and light competition; it applies to annual weed species (see section A in supplementary material online). Nondormant weed seeds close to the soil surface germinate after rain or tillage in moist conditions; only seeds close to the soil surface succeed in emerging. Dormant and/or buried seeds germinate little; their disappearance is mostly due to in situ mortality. Pre-emergent processes are simulated for an average m² of the simulated field. After emergence, both weed and crop plants are placed on a field sub-sample (e.g. $4 \times 4 \text{ m}^2$): the crop plants according to their sowing pattern (e.g. row-sown or broadcasted) listed in the input variables, and the weeds in patches. The above-ground part of plants is represented by a cylinder, with height, diameter and leafdistribution depending on the species, plant stage and past shading conditions which can lead to etiolation. Each day, light availability is calculated in each point of this 3D-canopy, resulting in biomass accumulation and subsequent plant-cylinder growth. At weed maturity, seed production is calculated as a function of biomass and the seeds added to the soil seed bank. FLORSYS also comprises a submodel from STICS to predict soil climate (Brisson et al., 1998) and another from DECIBLE to predict soil structure (Chatelin et al., 2005)

The relationships between the life-stages depend on environmental variables and management techniques (section A.2 in supplementary material online). For instance, tillage buries and Download English Version:

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