

Fuzzy assessment of herbicide resistance risk: Glyphosate-resistant johnsongrass, *Sorghum halepense* (L.) Pers., in Argentina's croplands



D.O. Ferraro^{a,*}, C.M. Ghersa^b

^a Cátedra de Cerealicultura, IFEVA, Facultad de Agronomía, Universidad de Buenos Aires, CONICET, Av. San Martín 4453, Buenos Aires 1417DSE, Argentina

^b Cátedra de Ecología, IFEVA, Facultad de Agronomía, Universidad de Buenos Aires, CONICET, Av. San Martín 4453, Buenos Aires 1417DSE, Argentina

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ABSTRACT

A fuzzy-logic based model was built in order to assess the relative influence of different ecological and management drivers on glyphosate resistance risk (GRR) in *Sorghum halepense* (L.) Pers. The model was hierarchically structured in a bottom-up manner by combining 16 input variables throughout a logical network. Input data were related to 1) herbicide usage, 2) crop rotation, 3) landscape characterization, 4) weed dispersal, and 5) mean maximum and minimum seasonal temperature. Mean maximum and minimum seasonal temperatures and the dominance of glyphosate use were the variables that showed the highest sensitivity to input changes. Application of the model at a regional scale resulted in a wide range of GRR values. The lowest range values (lower than 0 and between 0 and 0.25) were represented in 5.5% and 21.5% of the cropping area, respectively. Intermediate GRR range (between 0.25 and 0.5) were assessed in 57.3% of the cropping area whilst the highest GRR range values (0.5–0.7) were represented in only 15.6% of the studied area. The assessment of trade-offs between different ecosystem functions through expert opinion can complement traditional analyses for predicting herbicide resistance risk based on solely the genetic aspect of the evolutionary process.

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1. Introduction

During the last decades, herbicide-resistant weed populations are increasingly evolving creating problems around the world (Powles, 2008). Herbicide resistant weeds may be driven by genetic, ecological, and agronomic factors. These factors are included in both theoretical and empirical approaches for assessing the risk of herbicide resistance in weeds aimed at making accurate predictions of when, where and how much resistance will appear (Maxwell et al., 1990). Most of these approaches are based on the herbicide effects on both morphological and physiological weed traits that determine herbicide resistance. However, our knowledge about the relative magnitude of both the environmental factors or ecological characteristics of weed populations on the evolution rate of herbicide resistance is still vague or fuzzy (Neve et al., 2009). For example, we know that outbreeding annuals with large populations and without persistent soil seed banks are most likely to become resistant or that inbreeding perennials with low seed production or asexual

perennials are less likely to evolve resistance (Powles, 2008). However, it is difficult to use this information for real cases, even for particular species due to variability and the challenge of establishing clear-cut definitions for each of these characteristics that may be influenced by the interactions with other biological factors. Moreover, in order to go beyond the simplified assumption of random mating, the herbicide resistance models should incorporate spatial structure and processes so that the implications of spatial aggregation of seeds and gene flow should then be used (Neve et al., 2009).

In Argentina, some common weeds such as *Parietaria debilis*, *Petunia axillaris*, *Verbena litoralis*, *Verbena bonariensis*, *Hybanthus parviflorus*, *Iresine diffusa*, *Commelina erecta* and *Ipomoea* sp. have been reported to be glyphosate-tolerant (Papa, 2000). Moreover, over 16 million hectares in Argentina are dedicated to glyphosate-resistant (GR) soybean production (Binimelis et al., 2009). Recently, in some of the areas of transgenic glyphosate-resistant crops in Argentina, there are evolved GR populations of *S. halepense* (Powles, 2008). *S. halepense* is a C4 perennial and rhizomatous grass weed which reproduces by seeds and rhizomes, and became widely naturalized and weedy in Argentina (Valverde and Gressel, 2006). Currently, there are records from the province of Salta, northern Argentina, of appearance of GR *S.*

* Corresponding author. Tel.: +54 (0)1145248000.

E-mail address: ferraro@agro.uba.ar (D.O. Ferraro).

halepense biotype (Valverde and Gressel, 2006). However, a comprehensive risk assessment of glyphosate resistance risk has not been conducted. Based on these antecedents, we integrated eco-physiological and demographic information of *S. halepense* with data on cropping practices, landscape; and climatic characteristics of Argentina's main cropping as drivers for assessing the glyphosate resistance risk (GRR) for this weed. The model was built using a fuzzy logic framework (Zadeh, 1965), which provides a set of elements (i.e. membership functions, linguistic variables and rule sets) that allows handling the uncertainty by using interval-valued fuzzy sets instead of classifying membership as either true or false as in the classical (Boolean) logic system. The specific details about fuzzy modeling are described in Appendix A.

2. Methods

2.1. GRR assessment

The model for assessing GRR (GRR model) was built using data at plot level (see Section 3.1 Model structure). However, in order to obtain GRR regional predictions, the model was run at the landscape level with average regional variables. The average regional variables represent the modal conditions of a field crop for each production region (see below). Therefore, we created a GIS database and arranged the data for GRR model running, so data can flow from GIS-created database into GRR model and modeling results can be transferred to GIS for final presentation. A set of different GIS database components was built:

- 1) Production regions: A number of 21 productive regions were identified, covering nearly all the cropping areas of the country. Production regions were defined using existing GIS databases (Conte et al., 2007) along with feedback from AACREA (Argentine Association of Agricultural Experimentation Consortia), a nongovernmental association of farmers using ArcGIS 9.1 (ESRI Copyright© 2005).
- 2) Climate data: Maximum average and minimum average air temperature data were interpolated using universal krigging, whereby a polynomial is fit to the underlying spatial trend (Journel and Huijbregts, 1978). This dataset was developed by interpolating monthly historic climate observations (1961–2010) from 90 meteorological stations (SMN, 2010) to a similar resolution of the map of production regions (ca. 16 km resolution).
- 3) Landscape data: representative values of landscape characterization (i.e. shrub and tree hedge closeness) of each production region were empirically reconstructed. First, we determined the dominant biome in each of the production regions studied on the basis of existing GIS data (Burkart et al., 1999). Subsequently, we estimated an average value of the relative coverage of trees and shrubs in the surrounding landscape, based on physiographic description of each biome (Hauman et al., 1947). Thus, average values were obtained for hedge shrub closeness (% Sh), and hedge tree closeness (% Tr) for each productive region (see section 3.1.2). Finally, the values obtained were compared by consulting local experts and technicians to adjust the final values according to the most recent changes of the landscape structure. Thus, final landscape data of each productive region were based on the literature review and reflect both an amount of certainty as well as some uncertainty concerning the election of a single modal value of landscape configuration for the whole production region.
- 4) Management data: Data on crop rotation and management regime for each production zone were determined

analogously to landscape characterization. Therefore, we proceeded to empirically reconstruct both a modal crop rotation and management regime for each production zone. In Argentina, cropping schemes have developed for rainfed soybean (*Glycine max* Merr.) production that invariably employs no-tillage management. Often these schemes include growing soybean in a sequence of crops including wheat (*Triticum aestivum* L.); maize (*Zea mays* L.) and sunflower (*Helianthus annuus* L.) entailing an average of 88% of total cropping area among the production regions (SAGPyA, 2009). Regional variability in both crop rotation and management were reconstructed using agro-economic monthly databases (*Márgenes Económicos* and *Agromercado*) for each production region, as well as crop rotation records from SAGPyA (Secretary of Agriculture, Husbandry, Fishing and Feeding, Argentine Republic). Final crop rotation and management schemes were also adjusted according to the elicited expertise from technicians and farmers of each production zone. In order to assess the current risk level of glyphosate resistance in the agroecosystems studied, we included a set of management variables that represent the current cropping conditions in the studied regions. Thus, variables like mechanical weeding or irrigation were disregarded as they are not used in the study region. Moreover, other cropping system components (e.g. sowing date and density, variety ability for competition, intermediate crops) were omitted in order to build a more generic risk assessment.

2.2. Model sensitivity

A sensitivity analysis was performed to assess the relative effect of input variables on GRR assessment. Sensitivity of the dependent variable GRR on each input variable x was quantified by a modified sensitivity index I (Lenhart et al., 2002).

$$I_x = \frac{GRR_0 - GRR_1}{GRR_0} \times 100 \quad (1)$$

where I_x is the sensitivity index of the input variable x ; GRR_0 is the value of the dependent variable using all input variables at its baseline value; and GRR_1 is the value of the dependent variable when the input variable x were either increased or decreased. Because the behavior of the system can undergo important changes as a result of non-linear responses to input variables two independent tests were undertaken (Paterson et al., 2008): 1) Increasing GRR sensitivity analysis: Each input variable at a time was changed (increased or decreased); until the fuzzy proposition determined by its membership function becomes true, whereas all others were held at their baseline values. The baseline for this test is represented by all the input variables at the level where each fuzzy proposition become false (i.e. the lowest value for glyphosate resistance risk; $GRR_0 = -1$). This test evaluates the sensitivity of the model to increase the overall risk value (GRR) from the lowest risk condition ($GRR = -1$) when each variable takes the value corresponding to the maximum risk; 2) Decreasing GRR sensitivity analysis: Each input variable at a time was changed; until the fuzzy proposition determined by its membership function becomes false, whereas all others were held at their baseline values. The baseline for this test is represented by all the input variables at the level where each fuzzy proposition become true (i.e. the highest value for glyphosate resistance risk; $GRR_0 = 1$). This test evaluates the sensitivity of the model to reduce the overall risk value (GRR) from the highest risk condition ($GRR = 1$) when each variable takes the value corresponding to the minimum risk.

3. Results

3.1. Model structure

The first step in this model involves the formulation of the risk problem in a hierarchical structure (Fig. 1). In this model, climatic, geographic, agronomic, demographic, and eco-physiological data were used for assessing the fulfillment of three intermediate propositions related to risk for evolution of glyphosate-resistant *S. halepense*: 1) low system diversity; 2) high frequency of resistance alleles; and 3) high weed fecundity. The model criteria (i.e. the membership functions) are shown in Table 1

3.1.1. Low system diversity

Overall system diversity was the first factor to be considered for assessing the GRR evolution. According to thermodynamics, system diversity should lead to a complex ecosystem network. In agricultural system, a complex network entails a large number of species interactions and human decisions that progressively reduce the entropy dissipation and leads to higher level of system information and complexity. These complex systems typically show high dependence among their components which give them high resistance to modifications, or resilience (Holling, 1973). Overall, the model considered that more diverse cropping systems would lead to a higher resilience level that will reduce the risk of development of any functional or structural system change, including the increase in mutation frequency conferring herbicide resistance (Radosevich et al., 1992). We related two main dimension of system diversity to GRR evolution:

3.1.1.1. High glyphosate dependence. The intensity of glyphosate for weed management was used as a measure of herbicide diversity. The input variable (Fig. 1) was calculated as follows:

$$\% \text{ of Glyphosate use} = \frac{\text{number of glyphosate applications during the crop rotation}}{\text{total number of herbicides applications during the crop rotation}} \quad (2)$$

As a measure of risk assessment, the fuzzification of this variable was made through a membership function that defines a value of 80% of Glyphosate use for weed control as the situation where the proposition *High glyphosate dependence* is true (Table 1). One of the model assumptions is the use of herbicide (glyphosate) at the label dose. This assumption omitted the potential sublethal effect of reduced rates in increasing the evolution rate of herbicide resistance. This assumption is based on the fact that the Argentine cropping systems usually receive doses equal to or higher than that recommended by the manufacturer on the label.

3.1.1.2. Low crop genotype diversity. System diversity was also related to both the species richness in the crop rotation (# crop species) and the dominance of glyphosate-resistant (G-R) crops (% of Glyphosate-resistant crop species) (Fig. 1). Membership functions for these two input variables were represented in Table 1. Specifically, the fuzzy proposition *Monoculture* becomes false (truth value = -1) when the crop rotation include at least four different crops (Table 1). The fuzzy proposition *High G-R dominance* becomes totally true when the crop rotation exhibits at least 80% of G-R crops (Table 1).

3.1.2. High frequency of resistance alleles

The model relates three major determinants for assessing the risk of increasing the frequency of resistant alleles in the *S.*

halepense populations: 1) the gene flow; 2) the herbicide selection pressure, and 3) the weed seedbank turnover.

3.1.2.1. High gene flow. Resistant genotype frequencies are modified by gene flow (i.e. propagule immigration, seed bank dynamics, inbreeding, and random genetic drift) (Maxwell et al., 1990). Within this module, two main forces related to gene flow in agro-ecosystems were represented: a) the landscape structure and 2) the propagule dispersion. Landscape structure, through the fuzzy proposition *High landscape openness*, was represented by means of the relative contribution of both trees and shrubs for closing the landscape and acting as physical barriers for gene flow (Weinstoerffer and Girardin, 2000). Two fuzzy variables (Shrub and Tree presence, Fig. 1) were defined by using the input variables 1) % shrub hedge closeness (% Sh), and 2) % tree hedge closeness (% Tr). Both variables are defined in terms of the ease with which a given observer situated within a crop field can obtain an extensive view over the surrounding country, through both the shrub hedge and the tree edge of each crop field (Weinstoerffer and Girardin, 2000). Although these two variables are intrinsically qualitative, we defined a multi-set fuzzy variable for defining three different states of both shrub and tree presence (Appendix B). After both tree and shrub presences are assessed by their respective membership functions a final truth-value of the proposition *High landscape openness* was calculated using a rule node (Appendix B). Both the threshold values of each membership function and the rule node conclusions were based on both the literature review and the author's criteria about the influence of landscape structure on gene flow intensity for assessing final GRR values. The third input variable that influences the gene flow of *S. halepense* propagules is the influence of farm machinery dispersion (i.e. secondary dispersion) (Thill and Mallory-Smith, 1997). In Argentina, as the cropping systems becomes more intensive, the production processes are

dominated by managerial tasks performed by hired external economic agents (Manuel-Navarrete et al., 2009). Thus, we used the farm machinery ownership (FMO), as a proxy for the potential long-range dispersal due to farm equipment movement. We identified three FMO levels: 1) farm machinery owned by the landowner (Own), 2) farm machinery that is owned by a mid-size contractor, working within less than 100 km from the farm (Local) and 3) farm machinery that is owned by a large contractor, who works in an area exceeding 100 km away from the farm (Regional). The fuzzy proposition *Long-range propagule dispersion* uses a qualitative function that determines the total membership to the proposition when the farm machinery is hired from a large contractor (regional) and the null membership to the proposition when the farm equipment comes from the landowner. In the case that farm labor tasks were performed with a mixture of own and hired equipment, it should be considered which of the two models is the most dominant.

3.1.2.2. High herbicide selection pressure. The second logical node for assessing the frequency of resistance alleles in the *S. halepense* populations is the herbicide selection pressure. This pressure was assessed by means of the frequency and the efficiency of herbicide use. The number of glyphosate applications (# G applications) determined the intensity of glyphosate usage during the crop rotation (Table 1). We used the annual average number of

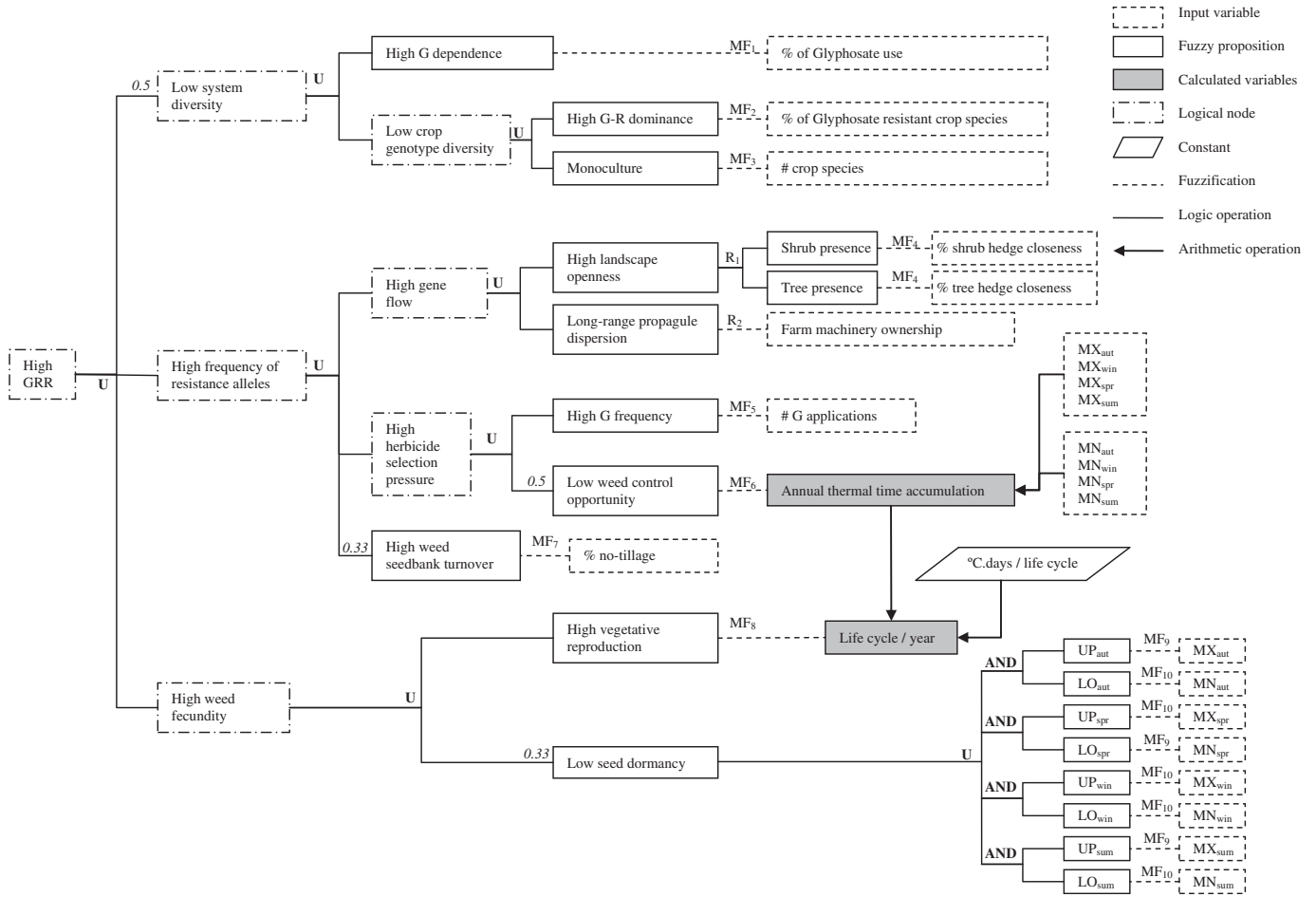


Fig. 1. Fuzzy-logic network structure for assessing the glyphosate resistance risk (GRR) in *Sorghum halepense*. The network includes the input and calculated variables, the membership functions (MF), the rule nodes (R), the fuzzy propositions, the logical nodes and the constants. Bold capital letters indicates the logical operator. Number in italics corresponds to the relative importance of each antecedent, when the relative importance of each antecedent in the logical node differed from 1 (see Technical Appendix, for details). MX and MN are maximum average and minimum average temperatures, respectively, for autumn (aut), winter (win), spring (spr) and summer (sum). Input variables and fuzzy propositions description are in Table 1.

glyphosate applications during the crop rotation, as the input variable for defining the fuzzy proposition *High G frequency*, is totally true value when the cropping systems reaches an average value of four Glyphosate application/year (Table 1). The other cause of weed mortality that was related to selection pressure was the efficiency of herbicide use. The perennial nature of *S. halepense* defines a critical period for herbicide control that depends on the functional

relationships between sprout emergence and environmental factors (Benech Arnold et al., 1992). In the cropping systems studied, failures in controlling weed populations are usually more associated with mismatch between the critical moment for controlling weed populations and the time of herbicide application, than the use of herbicide sub-doses. In *S. halepense*, the herbicide control efficiency increases as the application is closest to the period of

Table 1

Linear membership functions (MF) description for calculating a set of fuzzy propositions from the logic network structure of Fig. 1. I_t and I_f are the variable (V) level where the fuzzy proposition becomes totally true or false, respectively. See text for a full explanation of variable calculations.

MF	Input variable (V)	Code	Range/unit	Description	Fuzzy proposition	V value	
						I_t	I_f
1	% of Glyphosate use	% G	[0;100]	Measure of Glyphosate (G) dominance for weed control during the crop rotation	High G dependence	80	0
2	% of Glyphosate resistant crop species	% G-R	[0;100]	Measure of dominance of glyphosate resistant (G-R) crops used in the crop rotation	High G-R dominance	80	0
3	# crop species	# spc	[1;n]	Number of crop species in the crop rotation	Monoculture	1	4
5	# G applications	# G	[0;n]	Annual average number of G applications during the crop rotation	High G frequency	4	0
6	Annual thermal time accumulation	AnnTT	°C days	Proxy for assessing the effect of potential weed growth on the opportunity for weed control	Low weed control opportunity	750	250
7	% of no-tillage	% NT	[0;100]	Proxy for soil disturbance influence on herbicide resistance evolution	High weed seedbank turnover	100	0
8	Life cycle/year	# Cycle	[1;n]	Number of life cycles in one year	High vegetative reproduction	6	1

minimum rhizome biomass (Satorre et al., 1985). For this reason, any environmental condition that increases the *S. halepense* growth rate will necessarily shorten the time period (in days) of minimum rhizome biomass. In order to incorporate the effect of weed growth rate for defining the gap between maximal susceptibility and time of controlling (the weed control opportunity), we used the temperature regime (i.e. the thermal time accumulation) of each production zone as a proxy for the potential growth rate of *S. halepense* populations (Fig. 1). Annual thermal time accumulation (Table 1) was calculated as using a base temperature (at and below which the growth rate is zero) of 15 °C for *S. halepense* growth, and the ceiling temperature (at and above which the growth rate is again zero) was set at 35 °C (Ghersa et al., 1990). Instead of the usual thermal time calculation using daily mean temperatures, we derived monthly mean temperatures from the maximum and minimum monthly temperatures for calculating the growing degree days (GDD) as the independent variable in the modeling of *S. halepense* population dynamics. As the GDD increases, the risk of mismatch between the occurrence of critical control period and the herbicide application increases. Thus, we used the annual thermal time accumulation (in GDD) as an input variable for defining the fuzzy nature of the fuzzy proposition *Low weed control opportunity*. The membership function (Table 1) uses a linear transition between two threshold values: the false condition (250 °C day year⁻¹) and the true condition (750 °C day year⁻¹). These two values represent the annual thermal accumulation for completing 1 and 3 life cycle as seed–rhizome–seed in one year, respectively (Holshouser et al., 1996).

3.1.2.3. High weed seedbank turnover. In low soil disturbance no-till systems, weed seeds are concentrated on, or immediately below, the soil surface, compared with distribution in the soil profile at greater depths in systems with a greater amount of soil disturbance (Colbach et al., 2000). In no-till systems, weed seedlings largely resulted from seeds shed in the previous crop, with little buffering against resistance evolution from older seeds that might have susceptibility (Moss, 2002). Thus, weed seed bank turnover might interact with increased herbicide use in no-till systems to increase the risk of evolution of herbicide resistance in *S. halepense* populations. We simply used the percentage of no-till system in the crop rotation (% of no-till) as input variable for calculation the membership to the fuzzy proposition *High weed seedbank turnover* (Fig. 1).

3.1.3. High weed fecundity

A. S. halepense life-table can be divided in 1) genet (sexual origin) annual plants that develop from seed and produce new seeds and/or rhizomes; and 2) ramet perennial plants that originated from rhizome or crown buds that develop new rhizome buds and or seed. Also, the growing season for the seed annual cycle is shorter than for the rhizome perennial cycle, under the same environmental conditions. We used the GDD model (Ghersa et al., 1990) and climatic information to calculate and to map areas with particular growing seasons and to estimate both the number of generations for both genet and ramet plant populations and the conditions for dormancy termination (Benech Arnold et al., 1992). Particularly, the model is able to represent the effects of both vegetative and sexual reproduction (through the release of seed dormancy).

3.1.3.1. High vegetative reproduction. The potential vegetative growth conditions were assessed by means of the GDD model (Ghersa et al., 1990). This model calculates an amount of 250 °C days for completing the life cycle as seed–rhizome–seed (Ghersa et al., 1990; Satorre et al., 1985). The annual thermal time accumulation over the base temperature was used in order to

calculate the number of *S. halepense* life cycles due to vegetative growth. Using this value as input variable of the membership function (Fig. 1), it was possible to assess the fulfillment of the *High vegetative growth* fuzzy proposition (Table 1).

3.1.3.2. Low seed dormancy. Seed dormancy is important in the persistence of *S. halepense* in Argentinean cropping systems (Benech Arnold et al., 1992). This dormancy may be partly overcome by the stimulating effects of alternating temperatures, at a particularly 30/20 °C regime (Benech Arnold et al., 1992). In order to assess the alternating temperature effects, the model used the maximum and minimum average temperature value for each one of the annual season (autumn, winter, summer and spring) as input variables (Fig. 1). The fulfillment of the alternating temperatures regime was assessed using two membership functions that calculate both the full membership to the upper limit (UPi) and the lower limit (LOi) (Fig. 1). Finally, the AND and U logical connectives computed the annual average membership value (Fig. 1). This value range from –1 (null membership to alternating temperatures regime) to 1 (full membership to alternating temperatures regime) and it was used for assessing the truth value of the fuzzy proposition *Low seed dormancy* (Fig. 1).

3.2. Sensitivity analysis

The sensitivity tests (Fig. 2) showed that the relative change in output values (when input variables were changed over the entire input range) was below 40% for all variables (Fig. 2). GRR was most sensitive to changes in the variable that measures the relative participation of glyphosate in the overall herbicide used (% G) (Fig. 2). The model behavior against contrasting changes in % G (values from 0 to 80% G), were a change of 35% of the final value of GRR (Fig. 2). The air temperature variables also showed relatively high I values. However, this change only occurred in the scenario in which all variables were kept in the baseline condition for the minimum risk, and each of the temperature values were changed until the condition is equivalent to the maximum risk. The value obtained for these variables showed that, compared with more extreme changes in temperature values, the risk value of GRR increased by 19%, but only decreased by 1% (Fig. 2). This asymmetric pattern indicates that the fuzzy network was more reluctant to reduce the risk values than to increase them when the air temperatures are changed. The remaining input variables presented a symmetrical pattern of equal sensitivity both increased as compared to the decrease of GRR (Fig. 2).

3.3. Regional assessment

The GRR regional assessment covered a cropping area of 1,338,300 km² (Map 1) from the estimated 10 × 10 km grid created by kriging that contains 13,382 records. Climatic data from each point was calculated by kriging and crop sequence, management regime and landscape characteristics came from data at production zone level (see Appendix B). Results from the regional model application showed GRR values in the range of –0.24 to 0.74 (Map 1). However, only 5.5% of the area analyzed showed GRR values lower than 0 (Map 1). GRR values ranging between 0 and 0.25 were included in 21.5 percent of the remaining area; 57.3% appeared with values in the range of 0.25–0.5, and 15.6% had values in the range of 0.5–0.74 (Map 1). Regarding the geographic distribution of the GRR values, areas where glyphosate resistance risk was partially false (i.e. GRR < 0) were located in the southern part of the study area (the entire production zone 20 and part of the zone 18) and a small portion of extreme northwest of the map, which is characterized by sharp elevation change. These areas have the lowest values of

intensity of use of glyphosate with a low temperature thermal regime during the year (see Appendix B). Areas characterized by high risk values were located mainly in the northwest of the country (productive zone 0) and in the central region, the most productive and long-agricultural history area among the cropping areas of Argentina (productive zone 16) (Map 1). Another response pattern that resulted from the regional assessment was the low intrazonal GRR variability in north-central areas of the country (Map 1). This lower intrazonal variability was associated to low spatial variability of the temperature regime (data not shown), so GRR values mainly respond to changes in the variables measured at the production zone level (i.e. crop rotation, management regime and landscape characterization).

4. Discussion

In this paper we derived a novel analytical framework for modeling the relative influence of different ecological and management drivers on herbicide-resistance evolution rate. The novelty of this approach compared to other models proposed earlier to calculate the risk for herbicide evolution (i.e. classical parametric models) (Gressel et al., 1996) are mainly based in 1) a shift from probability theory to fuzzy logic for the management of uncertainty and 2) a clear and operational model structure since it uses easily available data and the rules; and inputs are totally explicit and can be changed or updated as our knowledge about the system improves. The modeling of the risk of herbicide resistance evolution in large areas entails a large number of interactions and uncertainties. In such highly complex systems, where both the statistical data and the physical knowledge required for a purely probabilistic risk analysis are scarce, a fuzzy logic approach for system modeling could provide a complementary modeling approach, by using degrees of belief and plausibility instead of a probabilistic approach where parameters are usually treated as fixed but unknown values (Karimi and Hüllermeier, 2007). Furthermore, these fuzzy approaches can easily evolve toward traditional probabilistic methods as information is collected and the risk assessment process develops.

Although we have no data for a rigorous model validation, the sites in which the model produced high GRR values (Northern Córdoba: productive zone 10, Southern Santa Fe Province: productive zone 13, Eastern Salta: productive zone 0, and Tucumán: productive zone 3) correspond to areas in which there are official reports of the occurrence of glyphosate resistance for this weed (Binimelis et al., 2009). Noteworthy is that similar risk values may result from different effect integration of variables. For example, in Eastern Salta (northern Argentina, productive zone 0) high risk values are driven by high temperatures; whereas in North Buenos Aires province (productive zone 16) the GRR values are determined by agroecosystem characteristics that enhance gene flow and the use of no-tillage. Despite that our model predictions indicated high risk values for both zones, there are still no reports of resistance in zone 16, which historically has received the highest accumulated glyphosate dose application in Argentina (Viglizzo et al., 2004). However, the model structure, by considering the multiple and complex interaction among system components, would predict the potential effects of both environmental and management drivers on the risk of herbicide resistance evolution (not the parametric assessment of a specific herbicide resistance evolution rate).

The GRR model results have both functional and practical implications. For example, in productive zone 16, occurrences of herbicide resistant biotypes may be restricted due to environmental conditions, basically temperature, which regulates population size and growth and directly affect the evolution rate (Jasieniuk and Maxwell, 1994). However, despite of the low probability, if resistant individuals would occur or are introduced into the zone through seed immigration the model predicts that they will remain and spread. Instead, in productive zone 0, there is a high probability for spontaneous occurrence of resistant populations that is driven by the environmental conditions that sustain high population size and fast growth rates and short generation times interacting with landscapes with high levels of agrochemical toxicity. Thus, in one case management should be oriented to reduce gene flow whilst in the other should focus in reducing the selective pressure.

Most of the available information to deal with resistance evolution is oriented toward handling the problem once it is detected.

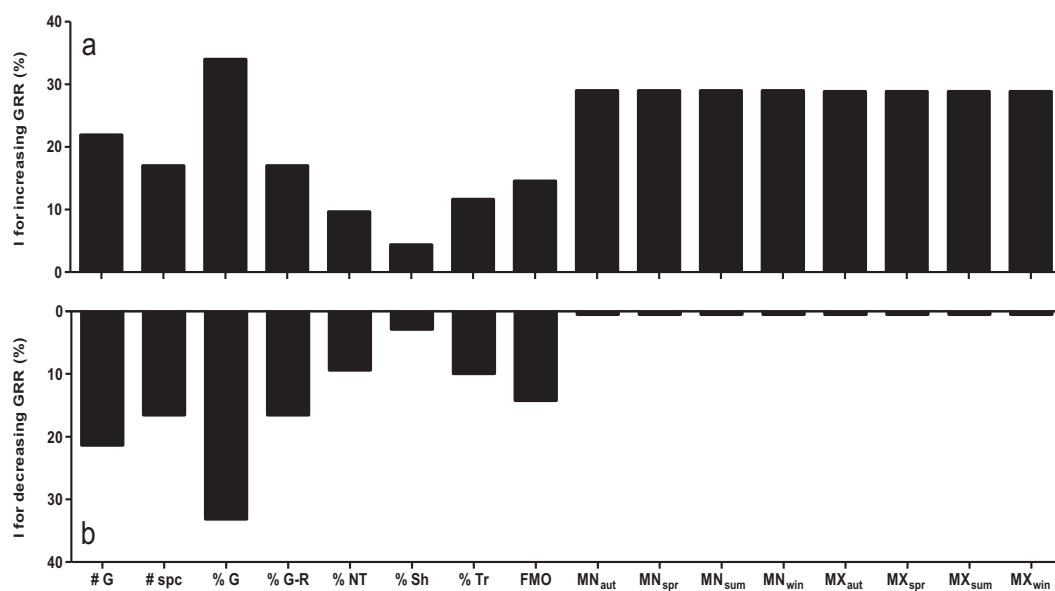
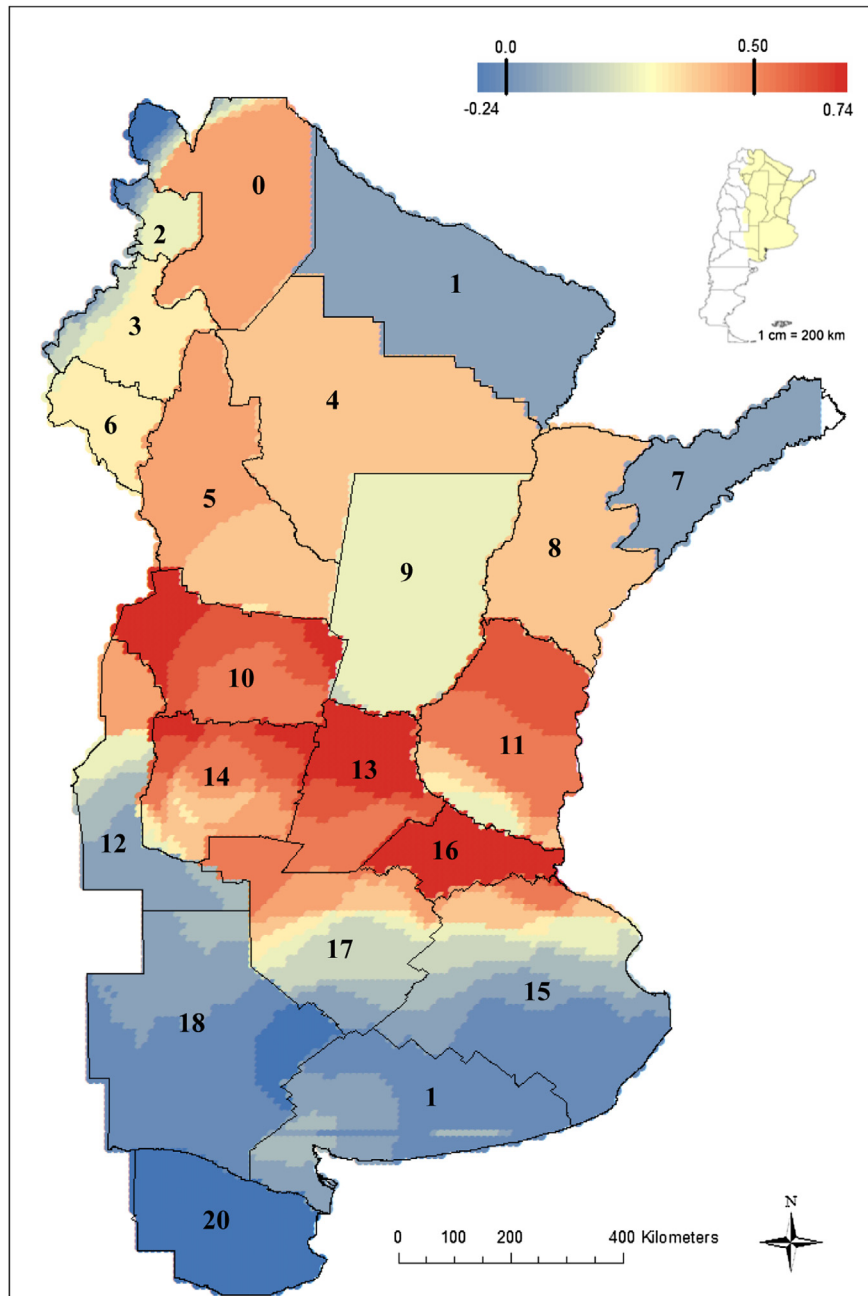


Fig. 2. Results of sensitivity index I calculations on each input variable. Sensitivity outcome was calculated by changing each input variable until the value of individual maximum risk using a baseline of $GRR = -1$ (minimum risk) (a); and by changing each input variable until the value of individual minimum risk, using a baseline of $GRR = 1$ (maximum risk) (b). Variable codes are in Table 1 and Fig. 1. % Sh and % Tr are shrub and tree closeness, respectively (see Fig. 1).



Map 1. Regional assessment of the glyphosate resistance risk (GRR) values. The color scale indicates the risk value for the range observed (−0.24–0.74). The numbers represent the code for each production region (zone code). (For interpretation of the references to color in this legend, the reader is referred to the web version of this article.)

This means that permanent monitoring and screening is advised for early detection of resistance and then various tools and practices are recommended to deal with the problem (Shane Friesen et al., 2000). However, many of these approaches are not incorporated because they are costly in terms of money, time and labor. The use of the fuzzy-logic based model developed in this work as prior for ecological models may improve this situation, as a useful cost-effective assessment tools for making exploratory predictions about the effect of multiple drivers on the risk of herbicide resistance evolution.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at <http://dx.doi.org/10.1016/j.cropro.2013.04.004>.

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