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A model-based approach to assist variety evaluation in sunflower crop

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Abstract¹

Assessing the performance and the characteristics (e.g. yield, quality, disease resistance, abiotic stress tolerance) of new varieties is a key component of crop performance improvement. However, the variety testing process is presently exclusively based on experimental field approaches which inherently reduces the number and the diversity of experienced combinations of varieties x environmental conditions in regard of the multiplicity of growing conditions within the cultivation area. Our aim is to make a greater and faster use of the information issuing from these trials using crop modeling and simulation to amplify the environmental and agronomic conditions in which the new varieties are tested.

In this study, we present a model-based approach to assist variety testing and implement this approach on sunflower crop, using the SUNFLO simulation model and a subset of 80 trials from a large multi-environment trial (MET) conducted each year by agricultural extension services to compare newly released sunflower hybrids. After estimating parameter values (using plant phenotyping) to account for new genetic material, we independently evaluated the model prediction capacity on the MET (relative RMSE for oil yield was 16.4%; model accuracy was 54.4 %) and its capacity to rank commercial hybrids for performance level (relative RMSE was 11 %; Kendall's $\tau = 0.41$, $P < 0.01$). We then designed a numerical experiment by combining the previously tested genetic and new cropping conditions (2100 virtual trials) to determine the best varieties and related management in representative French production regions. Finally, we proceeded to optimize the variety-environment-management choice: growing different varieties according to cultivation areas was a better strategy than relying on the global adaptation of varieties. We suggest that this approach could find operational outcomes to recommend varieties according to environment types. Such spatial management of genetic resources could potentially improve crop performance by reducing the genotype-phenotype mismatch in farming environments.

¹This is the post-print version of the manuscript published in *European Journal of Agronomy* (10.1016/j.eja.2016.09.001)

Introduction

The purpose of plant breeding programs is to develop new crop varieties with improved traits such as grain yield and quality across a range of environmental conditions. As newly released crop varieties will be grown in agro-ecologically diverse target regions, it is important to test candidate genotypes in a representative sample of environments (climate, soils, cropping systems) from the target region and to assess genotype-by-environment ($G \times E$) interactions. $G \times E$ interactions correspond to significant changes in the relative performance of the genotypes when they are evaluated in different environments. Such interactions could be substantial in sunflower crop as their contribution to total yield variance may range from 5 to 20 % (far less than the E contribution but generally more than the G contribution) (de la Vega et al., 2001; Foucteau et al., 2001; Marinković et al., 2011). Large and regional $G \times E$ interactions complicate selection for broad adaptation (de la Vega, 2012) but identifying specifically adapted genotypes could be promoted in advisory systems to optimize locally the variety choice (Jeuffroy et al., 2014).

New lines and varieties developed by breeders are usually subjected to multi-environment trials (MET) to evaluate their relative performance for a target population of environments (TPE) (DeLacy et al., 1996; Welham et al., 2010). Today, these trials still play a key role in variety testing during breeding programs as well as for providing recommendations to farmers by extension services. A range of stakeholders are involved in this experimental testing: seed companies, extension services, cooperatives, private consultants and public services in charge of the official registration, sharing common experimental designs and methodological questions but having also their own objectives and needs (Lecomte et al., 2010).

The schemes used for official variety testing of field crops are slightly different from one country to another. However, there is a common feature in Europe (Van Waes, 2009) where official variety trials are arranged by dedicated institutes for the examination of value for cultivation and use (VCU). These VCU trials aim to emulate practical cultivation conditions in areas suitable for each crop. Before its commercial release, each variety undergoes VCU trials for at least two years before entering in the National List of Plant Varieties. Thereafter the variety undergoes trials for another 2-3 years to identify the best performing new varieties under local conditions and provide descriptions of their main agronomic and quality characteristics. These trials result in the production of Recommended Variety Lists. The recommendations for variety cultivation are published either as national summaries or as regional bulletins. Altogether the testing of a variety in official variety trials takes 3 to 6 years depending on the countries and crops.

In France, a new variety is registered in the Official Catalog of Plant Varieties after two or three years of successful field testing (pre-registration) conducted by GEVES² (in charge of official seed and variety testing) using METs. Then newly released varieties are tested over a wider area and with more trials to determine their regional performances by technical institutes in charge of extension services (post-registration). Regarding sunflower, the French technical institute for oilseed crops (*Terres Inovia*³) is in charge of the post-registration activity. In parallel, seed companies and cooperatives also conduct private testing to enhance their own expertise.

However, these METs are conducted at great expense and there is potential to make greater and faster use of the information issuing from these numerous trials for registration and further recommendation. Focusing on sunflower, we identified several weaknesses of the current VCU design exclusively based on field testing in France (Debaeke et al., 2010, 2011):

- (1) Pre- and post-registration trials (respectively conducted by *GEVES* and *Terres Inovia*) are not pooled for a common analysis and the number of trials in each MET steadily decreases with time. Currently, each sunflower variety is thus assessed on 15 to 45 trials then the results are clustered in one to four regional pools for simplifying recommendations. When pooling all the maturity groups and oil composition types (linoleic vs oleic), about a hundred trials are carried out each year to assess the agronomical, technological and environmental value of newly released varieties. Consequently, the independent analysis of networks (and years) increase the risk of matching the wrong management or location to a variety, and also mean that a variety of value to a particular location might be discarded prematurely. Additionally, the crop management and soil conditions observed in evaluation networks does not match farmer's conditions where a greater proportion of shallow soils and low-input management conditions (no irrigation, low plant density) were observed

²Groupe d'Etude et de Contrôle des Variétés et des Semences

³Institut technique des oléagineux, des protéagineux et du chanvre industriel (formerly *CETIOM*)

(Debaeke et al., 2012). Consequently, the capacity of these METs to represent the target population of environments is decreasing from year to year, because of the sheer decrease of the number of trials, and because of their design. Although this experimental network covers the main regions of sunflower production in France, more diverse environmental conditions (soil, weather, crop management) would undoubtedly improve the assessment of yield stability.

- (2) In many cases, if yields are low at particular locations because of drought stress, the entire trial will be rejected because of increased error variances. We argue that when these data are discarded for statistical reasons, valuable information is lost. More importantly, released varieties can be biased towards those that perform well under ideal conditions, but run the risk of performing poorly when water is limiting (Pidgeon et al., 2006).
- (3) Only a few criteria are used to assess the performance of new sunflower varieties and they are restricted to final productivity, grain quality, earliness and tolerance to major diseases (Table 1). Although sunflower is a summer crop, grown without irrigation in shallow to moderately-deep soils, no routine evaluation of drought tolerance traits is performed (except earliness at anthesis which is a drought escaping trait). Therefore, current evaluation criteria underestimate the rusticity of some varieties, eventually performing better under water deficit. Moreover, there has been little, if any, sound characterization of the physical environment (e.g. available soil water) and of the constraints perceived by plants (water and nitrogen stresses, disease severity, ...). A proper characterization of the environments over the MET (e.g. Chenu et al., 2011) would facilitate the analysis of $G \times E$ interactions and the clustering of trials having similar stress patterns.
- (4) On each site, a single crop management system is tested, independently of variety-specific requirements, which impedes the proposal of a specific “variety-management” recommendation per type of environment. Therefore, MyVar, a decision support tool developed by *Terres Inovia* in 2014, does not provide cultivar recommendations for crop management but only indicates characteristics of suitable varieties.

Criteria	Entry	Levels	Details
General information	Breeding company	-	
	Year of release	3	<2005, 2005-2010, >2010
	Registration EU Country	2	France, Abroad
Plant phenology	Anthesis earliness	5	very early to late
	Maturity earliness	5	very early to late
Plant morphology	Plant height	3	short, medium, tall
Disease tolerance	Phomopsis stem canker	5	
	Sclerotinia head rot	4	
	Sclerotinia basal stalk rot	3	
	Verticillium wilt	4	
Downy mildew resistance	Resistance profile	3	RM9, RM8, other RMs
Herbicide tolerance	Technology employed	3	none, Clearfield, Express Sun
Seed characteristics	Thousand seed weight	3	low, medium, high
Oil characteristics	Oil concentration	4	Low, medium, high, very high
	Oil quality	2	high oleic, linoleic (mid-oleic)
Yield performance	Performance level	5	Scale depending on multi-location field trials

Table 1. Criteria available in France to choose a sunflower variety. These criteria are included in the MyVar web tool developed by Terres Inovia.

While all these stated problems increase the risk of matching the wrong management or location to a variety, they may also mean that a variety of value to a particular location is discarded prematurely. Consequently, statistical analysis of the data collected on METs has received a lot of attention, largely in response to the difficulties caused by $G \times E$ interactions (Malosetti et al., 2013; e.g. Piepho et al., 2012). Besides, in spite of their potential interest, dynamic crop models have not been used extensively to explain and predict $G \times E$ interactions (Bustos-Korts et al., 2016; Chapman, 2008; Chapman et al., 2002). Generally speaking, we may consider that environmental characterization and diagnosis of yield limiting factors are not sufficiently practiced by breeders and advisory services to exploit the $G \times E$ interactions

that could be detected. We assume that crop modeling and simulation could significantly improve the efficacy of this experimental assessment by its ability to explore untested conditions and by giving access to soil and plant variables that are not measured in variety trials. For instance, the SUNFLO crop model (Casadebaig et al., 2011; Lecoœur et al., 2011) was developed to simulate on a daily step the response of sunflower genotypes to various soil-weather environments and management options (sowing date, plant density, nitrogen fertilization, irrigation) and some applications in variety testing and plant breeding have been suggested (Casadebaig and Debaeke, 2011; Casadebaig et al., 2014; Jeuffroy et al., 2014).

In this study, we will explore how field-based assessment can leverage simulation, either to characterise environments (simpler, E problem) or to rank cultivars (harder, $G \times E$ problem). The objective of this contribution is to develop an integrated framework for variety evaluation of sunflower based on crop modeling in order to widen and complete the current information on sunflower varieties provided by official advisory, extension services or private seed companies for a range of environmental and agronomic conditions. The potential use of this framework will be illustrated as a proof of concept.

A framework to include crop modeling in the current variety evaluation process

A model-based approach was designed to assist variety evaluation in due time and to amplify the environmental and agronomic conditions in which the varieties are routinely tested. Four steps were identified and integrated in the current process of pre- and post-registration used in France by *GEVES* and *Terres Inovia*, targeting the extension services and seed companies to define the proper use of newly released varieties (Figure 1). For instance questions such as *In which pedo-climatic area should I promote this material? In association to which crop management ?* are addressed by this model-based approach.

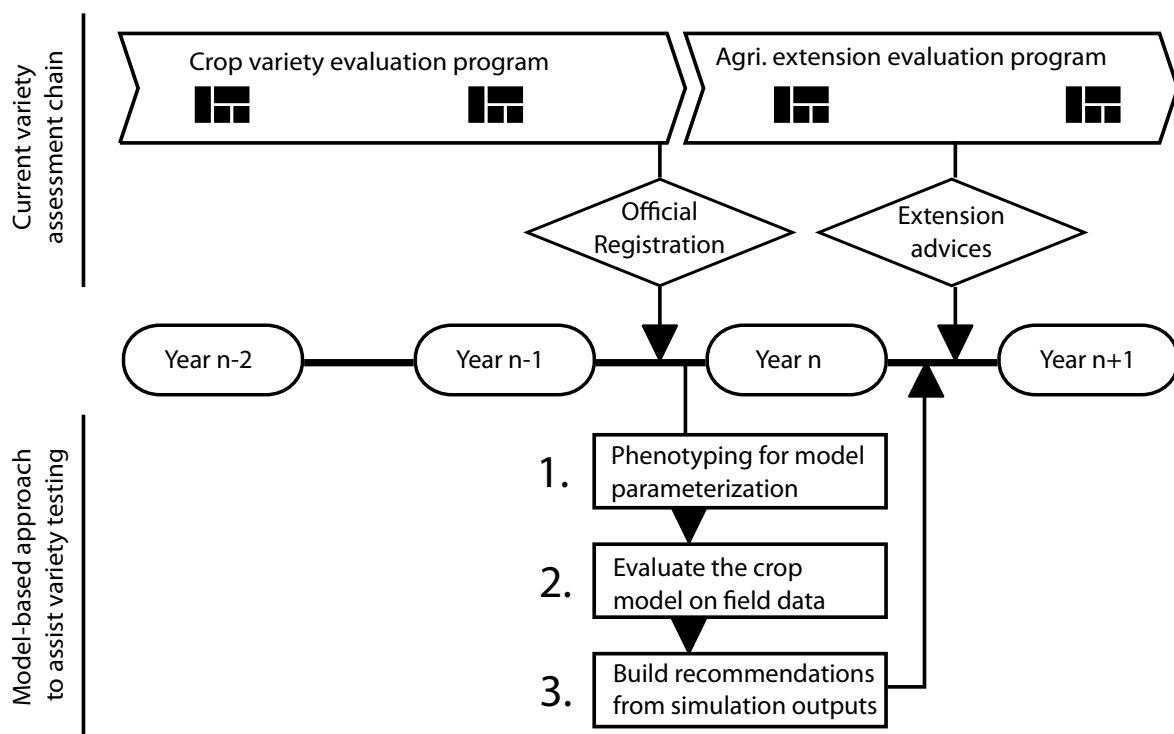


Figure 1. A framework to include crop modeling in the variety evaluation process.

The representation of the variety evaluation chain (upper part in the diagram) is based on the current French system, with two years on trials before variety release (variety evaluation MET), and two year after (agricultural extension MET). The presented approach leverage existing trials to get informations on tested varieties and to evaluate the crop model (steps 1-2). After designing numerical experiments, simulation would then provides recommendation for variety choice, accounting for the diversity of growing conditions and climatic uncertainty (steps 3).

Step 1. Phenotype newly released varieties to estimate parameter values. Phenotyping will be limited to newly released varieties, distributed for commercial development. Each year, about 15-25 sunflower varieties are registered by CTPS⁴ in France. Although the varieties have been already tested during two years by *GEVES* before their official registration, they will be tested during at least one more year over a larger MET network by *Terres Inovia* to evaluate their regional adaptation (Mestries and Jouffret, 2002). The usual phenotyping which is currently performed for variety evaluation is limited to five agronomic variables: anthesis date, plant height, achene moisture at harvest, grain yield and oil concentration (CTPS, 2014). In two selected field locations, newly released varieties will be examined in microplots to measure the 10 out of 12 of the genotype-dependent parameters of the SUNFLO crop model (Table 2). These specific trials target data on phenology, architecture and yield build-up. The response of leaf expansion and transpiration to soil water deficit (2 additional parameters) will be determined in controlled conditions (Casadebaig et al., 2008; Lecoeur et al., 2011).

Step 2. Evaluate the SUNFLO crop model using variety evaluation networks. Once parameterized to represent new varieties, the SUNFLO model will be evaluated on the *GEVES* and *Terres Inovia* networks to determine its predictive quality for this new genetic material. Depending on its performance, the model will be stated as valid or not for the range of commercial varieties. If valid, the model will be used to run numerical experiments in next step.

Step 3. Design numerical experiments and provide variety recommendation. Stakeholders will design numerical experiments combining varieties, target environments and management options. The SUNFLO model will then be run using 30 years of meteorological data to cope with climatic uncertainty. Simulated rankings (mean and standard deviation) will be produced on grain and oil yield for each combination of soil, climate and management. The previous computational results may be completed with other datasets not available through simulation, such as the tolerance of the varieties to abiotic factors (e.g. fungal diseases from Table 1). Advisers could choose the best varieties and the management to adapt and disseminate their recommendations through usual media (publications, web, meetings, ...). In this study, this final step will not be illustrated.

Materials and Methods

The SUNFLO crop model

The SUNFLO model is the core of the approach. SUNFLO is a process-based model for the sunflower crop which was developed to simulate the grain yield and oil concentration as a function of time, environment (soil and climate), management practices (irrigation, fertilization, crop density) and genetic diversity, through genotype-dependent parameters (Casadebaig et al., 2011; Debaeke et al., 2010; Lecoeur et al., 2011) (Figure 2, Table 2.). The model simulates the main soil and plant processes: root growth, soil water and nitrogen content, plant transpiration and nitrogen uptake, leaf expansion and senescence and biomass accumulation, as a function of main environmental constraints (temperature, radiation, water and nitrogen deficit).

This model is based on a conceptual framework initially proposed by Monteith (1977) and now shared by a large family of crop models (Brisson et al., 2003; Holzworth et al., 2014; Jones et al., 2003). In this framework, the daily crop dry biomass (DM_t) is calculated as an ordinary difference equation (eq. 1) function of incident photosynthetically active radiation (PAR , MJ m⁻²), light interception efficiency ($1 - \exp^{-k \cdot LAI}$) and radiation use efficiency (RUE , g MJ⁻¹, Monteith (1994)). The light interception efficiency is based on Beer-Lambert's law as a function of leaf area index (LAI) and light extinction coefficient (k). The SUNFLO model is based on a distributed approach of leaf expansion and senescence rather than a homogeneous canopy layer (*big leaf*) and intercepted radiation per LAI is used to drive leaf expansion response to cropping density (Rey et al., 2008).

$$DM_t = DM_{t-1} + RUE_t \cdot (1 - \exp^{-k \cdot LAI_t}) \cdot PAR_t \quad (1)$$

Thus, the simulated $G \times E$ interactions result from the impact of genotype-dependent traits (phenology, architecture, biomass allocation) on the capture of environmental resources (radiation, water, nitrogen) and on the differential responses of the genotypes to environmental constraints in a dynamic feed-back.

⁴Comité Technique Permanent de la Sélection des plantes cultivées

The model divides the crop cycle into 6 phenological phases using thermal time (base 4.8 °C, Granier and Tardieu (1998)): (1) sowing (A0) - emergence (A2), (2) emergence - floral initiation (E1), (3) floral initiation - early anthesis (F1), (4) early anthesis - early grain-filling (M0), (5) early to late grain filling (M3, physiological maturity) and (6) physiological maturity to harvest time (M4). Each phenological stage induces differential physiological processes. Water and nutrition uptake are simulated daily and computed stress variables impact crop phenology, plant transpiration, leaf expansion, and biomass accumulation. Yield is estimated through harvest index (HI, seed:aerial biomass ratio) rather than from yield components. Harvest index and oil concentration values at harvest are estimated using multiple linear regressions using two type of predictors: (1) simulated variables estimated in the process-based part of the model (e.g. sum of intercepted light, nitrogen and water deficit) and genotype-dependent parameters estimated in non-limiting field conditions (potential harvest index and oil content) from METs.

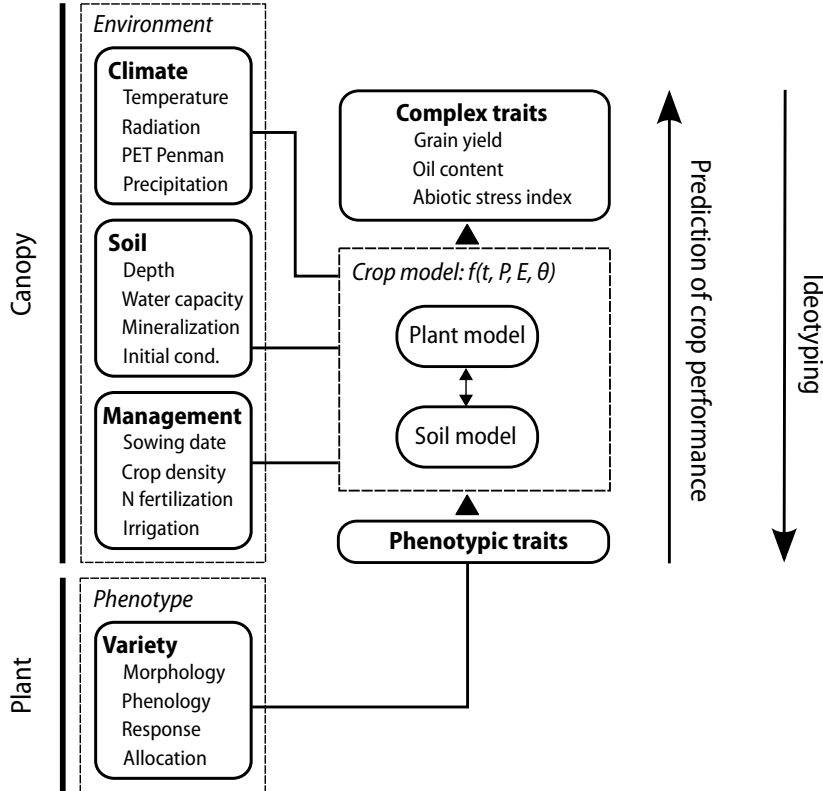


Figure 2. Schematic representation of the SUNFLO crop model. Soil-Plant system is described as a function of time, environmental inputs and phenotypic inputs (left column). Phenotypic traits are used as genotype-dependent parameters in the model.

Each variety is currently described by 12 parameters, i.e. phenotypic traits measurable in field and controlled conditions for newly released material (Casadebaig et al., 2008, 2014; Debaeke et al., 2010). The parameters can be sorted in four groups: phenology (4 parameters), leaf architecture (4), response to water constraint (2), and biomass allocation to the grains (2) (Table 2). Furthermore, we assumed that this set of 12 traits were sufficient to describe the adaptation of a variety to a location. Other traits, not accounted for in the crop model can also drive plant response to environment (such limitations are further discussed in Casadebaig et al., 2011).

Process	Symbol	Function	Unit	Field	Controlled	Model	MET	mean	min	max
Phenology	TDE1	Temperature sum to floral initiation	<i>C.d</i>	Possible	No	Yes	No	482	441	523
Phenology	TDF1	Temperature sum from emergence to the beginning of flowering	<i>C.d</i>	Yes	No	No	Yes	836	765	907
Phenology	TDM0	Temperature sum from emergence to the beginning of grain filling	<i>C.d</i>	Possible	No	Yes	No	1083	1012	1154

Process	Symbol	Function	Unit	Field	Controlled	Model	MET	mean	min	max
Phenology	TDM3	Temperature sum from emergence to seed physiological maturity	<i>C.d</i>	Yes	No	No	No	1673	1538	1831
Architecture	TLN	Potential number of leaves at flowering	<i>leaf</i>	Yes	Possible	No	No	29	22	37
Architecture	LLH	Potential rank of the plant largest leaf at flowering	<i>leaf</i>	Yes	Possible	No	No	17	13	21
Architecture	LLS	Potential area of the plant largest leaf at flowering	<i>cm²</i>	Yes	Possible	No	No	450	334	670
Architecture	K	Light extinction coefficient during vegetative growth	-	Difficult	No	Yes	No	0.89	0.78	0.95
Response	LE	Threshold for leaf expansion response to water stress	-	No	Yes	No	No	-4.4	-16	-2.3
Response	TR	Threshold for stomatal conductance response to water stress	-	No	Yes	No	No	-9.8	-14	-5.8
Allocation	HI	Potential harvest index	-	Yes	No	No	No	0.4	0.25	0.48
Allocation	OC	Potential seed oil content	%	Yes	No	No	Yes	55	48	61

Table 2. Phenotypic traits used as crop model inputs and the way to estimate them routinely. Mean, maximum, and minimum values observed on 89 cultivars phenotyped since 2008 are indicated.

Most of these parameters are directly measured at field level in microplots ($\sim 30 \text{ m}^2$) or in controlled conditions (greenhouse or outdoor platform) on isolated plants. Some parameters are indirectly estimated from observed traits: floral initiation and beginning of grain-filling dates are determined from flowering date; light extinction coefficient is estimated as a function of morphological parameters (plant height, leaf number, largest leaf height and size). Of course, the measured traits show phenotypic plasticity and thus their values change from site to site. We hypothesized that phenotypic information could be used as genotypic information (Casadebaig et al., 2011) after (1) assessing the trait phenotypic plasticity impact on variety rankings between sites and (2) using either the mean or maximum trait value as parameter value (depending on the parameter meaning), if rankings were not significantly affected (using Kendall's W test). Globally, these traits were stable enough to be used as genotype-dependent parameters (see Casadebaig et al., 2008 for response traits and Casadebaig (2008) p. 142-143 for phenological and morphological traits).

The soil is simply described by water holding capacity (mm) on the soil depth usually explored by roots and by the nitrogen mineralization rate (kg N per normalized day at 15°C). Daily weather used for simulation is composed of 5 common variables: maximum and minimum air temperatures (T, $^\circ\text{C}$), precipitation (P, mm), potential evapotranspiration (PET, mm), global radiation (GR, MJ m^{-2}).

Crop management is described by sowing date, plant density, timing and amount of nitrogen fertilization and irrigation. Detailed algorithm and equations of SUNFLO can be found in Casadebaig et al. (2011) and Lecoeur et al. (2011). The oil model was recently refined by Andrianasolo et al. (2014). SUNFLO was first developed on a commercial modeling platform (ModelMaker®) then it was implemented on the RECORD modeling platform from INRA (Bergez et al., 2013). Additional documentation is also available in the associated rsunflo R package (Casadebaig, 2013).

Step 1: Phenotyping and model parameterization

The estimation of growth and development parameters of SUNFLO is based on the direct measurement at field level of agronomic variables. The parameters representing the plant response to water deficit are rather measured in controlled conditions. The following phenotyping protocols were implemented on the varieties evaluated in the METs.

Field

In field, dense stands (6-7 plants m⁻²) were established at conventional sowing date on microplots of 30 m² replicated three times and well protected from birds, weeds, and diseases. Non limiting conditions for N and water were targeted. Two distinct types of field experiments were necessary. A first kind of experiment was carried out on a deep soil to estimate crop phenology and maximal leaf area development, provided that water and nitrogen were fully available for plant until anthesis. Practically, the experiments were conducted since 2008 on the *En Crambade* experimental station of *Terres Inovia* (Montesquieu-Lauragais, Haute-Garonne, latitude: 43.416 N, longitude: 1.629 E, altitude: 233m) on a deep clay soil where non-limiting conditions are observed each year. A second kind of experiment was carried out to limit vegetative growth before anthesis (through shallow soil). Then, irrigation at flowering allowed to maximize harvest index and oil concentration. The experiments were conducted since 2008 at the *Chambon* experimental station of *Terres Inovia* (Surgères, Charente-Maritime, latitude: 46.109 N, longitude: 0.752 W, altitude: 45 m) on a shallow, calcareous soil (*Groies*).

The phenological stages were regularly scored (emergence, early flowering, physiological maturity). At flowering, the following variables were measured for 5 plants per replicate: total leaf number (TLN), leaf area (LLS) and position of the largest leaf from the bottom (LLH), and plant height (for the estimation of the light extinction coefficient). At physiological maturity, 10 plants were sampled per plot for measuring the potential harvest index (HI). Achene oil concentration was determined by Nuclear Magnetic Resonance by *Terres Inovia* national laboratory in Ardon. Potential oil content (OC) was determined as the 9th decile of the distribution of oil concentration values measured in METs by *GEVES* and *Terres Inovia* during the pre- and post-registration process at national level.

Controlled conditions

Following Sinclair and Ludlow (1986) approach, we used a protocol in controlled conditions (Lecoeur and Sinclair, 1996) to determine the response of leaf expansion and transpiration at the plant scale after stopping watering and leaving the soil progressively drying (dry-down design) (Casadebaig et al., 2008). The objective was to monitor the response of ecophysiological variables (plant transpiration, stomatal conductance, leaf expansion) to increasing water deficit. For each tested genotype, a logistic model was proposed to describe the plant response (equation 2).

$$y = -1 + \frac{2}{1 + \exp^{(a \times x)}} \quad (2)$$

with y , relative plant transpiration rate or relative leaf area expansion rate (relatively to well irrigated control) and x , soil water deficit (indicated by the fraction of transpirable soil water, FTSW). The fitting of coefficient a gives the genotype-dependent parameter of plant response to soil water deficit used in the SUNFLO model (hereafter named *LE* for leaf expansion and *TR* for transpiration).

Step 2: Model evaluation

Data

We used the data available in the French post-registration MET from *Terres Inovia* to evaluate the predictive quality of SUNFLO. For this proof of concept, we focused on 52 locations in 2009 to compare measured and simulated oil yields with SUNFLO (Figure 3). Most of the locations came from Poitou-Charentes (16), Centre (9), Midi-Pyrénées (8) and Pays de Loire (7) regions, which represent about 75 % of the cultivated sunflower areas in France (Figure 3). Other regions covered by the network were Aquitaine (3), Auvergne (2), Languedoc-Roussillon (2), Rhône-Alpes (2), Provence-Alpes-Côte d’Azur (2) and Burgundy (1). In each location, one to four variety trials were conducted, corresponding to linoleic, oleic, early- or late-maturing panels of varieties, for a total of 80 trials performed over the network in 2009 (summarised in Table S1). Only the locations that could be reasonably described (nearby weather station, sufficient information on soil depth, reliable information on crop management) were kept for the evaluation step (80 out of 99 trials in the MET). Depending on the number of trials and the number of varieties that were sown, from 6 up to 26 varieties were compared on each location for a total of 35 distinct varieties tested over the MET. In each trial, measured variables were pooled from 3-4 replicates. Globally, 568 average plots (variety \times trial) were used for model evaluation on oil yield.

The data from the most representative weather stations were used as daily input data. At the national level, the 2009 growing season was characterized by rainfall shortage during grain filling period with contrasted impacts on yield according to soil depth and climatic area. This resulted in a climatic water deficit of 138 to 523 mm (sum of precipitation minus evapotranspiration). National grain yield was 2.4 t ha^{-1} in 2009 with variations from 1.9 to 2.9 t ha^{-1} between 1989 and 2014. Soil water capacity was estimated from European Soil Database Derived data (Hiederer, 2013) and *in situ* soil profiles and analysis when it was available. Available soil water content was ranging from 80 to 230 mm. Soil water content at sunflower planting was initialized at 80 % of available soil water content (based on soil analysis data before the sowing date). Sowing date was ranging from March, 26 to May, 7. Extreme values of plant densities were 4.8 and $6.5 \text{ plants m}^{-2}$. Supplemental irrigation ($< 60 \text{ mm}$) was applied only in 5 locations out of 52. The amount of nitrogen fertilizer applied was ranging from 0 to 92 kg N ha^{-1} . As residual N was generally not measured in most of the situations, a default value was fixed at 60 kg N ha^{-1} . This corresponds to the average value of N mineral at the end of winter simulated by EPICLES model in more than 200 farmer's fields from South-West France during two years (2007-2008) (Champolivier et al., 2011).

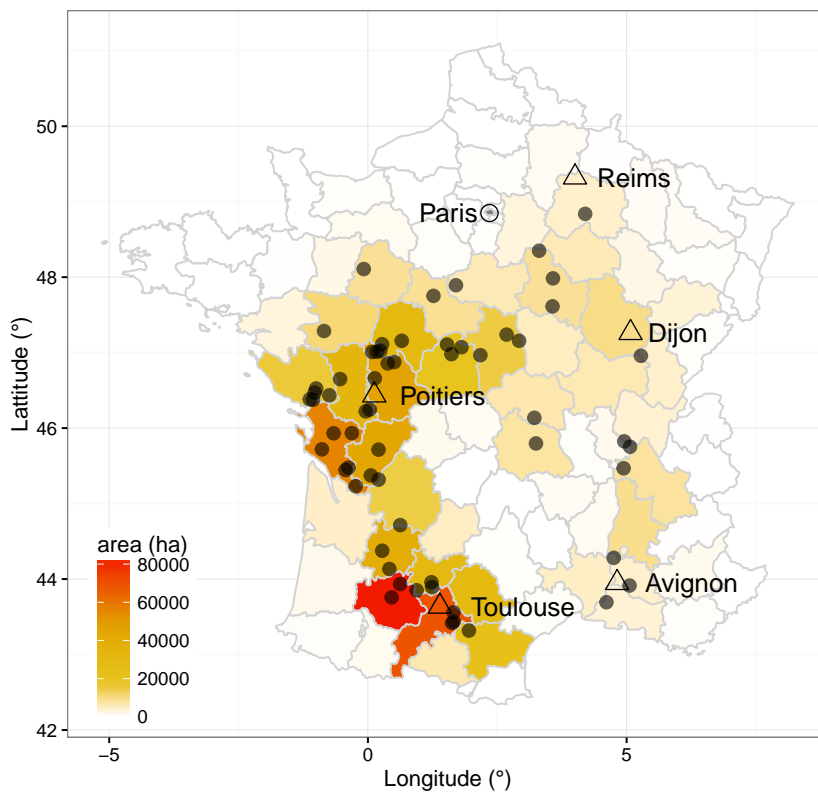


Figure 3. Distribution of the 52 experimental platforms from the post-registration network from CETIOM used for SUNFLO evaluation in 2009. The geographical distribution of experimental platforms (dots) is mapped in relation with the main sunflower producing regions in France. The five locations used in the numerical experiment are indicated with triangles (from North to South : Reims, Dijon, Lusignan, Avignon, Toulouse).

Methods

We provided a range of metrics allowing to get an overview of the crop model performance in this specific usecase, i.e. where input data and observed variables are more prone to uncertainty than in designed research trials. We evaluated the model prediction capacity using three approaches. First, a visualization of residuals (observed - simulated values) for environmental and genotypic main effects, along with the computation of several goodness-of-fit metrics (RMSE, bias, Kendall's τ) (as suggested in Wallach et al., 2014). We also evaluated the model capacity to rank each individual situations into three mutually

exclusive yield class (low, medium, high OY), based on 3-quantiles of yield distribution. We derived model accuracy (the proportion of exact predictions) and weighted Cohen's kappa (Cohen, 1968) from the contingency table (confusion matrix, i.e. counts of observed class as a function of predicted class). Cohen's κ is a measure of agreement between two qualitative variables (observation, simulation). Finally, to focus on G×E interactions we compared the model error with three kind of parameterizations, expressed as (1) $Y = f(E)$, i.e. averaging genetic variability; (2) $Y = f(G)$, i.e. averaging environmental variability and (3) $Y = f(G, E)$, i.e. actual parameterization. This last evaluation was carried both on this study dataset (*extension*) and a previous dataset where more distinct cultivars were evaluated on less contrasted locations (*genetics*) (described in Casadebaig et al., 2011).

Step 3: Model application

We designed a numerical experiment to illustrate the potential use of simulation to evaluate variety performance under different environments and management options. Five climatic stations covering the sunflower growing area were selected: Reims, Dijon, Lusignan, Avignon, Toulouse (Figure 3). 35 years (1978-2012) of daily climate data were used for representing climatic variability. Soil variation in each region was summarized by two soil depths corresponding to values of available soil water content of 100 and 200 mm. Options of crop management were simplified: two different sowing dates (April 1 ; April 30) and a range of plant densities observed in practice (3, 5 and 7 plants m⁻²). Each of the 35 phenotyped varieties were simulated on 350 pedo-climatic environments (5 locations × 2 soils × 35 years) on which 6 crop management options were applied. The whole exercise resulted in 2100 virtual trials and 73500 model runs.

Our operational aim was to provide recommendations for the cultivated genetic material according to broad cultivation conditions in order to reduce the phenotype-environment mismatch. For that, the target population of environments was grouped in 10 broad environments, corresponding to location × soil conditions. Data from the simulated multi-environment trial was summarized by ranking the varieties according to their mean oil yield (averaged over 35 years and 6 management conditions), for each of these 10 environments. Additionally, each environment was characterized by mean climatic water deficit (ET:PET ratio, %) and mean performance level (oil yield, t ha⁻¹). Concerning recommendations for coupled variety-management options, we proceeded by ranking management options for each broad environment × variety combinations (350 cases). We presented these results with a subset of five contrasted varieties from different seed companies (ES Biba, Extrasol, NK Kondi, SY Listeo, Vellox) and two broad environments (North deep soil, South shallow soil). Kendall's coefficient of concordance (Kendall, 1948) was used to test the agreement in variety or management rankings among the 10 environments.

Results

Step 1: Phenotyping and model parameterization

Phenotypic variability among a range of commercial varieties

In 2009, the performance of 35 varieties (oleic and linoleic) was tested at field level over a range of environments in France (post-registration MET from *Terres Inovia*). The variety panel included 12 control varieties and 23 newly registered varieties. The crop model parameters for this panel were previously obtained in 2008 and 2009, in dedicated experiments in field (Debaeke et al., 2010) and controlled conditions (Casadebaig et al., 2008).

We have illustrated (in Table 2 and Figure 4) the phenotypic variability for the crop model parameters with all the varieties phenotyped so far (89 cultivars since 2008). If differences in phenology and achene oil concentration were expected (Figure 4, panels A and D), less information was available on the components of plant leaf area (TLN, LLH, LLS) and on potential harvest index (HI) on newly released varieties. Considering traits related to plant leaf area, leaf number ranged from 22 to 37, with different position or size for the largest leaf. The largest leaf was positioned from nodes 14 to 21 corresponding to two contrasting canopy morphologies referred as *fir tree* (largest leaves at the middle-bottom) or *parasol pine* (largest leaves at the middle-top) respectively (Triboi et al., 2004). This variability was modeled by a wide range of leaf area profiles (Figure 4, panel B). The potential harvest index ranged from 0.33 to 0.48 (Table 2). The response of physiological processes to water deficit illustrates two contrasted strategies observed

among recent varieties: a *conservative* strategy, where the plants react to drought stress by reducing leaf expansion and closing their stomata when FTSW is still relatively high, and a *productive* strategy, whereby the crop keeps expanding and transpiring despite increasing drought (Sinclair and Muchow, 2001). This difference in genotypic response may induce $G \times E$ interactions depending on timing and duration of drought scenario (Casadebaig and Debaeke, 2012), e.g. the *productive* strategy may deplete soil water too rapidly and expose the crop subsequent water deficit in drought-prone conditions.

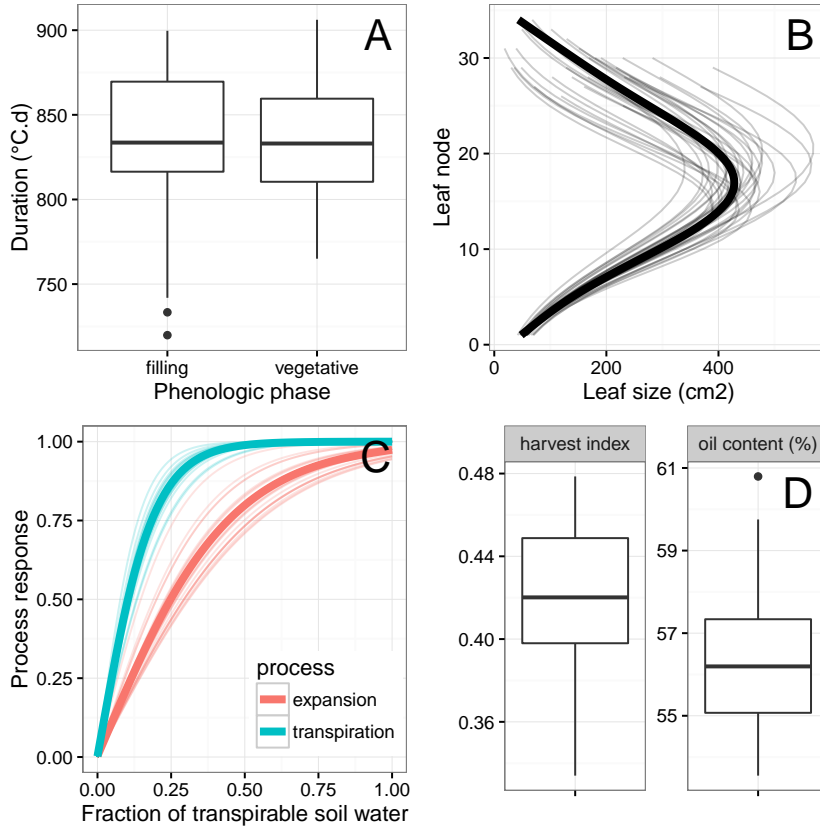


Figure 4. Phenotypic diversity in recent cultivated hybrids. Parameters are grouped by main physiological processes and we represented either their distribution or their effect in the crop model. Panel A represent crop development expressed in thermal time from emergence to phenologic phase ($TDF1$, $TDM3$). Panel B represent the genotypic variability of leaf spatial distribution on stem (TLN , LLH , LLH). Panel C represent the genotypic variability in plant transpiration (blue) and expansion (red) response to water deficit. Panel D represent potential biomass allocation to grain (HI) or potential oil content (OC)

Step 2: Model evaluation on post-registration MET

The SUNFLO model was run on each of the 80 trials of the 2009 MET for the varieties grown in each location. In this study, the evaluation of the model performance focused on oil yield (grain yield \times oil concentration) as it corresponds to the final commercial product and is the most integrated variable available. The model was evaluated on its ability to characterize abiotic stress, reproduce main environmental and genotypic effects (Figure 6) and simulate $G \times E$ interactions (Figure 7).

Environmental characterization

Water availability is the main limiting factor of sunflower crop in France (Champolivier et al., 2011; Merrien, 1992; Quere, 2004). We used the SUNFLO model to simulate water stress dynamics for each variety \times environment combination, from which we computed the actual to potential evapotranspiration ratio (ET:PET) over the three growth period (vegetative, flowering, grain filling) as an indicator of water stress at the plant level. Because this indicator depends on genotype (because of phenology, architecture

and/or water response differences as determined above), we used the mean value of ET:PET ratio for the varieties present in the trial.

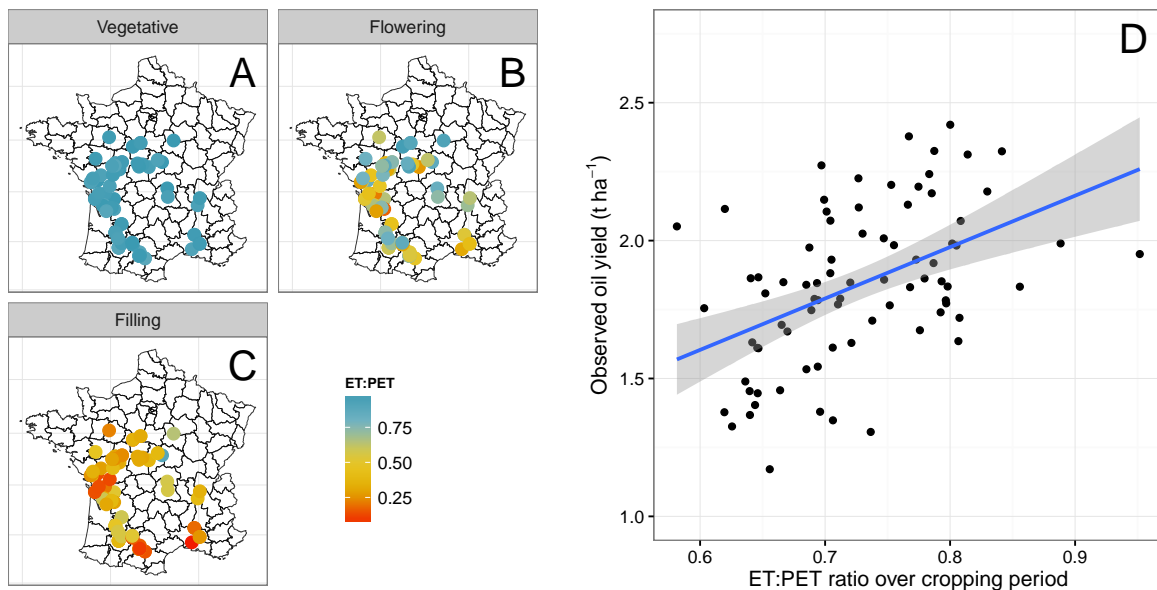


Figure 5. Characterization of the water stress level across the multi-environment network. The SUNFLO crop model was used to simulate water stress dynamics for each genotype x environment combination and we computed the mean ET:PET ratio over the considered growth period as an indicator of water stress. Maps in panels A-C represent the location of trials and the water stress level experienced by varieties during the main crop periods: vegetative (A), flowering (B) and grain filling (C). Panel D shows the correlation ($r = 0.47$, *** $P < 0.001$) between observed oil yield and simulated water stress index, for each trial.

Figure 5 illustrates the distribution of water stress patterns at national level. In 2009, as a result of differences in weather, soil and management, ET:PET ranged from 0.58 to 0.95 when considering the whole cropping period. Water stress progressively settled during pre-flowering and contrasting water stress intensities were observed during flowering and grain filling. Oil yield was significantly correlated to simulated ET:PET ($r = 0.47$; *** $P < 0.001$) when considering the 80 trials. This suggests that mean oil yield (OY) per trial can be used as an indicator for estimating model performance for ranking environments.

Environmental and genotypic main effects

The ability of SUNFLO model to rank environments and sunflower varieties is illustrated on Figure 6 where model residuals (observed minus simulated values) are plotted against simulated values for each trial (panel A) or varieties grown in 2009 (panel B). We used four metrics to evaluate prediction capacity: the root-mean-square error (RMSE), the relative RMSE (RMSE divided by observed mean), bias and Kendall's rank correlation coefficient which measures the similarity between simulated and observed rankings. Concerning environmental effects (panel A), relative RMSE was 13.1 % and Kendall's τ was 0.48 (*** $P < 0.001$). The model residuals were unbalanced, indicating a global underestimation of oil yield (positive biases of 0.13 t ha^{-1}) but no particular structure can be identified. The simulated yield range was lower than the observed one: the simulated yield standard deviation was 32% lower than the observed one. Concerning genotypic effects (panel B), relative RMSE was 11 % and Kendall's τ was 0.41 (** $P < 0.01$). The model residuals were unbalanced with a linear structure, indicating a systematic error, i.e. underestimation decreased with the level of cultivar performance (positive biases of 0.15 t ha^{-1}). In both cases, the prediction error was accurate enough to allow a significant ranking (Kendall's τ) of varieties or environments across the MET.

Moreover, we found a weak correlation between oil yield prediction error per environment and distance between trial and climatic station ($r = 0.19$; $P = 0.10$) meaning that prediction error was slightly lower when climate data were measured in the field neighbourhood.

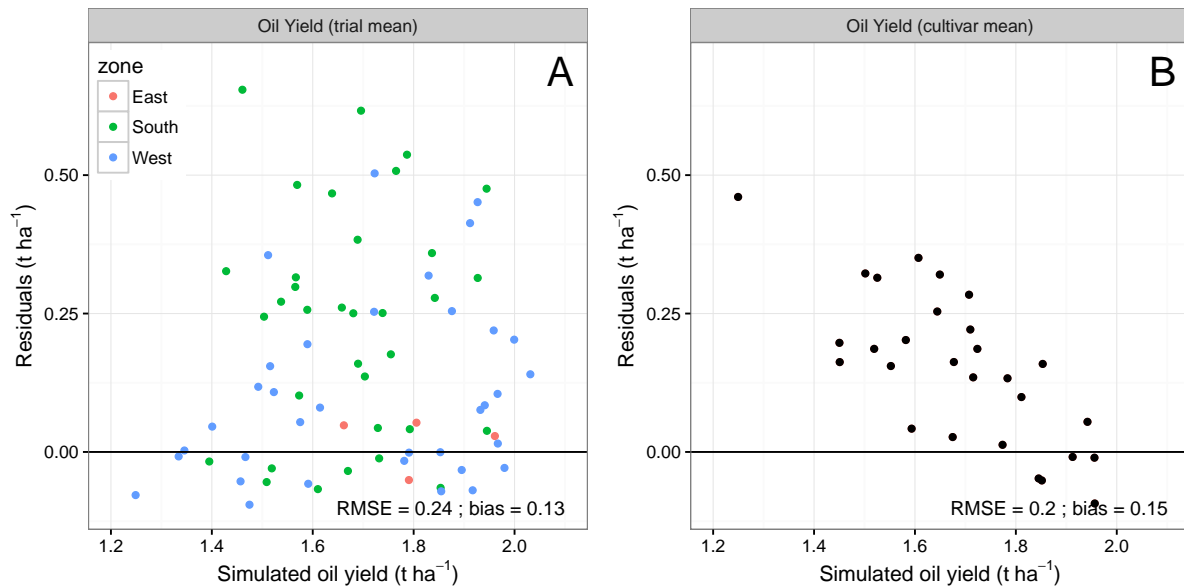


Figure 6. Model evaluation on an independent multi-environment network: environmental and genotypic main effects. In both panels, residuals (observed values minus simulated values) are plotted against simulated values. Panel A displays the model capacity to discriminate between environments (average yield value per trial, $n=80$). Relative RMSE was 13.1 % ; Kendall's τ was 0.48 (** $P < 0.001$). Panel B displays the model capacity to discriminate between genotypes (average yield value per genotype, $n=28$). Relative RMSE was 11 % ; Kendall's τ was 0.41 (** $P < 0.01$)

Genotype \times environment interactions

In this evaluation approach, we used all individual situations (568 plots resulting from a subset of 35 varieties grown on 80 trials) to evaluate the residual error (Figure 7A). Simulated oil yield ranged from 1 to 2.31 t ha⁻¹ while observed values ranged from 0.99 to 2.6 t ha⁻¹ with a simulated standard deviation 21 % lower than the observed one. The model RMSE was 0.3 t ha⁻¹ (RRMSE = 16.4 %) where Southern situations were mainly responsible for under-estimation (RRMSE = 18.8 %, bias = 0.23 t ha⁻¹ on trials in this subset - in green in Figure 7A). The model residuals were moderately unbalanced toward under-estimation of oil yield without particular structure.

The confusion matrix (Figure 7B) displays the proportion of actual G \times E combinations that were correctly predicted (diagonal) and errors (other cells). This information was summarized with two metrics: the model accuracy, i.e. the proportion of exact predictions (54.4 %) and weighted Cohen's kappa (0.5, *** $P < 0.001$) (Cohen, 1968). According to Landis and Koch (1977), a kappa value > 0.40 denotes a moderate agreement between two raters.

We also focused on the prediction capacity of the G \times E interactions component. Figure S1 indicated that, in the studied MET (*extension network*), the global prediction error (RMSE) was similar whether we used a genotype-dependent parameterization or not; although the bias was reduced in the first case. However, it was not the case when evaluating the model with another dataset (Casadebaig et al., 2011), where the genotype-dependent parameterization led to more accurate predictions (Figure S1, *genetics network*).

From these agreement methods, we can conclude that SUNFLO succeeded in representing roughly variety ranking in sunflower. Moreover, Figure 7B also indicated that the model was able to separate the less productive varieties from the best ones: the proportion of exact predictions was higher in low (C) or high (A) yield class than medium class (B).

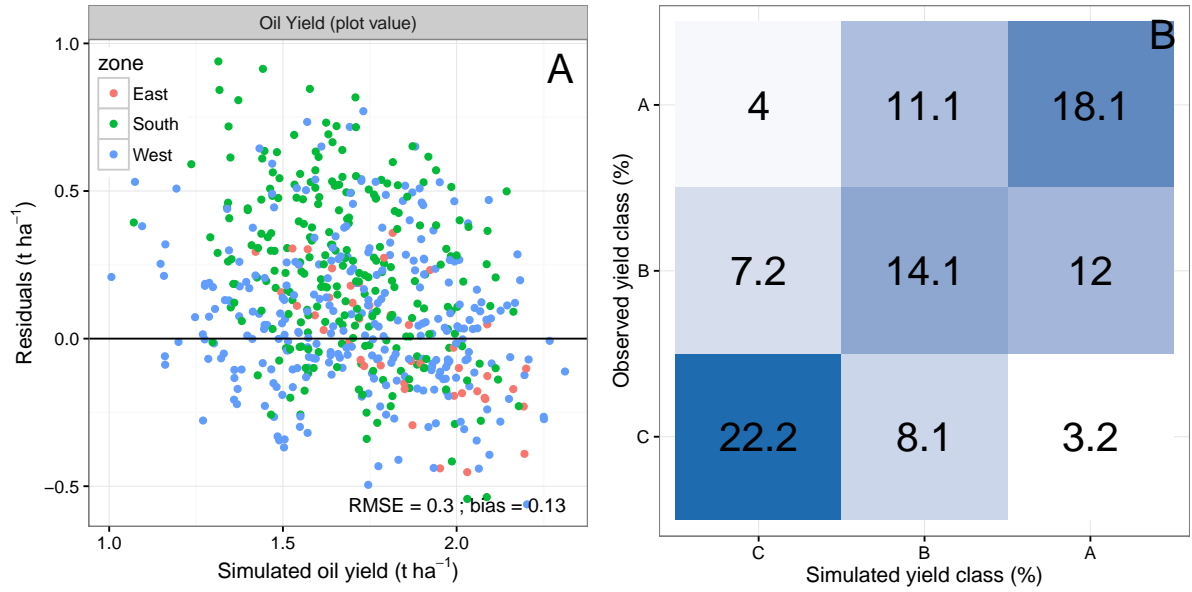


Figure 7. Model evaluation on an independent multi-environment network: global quantitative and qualitative evaluation. Panel A displays the model prediction capacity on the complete MET ($n=568$ genotype \times environment combination), with colors indicating large climatic zone in the French sunflower growing area. Relative RMSE was 16.4 %. Panel B displays the confusion matrix of the model capacity to qualitatively predict crop oil yield on the same dataset. Observed and simulated values were divided into 3 performance class from A (top third) to C (low third). The confusion matrix represents the proportion of actual $G \times E$ combinations that were correctly predicted (diagonal) and errors (other cells). Model accuracy was 54.4 % (exact predictions) and weighted Cohen's kappa was 0.49 (** $P < 0.001$).

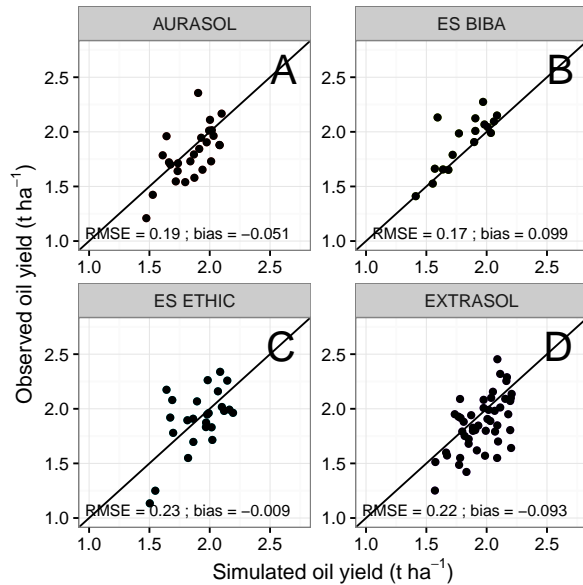


Figure 8. Model evaluation on an independent multi-environment network: subset for control varieties. Panels A-D display the model prediction capacity for a subset of four control varieties well represented across the MET, where each point is an individual plot. On this subset, the relative RMSE was ranging from 9 to 12 % ; Kendall's τ was ranging from 0.32 (* $P < 0.05$) to 0.59 (** $P < 0.001$).

Finally, we focused evaluation on a subset of 4 control varieties (*Aurasol*, *ES BIBA*, *ES ETHIC*, *EXTRASOL*) which were more frequently phenotyped ($n \in [4 - 10]$ trials, see section *Phenotyping and model parameterization*) and more represented ($n \in [17, 48]$) across the MET (Figure 8, A-D) than other

tested varieties. On this subset, the prediction error was lower than in the global dataset.

Step 3: Model application

For this study, we proposed a simple description of the target population of environments for sunflower in France. We used the SUNFLO crop model to simulate a numeric multi-environment trial network for all of the 35 phenotyped varieties, i.e. 2100 virtual trials widening the original evaluation network of 80 trials.

Providing recommendation for variety choice

Current recommendations for variety choice are mainly based on sowing date adjustment to variety earliness, i.e. an adaptation to the sum of temperature available in the growing location. Our results confirmed this trend: considering the two overall best performing varieties (legend in Figure 9), the late-maturing one performed better in colder environments, even if earliness was in the middle range of the considered genotypic diversity. We also observed that the variety rankings for the considered broad cultivation conditions were different (Figure 9). This result illustrated that the model successfully simulated $G \times E$ interactions (variety ranking is different from site to site) and could support the recommendation of varieties performing better on specific growing condition (variety in the top row are different). We formally tested this hypothesis by comparing the agreement between variety rankings with Kendall's coefficient of concordance (Kendall, 1948), which indicated a low agreement among cultivation conditions (0.25, $p = 0.038$), i.e. supported specific recommendations. However, the quantitative differences between ranks were more important in either dry or humid conditions than in mild climates, where a sub-optimal variety choice had less consequences on crop productivity (Figure 9, white figures in cells).

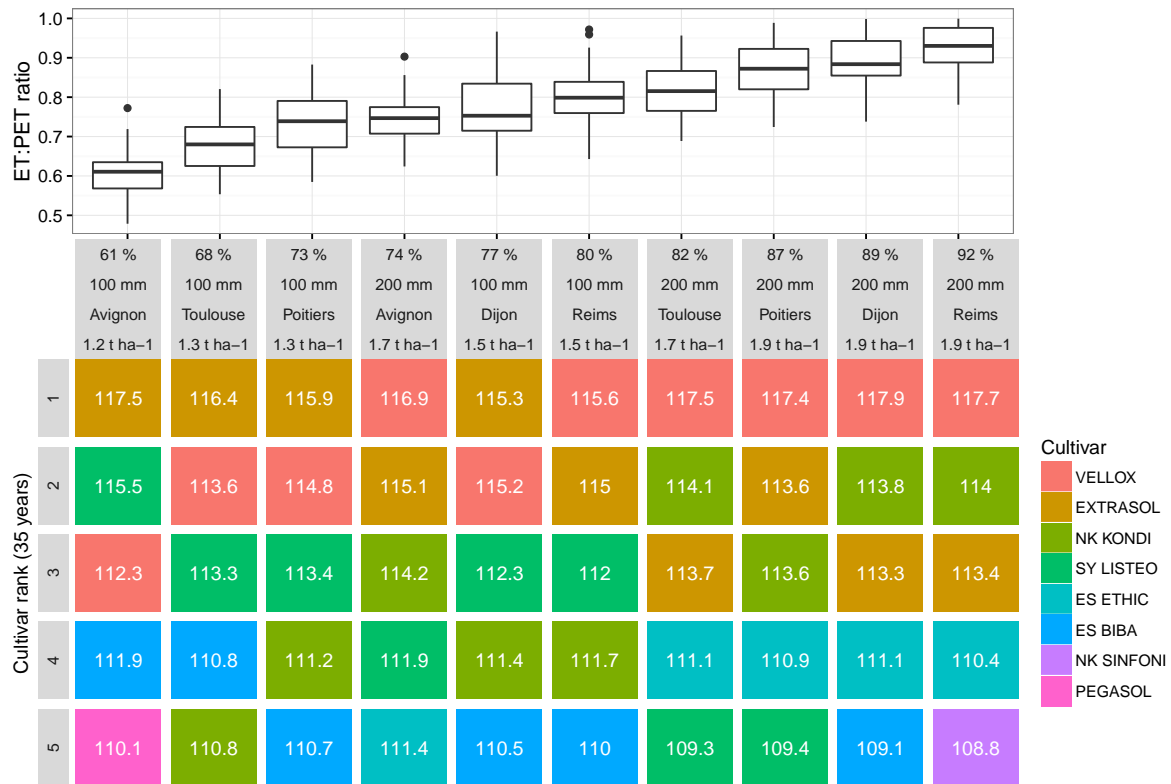


Figure 9. Using crop modeling to improve variety recommendations in broad cultivation conditions 35 varieties were ranked according to mean crop oil yield (over 35 years), for each of the 10 site \times soil conditions. The overall variety ranking in the TPE is indicated in the legend. Those 10 broad cultivation conditions were sorted by decreasing water deficit (mean ET:PET ratio) from left to right (top boxplot). The figure presents the top five cultivars (y-axis, decreasing performance from rank one to five) for each broad cultivation condition (x-axis, soil water capacity, site and mean performance in column headers). Quantitative differences between ranks are indicated in the in cells (white figures) as

variety performance relatively to mean performance in columns (%). Kendall's W coefficient of concordance (Kendall, 1948) is 0.25 (* $P < 0.05$) indicating a low agreement in cultivar ranking among cultivation conditions, i.e the possibility for location-specific recommendations.

Providing recommendations for coupled variety-management choices.

Globally, when considering all possible varieties \times broad environments (350 cases), the management had a weak impact on crop performance (white figures in Figure 10) and all management options were found to be similar ($W=0.15$, *** $P < 0.001$). In this case, a global recommendation would be to prioritize early sowings with a planting density around 7 plants m^{-2} , which happens to be similar to advices issued from agricultural extension services (Terres Inovia, 2016).

However, when focusing on more contrasted conditions, i.e. a subset of five varieties from different seed companies (cultivars *VELLOX*, *EXTRASOL*, *NK KONDI*, *SY LISTEO*, *ES BIBA*) and two broad environments (North deep soil, South shallow soil) simulation brought evidence for linking management options to the variety choice. In figure 10, we illustrated that management options were significantly dependent on variety choice and cultivation conditions ($W=0.29$, $p = 0.011$), with interactions between variety and planting density in locations more exposed to water deficit (Toulouse, 100 mm AWC) and interactions between varieties and sowing date in more favorable locations.

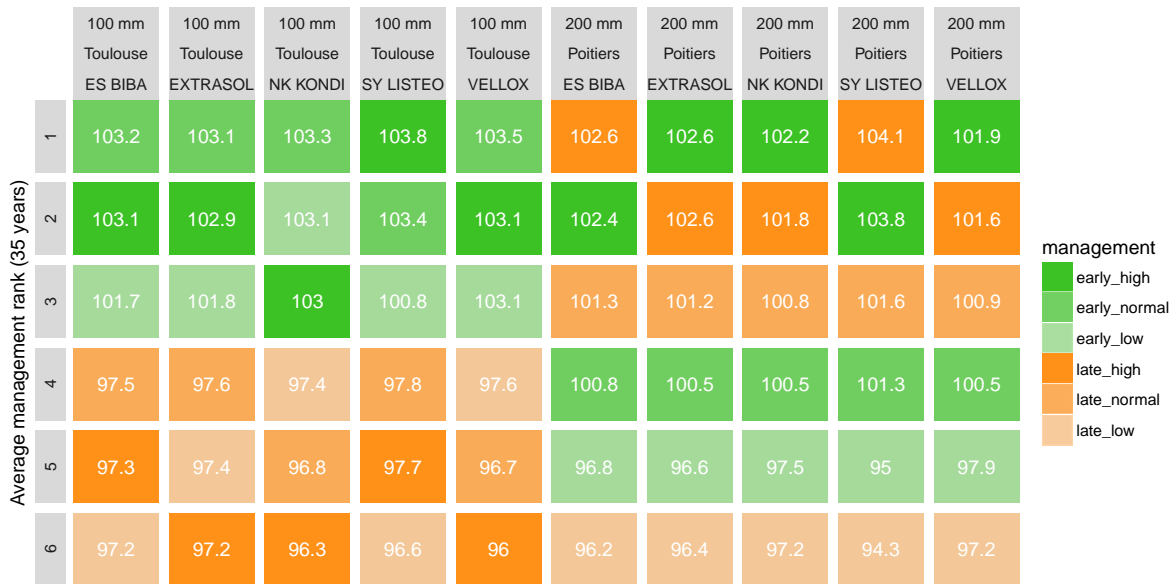


Figure 10. Using crop modeling to adapt crop management to variety choice. Six management options were ranked according to mean crop oil yield (over 35 years), for each of the 10 site \times soil \times variety conditions. The figure is based on a subset of five contrasted varieties from different seed companies and two broad environments (North deep soil - Poitier 200 mm SWC, South shallow soil - Toulouse 100 mm SWC). Quantitative differences between ranks are indicated in the in cells (white figures) as management performance relatively to mean performance in columns (%). Hue indicates early (green) or late (orange) crop sowings, while saturation indicates the sowing density.

Discussion

Predicting $G \times E$ interactions with a simulation model calibrated with measurable genotype-dependent parameters is an important specificity of our approach. In this method, the uncertainty in parameters values is driven solely by data rather than by both model and data. In many other crop models, genotype-dependent parameterization results from model fitting on intermediary or final variables (Jeuffroy et al., 2014). Moreover, as varieties are phenotyped the same year as their release, it allows model-based studies to keep pace with genetic progress; a concern raised in a recent modeling impact review (Robertson et al., 2015). We also aim to further integrate this direct parameterization approach with the official variety evaluation chain thereby improving transparency in model parameters.

In return, simulation could increase the efficiency of variety evaluation because (1) phenotyping and modeling steps are adapted to the number of varieties and trials of registration process and (2) of the possibility to conduct numerical experiments in order to test un-encountered situations and widen the climatic variability when evaluating varieties.

The model accuracy was sufficient to characterize environments and rank varieties in a national evaluation network.

The SUNFLO crop model simulated oil yield of different sunflower hybrids in various cropping environments with a reasonable accuracy (54.4 %) once (1) considered varieties were phenotyped to provide genotype-dependent parameters and (2) soil, management and climatic conditions were correctly characterized. This performance is similar to most of the published crop models often more complex than SUNFLO (Martre et al., 2015; Rosenzweig et al., 2013). However, if the model successfully ranked cultivated varieties displaying a large genetic variability, this study pointed out a lack of accuracy to discriminate those closer in terms of productivity (Figure S1 and Casadebaig et al. (2011)). The model prediction error came from the uncertainty in the input dataset (e.g. pedo-climatic data) but also from the model structure, i.e. how the physiological processes and the limiting factors are represented or not.

The uncertainty in the characterization of trial environments impacted prediction quality. For instance, when using the distance between trial and climatic data measurement location as a proxy for data quality, we showed an impact on prediction error. Representative daily climatic data (especially precipitation) are therefore absolutely necessary. We also made strong assumptions on soil nitrogen availability. Except for N fertilization which was described in crop management, we considered constant values for residual N (60 kg N ha^{-1}) and potential N mineralization ($0.7 \text{ kg N normalized day}^{-1}$) in the absence of information for each location. In field surveys, initial N at sunflower sowing could range from 30 to 130 kg ha^{-1} N depending of the cropping system and potential mineralization from 0.4 to $1.8 \text{ kg N normalized day}^{-1}$ (Valé et al., 2007). The use of a soil map (Hiederer, 2013) jointly with data from local soil analysis allowed to reduce uncertainty on soil water capacity estimation. However, soil water capacity may have been under-estimated in shallow soils with cracked subsoil, leading to underestimation of crop performance (indicated by a negative bias in model evaluation). As model prediction quality is affected by inaccurate determination of water and nitrogen availability but also initial amounts, we suggest to measure LAI on control varieties and estimate input data with numerical optimisation (Debaeke et al., 2012). Additionally, observed data are also uncertain. Experimental design based on microplots (30 m^2) tends to overestimate grain yield compared to farmers field conditions. A small number of experimental location (2/54) where grain yield was over 4.5 t ha^{-1} were not considered in evaluation because the crop model was not designed for such outliers in performance level.

The modeling options, i.e. the processes included or not in the SUNFLO crop model also impacted prediction quality. This matter was previously discussed in details during the model development (Casadebaig et al., 2011) and the key points were related to the modeling of abiotic stresses interaction and not considering biotic factors. Abiotic stresses were represented with scalars and their interaction was modeled with a multiplicative approach which tends to overestimate stress effects, leading to yield underestimation in environments most exposed to abiotic stresses (e.g. Southern environments in Figure 7A). Biotic factors were not considered in the model because the usual crop management aims to limit pests damage, particularly in variety evaluation networks. However, the occasional yield overestimation by the model was probably due to uncontrolled limiting factors, where predation (mainly by birds) during crop emergence and harvest may cause severe yield losses. As with most of the crop models, there is no efficient solution to predict yield losses caused by numerous biotic factors (e.g. for fungal diseases phoma, sclerotinia, phomopsis, verticillium). Attempts to couple detailed simulation model for plant growth and pest infection, injury and damage (Boote et al., 1983; Rouse, 1988; Savary et al., 2000; Willocquet et al., 2008) did not yet led to tools easily usable outside of specific pathosystems. Statistical or multi-criteria aggregative approaches (such as Aubertot and Robin, 2013) might be used in conjunction with crop models to represent the inherent complexity of agroecosystems.

Overall, the SUNFLO model was able to simulate trials from a MET network using accessible inputs (open-sourced soil map and climate data) and without a numerical calibration step targeting genotype-dependent parameters. On this dataset, the model performance was comparable to other crop models calibrated and evaluated on a small number of good experimental data (García-López et al., 2014; e.g. for sunflower Leite et al., 2014).

Plant phenotyping to keep pace with genetic progress and reduce uncertainty model inputs.

The model parameters chosen to represent varieties focused on key physiological processes (phenology, light interception, water response) but their number was kept compatible with manual field phenotyping protocols. These protocols are now routinely used by *Terres Inovia* extension service since 2008 to parameterize new varieties. We found that two environments generating contrasted growth conditions (one for potential canopy development, one for potential biomass allocation) are necessary and sufficient to determine the parameters of potential growth. This experimental design could be improved by including a small set of precisely phenotyped control varieties in each experiment to control the environmental effect (years and locations).

However, the recent development of high-throughput plant phenotyping could question this approach, potentially reducing uncertainty in the measurement of genotype-dependent parameters and allowing to consider new processes or parameters. Initially, we suggested a complete determination of SUNFLO parameters on isolated plants grown in greenhouse (Lecoeur et al., 2011). Although the correlation with field plants is acceptable, considering only phenotyping platforms operating in controlled conditions would failed to represent plant functioning in late grain filling stages and in dense stands. Consequently, an open-air pot platform is currently in development aiming to automatize daily measurements for water deficit, leaf area and transpiration (Blanchet et al., 2016). Such platform will target mainly the phenotyping of response traits (LE , TR) but architectural trait will also be evaluated. Some phenotyping methods might also be directly usable on MET used for variety evaluation, such as using unmanned aerial vehicles and image analysis to estimate phenological stages or multispectral camera for canopy architecture (Baret and Buis, 2008; Verger et al., 2014).

Generally, we suggest that model calibration targeting genotype-dependent parameters should be avoided both for conceptual and technical reasons. From a conceptual point of view, such parameters (in fact, phenotypic traits), are supposed to represent genotype and thus their value should not vary among environments. Secondly, it is possible to directly measure such parameters by limiting their number and designing phenotyping methods during model development.

Toward decision support systems based on modeling and simulation

The simulation of phenotypic plasticity enables a set of applications for breeders and advisers where variety evaluation is a central process (Jeuffroy et al., 2014). We briefly illustrated two of these applications: (1) the characterization of water stress constraints perceived at the plant level, in each trial environment (Figure 5) and (2) the determination of agronomic suitability of registered varieties, including variety-dependent management recommendations (Figures 9-10). In the later numerical experiment, we designed a simple scenario, using only 10 site x soil conditions to describe the actual sunflower growing area. Nevertheless, we illustrated that (1) distinct varieties could be recommended according to local pedo-climatic context and that (2) this recommendation could led to crop performance increase under climatic uncertainty (35 years of historical data). Our case study also illustrated that even if there was evidence for a variety-dependent crop management (sowing date and plant density), its impact on crop performance was modest (+ 3% compared to average management).

Simulation also enables new applications for variety evaluation. Because recurrent field trials (Figure 1) are dependent of climate variability (and in longer term, climate change), varieties released in different years were not evaluated in the same conditions. By designing a virtual MET to compare those varieties under the same climatic variability, it is possible to compare them and to assess the rate genetic progress independently of climate change. Before considering such applications, we need to develop a framework linking crop simulation with genotypes, soil and climate datasets so that involved stakeholders can design numerical experiments adapted to their specifications. Such operational decision tools should focus on parsimonious models and deliver integrated outputs easy to interpret.

Conclusions

Our aim was to present a model-based approach to assist the variety evaluation process. Although this approach was implemented on sunflower crop, it is not limited to a specific crop if the simulation model

is adapted. We showed that few phenotypic traits used as genotype-dependent parameters are sufficient to predict phenotypic plasticity observed for recent hybrids tested in evaluation networks. Nevertheless, we found that the model performed better for assessing abiotic stress (G, E component) than for ranking cultivars (G×E interactions component), especially in an agricultural extension network with inherent uncertainty in input data. Linking official variety evaluation multi-environment trials and crop modeling allowed to amplify the environmental and agronomic conditions in which the varieties are routinely tested. We suggest that this approach could find operational outcomes to recommend varieties according to environment types. Such spatial management of genetic resources could potentially improve crop performance by reducing the genotype-phenotype mismatch in farming environments.

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Supplementary material

#	site	lat	lon	SCWD	AWC	density	sowing	harvest	irrigation	fertilization
1	Saulzet	46.14	3.22	-138	121	5.6	Mar-27	Sep-07	0	85
2	Castelnaudary	43.32	1.95	-473	157	5	May-04	Sep-07	0	40
3	Castelnaudary	43.32	1.95	-478	157	6.5	May-07	Sep-07	0	60
4	Champniers	45.71	0.21	-281	148	5.6	Apr-20	Sep-07	60	50
5	Tusson	45.32	0.21	-283	86	6	Apr-01	Aug-27	0	50
6	Gibourne	45.93	-0.31	-332	130	5.6	Apr-07	Sep-02	0	80
7	Reaux	45.48	-0.37	-280	121	5.6	Apr-25	Sep-10	0	60
8	Sablanceaux	45.72	-0.89	-282	98	6.5	Apr-14	Sep-08	0	60
9	Jonzac	45.45	-0.43	-229	185	5.6	Apr-06	Sep-08	0	55
10	Civray	46.97	2.17	-247	73	5.2	Apr-06	Sep-09	0	46
11	Montigny	47.24	2.68	-238	73	6.5	Apr-14	Sep-11	0	60
12	Pecdorat	44.71	0.62	-218	140	5.6	Mar-31	Aug-27	0	60
13	Fourques	43.69	4.61	-523	158	4.8	Apr-25	Sep-07	0	42
14	Montesquieu Lauragais	43.42	1.63	-348	217	5.4	May-12	Sep-03	0	80
15	Montesquieu Lauragais	43.42	1.63	-357	217	6.5	May-05	Sep-03	0	60
16	Lanta	43.56	1.65	-453	217	6.5	May-05	Sep-17	0	60
17	Villenouvelle	43.44	1.66	-370	169	6.5	May-05	Aug-29	0	60
18	Jegun	43.76	0.46	-339	121	6.5	May-05	Sep-02	0	60
19	Jegun	43.76	0.46	-339	121	6.5	May-05	Sep-02	0	60
20	Vatan	47.07	1.81	-257	101	6.2	Apr-17	Sep-14	0	45
21	Ligré	47.11	0.27	-312	82	5.6	Apr-02	Sep-04	0	0
22	Ligré	47.11	0.27	-326	82	6.5	Apr-14	Sep-04	0	60
23	Ste Catherine De Fierbois	47.16	0.65	-347	158	6.5	Apr-14	Sep-04	0	60
24	Saint Sorlin De Vienne	45.47	4.94	-415	189	5.9	Apr-21	Sep-11	0	50
25	Rhodon	47.75	1.27	-265	158	6.5	Apr-15	Sep-11	0	60
26	Huisseau	47.89	1.7	-265	175	6.5	Apr-06	Sep-10	0	60
27	Villeton	44.38	0.28	-323	189	6.5	Apr-24	Sep-09	0	60
28	Villeton	44.38	0.28	-323	189	6.5	Apr-24	Sep-09	0	60
29	Calignac	44.13	0.42	-342	217	6.5	Apr-24	Sep-14	0	60
30	Calignac	44.13	0.42	-342	217	6.5	Apr-24	Sep-14	0	60
31	Pont Du Château	45.8	3.25	-277	106	6	May-06	Sep-25	0	40
32	Pusignan	45.75	5.07	-433	189	5.8	Apr-07	Aug-27	0	45
33	Tennie	48.11	-0.08	-341	158	6.5	Apr-15	Sep-10	0	60
34	Monbequi	43.89	1.24	-365	118	6.5	May-05	Sep-11	0	60
35	Montech	43.96	1.23	-370	178	6.5	May-05	Sep-14	0	60
36	Bollene	44.28	4.75	-393	189	5.6	Mar-31	Aug-27	0	60
37	Bollene	44.28	4.75	-441	189	6.5	Apr-10	Aug-27	0	60
38	Isle Sur La Sorgue	43.91	5.06	-475	209	5.6	Apr-09	Sep-08	0	40

#	site	lat	lon	SCWD	AWC	density	sowing	harvest	irrigation	fertilization
39	Isle Sur La Sorgue	43.91	5.06	-472	209	6.5	Apr-10	Sep-08	0	60
40	St Martin De Fraigneau	46.43	-0.74	-341	148	5.4	Apr-22	Sep-10	0	50
41	Ste Radegonde Des Noyers	46.38	-1.06	-329	171	5.6	Apr-02	Aug-26	0	40
42	Nalliers	46.47	-1.03	-330	119	5.6	Apr-22	Sep-10	0	20
43	Usseau	46.88	0.51	-314	175	5.7	Apr-10	Sep-09	0	66
44	Sossay	46.86	0.38	-311	121	5.6	Apr-06	Sep-10	0	60
45	Esnon	47.98	3.58	-215	158	6	Apr-03	Sep-08	0	50
46	St Martial	45.37	0.06	-249	150	5.6	Apr-21	Sep-07	0	46
47	St Martial	45.37	0.06	-254	150	6.5	Apr-17	Sep-07	0	60
48	Orignolles	45.23	-0.24	-274	78	5.6	Apr-23	Sep-16	0	72
49	Sablonceaux	45.72	-0.89	-335	98	5.6	May-05	Sep-14	35	74
50	Les Nouillers	45.93	-0.66	-341	130	5.6	Apr-21	Sep-08	0	69
51	St Martin Des Champs	47.16	2.92	-203	243	5.8	Mar-26	Aug-28	0	50
52	Montigny	47.24	2.68	-235	97	5.6	Apr-14	Sep-11	0	39
53	Pecclorat	44.71	0.62	-218	140	5.6	Mar-31	Aug-27	0	60
54	Montesquieu Lauragais	43.42	1.63	-351	155	6.5	May-06	Sep-07	0	60
55	Montesquieu Lauragais	43.42	1.63	-351	155	6.5	May-06	Sep-07	0	60
56	Lanta	43.56	1.65	-452	155	5.4	May-07	Sep-17	0	30
57	Villeneuve	43.44	1.66	-286	112	5.3	Apr-06	Aug-29	0	50
58	Jegun	43.76	0.46	-294	112	5.6	Apr-09	Sep-02	0	69
59	Jegun	43.76	0.46	-341	141	6.5	May-05	Sep-02	0	60
60	Lectoure	43.93	0.62	-311	224	5.6	Apr-09	Aug-31	0	61
61	Levroux	46.98	1.61	-262	158	5.6	Apr-16	Sep-11	35	54
62	Vicq Sur Nahon	47.11	1.53	-259	158	6	Apr-19	Sep-14	0	36
63	Ligré	47.11	0.27	-327	101	6.5	Apr-14	Sep-04	0	60
64	Ste Catherine De Fierbois	47.16	0.65	-313	158	5.2	Apr-21	Sep-03	0	65
65	Rhodon	47.75	1.27	-249	158	5.6	Apr-10	Sep-09	60	60
66	Huisseau	47.89	1.7	-276	175	5.6	Apr-23	Sep-16	0	54
67	Villeton	44.38	0.28	-319	189	5.6	Apr-23	Sep-09	10	70
68	Villeton	44.38	0.28	-323	189	6.5	Apr-24	Sep-09	0	60
69	Calignac	44.13	0.42	-343	217	5.6	Apr-24	Sep-14	0	92
70	Ste Christine	47.29	-0.85	-306	189	6	May-05	Sep-14	0	45
71	St Vincent La Chatre	46.22	-0.04	-348	131	5.4	Apr-27	Sep-14	0	72
72	Sainte-Blandine	46.65	-0.54	-310	103	6	Apr-21	Sep-09	0	50
73	Monbequi	43.89	1.24	-368	130	5.5	May-07	Sep-11	0	80
74	Monbequi	43.89	1.24	-366	130	6.5	May-05	Sep-11	0	60
75	Montech	43.96	1.23	-321	240	6	Apr-10	Sep-14	0	50
76	Champagne Les Marais	46.38	-1.12	-318	94	5.6	Apr-02	Sep-02	0	50
77	St Etienne De Brillouet	46.53	-1	-333	189	5.6	Apr-22	Sep-10	0	20
78	Frozes	46.66	0.13	-307	189	5.4	Apr-22	Sep-10	0	50
79	Ceaux En Loudun	47.03	0.24	-385	161	5.4	May-06	Sep-14	0	50
80	Loudun	47.01	0.08	-360	166	5.5	Apr-15	Sep-10	0	60

Table S1: Description of locations and management practices on the multi-environment trial. Headers indicates the locations and years of trials, the climatic water deficit (SCWD, mm) i.e. the sum of precipitation minus sum of potential evapotranspiration, the plant available water capacity (AWC, mm) i.e the amount of soil water reserves, the plant density at sowing (plants m⁻²), the sowing and harvest dates, the amount of irrigation (mm) and nitrogen fertilization (kg ha⁻¹ eq. mineral nitrogen).

zone	site	lat	lon	ST	SCWD_m	SCWD_sd
East	Dijon	47.3	5.1	2646.0	-263.5	113.3
East	Reims	49.3	4.0	2454.6	-229.5	78.9
South	Avignon	44.0	4.8	3178.7	-524.1	120.9
South	Toulouse	43.6	1.4	2958.0	-405.2	135.6
West	Poitiers	46.4	0.1	2586.6	-294.5	102.4

Table S2: Description of locations on the simulated multi-environment trial Headers indicate the locations of trials; the sum of temperatures (ST, °C), the mean climatic water deficit (SCWD_m, mm) and standard deviation (SCWD_sd, mm) i.e. the sum of precipitation minus sum of potential evapotranspiration.

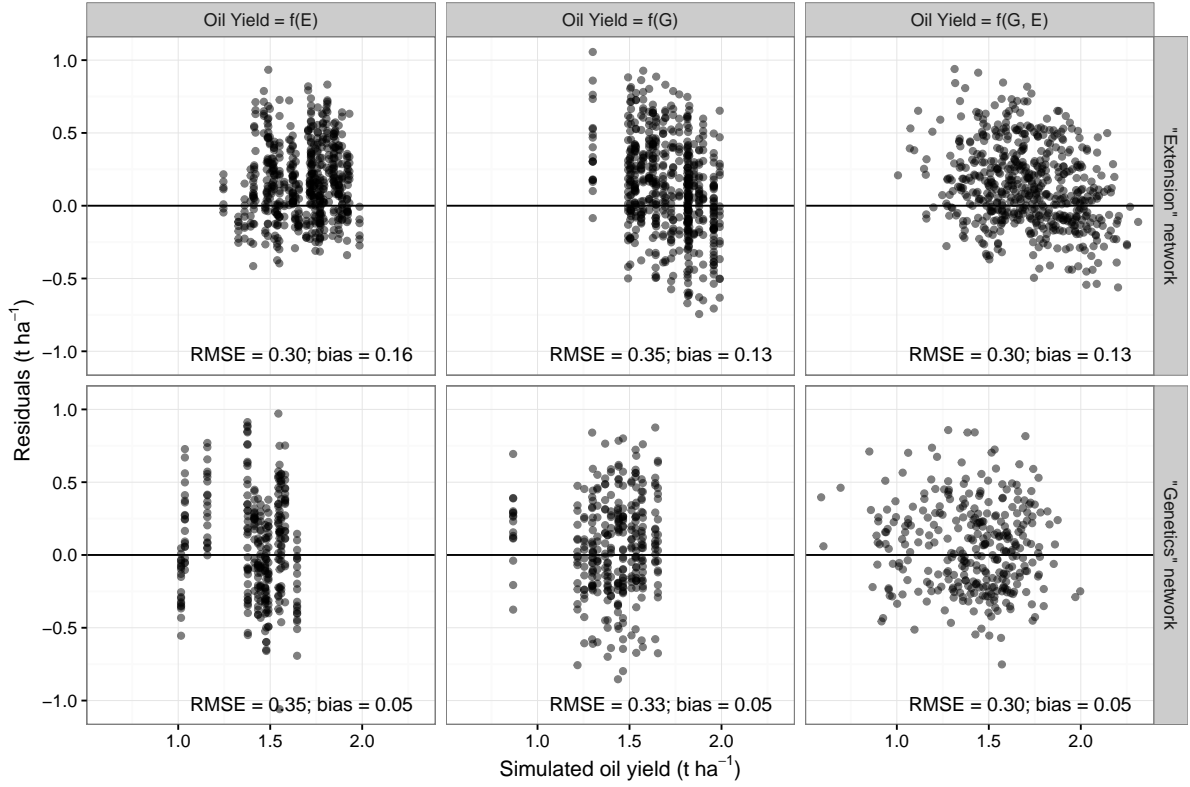


Figure S1: Evaluation of simulation of $G \times E$ interactions in two contrasted multi-environment trial networks. We compared the model error with three kind of parameterizations (in columns) and two datasets (lines). Different parameterization were expressed as (1) $Y = f(E)$, i.e. averaging genetic variability; (2) $Y = f(G)$, i.e. averaging environmental variability and (3) $Y = f(G, E)$, i.e. actual parameterization. Two dataset were used : this study (*extension*) and a MET in which more distinct cultivars were evaluated on less contrasted locations (*genetics*) (described in Casadebaig et al., 2011).

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