INTEGRATING BIOTREATED WASTEWATER REUSE AND VALORIZATION WITH ENHANCED WATER USE EFFICIENCY TO SUPPORT THE GREEN ECONOMY IN EU AND INDIA

Work Programme 2012 "COOPERATION"

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Water4Crops - EU

Work Package 4
Improving WUE and drought tolerance of maize, sorghum, millet and tomato via genomics approaches and modelling

Deliverable D4.5
Models for maize, sorghum and millet growth and production under different water regimes and climatic scenarios

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1. INTRODUCTION

A crop model with explicit genetic variability can potentially simulate crop production for hundreds of genotypes, sites, and years, resulting in the indication on where and when a given combination of trait /alleles confers a positive effect (Parent and Tardieu, 2014). However, most current crop models have been developed for predicting the effects of current or future climate and cultivation techniques on a single genotype. New models with genetic parameters have to be developed if one wants to simulate real genotypes or the effects of the genetic variability. This is now more and more feasible because genotypic values of model parameters can now be measured in high throughput phenotyping platforms for hundreds of genotypes.

The Water 4 Crops project involves the analysis of the comparative advantages of several traits/alleles linked to Water Use Efficiency (WUE) and leaf growth on the performances of maize, sorghum and millet genotypes in various conditions of evaporative demand (VPD) and soil water deficit.

This aim had to face several challenges. (i) First, a comparative analysis of the genetic variability in these three species is not available and the framework of analysis had to be entirely built. Indeed, the framework of analysis previously developed at INRA for leaf expansion in maize was not adapted to sorghum and millet. (ii) The crop model had to explicitly consider leaf expansion of individual leaves for genotypes varying in leaf development, number of leaves and flowering time. A previous leaf expansion model coupled with a model of leaf development is available in APSIM (Chenu *et al.*, 2008, 2009). However, this model had too many parameters which were not measurable in the field or in phenotyping platforms and this model was adapted to a constant cycle duration only (and a unique number of leaves). A new model, adapted to the three species, for genotypes differeing in their number of leaves and with measurable parameters had to be developed and inserted into the crop model APSIM.

In this project, we developped a new multi-species, multi-genotypes model based on APSIM, able to simulate the effects of the genetic variability on traits linked to WUE and leaf growth on plant productions in multiple climatic scenarios and irrigation strategies:

-We first selected 3 micro panels (20-30 genotypes / species) of maize (tropical and temperate accessions), sorghum and pearl millet taking into account their origins, groups, and responses to evaporative demand and / or soil water deficit determined in previous study at INRA and ICRISAT (selection has been done jointly with ICRISAT).

-We developed a framework for analysing plant and leaf development, transpiration and leaf expansion and their sensitivity to soil water deficit and evaporative demand in the three species with 4 experiments carried out in both the *PhenoDyn* and *PhenoArch* phenotyping platforms of Montpellier.

-The three micropanels were phenotyped together in three experiments in the *PhenoDyn* platform. Model parameter values for each genotype were analysed.

-We developed a new model of leaf development and sensitivities to soil water potential and evaporative demand valid in the three species for genotypes with different numbers of leaves. Parameters can all be measured in phenotyping platforms. Values of model parameters for genotypes of the micropanels measured in the *Phenodyn* platform can be inserted in the model. This model was tested over Europe with maize temperate accessions in a network of field trials of a companion project (EU FP7 DROPS). A field trial performed by Horta in Italy in 2016 with genotypes of both sorghum and maize of the micropanels under well-watered conditions and water deficit provided data which still have to be compared to simulated data.

-We simulated the effect on crop production of the observed genetic variability on measured parameters within the micropanel. The observed range of variation on parameter values was inserted in the new model and the combination of 59 sites x 30 years x 9 virtual genotypes x 3 irrgation scenarios x 2 soil depths was simulated. In total, we run 114696 simulations. In each situation, European maps of the comparative advantage of each parameter values compared to the control genotypes were built.

2. Selection of mini panels of maize, sorghum and pearl millet differing in origin and sensitivity to soil water deficit and evaporative demand and from major genetic groups

(this has been carried out together by INRA and ICRISAT-India)

The genetic material has been selected in a consistent way in the three species. The process was (i) to start with a large panel maximizing the genetic diversity in each species, and (ii) to maximize the diversity of phenotypic responses to drought or VPD, but keeping a genetic diversity as large as possible and comprising most of the subfamilies within each species.

Because we have access to inbred lines in sorghum, we have decided to use inbred lines in all species. The original genetic material has been selected in GCP projects in each species for the tropical material. In temperate maize, this collection originates from the projects DROPS and Cornfed (UE).

-In maize, the original panel comprised 89 lines with different origins, breeding histories and responses to drought. The whole set has been phenotyped for the response of leaf elongation to soil water potential and VPD before the beginning of the project. Within this set, a subset of 30 lines (15 tropical and 15 temperate), maximizing the phenotypic diversity, has been selected for analysis at INRA, HORTA, and ICRISAT (Appendix 3).

-In Sorghum, the original panel comprised 152 lines, out of the 380 entries of the reference collection, maximizing the genetic diversity of tropical sorghum. These lines were initially selected for a narrow window of flowering time and tested under lysimetric conditions for a number of drought-related characteristics including water use efficiency. Twenty lines were selected because of their high contrast of response to evaporative demand. The whole set (20) has been analyzed at INRA and ICRISAT (Appendix 1).

-In Millet, the mini panel comes from a collection of 264 lines maximizing the genetic variability. Before the beginning of the project, these lines have been tested under lysimetric conditions to identify those having the largest contrast for transpiration efficiency. A subset of 20 lines has been selected with a procedure similar to that of tropical sorghum. The whole set has been analysed at INRA and ICRISAT (Appendix 2).

It has been checked in all species that the selection process did not eliminate any origin or historic class of genotype.

3. Phenotyping framework for measuring model parameter values in the three species.

A framework of analysis was previously developed for maize for measuring parameter values of leaf expansion and its sensitivity to evaporative demand and water deficit in the phenotyping platform *PhenoDyn* at INRA-Montpellier (Welcker *et al*., 2011). The *Phenodyn* platform allows to monitor leaf expansion rate, transpiration and environmental conditions at the time step of 15 min for more than 400 plants. The analysis framework considered a stable maximum leaf expansion rate during a week, and a rapid decline after that. During this long stable period, any deviation from the maximum rate was considered as the effect of the environment. First, the temperature effects were removed by expressing leaf expansion as a rate per thermal time unit, using the conventional approach of linear thermal time (degree day). The effects of evaporative demand was measured with the difference between day values under high evaporative demand and leaf expansion at the end of the night (when evaporative demand is null). The effect of soil water potential was calculated as the slope of the relationship between soil water potential and leaf expansion rate during the night for plants in drying conditions.

However, this framework was not adapted to the comparative analysis of the three species. First (i), growing condition and analysis framework had to be common for the three species. (ii) Thermal time calculation differs between these species. (iii) The period of stable maximum leaf expansion is very short (if there is any) in millet and sorghum, and the decline is slow. In maize, most of the final leaf length has been grown during the stable leaf expansion rate and the hypothesis of a stable growth and a rapid decline is close to reality. This was not the case in millet and sorghum.

In a first experiment, 188 plants of maize, sorghum and millet with 2 lines per species have been analyzed under well-watered conditions with a new protocol, mixing the use of the two phenotyping platforms, “PhenoArch” and “Phenodyn”. Growing conditions were adequate for all species (pots, substrate, moisture, fertilizer, and photoperiod). The protocol was adapted (sowing date, number of plants per pot, number of measured leaves, etc.) , to conduct a second experiment, under water deficit.

In this second experiment, two levels of water supply have been tested on 188 plants of maize, sorghum and millet with the same 2 genotypes per species. The protocol based on the use of both platforms proved to be adequate for the three species. This experiment allowed to select the range of water deficit similar in the three species in larger experiments on the genetic variability.

In the third experiment, 600 plants have been grown under two levels of water supply and leaf expansion of all growing leaves on main stem and tillers were monitored.

A new framework of analysis has been developed based on this complete dataset of three experiments with the three species. A set of software applications suited to this protocol has been developed in the R language.

1) Leaf expansion was monitored for successive leaves (5 to 10) and not for leaf 6 only (Figure 1).
2) Thermal time was calculated using the concept of day at 20°C (Parent et al., 2010). Parameters for each species were those of Parent et al. (2012). With this framework, leaf expansion of each species was compared on a similar basis, namely the equivalent leaf expansion at 20°C.
3) For a considered leaf number of each genotype, the time course of night leaf elongation for well-watered plants was averaged between replicates, using thermal time units and starting at leaf appearance. This curve was considered as the potential leaf elongation rate for this leaf number and for this genotype. Any deviation from this curve for well-watered plants during the day was considered as the effect of evaporative demand. Any deviation during the night was considered as the effect of soil water potential.
4) Model parameters were extracted from these time courses.

   -Phyllochron was calculated directly from data of leaf appearance

   -Maximum leaf expansion rate calculated as the average value of the curve of potential leaf elongation rate before a 10 % decrease.

   -Sensitivity to evaporative demand was the slope of the relationship between VPD and relative leaf expansion rate (leaf expansion rate / potential leaf expansion rate at a similar thermal time after leaf appearance) for well-watered plants.

   -Sensitivity to soil water potential was the slope of the relationship between soil water potential and relative leaf expansion rate during the night (leaf expansion rate / potential leaf expansion rate at a similar thermal time after leaf appearance).

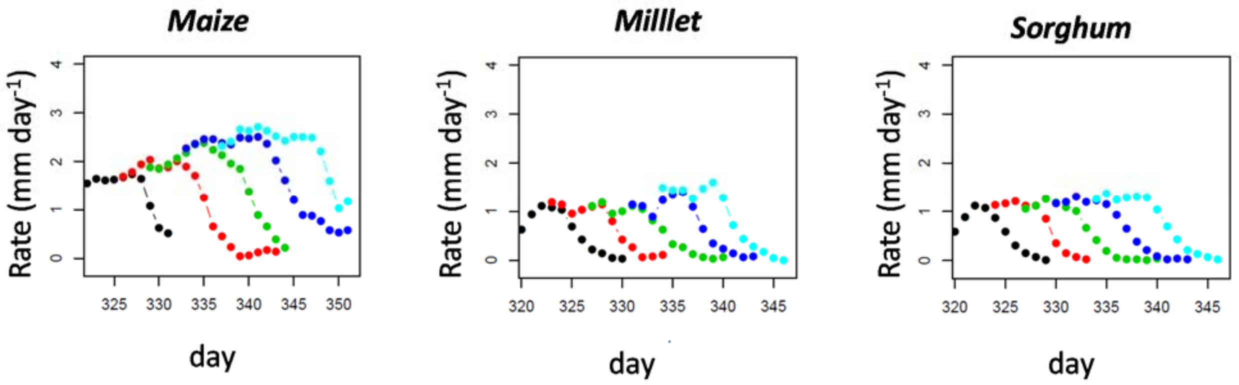


Figure 1. Time courses of night time leaf expansion for successive leaves in the three species. One plant of one genotype of each species is presented here. Each point is the average value of leaf expansion during one night. Leaves 5, 6, 7, 8, 9 are respectively drawn in black, red, green, dark blue, light blue.

4. Model parameter values in the three species.

The mini panels of the three species have been evaluated for growth and transpiration responses under contrasting environmental conditions in 3 experiments in the *PhenoDyn* platform. The three experiments were similar but allowed 4 replicates per genotype per water scenario. Overall, all genotypes were analysed under 2 water scenarios with 4 replicates / genotype (total = 1350 plants). Environmental conditions, soil water status, growth and transpiration were monitored until the leaf-10 stage. Phyllochron, potential leaf expansion rate, sensitivity to VPD and sensitivity to soil water deficit have been determined in all genotypes of the 3 micro panels.

- The phyllochron was estimated in the 3 micro-panels of the three species in the platform. Expressed with thermal time unit, this measurement is stable over experiments. In maize, phyllochron values measured in the platform were compared to results in the field and were very close.

-Maximum leaf expansion rate was calculated from the curve of potential leaf elongation rate during the night as explained above. Within the micropanels, average value for leaf 6 of each species was higher in maize compared to sorghum and millet (Fig.2). However, maize genotypes with the slower leaf expansion rate had maximum leaf expansion rate as low as the slowest genotypes of millet and sorghum. The range of genetic variation was similar in the three species (around ± 17%, Fig.2).

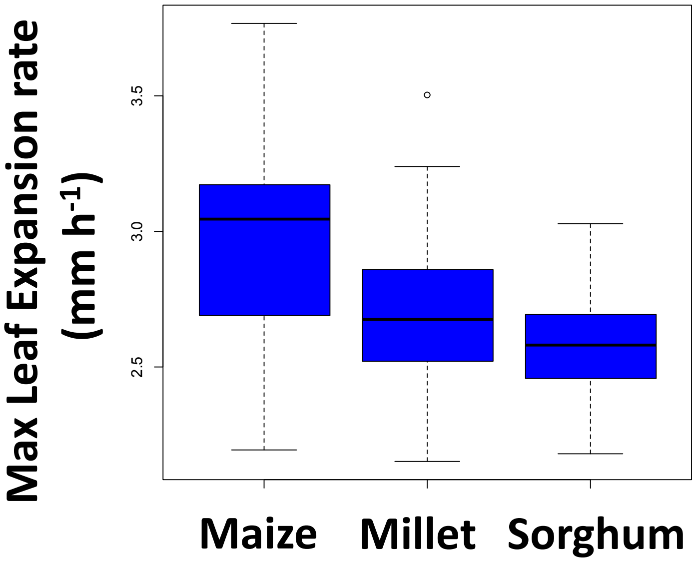


Figure 2: Range of variation of maximum leaf expansion rate for leaf 6 observed in the three micro panels in the three species .

- Sensitivities to evaporative demand and soil water potential were calculated in all genotypes of the three species (Appendix 4). First, the response curves were determined in each genotype. The relationship between soil water potential and leaf expansion during the night (relative to the potential leaf expansion, see above) was drawn in all genotypes (Fig.3). The range of soil water potential differed between genotypes because of different rates of transpiration and this range was limited to 0 - to -0.6 MPa in order to avoid range effects. The response was linear and the slope of the relationship was calculated in each genotype (Fig.3). Within the micropanels, average value of the sensitivity to soil water potential was higher in maize compared to sorghum and millet (Fig.4). However, we observed large overlaps between the ranges of sensitivity of the three species with sensitive or less sensitive genotypes observed in all species. The range of genetic variation was slightly larger in maize compared to sorghum and millet.

Parameter values for all genotypes are available on request for partners.

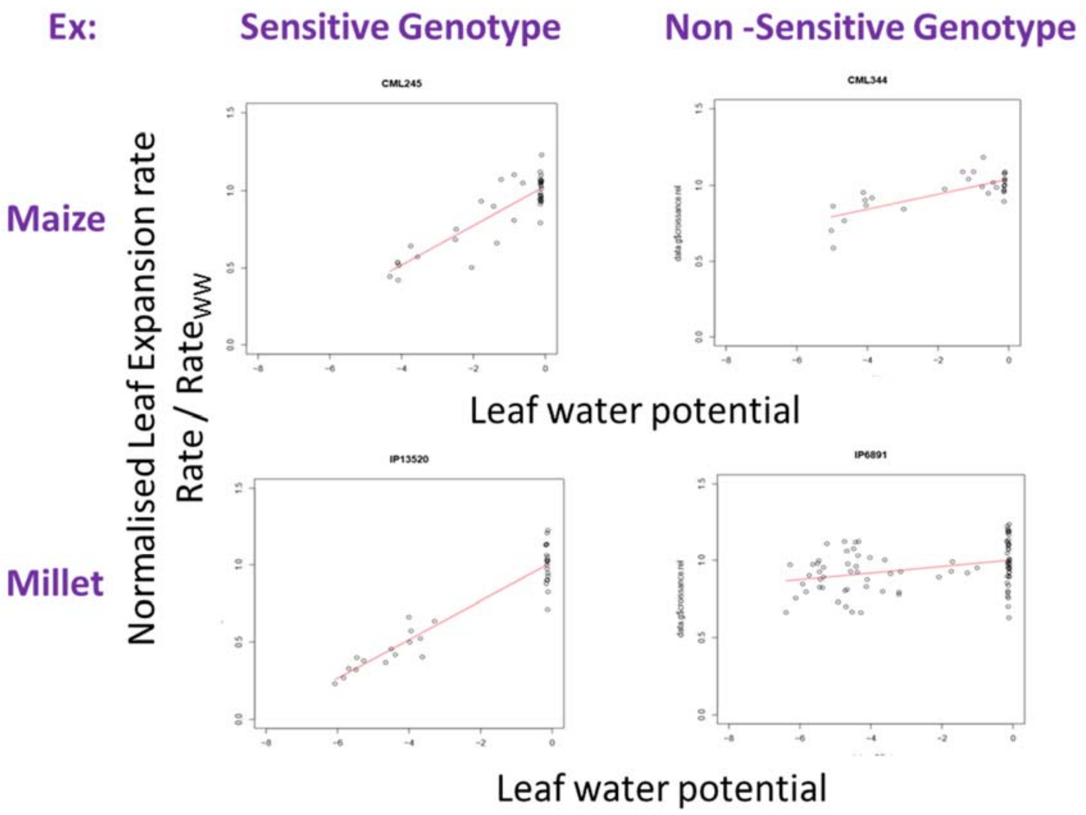


Figure 3: Example of sensitivities of leaf expansion to water deficit in maize and millet .

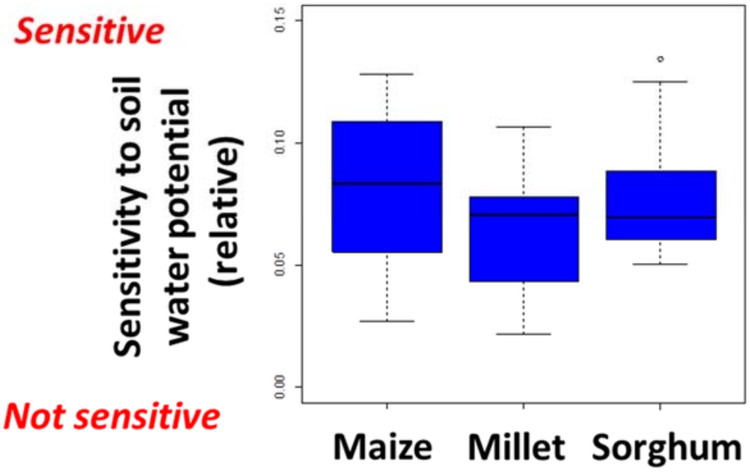


Figure 4: Range of variation of sensitivity of leaf expansion to water deficit in the three species .

5. Model development

We have worked on an existing leaf expansion model developed in APSIM, which applied to virtual genotypes differing only on maximum leaf growth rate and its sensitivity to soil water deficit and vapour pressure deficit (Chenu et al., 2008, 2009). This model included many parameter which were not measurable in the field or in phenotyping platform or measurable but with technics which were not adapted to large panels (ex: timing of leaf initiation). In addition, this model was adapted only to genotypes with a constant number of leaves. We have extended it to represent real genotypes differing in maximum number of leaves, timing of leaf initiation, appearance and duration of leaf expansion, shape of leaves (length *vs*. width) and sensitivity to water deficit and evaporative demand.

The part of the model considering leaf development has been completely changed. We paid special attention to minimize the number of parameters in formalisms with only easily measurable parameters. For example, the timing of leaf initiation is not anymore a model parameter, but is calculated from the timing of leaf appearance (phyllochron). The same apply to other non-measurable timings of leaf development such as the end of the phase of linear leaf expansion which now depends on the timing of the ligule appearance. The resulting model uses four genotypic parameters to simulate leaf development (Fig.5), namely: final leaf number, phyllochron, the slope of the progression of leaf ligulation with thermal time and thermal time at emergence.

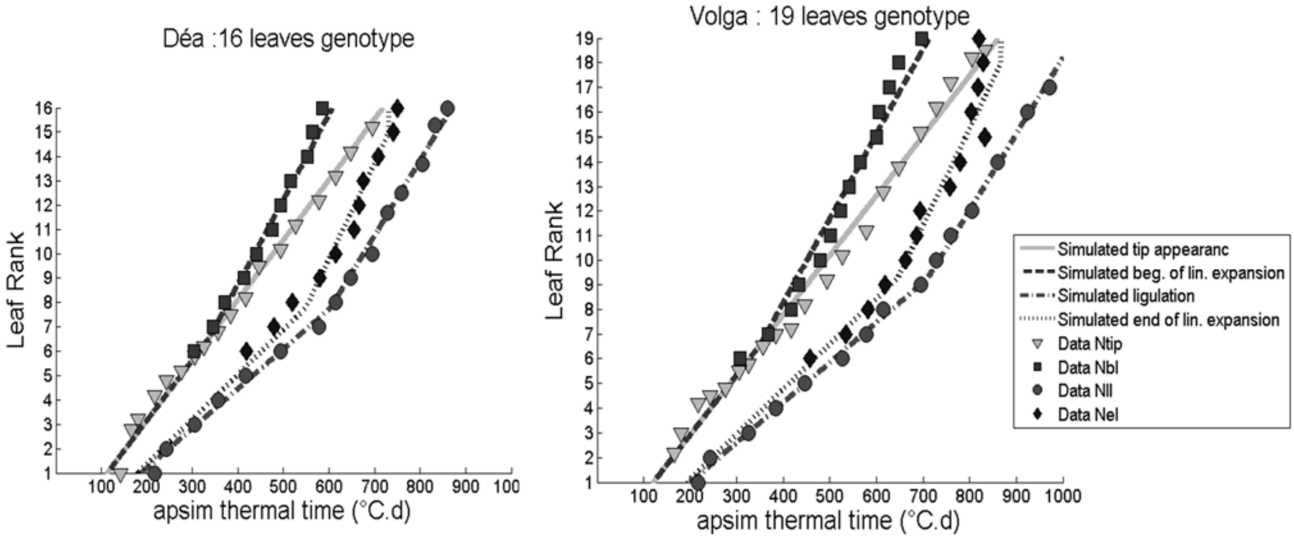


Figure 5: Simulated and measured data for 16 and 19 leaves maize genotype for leaf appearance, beginning of linear elongation, end of linear elongation and ligulation.

The part of the model considering the responses to soil water has been slighly changed. Because we observed a strong relationship between the sensitivities to soil water potential and evaporative demand, these sensitivities have been changed in the model to be dependant on a common parameter only. Maximum leaf elongation rate was assumed to vary between successive leaves in a way that only depends on final leaf number. Sensitivities to evaporative demand and soil water potential were assumed to be common to all leaves. Leaf width now depends on a genetic parameter and sensitivity to light.

Codes are available on request for partners.

We have tested the adapted model in relation with observed values in a network of 30 experiments of maize in the field (from a companion project EU FP7 DROPS) to investigate its capacity of simulating genotype by environment interactions with good correlation in well-watered field trials. A field trial performed by Horta in Italy in 2016 with genotypes of both sorghum and maize of the micropanels under well-watered conditions and water deficit provided data which are currently under analysis (Fig.6). It will allow to test if the model could be used in comparative studies.

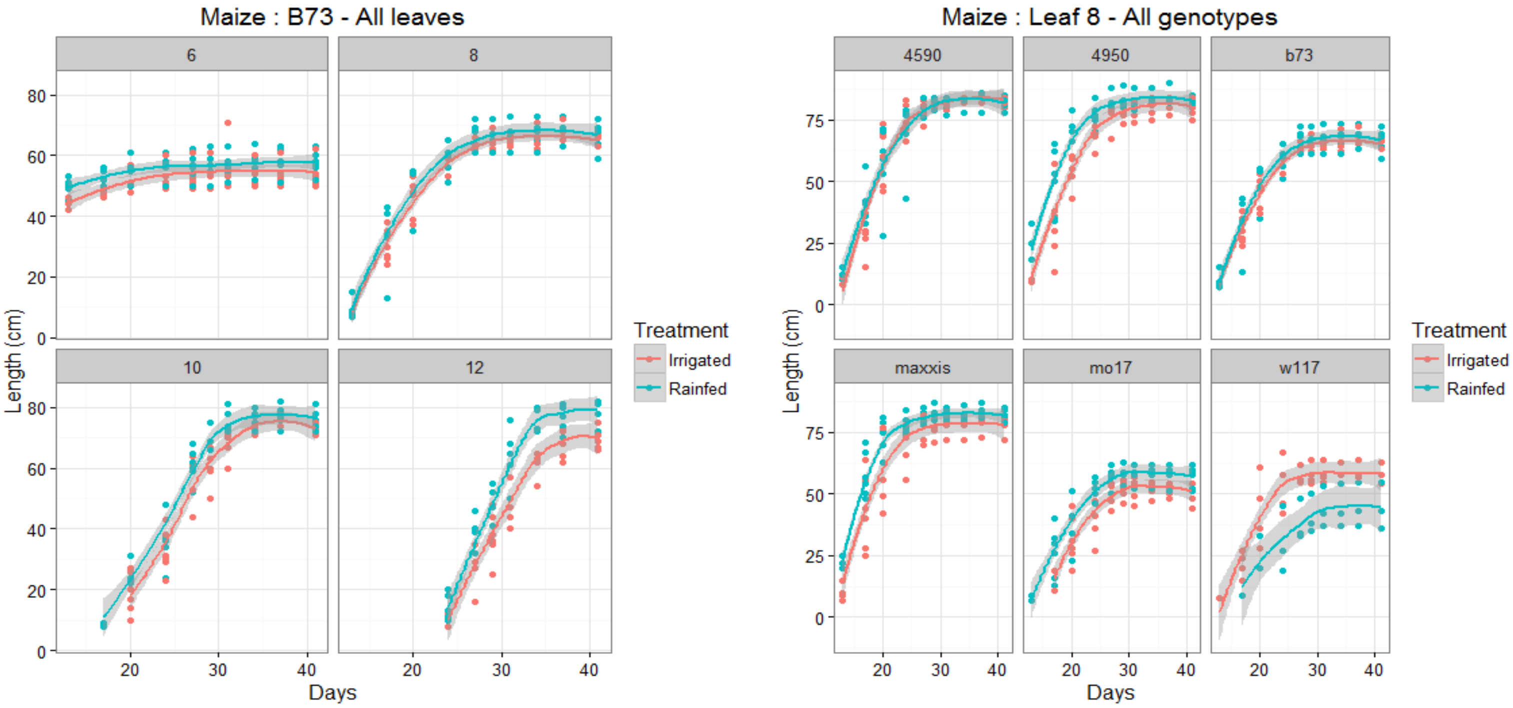


Figure 6: First analysis of leaf expansion of maize genotypes grown in well-watered or rainfed conditions in the field. Measurements have been carried out by Horta.

6. Simulation of the effect of Genotype x Environment x Irrigation on crop production

We have simulated the effect on yield of the interaction between various genotypes of maize and irrigation techniques under typical climates of Europe, using this new model. Simulations were run for 59 Europeans sites during 36 years in 2 soil depths (60cm and 150cm). In total, we run 114696 simulations.

Simulation Plan

Nine genotypes were simulated, each one characterized by (i) leaf growth potential and (ii) a sensitivity to soil water potential and VPD. Three levels for each parameter were defined (high, middle and low). Three watering scenarios were tested: (i) Rainfed, (ii) Well-watered, (iii) Optimized. Simulations were run for 59 Europeans sites during 36 years in 2 soil depths (60cm and 150cm).

Watering scenarios

Three water scenarios were tested for each situation:

-The control scenario, called “rainfed” with no irrigation.

-The “well-watered” scenario was characterized by a regular irrigation of 30 mm every 7 days during all the irrigation period of maize, i.e. between the stage “10 leaves” and the stage “50 % humidity in the grain”.

- The optimized scenario consisted in reducing the irrigation period, the number and the quantity of the irrigation. Four irrigations of 25 mm during a period of 30 days around the flowering.

Genotypes

We tested genotypes differing in potential leaf elongation rate (parameter “a”) and sensitivity to soil water potential and evaporative demand (parameters “b”) in the range of the observed value for the micropanel.

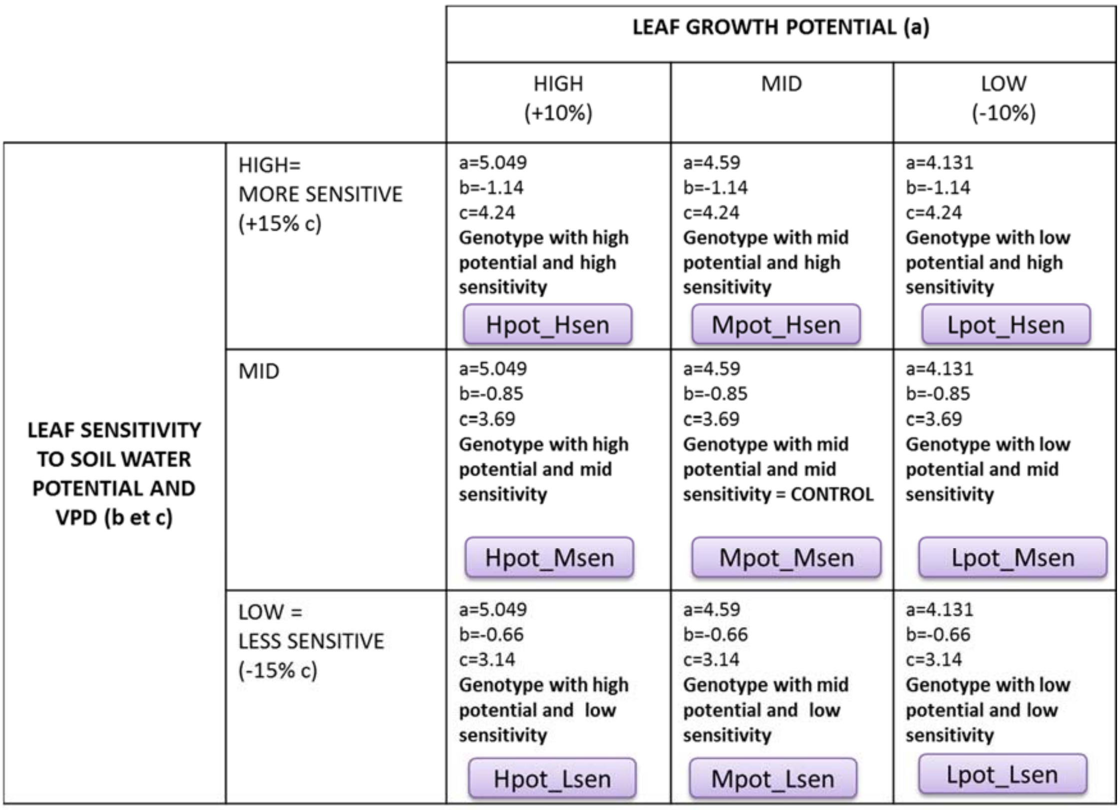
We defined three levels for each parameter: high, medium and low.

-Medium values for all parameters were set from the maize genotype B73 but with different leaf number depending on latitude. This initial genotype B73 is different for each site. A previous work allowed us to choose for each site the final leaf number adapted for each site (and consequently, a cycle duration). This optimized genotype was selected in well-watered condition. This genotype was the control of our study (Mpot_Msen).

-Genotypes with high (Hpot) or low (Lpot) leaf growth potential were characterized respectively by a rise or a decrease of 10% of the parameter “a”.

-Genotypes with high sensitivity (Hsen) or low sensitivity (Lsen) were characterized respectively by a rise or a decrease of 15% of the parameter “b”.

9 genotypes were defined crossing three levels of the two parameters (Fig.7).



		LEAF GROWTH POTENTIAL (a)		
		HIGH (+10%)	MID	LOW (-10%)
LEAF SENSITIVITY TO SOIL WATER POTENTIAL AND VPD (b et c)	HIGH= MORE SENSITIVE (+15% c)	a=5.049 b=-1.14 c=4.24 **Genotype with high potential and high sensitivity** Hpot_Hsen	a=4.59 b=-1.14 c=4.24 **Genotype with mid potential and high sensitivity** Mpot_Hsen	a=4.131 b=-1.14 c=4.24 **Genotype with low potential and high sensitivity** Lpot_Hsen
	MID	a=5.049 b=-0.85 c=3.69 **Genotype with high potential and mid sensitivity** Hpot_Msen	a=4.59 b=-0.85 c=3.69 **Genotype with mid potential and mid sensitivity = CONTROL** Mpot_Msen	a=4.131 b=-0.85 c=3.69 **Genotype with low potential and mid sensitivity** Lpot_Msen
	LOW = LESS SENSITIVE (-15% c)	a=5.049 b=-0.66 c=3.14 **Genotype with high potential and low sensitivity** Hpot_Lsen	a=4.59 b=-0.66 c=3.14 **Genotype with mid potential and low sensitivity** Mpot_Lsen	a=4.131 b=-0.66 c=3.14 **Genotype with low potential and low sensitivity** Lpot_Lsen

Figure 7. Summary of the 9 virtual genotypes simulated in this study.

In each condition, each genotype was compared to the control and the difference between the average values over 36 years were displayed on maps of Europe. (46 maps in total). All maps and result from the simulations are available on request for partners.

7. Results

Effect of irrigation techniques and soil depth on yield

- ✓ Irrigation allows an increase of yield in most part of Europe in deep or superficial soil.
- ✓ In deep soil and for the control genotype, optimized irrigation scenario does not improve yield compared to rainfed conditions.
- ✓ In deep soil, the well-watered scenario allows a yield rise in south of Europe (2.5 to 10 t/ha) while the yield is constant in northern Europe.
- ✓ In superficial soil, optimized irrigation of the control seems to be a better solution to increase yield in north Europe. Indeed, between the two watering scenarios the rise is similar for a smaller quantity of water.

Effect of the genetic variability in rainfed conditions

- ✓ In rainfed conditions, genotypes which are the less sensitive to soil water deficit are the most productive in all environments (Fig.8).
- ✓ In northern Europe, this low sensitivity combined with a high growth potential gave the highest yield.
- ✓ In southern Europe, highest yield are observed for genotypes with low sensitivity but also low growth potential.

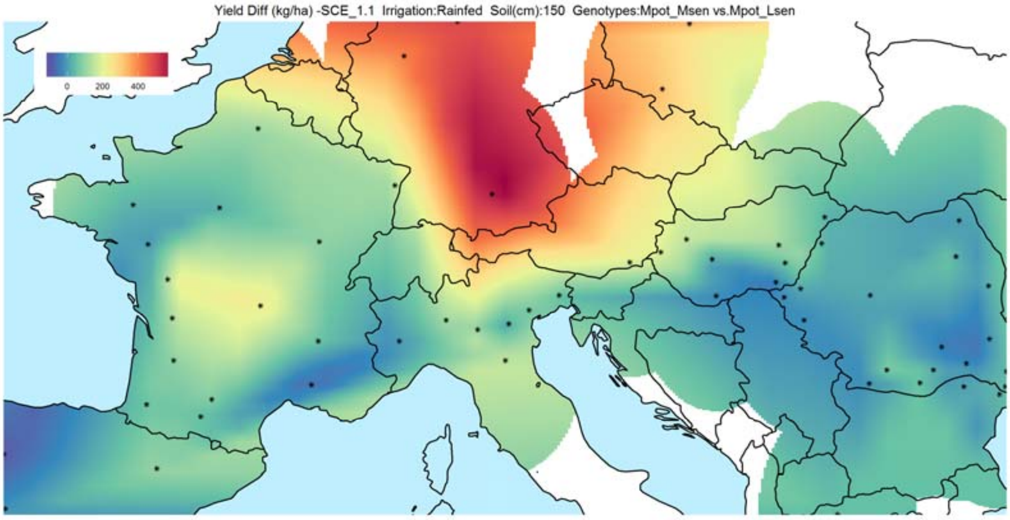


Figure 8: Effect of a low sensitivity to soil water deficit in rainfed conditions for deep soils.

Effect of the genetic variability for well-watered conditions

- ✓ Under well-watered conditions, the combination of a high growth potential and a low sensitivity increases yield all over Europe (fig 9).

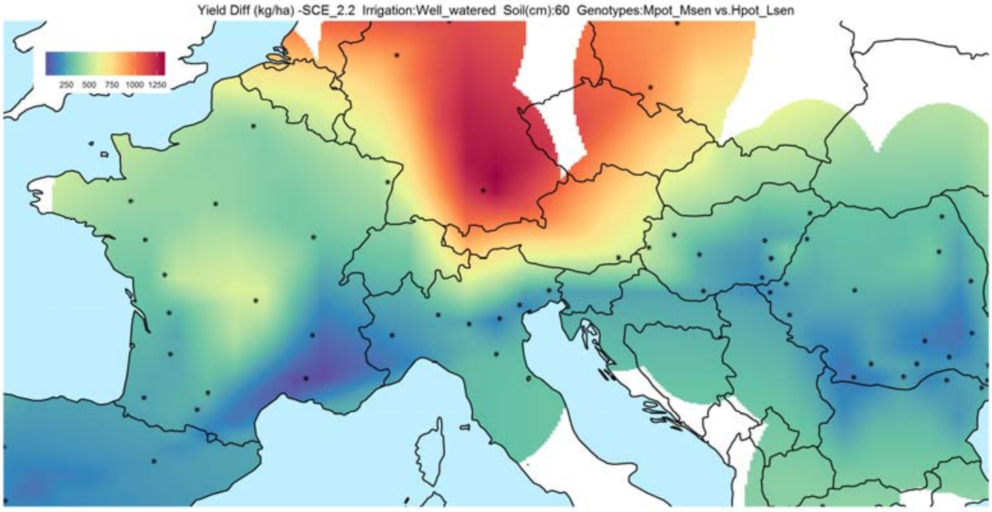


Figure 9: Effect of a high growth potential and a low sensitivity to soil water deficit in well-watered conditions in shallow soils.

Effect of the genetic variability for optimized irrigation

- ✓ Under optimized scenario of irrigation, genotypes with high growth potential combined with a low sensitivity to soil water deficit increases yield in most part of Europe (Fig. 10).
- ✓ However, genotypes with a low growth potential and a low have higher yield in the south Europe (Fig. 11)

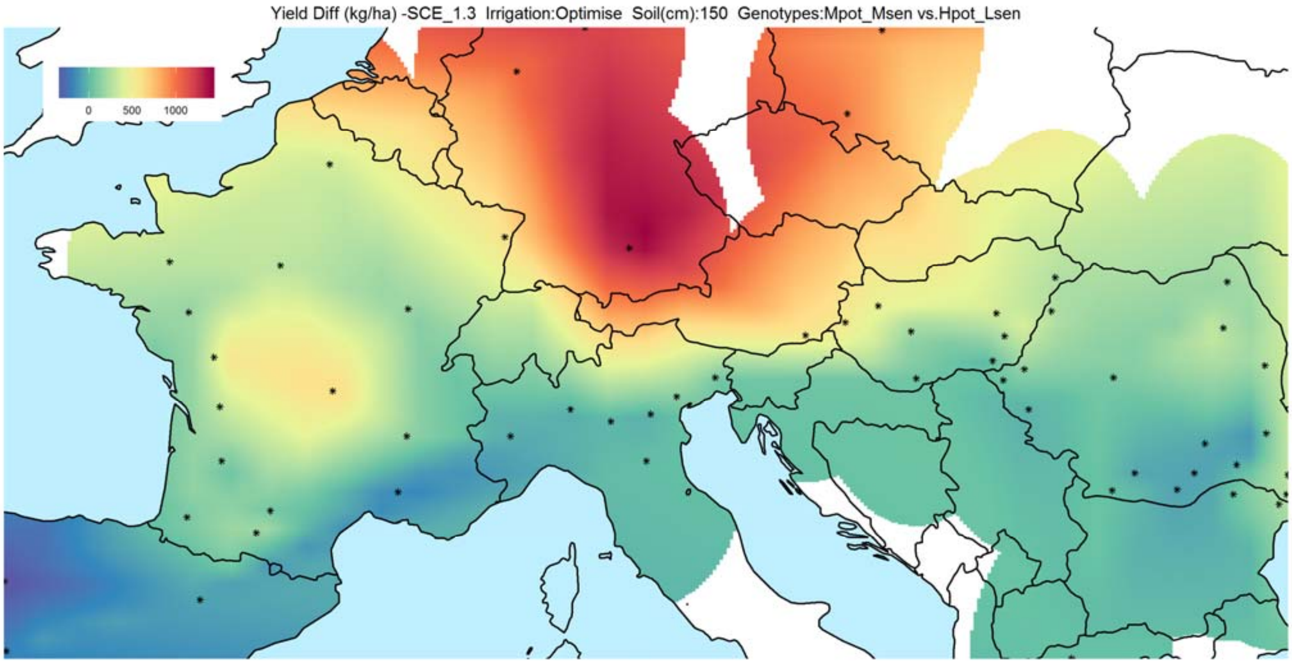


Figure 10: Effect of a high growth potential and a low sensitivity to soil water deficit in optimized irrigation conditions in deep soils.

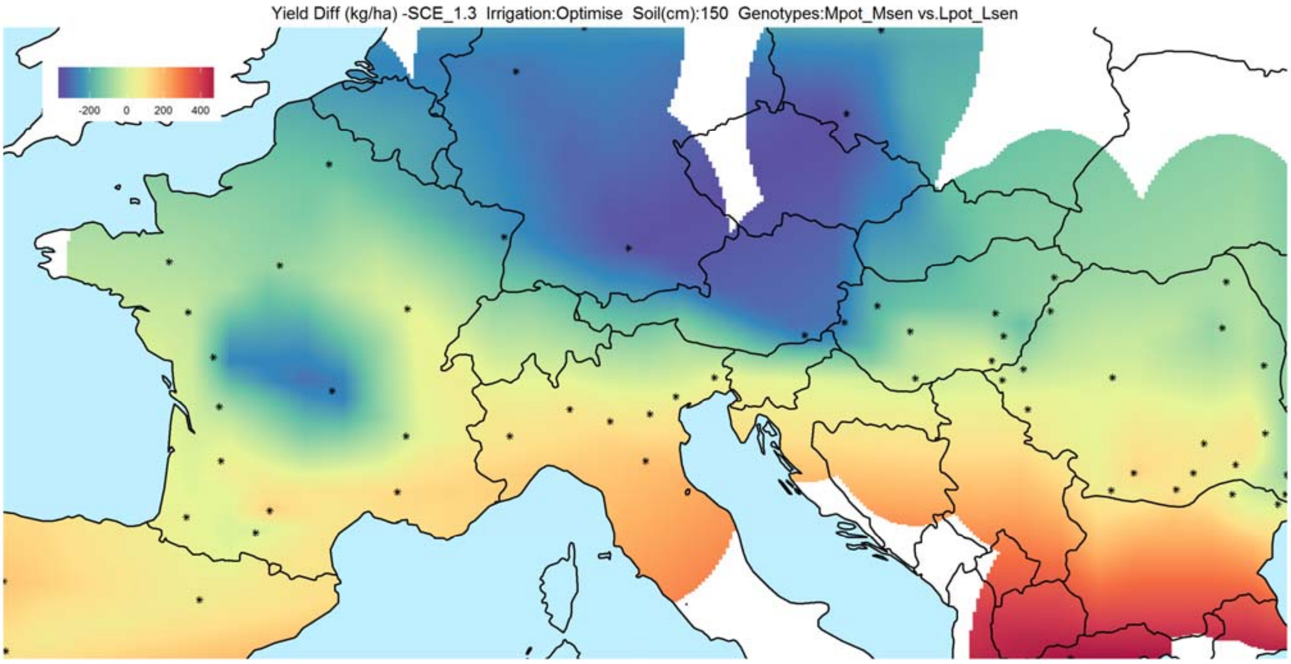


Figure 11: Effect of a low growth potential and a low sensitivity to soil water deficit in optimized irrigation conditions in deep soils.

8. CONCLUSIONS

The WP4 of the “Water 4 Crops” project aimed at improving water use efficiency of maize, sorghum and millet. For adapting water use in different climatic scenarios, plant can change their stomatal conductance and leaf expansion. However, one trait value can have positive or negative effects depending on environmental conditions and crop management. Developing a crop model with explicit genetic variability on such traits and simulating crop production in large ranges of climatic scenarios and crop management can therefore be a solution to indicate where and when a given combination of trait confers a positive effect.

In this project, we first selected micropanels representing the genetic variability in three species (maize, millet and sorghum). We developed a new model of leaf expansion and sensitivities to soil water deficit and evaporative demand valid for real genotypes with different maximum leaf numbers. We developed a framework of analysis valid in the three species to measure model parameter values and we used it for phenotyping genotypes of the three micropanels. We used the observed range to simulate the effects of the genetic variability observed in maize on crop production over Europe for different irrigation strategies.

Trait values, codes of the model and simulated data are available to partners. In addition to the intrinsic value of such data, these results could have a large impact for breeding by indicating the best combination of trait values in each combination of site by irrigation strategy.

Appendix 1: Micro- panel selected in Sorghum

	IS Number	**Institution**	**Race**	**Country**	**Continent**	response Tr
1	IS 393 (411) 659					Strong
2	IS 8347	ICRISAT	G	PAK	India	Strong
3	IS 20743	ICRISAT	B	USA	AmericaN	Strong
4	IS 25910	ICRISAT	G	MLI	AfricaW	Strong
5	SSM 275	Agropolis-Cirad	Gma	BFA	AfricaW	Strong
6	IS 20763	ICRISAT	CB	USA	AmericaN	Strong
7	IS 30619	ICRISAT	C	CMR	AfricaC	Strong
8	IS 14276	ICRISAT	C	ZAF	AfricaS	Strong
9	IS 27791	ICRISAT	DB	DEU	Europa	Strong
10	IS 29472	ICRISAT	K	LSO	AfricaS	Strong
11	IS 31693	ICRISAT	CB	DZA	MediterB	Low
12	IS 16044	Agropolis-Cirad	C	CMR	AfricaC	Low
13	IS 16173	Agropolis-Cirad	C	CMR	AfricaC	Low
14	IS 8348	ICRISAT	D	PAK	India	Low
15	IS 14556	ICRISAT	GC	ETH	AfricaE	Low
16	IS 15428	ICRISAT	C	CMR	AfricaC	Low
17	IS 10876	Agropolis-Cirad	GC	NGA	AfricaW	Low
18	IS 3583	ICRISAT	C	SDN	AfricaE	Low
19	IS 10978	ICRISAT	D	USA	AmericaN	Low
20	IS 3147	ICRISAT	CB	ZAF	AfricaS	Low

Appendix 2: Micro- panel selected in Millet

🟧 **low TE**
🟩 **high TE**

Entry number	Entry	Mat Group	GCP Entry
1	🟧 25	1	Okashana 1 (ICMV 88908)
2	🟧 43	1	IP 6179
3	🟧 3	1	IP 13520
4	🟧 75	2	IP 20349
5	🟧 245	4	IP 3110
6	🟧 249	4	IP 14311
7	🟧 147	3	IP 6101
8	🟧 238	4	IP 15857
9	🟧 169	3	IP 8647
10	🟧 248	4	IP 6125
11	🟩 125	2	IP 6891
12	🟩 179	3	IP 9651
13	🟩 166	3	IP 3471
14	🟩 103	2	IP 9391
15	🟩 83	2	IP 13363
16	🟩 78	2	IP 12395
17	🟩 111	2	IP 9351
18	🟩 22	1	IP 4542
19	🟩 53	1	IP 4979
20	🟩 4	1	Check

Appendix 3: Micro- panel selected in Maize

Line	**Origin**
MBS847	*Dent*
B73	*Dent*
FV-252	*Dent*
KY21	*Dent*
MO17	*Dent*
W117U	*Dent*
A188	*Dent*
W64A	*Dent*
CH10	*Flint*
EA1197	*Flint*
EP1	*Flint*
FC16	*Flint*
FV-2	*Flint*
FV-76	*Flint*
LP1233	*South-American Flint*
CLA17	*Tropical*
KUI3	*Tropical*
CML69	*Tropical*
LPSC7-F86	*Tropical*
CML254	*Tropical*
CML287	*Tropical*
CML312	*Tropical*
CML341	*Tropical*
CML344	*Tropical*
CML444	*Tropical*
CZL04006	*Tropical*
DTPYC9-F74	*Tropical*
CML245	*Tropical Highlands*
SCMALAWI	*Subtropical*
ZN6	*Subtropical*

Appendix 4: Parameter values of potential leaf expansion rate and sensitivity to soil water potential in the three species

Genotype	Species	Potential leaf expansion rate (mm $h_{20°C}^{-1}$)	Sensitivity to soil water potential (Mpa^{-1})	Range of Soil water potential (MPa)	number of data
CML69	maize	2.97	0.27	0.029737347	47
DTPYC9-F74	maize	3.16	0.32	0.031592204	42
A188	maize	2.19	0.39	0.021937039	41
CML344	maize	3.17	0.50	0.03168115	31
CML254	maize	3.05	0.50	0.030467101	41
CML444	maize	3.08	0.55	0.030806461	29
CZL04006	maize	2.73	0.67	0.027267431	40
CML341	maize	3.08	0.67	0.03083441	48
FC16	maize	3.72	0.73	0.037179065	32
B73	maize	3.20	0.79	0.031970413	44
EP1	maize	2.70	0.81	0.026990199	37
KUI3	maize	2.39	0.85	0.023861546	41
Ky21	maize	3.17	0.88	0.031744814	37
CML287	maize	3.29	0.88	0.032896504	38
FV252	maize	2.84	1.06	0.028359947	26
LPSC7-F86	maize	3.29	1.08	0.032916031	39
LP1233	maize	2.94	1.09	0.029441567	36
CML312	maize	2.64	1.09	0.02636194	29
W64A	maize	2.90	1.12	0.0290146	31
MBS847	maize	2.62	1.13	0.026183862	18
MO17	maize	2.46	1.20	0.024626228	27
CML245	maize	2.68	1.28	0.026839925	42
W117U	maize	3.12	NA	0.031210065	27
FV2	maize	3.12	NA	0.031240309	19
CLA17	maize	3.77	NA	0.037678806	28
FV76	maize	2.40	NA	0.024030082	19
ZN6	maize	3.21	NA	0.032117619	23
IP6891	millet	2.15	NA	0.021507905	90
IP6125	millet	2.20	0.22	0.022019976	35
IP6179	millet	3.20	0.24	0.032024804	81
IP4979	millet	2.30	0.30	0.023047406	15
IP7953	millet	2.60	0.34	0.026013323	36
IP3471	millet	2.52	0.41	0.025207668	20
IP13363	millet	2.60	0.46	0.025999517	42
IP22278	millet	2.68	0.52	0.026760803	80
IP20349	millet	3.09	0.58	0.030870357	53
IP12395	millet	2.81	0.60	0.028143505	67

106-AF	millet	2.69	0.71	0.026949708	116
IP8647	millet	3.05	0.71	0.030456777	38
87-AF	millet	2.57	0.71	0.025710217	57
IP9391	millet	2.57	0.74	0.025720343	35
110-AF	millet	2.70	0.75	0.027037359	65
IP15857	millet	2.78	0.80	0.027826651	83
IP9351	millet	2.86	0.89	0.028573939	46
IP4542	millet	3.50	0.91	0.03503057	60
IP14311	millet	2.35	0.95	0.023534665	55
IP3110	millet	2.33	1.06	0.023332179	77
IP13520	millet	3.24	NA	0.032376991	36
IS10978	sorghum	2.26	NA	0.022623704	31
IS31693	sorghum	2.48	NA	0.024781947	23
IS20743	sorghum	2.20	NA	0.021977637	27
IS3583	sorghum	2.67	0.50	0.026745983	44
SSM275	sorghum	2.60	0.58	0.026018179	24
IS15428	sorghum	2.72	0.58	0.027247068	38
IS16044	sorghum	2.80	0.59	0.028019114	26
IS10876	sorghum	2.51	0.62	0.025138677	35
IS16173	sorghum	3.03	0.65	0.030282444	39
IS30619	sorghum	2.61	0.68	0.026116719	28
IS25910	sorghum	2.30	0.69	0.022998744	31
IS 20763	sorghum	2.97	0.73	0.029691766	32
IS27791	sorghum	2.44	0.76	0.024356782	24
IS8348	sorghum	2.56	0.76	0.025612333	25
IS3147	sorghum	2.58	1.01	0.025795823	14
IS14556	sorghum	2.70	1.03	0.026987248	34
IS14276	sorghum	2.69	1.25	0.026914498	42
IS8347	sorghum	2.57	1.34	0.025726227	32
IS29472	sorghum	2.18	NA	0.021792905	18