TOWARDS AN UNIVERSAL SET OF DIFFERENTIAL SUNFLOWER GENOTYPES FOR PRECISE BROOMRAPE RACE IDENTIFICATION

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SUNFLOWER BROOMRAPE IS AN UNIQUE PARASITIC PLANT

- ✓ *Orobanche cumana* is a recent case of the new encounter of a non-weedy parasite with a crop

- ✓ *O. cumana* is to date the only broomrape species in which races have been described

- ✓ Major genes (*Or*) are used in breeding programs

Rubiales (2018)

Picture: Corteva Agriscience™

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BROOMRAPE RACIAL DISTRIBUTION

O. cumana populations are classified into physiological races using differentials mostly with qualitative resistance

Racial situation of sunflower broomrape is dynamic and becoming more complex

Race G+ populations (infect *Or7* hybrids) are increasing in all Europe

Precise knowledge of the parasite and the plant-parasite interaction are essential concepts to develop strategies of durable resistance

Martin-Sanz et al (2016); Velasco et al (2016)
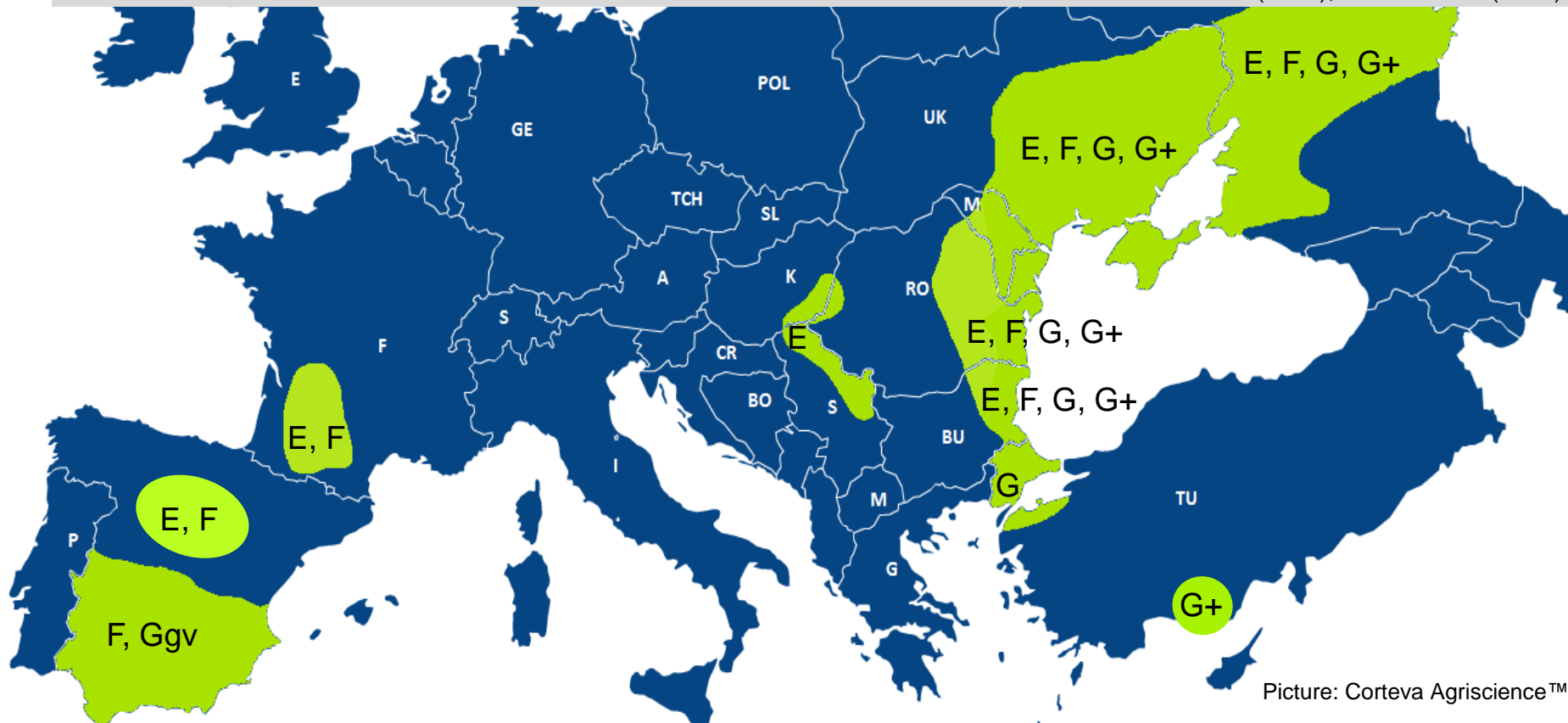
Picture: Corteva Agriscience™

BROOMRAPE-SUNFLOWER INTERACTION: PHYSIOLOGICAL RACES

1980's: races A to E were identified using five differential lines with monogenic dominan genes (*Or1* to *Or5*) (Vrânceanu et al (1980))

1990's: Broomrape populations overcoming *Or5* (race F) were identified in Spain, Romania, Bulgaria, Ukraine, Russia and Turkey (Molinero et al, 2015).

From **2000's** race G and H have been described in Black Sea area and recently in Spain and Morocco. Racial situation in these areas is unclear at this moment because the same races may differ in virulence (Molinero et al, 2015; Martin-Sanz et al, 2016; Nabloussi et al, 2018).

The aim of this study was to clarify this situation and proposed genotypes that allows precise identification of the different pathogenic races in the most important broomrape areas.

Table 2. Proposal for standardized characterization and nomenclature of *Orobanche cumana* populations using the coded triplets system, which is based on the use of eight sunflower lines -termed differentials-, grouped into three sets

Population of *O. cumana*	Group # 1		Group # 2		Group # 3	
	Differentials	Value if susceptible reaction	Differentials	Value if susceptible reaction	Differentials	Value if susceptible reaction
	AD66 (-)	1	Record (*Or3*)	1	LC1093 (*Or6*)	1
	K A-41 (*Or1*)[b]	2	S1358 (*Or4*)	2	P96 (*Or5, Or6, Or7*)	2
	J8281 (*Or2*)	4	P1380 (*Or5*)	4		
Code[a]:	Total in group # 1		Total in group # 2		Total in group # 3	

[a] Each population is identified by a code of three digits which are obtained by totals due to susceptible reactions of each of the lines into the set. Resistant reactions impart 0. [b] Gene/s governing resistance in each line according to Vrânceanu *et al.* (1980), Akhtouch *et al.* (2002), Pacureanu *et al.* (2004), and Pérez-Vich *et al.* (2004).

Molinero et al (2015)

Key differentials for races above E:

- Martín-Sanz et al (2016): P96, DEB2 and hybrids
- Molinero Ruíz et al (2014): P96 and L86
- Antonova et al (2014): P96 and VT62 (*Or7*)
- Shindrova & Penchov (2012): hybrids
- Burlov & Burlov (2010): inbred lines
- Pacureanu et al (2008, 2009): hybrids and inbreds (LC-1093)

PHENOTYPIC EXPERIMENTS

GENOTYPE	GENETICS	RESISTANCE
B117	No Or	None
S-1358	Or4 hom	A-D
NR5	Or5 hom	A-E
P96	Complex	A-F
Or7 inbred	Or7 hom	A-G
DEB2	Or_Deb2 hom	A-H
L86	Unknown	?
LC1093	Unknown	A-F
Hybrid 1	?	A-F
Hybrid 2	?	A-F
Hybrid 3	Or5Or7 het	A-G

Broomrape samples:

34 BR populations * 11 Sunflower genotypes * 13 reps = 4862 plants

Experiments were conducted on multi-pot trays with a pot volumen of 40cm3 with 0.28mg of seeds per g of soil
Plants were grown during 55 days in a greenhouse at 25/20ºC (day/night) with 14h of photoperid
Susceptibility is is considered when % Sus > 50% and average nodules >2

RESULS: identification 8 different pathogenic races

DIFFERENTIAL	RESISTANCE	RESISTANCE-SUSCEPTIBILITY PROFILE							
B117	None								
S-1358	A-D								
NR5	A-E								
P96	A-F								
Or7 inbred	A-G								
DEB2	A-H								
L86	?								
LC1093	A-F								
Hybrid 1	A-F								
Hybrid 2	A-F								
Hybrid 3	A-G								
RACE		E	F_CU	F	F-P96	G	G_GV	G+	H
Number of samples		4	1	3	6	4	3	8	5
COUNTRIES		Hungary France Spain	Spain	Spain Bulgaria	Russia Ukraine Greece Bulgaria	Morocco Bulgaria Turkey	Spain Russia	Bulgaria Russia Romania Turkey	Bulgaria Ukraine Romania

Table: Proposed codes for *O. cumana* races

Line of sunflower	100	300	700	710	730	770	771	773
AD66	S[a]	S	S	S	S	S	S	S
K A-41	R	S	S	S	S	S	S	S
J8281	R	R	S	S	S	S	S	S
Record	R	R	R	R	S	S	S	S
S1358	R	R	R	R	R	S	S	S
P1380	R	R	R	R	R	S	S	S
LC1093	R	R	R	R	R	R	S	S
P96	R	R	R	R	R	R	R	S
Historical race	A	B	C	D	E	F	F or G?	F or G?

[a] S: susceptible, R: resistant.

Numerical system like in downy mildew

Molinero et al (2015)

It is needed to change the race nomenclature to be able to discriminate between the different pathotypes!!!

We proposed to change that differentials by those ones:

B117   **L86/LC1093B**   **Hybrid 3**
S1358   **P96**   *Or7* **inbred**
NR5   **Hybrid 1**   **DEB2**

BROOMRAPE RACE IDENTIFICATION PROPOSAL USING A NUMERICAL SYSTEM

			New race name							
			310	700	710	730	751	770	771	773
D1	(+1)	B117								
D2	(+2)	S1358								
D3	(+4)	NR5								
D4	(+1)	L86								
D5	(+2)	P96								
D6	(+4)	Hybrid 1								
D7	(+1)	Hybrid 3								
D8	(+2)	Or7 inbred								
D9	(+4)	DEB2								
Old race name			E	F_CU	F	F-P96	G_GV	G	G+	H
Number of samples			4	1	3	6	3	4	8	5
Countries			Hungary France Spain	Spain	Spain Bulgaria	Russia Ukraine Bulgaria Greece	Spain Russia	Morocco Bulgaria Turkey	Bulgaria Russia Romania Turkey	Bulgaria Ukraine Romania

✓ Races 310, 710 and 770 would correspond to the classical races E, F and G, respectively

✓ Races 730 and 751 are like variants of what has been called before race G

✓ Race 771 corresponds to the race G+, characterized by infecting *Or7* gene in hybrids but not in inbreds.

✓ Race 773 is able infect all the genotypes except DEB2

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CONCLUSIONS

- This study presented preliminar data about pathogenic diversity of several broomrape populations along European countries. Final results will be presented in the next Sunflower Conference

- Racial situation has become much more complex than it was until race E. Different "versions" of race F and G have been identified. In total, 8 races have been characterized of which 7 are above race E.

- A new system for broomrape race identification should be proposed to be able to cover the pathogenic diversity found in this study. The new system of differentials may include the inbred lines B117, L86, S-1358, NR5, P96, *Or7* line*, and DEB2*, and the hybrids 1* and 3*.

- We propose to use a system similar to downy mildew, as described before by Molinero-Ruiz at al (2015), but changing some of the differentials.

THANK YOU FOR YOUR ATTENTION!