



# I Simposio Español de Fisiología y Mejora de Cereales

Zaragoza, 9-10 de abril de 2018



Organizado por:

**Red Temática  
AGL2016-81855-REDT**



**Red de Cereales y Leguminosas  
del CIHEAM**



Con el patrocinio de:



Oro



Plata

Con el auspicio de:

*Sociedad Española de Fisiología Vegetal*

*Sociedad Española de Genética*

*Asociación Española de Técnicos Cerealistas*

*Fundación Española de Cereales*



**I Simposio Español de Fisiología y Mejora de Cereales**  
**I Spanish Symposium on Cereal Physiology and Breeding**  
*Zaragoza 9-10 April 2018*

Organized in the framework of the (i) Thematic Network AGL2016-81855-REDT “*Fisiología del Rendimiento y Calidad para la Mejora de Cereales*” and (ii) the Network of “Red de Cereales y Leguminosas” del CIHEAM

The program of the I Spanish Symposium on Cereal Physiology and Breeding starts with an opening session followed by four thematic sessions (Crop development, Yield potential, Abiotic stresses, and Biotic stresses) and closed by a “wrapping up” discussion session. Each session is opened by an invited keynote presentation followed by a number of oral presentations selected from those submitted voluntarily by the participants and with a poster session (joining two sessions in each of the two poster sessions scheduled). The different size of each of the sessions respond to the number of abstracts submitted for each of them. In each session there will be two spaces open for discussions, one following the invited keynote presentation and another one closing the session after all oral communications have been delivered. The exception would be the last session that due to the limited number of abstracts submitted both discussions spaces were merged. We expect these open discussion spaces could include discussions not only on the particular presentations offered but also more openly (though within the issue under discussion). The core of the Symposium will be the communications of the scientific work in the four thematic sessions.

**Communications:** There will be a keynote presentation opening the session and then oral communications as well as a ‘new’ format of oral “quick-and-effective” TWO-minutes poster ‘flash presentations’ (before the actual poster session)

**1. “Regular” Oral communications** will be allocated a slot of 12’. As it will take c. 1’ for the chair to introduce the speaker and for him/her to take place to start his/her presentation, each oral communication must be prepared (and rehearsed!) to be delivered in no more than 11 minutes. Each presenter of an oral communication must be extremely rigorous in respecting the restriction to deliver a talk in 11 minutes (or less), as the chairpersons will be very strict on maintaining this limit and will inflexibly cut presentations exceeding this upper threshold (thus it is expected that each presenter will show his/her respect to the other presenters and to the audience by having well prepared the presentation to be delivered within the 11 minutes required). There will be a slot for open discussions closing all the oral presentations where issues from the different talks will be discussed further.

**2. TWO minutes poster ‘flash presentations’:** There is a global “*Three Minute Thesis*” competition (that started a decade ago in Queensland and is held in more than 200 universities worldwide nowadays). If people can tell significant things of a whole thesis in 3’, there would be plenty of time for our poster presenters to attract visitors to their posters (or to engage people in discussions over meals and coffee breaks, or even beyond the Symposium) from a very quick (and effective) **TWO-minute ‘flash presentation’ of each poster**. This will open each of the two poster sessions and will be organised as a ‘Carousel’ of presentations immediately before the poster viewing session. Brevity creates excitement; and our poster presenters will profit the opportunity for “advertising” their posters for following poster viewing session.

Requirements for the ‘**flash presentations**’: There will be **ONLY TWO power-point slides per poster** allowed: a first slide –holding the title- presenting the issue, a second slide with the key results and conclusion(s). Presentations not respecting these conditions will NOT be uploaded and will then NOT be shown in this “carousel of ‘flash presentations’ of posters”. Everybody knows that in the poster (and particularly through discussing with the authors) there will be plenty more to see, learn, discuss and enjoy. This **TWO-minute presentation** is NOT the last opportunity for discussing your work in the Symposium (and beyond), it is only the attraction to engage people in such discussion.

Chairpersons will be VERY strict in controlling that (i) each poster is summarised in only two slides with the content established above, (ii) each presenter will NOT use more than 2 minutes in that “flash presentation”. If you are one of our poster presenters, be thrilled to excel in this challenge!. Regarding the poster itself, please follow the indications suggested, and respect strictly the dimensions established, in the website (<http://networks.iamz.ciheam.org/cerealsnetwork/en/index.html>; see on the right-hand under “News”).

<b>Monday 9 April</b>		
13.30	Bus Departure from Zaragoza downtown ( <i>Calle del Coso, 80</i> ) to IAMZ Entrance	
14.00-14.20	Registration	
<b>Opening Session</b>		
<i>Chairpersons: Ramzi Belkhodja (IAMZ) &amp; Josefina Sillero (IFAPA)</i>		
14.20-14.30	Javier Sierra, IAMZ Director; Angel Ruiz, CSIC's AGR Coordinator	<b>Welcoming words</b>
14.30-14.45	Ana Casas (EAD-CSIC) Gustavo A. Slafer (ICREA/AGROTECNIO/UdL)	<b>Introduction. Why physiology and breeding of cereals?</b>
14.45-15.00	Octavi Quintana, PRIMA	<b>La iniciativa PRIMA</b>
<b>Session 1: Crop development</b>		
<i>Chairpersons: Ana Casas (CSIC) &amp; Francisco Ciudad (ITACyL)</i>		
15.00-15.30	Ernesto Igartua, EAD-CSIC, Zaragoza	Invited keynote paper: “ <b>Winter, spring and those in between. Growth habit unexplored possibilities and unexpected consequences</b> ”
15.30-15.40	Open discussion on Crop Development keynote paper	
15.40-15.52	Ochagavia et al.	Earliness per se effects on developmental traits in hexaploid wheat grown under field conditions
15.52-16.04	Vicente et al.	Transcriptome analysis of durum wheat flag leaves reveals a coordinated regulation of primary and secondary metabolism under the future climatic scenario
16.04-16.16	Berenguer et al.	New strategies with epigenetic and autophagy modulators to increase microspore embryogenesis efficiency for DH production in barley
16.16-16.28	Basavaraddi et al.	Does the QTLHeadingon wheat chromosome7D affect other traits?
16.28-16.40	Monteagudo et al.	Light quality influences rate of development and flowering genes expression in barley
16.40-16.52	Pérez de Luque et al.	Wheat genotype influences root symbiosis with mycorrhiza and rhizobacteria
16.52-17.04	Contreras et al.	Pan-genomes: estimating the true genomic diversity of species
17.04-17.16	Open discussion <i>Crop development</i>	
17.16-17.40	Coffee-break	
<b>Session 2: Yield potential</b>		
<i>Chairpersons: Ignacio Romagosa (AGROTECNIO/UdL) &amp; Rosa Morcuende (CSIC)</i>		
17.40-18.10	Thorsten Schnurbusch, IPK-Germany	Invited keynote paper: “ <b>A genetic playground for enhancing the yield potential of wheat</b> ”
18.10-18.20	Open discussion of Yield Potential keynote paper	
18.20-19.10	‘Carousel’ of TWO –MINUTES poster presentations (of posters sessions 1 and 2)	
19.10-20.00	<b>Viewing/discussing posters of sessions 1 and 2 (with authors by their posters)</b>	
20.00	Bus Departure from IAMZ Entrance to Zaragoza downtown	
21.30-23.00	<b>Symposium dinner</b> (TRES MARES - Restaurante Náutico; at Paseo Echegaray y Caballero s/n)	

<b>Tuesday 10 April</b>		
08.30	Bus Departure from Zaragoza downtown ( <i>Calle del Coso, 80</i> ) to IAMZ Entrance	
<b>Continue Session 2: Yield potential</b>		
<i>Chairpersons: Ignacio Romagosa (AGROTECNIO/UdL) &amp; Rosa Morcuende (CSIC)</i>		
09.00-09.12	Fernández-Gallego et al.	Wheat and barley ear counting in-field conditions, low-cost approach using RGB images.
09.12-09.24	Marcos-Barbero et al.	Exploring the genetic diversity in wheat performance at the high temperature and CO <sub>2</sub> concentration foreseen with climate change through the identification of key markers of growth and central metabolism.
09.24-09.36	Vergara-Diaz et al.	Metabolite profiles in leaves and spikes of field-grown wheat are related with crop yield and can be derived from hyperspectral readings
09.36-09.48	Kefauver et al.	UAV and Proximal Sensing for Phenotyping Maize in African Breeding Programs
09.48-10.00	Zouari et al.	Potential Associations Between Grain Yield, Drought Indexes and some Agronomic Traits of a Durum Wheat Collection
10.00-10.25	Open discussion <i>Yield potential</i>	
10.25-10.50	Coffee-break	
<b>Session 3: Abiotic Stresses</b>		
<i>Chairpersons: Jose L Araus (UB) &amp; Roxana Savin (AGROTECNIO/UdL)</i>		
10.50-11.20	John Foulkes, University of Nottingham-UK	Invited keynote paper: “ <b>Genetic diversity for rooting traits and tolerance of water and nutrient stresses in wheat</b> ”
11.20-11.30	Open discussion of Abiotic Stress keynote paper	
11.30-11.42	Lopes et al.	Optimizing winter wheat traits to improve resilience to a changing environment in rainfed crop systems of Turkey and Iran
11.42-11.54	Martínez-Subira et al.	Synthesis of bioactive compounds in barley during grain filling in response to late abiotic stress
11.54-12.06	Vicente et al.	Carbon and nitrogen metabolism in laminar and non-laminar photosynthetic organs under contrasting water regimes in low- and high-yielding durum wheat
12.06-12.18	Martignago et al.	Genome editing in Sorghum: a vanguard cereal to study drought stress
12.18-12.30	Soba et al.	Elevated CO <sub>2</sub> effect on wheat grain quality evolution during grain filling period
12.30-12.50	Open discussion on <i>Abiotic stresses</i>	
12.50-14.00	Lunch (Aula Dei Cafeteria)	
<b>Session 4: Biotic Stresses</b>		
<i>Chairperson: Alejandro Pérez Luque (IFAPA) &amp; Nieves Aparicio (ITACyL)</i>		
14.00-14.30	Elena Prats, IAS-CSIC, Córdoba	Invited keynote paper: “ <b>Plant physiological dysfunctions at the crossroad between disease resistance and resistance cost</b> ”
14.30-14.42	Ciudad- Bautista et al.	Incidence of <i>Oscinella frit</i> L (Diptera: Chloropidae) in Castilla y León
14.42-14.56	Pallavicini et al.	Aerial platforms as a new approach to select resistant lines for yellow rust in bread wheat breeding program
14.56-15.30	Open discussion on the whole session (keynote and oral presentations) of <i>Biotic stresses</i>	
15.30-15.55	‘Carousel’ of TWO –MINUTES poster presentations (of posters sessions 3 and 4)	
15.55-16.40	<b>Viewing/discussing posters of sessions 3 and 4 (with authors by their posters)</b>	
16.40-17.00	Ana Casas (EAD-CSIC) Ignacio Romagosa (AGROTECNIO/UdL)	<b>Wrapping up, conclusions and closing words</b>
17.00-17.25	Coffee-break & Farewell	
17.30	Bus Departure from IAMZ Entrance to Zaragoza downtown (and CSIC Delegation in Zgz)	

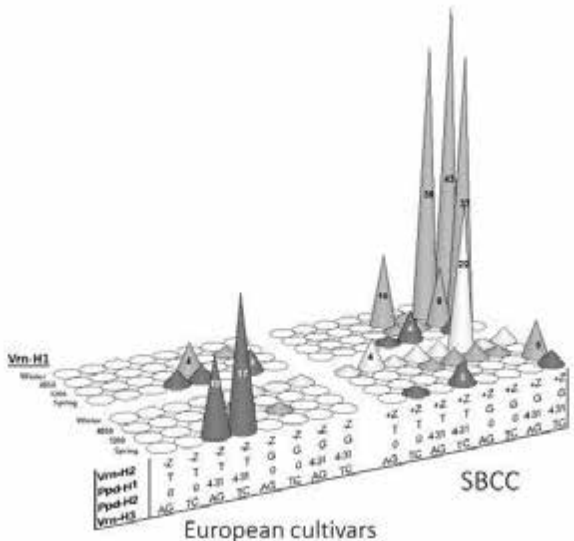
## **Posters of sessions 1 and 2**

- Poster # 01. **Ochagavía et al.** Earliness per se x temperature interaction on wheat developmental traits
- Poster # 02. **Lopez-Malvar et al.** Genome wide association analysis for cell wall bound hydroxycinnamates
- Poster # 03. **Solé et al.** Variability for glutamine synthetase 1 homoeogenes and N dose response in *Triticum* spp.
- Poster # 04. **Sánchez-León et al.** Engineering the major coeliac disease immunogenic complex in wheat by CRISPR/Cas9
- Poster # 05. **Figueroa-Garrido et al.** Combining abilities for cell wall components in corn hybrids
- Poster # 06. **Atienza et al.** Potential utilization of durum wheat landraces for breeding
- Poster # 07. **Ben Mariem et al.** Impact of N fertilization in agronomic and flour nutritional traits.
- Poster # 08. **Cantalapiedra et al.** Copy-number variation through k-mer count analysis
- Poster # 09. **Mattera et al.** Carotenoid accumulation patterns and lutein esterification process during grain development
- Poster # 10. **Saiz-Fernández.** High nitrate supply alters root and shoot metabolism and overall growth of maize plants
- Poster # 11. **Avila et al.** Exploring synteny relationships of *Hordeum chilense* genome for *Tritordeum* breeding
- Poster # 12. **Calderón et al.** Unzipping how homologous chromosomes can recognise and associate in pairs in wheat
- Poster # 13. **Fellahi et al.** Allelic variation of Rht, Vrn and Ppd genes in a set of bread wheat (*Triticum aestivum* L.) lines cultivated in eastern Algeria
- Poster # 14. **Ruiz et al.** Variation for root architecture in a core collection of durum wheat and their relation with eco-geographical and agronomic traits
- Poster # 15. **García-Molina et al.** Gluten proteins in low-gliadin wheats: effects of different nitrogen levels during fertilisation
- Poster # 16. **Gracia-Romero et al.** Remote sensing phenotyping for estimating genotypic variability in grain yield of durum wheat under different water and temperature conditions
- Poster # 17. **Chairi et al.** Post-Green Revolution genetic advance in durum wheat: the case of Spain
- Poster # 18. **Ayadi et al.** Comparative response of nitrate reductase activity, nitrogen utilisation efficiency (NutE) and nitrogen physiologic efficiency (NPE) in Tunisian durum wheat cultivars
- Poster # 19. **Garcia et al.** Fruiting efficiency differences between winter cereals
- Poster # 20. **Martínez-Peña et al.** Canopy vegetation indices to assess yield in durum wheat
- Poster # 21. **Caicedo et al.** Maize breeding for delayed senescence “STAY GREEN”
- Poster # 22. **Álvaro et al.** Bread wheat improvement to meet the requirements of the Spanish agrofood sector
- Poster # 23. **Kim et al.** Composite cross populations (CCPs) of wheat: The intensive use of genetic variation in the future wheat breeding

## **Posters of sessions 3 and 4**

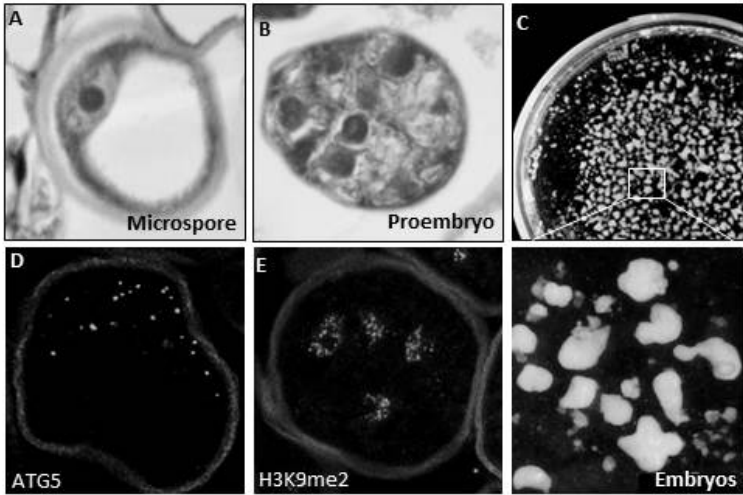
- Poster # 24. **Rezzouk et al.** Early assessment of the effect of irrigating with saline water in the agronomical performance of the pseudocereal *Chenopodium quinoa*: comparing different approaches
- Poster # 25. **Rispail et al.** Genetic plasticity of oat agronomic traits associated with climate variable changes
- Poster # 26. **Thameur et al.** Characterization of antioxidant enzymatic response of five barley genotypes under drought stress
- Poster # 27. **Bermejo-Bermejo et al.** An assessment of O<sub>3</sub>-sensitivity of Spanish bread wheat (*Triticum aestivum* L.) varieties
- Poster # 28. **Canales et al.** Encourage spending or saving water? A strategy for coping with drought in oats involve abscisic acid mediated modulation of transpiration coupled with improved root hydraulics
- Poster # 29. **Canales et al.** A novel role for OPDA (12-oxo Phytodienoic Acid) for coping with drought in oat by modulating root growth
- Poster # 30. **Jallouli et al.** Screening for drought tolerance in durum wheat genotypes in seedling stages
- Poster # 31. **Córdoba et al.** Acclimation to elevated CO<sub>2</sub> is improved by low Rubisco and carbohydrate content, and enhanced Rubisco transcripts in the G132 barley mutant
- Poster # 32. **Hannachi et al.** Genetic analysis of F<sub>2</sub> diallel crosses in durum wheat (*Triticum durum* Desf.) under semi-arid conditions
- Poster # 33. **Vicente et al.** Characterization of the transcript and metabolite responses of durum wheat to elevated CO<sub>2</sub> and high temperature at two nitrogen supplies using a qRT-PCR platform for central metabolism-related genes
- Poster # 34. **Martínez-Moreno et al.** Resistance to leaf rust in a core collection of ancient Spanish tetraploid wheats
- Poster # 35. **Montilla-Bascón et al.** New players in the cost of resistance: chlorophyll degradation pathway and photosynthetic dysfunctions in mlo resistant barleys
- Poster # 36. **Pallavicini et al.** Effect of yellow rust on agronomical traits in bread wheat

## **Session 1: *Crop development***

Title	Winter, spring and those in between. Growth habit unexplored possibilities and unexpected consequences
Authors	<p>E. Igartua<sup>1</sup>, M.P. Gracia<sup>1</sup>, F.J. Ciudad<sup>2</sup>, A. Monteagudo<sup>1</sup>, C.P. Cantalapiedra<sup>1</sup>, B. Contreras-Moreira<sup>1,3</sup>, A.M. Casas<sup>1</sup></p> <p><sup>1</sup>CSIC, EEAD. Avenida de Montañaña, 1005, 50059, Zaragoza, SPAIN</p> <p><sup>2</sup>Instituto Tecnológico Agrario de Castilla y León, ITACYL. Carretera de Burgos, km 119, 47071, Valladolid, SPAIN</p> <p><sup>3</sup>Fundación ARAID. Avenida de Ranillas, 1-D, planta 2<sup>a</sup>, oficina B, 50018, Zaragoza, SPAIN</p>
Keywords	barley, growth habit, adaptation
Abstract	
<p>This contribution will review the types of growth habit in barley, their genetic control, adaptive meaning, and avenues for its use in crop improvement. The main message is that the traditional winter-spring-facultative classification of barley cultivars is too narrow to contain the variety of adaptation formats that are possible in the species. Current and future climate conditions are already challenging conventional wisdom about the most appropriate growth habits for many regions. The talk will cover a re-appraisal of the possibilities at hand to shape the adaptive response of barley, and the genes and mechanisms at play. This knowledge will contribute to widen the catalogue of choices to produce cultivars best suited to a shifting environment. Winter barleys (same as winter wheats) are sown in autumn, and must carry mechanisms to survive frosts. One of these mechanisms is related to vernalization, i.e., the need of a cold period of specific length in order to reach flowering in due time. Spring barleys, in turn, are usually sown in late winter or spring, and do not need frost tolerance. Growth habit and adaptive pattern of adaptation depend on allelic combinations at genes <i>VrnH1</i>, <i>VrnH2</i>, <i>VrnH3</i>, <i>PpdH1</i>, <i>PpdH2</i>, and <i>HvCEN</i>, at least, and possibly others. These genes have been evaluated in Spanish landraces, and their alleles tested in a variety of experiments and populations over the years, revealing the existence of particular adaptive formats in Mediterranean barley, different from the more familiar ones of cultivars bred in countries that are more northern (Fig. 1). The results of the study of these landraces and of over 20 years of barley breeding in Spain will be shown in the light of breeding for Mediterranean conditions.</p>	
	
Legend	Figure 1. Main adaptation genes of the Spanish Barley Core Collection and a set of winter and spring European cultivars.

Title	EARLINESS PER SE EFFECTS ON DEVELOPMENTAL TRAITS IN HEXAPLOID WHEAT GROWN UNDER FIELD CONDITIONS																									
Authors	H Ochagavía <sup>1</sup> , P Prieto <sup>1</sup> , R Savin <sup>1</sup> , S Griffiths <sup>2</sup> , G.A Slafer <sup>1,3</sup> <sup>1</sup> University of Lleida, Department of Crop and Forest Science & Agrotecnio. Avenida Alcalde Rovira Roure, 191, 25198, Lleida, SPAIN <sup>2</sup> John Innes Centre. Norwich Research Park, Colney Ln, NR4 7UH, Norwich, UNITED KINGDOM <sup>3</sup> ICREA, Catalanian Institution for Research and Advanced Studies. Passeig de Lluís Companys, 23, 08010, Barcelona, SPAIN																									
Keywords	Eps, Anthesis, Vegetative, Reproductive, Final leaf number																									
Abstract	<p>Earliness per se (Eps) genes are critical for fine-tuning flowering time and likely to also modify slightly other developmental traits. Effects of Eps alleles on components comprising flowering time of hexaploid wheat have not been studied. We evaluated the effects of Eps alleles on flowering time and on a number of developmental traits using four groups of near isogenic lines (NILs) with contrasting Eps alleles (late vs early alleles). The NILs groups were derived from the Avalon x Cadenza (AxC) cross with the Eps gene on either chromosome 1D or 3A and from the Spark x Rialto (SxR) cross with the Eps gene on chromosome 1D. Eps1D-late alleles reached later flowering time (though the effect was stronger in AxC than in SxR); while Eps3A did not have any effect on flowering time. The latter conflicts with the results observed in the UK (where these NILs were produced and characterised), likely indicating that there may be Eps x temperature interactions. Differences on flowering time produced by Eps1D were mainly associated with changes on length the late reproductive phase. However, the effects of Eps1D on other developmental traits were different depending on the specific cross. Eps1D-early allele from AxC did not affect final leaf number (FLN), reduced spikelet initiation phase and, in turn, decreased the spikelet number (though less than proportionally as it accelerated the rate of spikelet initiation as well), whilst Eps1D-early allele from SxR affected marginally FLN, but had no effects on either spikelet initiation phase or spikelet number. These results provide new tools to wheat breeders as Eps alleles modified flowering time with changes on late reproductive phase improving the likelihood of floret primordia to end setting grains and with possibility to improve the adaptation without reducing yield capacity.</p>																									
	<p>Figure A: Bar chart showing anthesis time (°C d) for late and early alleles of different NILs. The x-axis represents Anthesis time (°C d) from 0 to 2000. The y-axis lists NIL groups: AxC 1D, AxC 3A, and SxR 1D. For each group, late alleles are shown in black and early alleles in white. Statistical significance is indicated by asterisks (***) or 'ns'.</p> <table border="1"> <caption>Approximate data for Figure A: Anthesis time (°C d)</caption> <thead> <tr> <th>NIL Group</th> <th>Allele Type</th> <th>Anthesis time (°C d)</th> <th>Significance</th> </tr> </thead> <tbody> <tr> <td rowspan="2">AxC 1D</td> <td>Late</td> <td>~1700</td> <td>***</td> </tr> <tr> <td>Early</td> <td>~1500</td> <td>***</td> </tr> <tr> <td rowspan="2">AxC 3A</td> <td>Late</td> <td>~1600</td> <td>ns</td> </tr> <tr> <td>Early</td> <td>~1600</td> <td>ns</td> </tr> <tr> <td rowspan="2">SxR 1D</td> <td>Late</td> <td>~1600</td> <td>*</td> </tr> <tr> <td>Early</td> <td>~1500</td> <td>*</td> </tr> </tbody> </table> <p>Figure B: Scatter plot showing the relationship between anthesis time (°C d) and duration of the phase (°C d). The x-axis is Duration of the phase (°C d) from 0 to 1000. The y-axis is Anthesis time (°C d) from 1500 to 1800. Three data series are shown with different symbols: filled triangles, filled squares, and open squares. Regression lines are shown for each series with R-squared values: R<sup>2</sup>=0.28, R<sup>2</sup>=0.28, and R<sup>2</sup>=0.91**.</p>	NIL Group	Allele Type	Anthesis time (°C d)	Significance	AxC 1D	Late	~1700	***	Early	~1500	***	AxC 3A	Late	~1600	ns	Early	~1600	ns	SxR 1D	Late	~1600	*	Early	~1500	*
NIL Group	Allele Type	Anthesis time (°C d)	Significance																							
AxC 1D	Late	~1700	***																							
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AxC 3A	Late	~1600	ns																							
	Early	~1600	ns																							
SxR 1D	Late	~1600	*																							
	Early	~1500	*																							
Legend	Duration (in thermal time) of the whole period from sowing to anthesis for late (black and dark grey bars) and early (white and light grey bars) alleles of different NILs (A). Relationship between anthesis and developmental phases (B).																									

Title	Transcriptome analysis of durum wheat flag leaves reveals a coordinated regulation of primary and secondary metabolism under the future climatic scenario
Authors	R. Vicente <sup>1,2</sup> , A. M. Bolger <sup>3</sup> , R. Martínez-Carrasco <sup>1</sup> , P. Pérez <sup>1</sup> , B. Usadel <sup>3</sup> , R. Morcuende <sup>1</sup> <sup>1</sup> Institute of Natural Resources and Agrobiological of Salamanca, IRNASA-CSIC. Cordel de Merinas, 40-52, 37008, Salamanca, SPAIN <sup>2</sup> Max Planck Institute of Molecular Plant Physiology, System Regulation. Am Mühlenberg, 1, 14476, Potsdam, GERMANY <sup>3</sup> RWTH Aachen University, Institute for Biology 1. Worringer Weg, 3, 52074, Aachen, GERMANY
Keywords	Climate change, Elevated CO <sub>2</sub> , High temperature, Transcriptome, Durum wheat
Abstract	<p>Atmospheric [CO<sub>2</sub>] and the earth's average temperature are rising due to anthropogenic activities, and their predicted changes may adversely affect plant growth and productivity, particularly in the Mediterranean basin. The use of molecular techniques to study gene-level responses to environmental changes in non-model organisms is increasing. To improve our mechanistic understanding of durum wheat response to elevated CO<sub>2</sub> and high temperature, we performed transcriptome RNA-seq analyses combined with physiological and biochemical studies in the flag leaf of plants grown in field chambers at ear emergence stage. Enhanced photosynthesis by elevated CO<sub>2</sub> was accompanied by an increase in biomass and starch and fructan content, and a decrease of N compounds (chlorophyll, soluble proteins and Rubisco content) in association with a decline of nitrate reductase and Rubisco activities. Whilst high temperature led to a decline of chlorophyll, Rubisco activity and protein content, glucose content increased and starch decreased. Furthermore, elevated CO<sub>2</sub> induced several genes involved in mitochondrial electron transport, a few genes for photosynthesis and fructan synthesis, and most of the genes involved in secondary metabolism, gibberellin and jasmonate metabolism, whereas those related to light harvesting, nitrogen assimilation and other hormone pathways were repressed. High temperature repressed genes for carbon, energy, nitrogen, lipid, secondary and hormone metabolisms. Under both environmental factors, the transcript profile resembled that previously reported for high temperature, although it was partly compensated by elevated CO<sub>2</sub>. Our results suggest that there was a reprogramming of primary and secondary metabolism under the future climatic scenario, leading to coordinated regulation of C-N metabolism towards carbon-rich metabolites at elevated CO<sub>2</sub> and a shift away from carbon-rich secondary metabolites at high temperature. Other novel genes potentially involved in regulation, including protein kinases, receptor kinases and transcription factors, were differentially expressed. Acknowledgments: M.A. Boyero and A.L. Verdejo for technical assistance. Funding: AGL2009-11987, AGL2013-41363-R, BES-2010-031029.</p>
	<div style="display: flex; justify-content: space-around;"> <div style="text-align: center;"> <p><b>A</b></p> </div> <div style="text-align: center;"> <p><b>B</b></p> </div> </div>
Legend	(A) Venn diagram analysis of the differentially expressed (DE) transcripts and (B) number of up or downregulated DE transcripts under elevated CO <sub>2</sub> , high temperature and their interaction relative to ambient CO <sub>2</sub> and temperature in wheat flag leaves

Title	New strategies with epigenetic and autophagy modulators to increase microspore embryogenesis efficiency for DH production in barley
Authors	E. Berenguer <sup>1</sup> , I. Bárány <sup>1</sup> , Y. Pérez-Pérez <sup>1</sup> , M.T. Solís <sup>1,2</sup> , C. Jiménez <sup>1</sup> , M.C. Risueño <sup>1</sup> , P.S. Testillano <sup>1</sup> <sup>1</sup> Pollen Biotechnology of Crop Plants group. Biological Research Center, CIB-CSIC. Ramiro de Maeztu, 9, 28040, Madrid, SPAIN <sup>2</sup> Dept. of Genetics, Physiology and Microbiology (Plant Physiology) Complutense University of Madrid, UCM. Faculty of Biology. José Antonio Novais, 12, 28040, Madrid, SPAIN
Keywords	Doubled-haploids, Microspore embryogenesis, autophagy, epigenetics, DNA methylation
Abstract	<p>Microspore embryogenesis is the fastest way to achieve complete homozygosis fixed in a single generation, reducing time and costs of cereal breeding programs. In vitro, stress treatments can induce haploid microspore to reprogram, acquire totipotency and produce embryos, which further generate doubled-haploid plants. Cell death and low reprogramming efficiency highly reduce the process yield, at early stages. In this work, we demonstrate that barley microspore reprogramming and embryogenesis initiation is epigenetically regulated. Erase of the gametophytic program and initiation of the new embryogenic program is associated with global DNA hypomethylation, correlating with HvMET1 DNA methyltransferase down-regulation, and low levels of H3K9 methylation. Treatments with epigenetic modulators like azacytidine (DNA de-methylating agent) and BIX-01294 (inhibitor of H3K9 methylation) promote microspore reprogramming, leading to higher proportion of embryogenesis initiation. Stress treatment that induces embryogenesis also causes cell death in a proportion of microspores. Autophagy is a catabolic process to recycle cytoplasmic components that also plays a role in the initiation and/or execution of cell death. Our results reveal the activation of autophagy and cathepsin proteases during microspore embryogenesis induction in barley, as well as their role in cell death of microspores. In vitro treatments using autophagy inhibitors (3-MA, E-64, concanamycin A), allow reducing cell death levels and, consequently, increasing the efficiency of in vitro microspore embryogenesis. These findings open up a completely new intervention pathway to increase the in vitro production of embryos and doubled-haploid plants in cereals and other crop species, especially those recalcitrant, for breeding programs. Bárány et al. 2018. J. Exp. Bot. DOI: 10.1093/jxb/erx455. Berenguer et al. 2017. Front. Plant Sci. 8, 1161. Solís et al. 2015. Front. Plant Sci. 6, 472. Supported by projects AGL2014-52028-R, AGL2017-82447-R granted by Spanish MINECO and European ERDF/ FEDER.</p>
	 <p>The figure consists of five panels labeled A through E. Panel A shows a single microspore with a clear nucleus. Panel B shows a proembryo with multiple nuclei. Panel C shows a petri dish containing a large number of small, dark embryos. Panel D shows a microspore with numerous bright spots indicating the localization of ATG5, a marker for autophagosomes. Panel E shows a proembryo with bright spots indicating the distribution of dimethylated histone H3K9 in the nuclei.</p>
Legend	Microspore embryogenesis in barley: microspore before induction (A), proembryo (B), advanced embryos (C). Localization of autophagosomes, labelled by ATG5 (D). Dimethylated histone H3K9 distribution in proembryo nuclei (E).

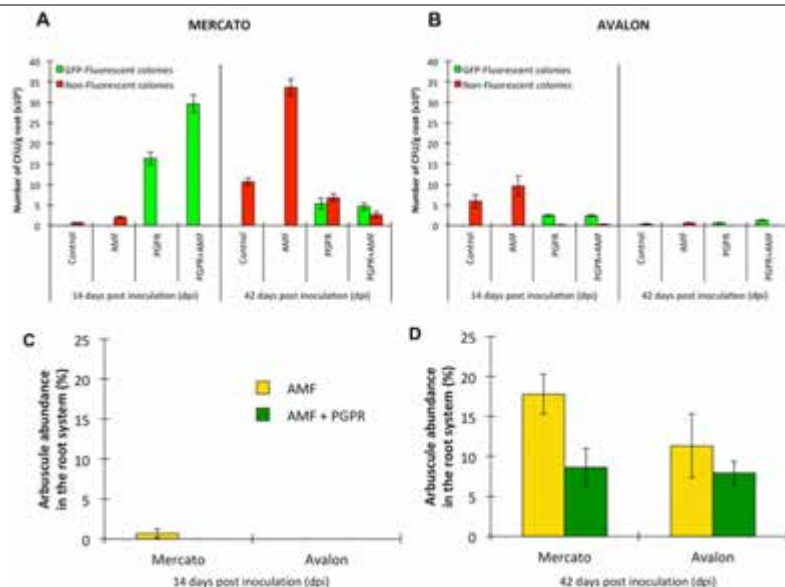
Title	Does the QTLHeadingon wheat chromosome 7D affect other traits?
Authors	P. A Basavaraddi <sup>1</sup> , R Savin <sup>1</sup> , S Griffiths <sup>2</sup> , G. A Slafer <sup>1,3</sup> <sup>1</sup> University of Lleida, Department of Crop and Forest Science & Agrotecnio. Av. Rovira Roure 191, 644747183, 25198, Lleida, SPAIN <sup>2</sup> John Innes Centre. Norwich Research Park, Colney Ln, NR47UH, NORWICH, UNITED KINGDOM <sup>3</sup> ICREA, Catalanian Institution for Research and Advanced Studies. Passeig de Lluís Companys, 23, 08010, Barcelona, SPAIN
Keywords	Fruiting efficiency, Late reproductive phase (LRP), Spike dry weight, Grain number
Abstract	<p>A QTL on chromosome 7D of wheat has been identified to affect adaptation through changes in time to anthesis. It seems relevant to know which specific phases (if any) were responsible for the effect on time to anthesis, as well as if the QTL has any effect on the number of organs initiated during these phases through tuning the rate of development, beyond the function it is known for. We ran a field experiment with 6 lines derived from the Paragon x Baja cross, differing in the possession of the QTL from each parent in their 7D chromosome, three lines with the QTL7D of Paragon (late flowering) and the other three with QTL of Baja (early flowering). We determined time taken to a number of stages, rates of initiation and/or appearance of particular organs, and growth/partitioning. As expected, lines with the QTL7D of Paragon flowered c. 100°C d later than those with the QTL7D of Baja. All the differences were expressed during the late reproductive phases, as lines with the QTL7D of Paragon and of Baja reached terminal spikelet (TS) with negligible (less than 10°C d) and non-significant difference. Within the period of TS-anthesis, the QTL was found more responsive in tuning the first part, which is up to the appearance of the flag leaf, with a minor (yet significant) effect on the duration from flag leaf to anthesis. These differences in development during the late reproductive phase were not followed by consistent (nor significant) differences in either of the components of grain number (i.e. lines with contrasting QTL7D did not differ in spike dry weight at anthesis nor in fruiting efficiency). It seems that fine-tuning time to anthesis with this QTL7D would allow improving adaptation with no penalties in yield-physiological traits.</p>
	<p>Figure (a) is a stacked bar chart showing Thermal Time (°C d) for Paragon and Baja. The y-axis ranges from 0 to 1400. The x-axis shows Paragon and Baja. The legend indicates Sowing-TS (black) and TS-Anthesis (grey). For Paragon, Sowing-TS is approximately 600 and TS-Anthesis is approximately 700. For Baja, Sowing-TS is approximately 600 and TS-Anthesis is approximately 500.</p> <p>Figure (b) is a grouped bar chart showing Spike dry weight (g m<sup>-2</sup>) and Fruiting Efficiency (Grains B.p.a.r<sup>-1</sup>) for Paragon and Baja. The y-axis ranges from 0 to 200. The x-axis shows Paragon and Baja. The legend indicates SDW (black) and FE (grey). For Paragon, SDW is approximately 100 and FE is approximately 50. For Baja, SDW is approximately 100 and FE is approximately 70.</p>
Legend	Stacked bar graph indicates that differences in time to anthesis between QTL7D of Paragon and Baja were evident only in the late reproductive phase (a); and differences in phenology were not significant in components of grain number (FE and SDWAnthesis; b)

Title	Light quality influences rate of development and flowering genes expression in barley
Authors	A. Monteagudo <sup>1</sup> , I. Karsai <sup>2</sup> , A. M. Casas <sup>1</sup> , E. Igartua <sup>1</sup> <sup>1</sup> EEAD-CSIC, Genética y Producción Vegetal. Avda. Montañana, 1005, 50059, Zaragoza, SPAIN <sup>2</sup> Centre for Agricultural Research, Hungarian Academy of Sciences. Brunszvik u., 2, H-2462, Martonvásár, HUNGARY
Keywords	Light quality, Flowering, Barley, Gene expression
Abstract	In winter cereals, vernalization and photoperiod are the main environmental signals that coordinate the flowering date. Genes HvVRN1, HvVRN2 and HvFT1 integrate these signals and interact to allow flowering in the right moment, together with photoperiod response genes, HvFT3 and PPD-H1. Crop responses to light quality and intensity are not fully understood. Biological processes such as seed germination, circadian rhythm, shade avoidance and flowering development are under influence of light spectrum. The objective was to study the effect of light quality using two different light bulbs (metal halide (M) and incandescent (I) lamps) and the interchange between both treatments in development and gene expression. Eleven varieties with known allelic variants for the major flowering time genes were evaluated under controlled conditions (16 h light, 300 $\mu\text{mol m}^{-2} \text{s}^{-1}$ ). Two independent experiments were carried out with fully-vernalized plants: 1) control treatments (M, I); 2) shifting chambers 10 days after the start of the experiment (M-I, I-M). In general, varieties developed faster the longer the exposure to M conditions. The analysis of 19 phenology traits classified the varieties in three groups, showing different sensitivity to light quality changes (Figure 1). Partition of the stem elongation phases showed that major differences between control treatments (I and M) were due to the duration of the period from appearance of first node (Z31) to pseudo-stem elongation (Z30). Expression levels of flowering promoters (HvVRN1, HvFT1 and PPD-H1) were high in M, while HvFT3 and HvVRN2 were higher under I conditions. The expression under shift treatments revealed also a high correlation between HvVRN1 and PPD-H1 transcript levels. Expression was higher under I conditions in the insensitive varieties, 'Kold' and 'Haruna Nijo', suggesting a similar pathway, probably with a common upstream photoreceptor governing the whole process.
	<p style="text-align: center;"><b>Cluster Dendrogram</b></p>
Legend	Phenotypic diversity between the 11 barley cultivars, based on 19 phenology traits, expressed as values relative to the metal halide treatment, used as control.

Title	Wheat genotype influences root symbiosis with mycorrhiza and rhizobacteria
Authors	A. Pérez-de-Luque <sup>1</sup> , J. Ton <sup>2</sup> , D. D. Cameron <sup>2</sup> <sup>1</sup> IFAPA, Centro Alameda del Obispo, Área de Genómica y Biotecnología. Avda. Menéndez Pidal, s/n, 14080 , Córdoba, SPAIN <sup>2</sup> University of Sheffield, Department of Animal and Plant Sciences. Western Bank, Alfred Denny Building, S10 2TN, Sheffield, UNITED KINGDOM
Keywords	Rhizobacteria, Mycorrhiza, Plant genotype, Wheat

**Abstract**

Plant breeding programmes usually focus on yield and resistance against biotic and abiotic stress as the main elements for genotype selection. However, during the last years new factors are gaining importance in order to be considered within these programmes. That is the case of the ability of crops for developing symbiotic relationships with beneficial soil microorganisms, such as arbuscular mycorrhiza fungi (AMF) and plant growth-promoting rhizobacteria (PGPR). Those organisms have proven to enhance plant growing, not only facilitating nutrient acquisition, but also priming plant defences and improving the health status of the crops. For that reason, application of these microorganisms to the soil (biofertilization) is becoming popular between farmers. Nevertheless, several parameters can affect the efficacy of such treatments, and genotype appears as an important one. Host plants strongly influence the extent to which AMF and PGPR colonize their roots through exudation of different metabolites that can attract specific organisms to the rhizosphere. For example, strigolactones are known to play a key role in recruiting AMF and benzoxazinoids have been shown to induce positive chemotaxis in the case of the PGPR *Pseudomonas putida*. Because these traits (the ability to form mycorrhiza and to attract rhizobacteria) have never been taken into account for breeding, a great variability can be found nowadays in crops (for example, in wheat and maize), hampering the efficacy of biofertilization treatments, and hindering the possibility for using these microorganisms as a complement for reducing conventional agrochemical applications. In this work, we present data about the differential behaviour of two wheat cultivars ('Mercato' and 'Avalon') respect to the colonisation of their roots by PGPR and AMF, and how it is affected by the interaction between both microorganisms.



Legend	Rhizobacterial and mycorrhizal colonisation of wheat roots
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Title	Pan-genomes: estimating the true genomic diversity of species
Authors	B. Contreras-Moreira <sup>1</sup> , C.P. Cantalapiedra <sup>1</sup> , M.J. García-Pereira <sup>1</sup> , S.P. Gordon, J.P. Vogel, P. Catalán, P. Vinuesa, E. Igartua <sup>1</sup> , A.M. Casas <sup>1</sup> <sup>1</sup> EEAD-CSIC. Av Montañana, 1005, 50059, Zaragoza, SPAIN
Keywords	pan-genome, plant genome, accessory genes, core genes
Abstract	<p>A pan-genome is defined as the union of all the genes and non-coding DNA found in all individuals of a species. While pan-genomes have been extensively studied in bacteria, and related to their ecological and pathogenic properties, our knowledge of pan-genomes in wild plants and crops is still limited. In this talk I will review how genome and RNA sequencing of both monocot and dicot models (<i>Brachypodium distachyon</i> and <i>Arabidopsis thaliana</i>) and crops (<i>Hordeum vulgare</i>) show that plants, as microorganisms, contain core genes, detected in all accessions, and also accessory sequences, which are present only in some of them. Core genes are more likely to be involved in essential biological functions, whereas accessory loci evolve faster and are conditionally expressed with roles in defense and development. Comparison of de-novo genome assemblies of <i>B. distachyon</i> accessions indicates that accessory genes accumulate in pericentromeric regions, close to transposable elements, in agreement with expression and enrichment analyses in barley. Our results demonstrate that pan-genomes are useful to explore germplasm diversity and show that mobile genetic elements play a key role in shaping plant genomes.</p>
	<p>S+ España y Mediterráneo occidental T+ Turquía y Mediterráneo oriental EDF+ ecotipos de floración tardía</p>
Legend	Phylogenomic tree of 54 ecotypes of <i>Brachypodium distachyon</i> allocated to Extremely Delayed Flowering (EDF+), E Mediterranean (T+) & W Mediterranean (S+) groups. Venn plot shows genes shared among them.

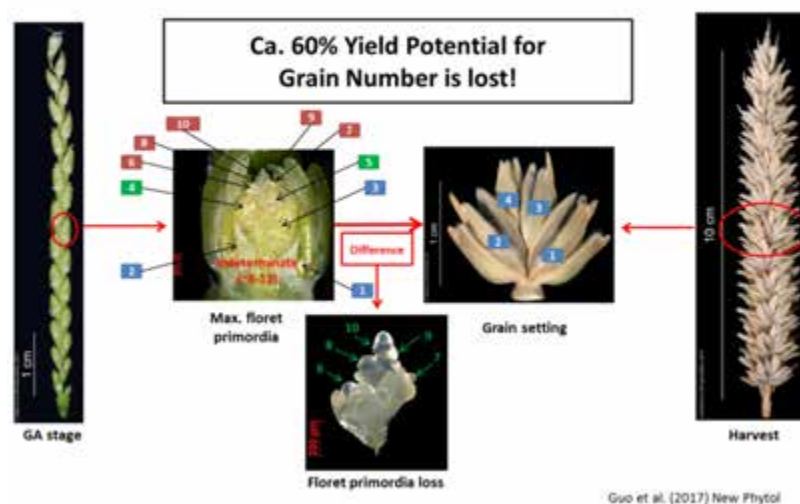
## **Session 2: *Yield potential***

Title	A genetic playground for enhancing the yield potential of wheat
Authors	T. Schnurbusch <sup>1</sup> <sup>1</sup> Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Independent HEISENBERG-Research Group Plant Architecture. Corrensstr., OT Gatersleben, 3, 06466, Seeland, GERMANY
Keywords	Grain number

**Abstract**

Increasing the grain yield remains the main goal of wheat breeding. Grain number is a crucial trait for determining grain yield, and floret fertility plays an important role in the determination of grain number. Floret fertility is governed by the allocation of assimilates to spikes and the distribution of assimilates within spikes. My lab is interested in the molecular-genetic elucidation of floret fertility in wheat. To better understand this process, we studied the maximum number of floret primordia per spikelet (MFS), fertile florets per spikelet (FFS), and number of grains per spikelet (GS) in a diverse wheat panel, two growth conditions and three spikelet positions. FFS was closely associated with floret survival and only weakly related to MFS. We also found that the post-anthesis process of grain set/abortion was important in determining genotypic variation in GS; an increase in GS was mainly associated with improved grain survival. The ovary size of more distal florets (F4 and beyond) seemed to act as a decisive factor for grain setting and effectively reflected pre-anthesis floret development, suggesting that assimilates allocated to distal florets may play a critical role in regulating grain set. Moreover, we systematically phenotyped 54 agronomic and fertility-related traits exhibiting assimilate distribution. By performing a genome-wide association study (GWAS) on all 54 traits, we identified novel quantitative trait loci (QTLs) and candidate genes that are involved in assimilate partitioning, floret fertility, spike morphology and ultimately in the determination of grain number, allowing us to propose a genetic network underlying floret fertility and related traits. Here, I will share our latest results relating to genes which alter spikelet fertility in wheat. Collectively, I will provide new insights into the genetic basis of spike architecture in wheat and may disclose newly discovered targets for boosting yield potential.

**Wheat Yield Potential and Floret Abortion**



**Legend** Figure 1: Spike and spikelet structure during the Green Anther stage and harvest showing floret loss.

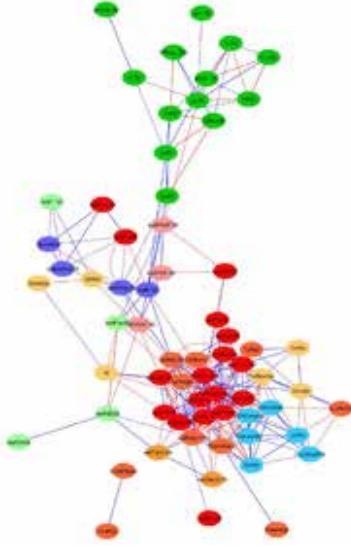
Title	Wheat and barley ear counting in-field conditions, low-cost approach using RGB images.
Authors	J.A. Fernandez-Gallego <sup>1</sup> , S.C. Kefauver <sup>1</sup> , N. Aparicio Gutiérrez <sup>2</sup> , M.T. Nieto-Taladriz <sup>3</sup> , S. Kerfal <sup>4</sup> , A. Lopez <sup>4</sup> , J.L. Araus <sup>1</sup> <sup>1</sup> University of Barcelona, Department of Plant Biology. Av. Diagonal, 645, 08028, Barcelona, SPAIN <sup>2</sup> Instituto Tecnológico Agrario de Castilla y León (ITACyL). Ctra. Burgos, Km. 119, 47071, Valladolid, SPAIN <sup>3</sup> Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA). Coruña, Km. 7.5, 28040, Madrid, SPAIN <sup>4</sup> Syngenta España. Calle de la Ribera del Loira, 8-10, 28042, Madrid, SPAIN
Keywords	Wheat, Barley, ear counting, image processing

**Abstract**

Number of ears per unit ground area is in most cases the main agronomic yield component. A fast evaluation of this attribute may contribute to monitor the efficiency of crop management practices, to an early prediction of grain yield or as a phenotyping trait in breeding programs. Currently the number of ears is counted manually, which is time consuming. This work uses zenithal RGB images taken from above the crop in natural light conditions by holding the camera by hand. Figure 1 shows the image acquisition system. Wheat field trials were carried out in two sites (Aranjuez and Valladolid, Spain) during the 2014/2015 crop season. Barley field trials were carried out in two sites (Arazuri and Valladolid, Spain) during the 2015/2016 crop season. A set of 24 varieties of durum wheat in two growing conditions with three dates of measurement and a set of 15 varieties of barley in rainfed conditions with one date of measurement were used to create the image database. The algorithm for ear counting uses three steps: (i) Laplacian frequency filter (ii) median filter (iii) segmentation using Find Maxima. We have calculated the corresponding ear counting per image number (ears/image) in terms of ears per square meters (ears/m<sup>2</sup>) in order to normalize the square meter size captured by the different types of cameras used. The results, on the one hand, demonstrate high accuracy between the algorithm counts and the manual (image-based) ear counts, higher than 90% and near to 90%, for wheat and barley, respectively. On the other hand, for wheat trials, the relationship between algorithm ear counting and grain yield were also significant and higher than the corresponding relationship using the manual counting. In this approach, results demonstrate that automatic ear counting performed on data captured around anthesis correlated better with grain yield than with images captured at later stages.



**Legend** Fig 1. Hand-help image acquisition

Title	Exploring the genetic diversity in wheat performance at the high temperature and CO2 concentration for resilience with climate change through the identification of key markers of growth and central metabolism.
Authors	E. Marcos-Barbero <sup>1</sup> , P. Pérez <sup>1</sup> , R. Martínez-Carrasco <sup>1</sup> , J.B. Arellano <sup>1</sup> , Y. Gibon <sup>2</sup> , R. Morcuende <sup>1</sup> <sup>1</sup> Institute of Natural Resources and Agrobiolgy of Salamanca (IRNASA), Abiotic Stress. C/ Cordel de Merinas, 40/52, 37008, Salamanca, SPAIN <sup>2</sup> INRA Bordeaux-Aquitaine, Biologie du Fruit et Pathologie. Edouard Bourlaux, 71, 33882, Villenave d'Ornon, FRANCE
Keywords	Elevated CO2 and temperature, Wheat genotypes., Physiological traits., Metabolites., Enzyme activities.
Abstract	
<p>Agricultural production is highly dependent on climate, and improved crop varieties that could counteract the effects of climate change will be required in the future. To date, the evaluation of the natural genetic diversity for the improvement of crop yield in the future climatic scenario is largely unexplored. We assessed the natural variation in tolerance to high temperature and CO2 concentration in a population of 60 wheat genotypes from the CIMMYT 8TH HTWSN collection, preselected at high temperature, with rapid and non-destructive phenotyping techniques. Considerable variations among genotypes in photosynthetic capacity, biomass and grain yield were detected in response to the future climatic scenario, although no consistent correlation was found between grain yield and photosynthetic rate per unit area when all genotypes were compared. The main factor contributing to yield variability was the growth length, the higher yielding genotypes being those with faster development, which avoid the increase of temperatures during grain filling. We also explored the variation in performance under elevated CO2 and high temperature across a set of ten wheat lines with different productivity using an integrated approach, that combines the study of the relationship of physiological characteristics with transcript, metabolite and enzyme activity profiles at critical developmental stages. At ear emergence, the connectivity between traits showed that an increase of starch and nitrate content in the flag leaf, together with a lower activity of enzymes involved in glycolysis, tricarboxylic acid cycle and N assimilation could be considered as positive markers for selection of high yielding wheat lines under climate change. Our study revealed that the determination of PSII operating quantum efficiency is an excellent marker of the photosynthetic variability between wheat lines. Acknowledgments: Grants AGL2013-41363-R, CSI083U16, AGL2016-79589-R (ERDF). Marcos-Barbero had a JCyL fellowship. Boyero, Verdejo, Calvo and González for technical assistance.</p>	
	
Legend	Correlation network for physiological and C-N metabolism traits in ten wheat lines with different productivity in response to elevated CO2 and temperature at ear emergence. Positive (blue edges) and negative (red edges) correlations between traits.

Title	Metabolite profiles in leaves and spikes of field-grown wheat are related with crop yield and can be derived from hyperspectral readings
Authors	O Vergara-Diaz <sup>1</sup> , T Vatter <sup>1</sup> , T Obata <sup>2</sup> , SC Kefauver <sup>1</sup> , A Fernie <sup>2</sup> , JL Araus <sup>1</sup> <sup>1</sup> University of Barcelona, BEECA - Plant Physiology Section. Diagonal , 643, 08028, Barcelona, SPAIN <sup>2</sup> Max Planck Institute of Molecular Plant Physiology. Am Mühlenberg , 1, 14476, Potsdam, GERMANY
Keywords	metabolite profile, spectroscopy, yield, wheat, water stress

#### Abstract

The advance on metabolomics has led to a better understanding of plant-environment interactions and how the levels of specific metabolites may be used as indicators of plant performance. In cereals, the accumulation of certain metabolites -such as proline and sugars- has been related with water stress and drought tolerance/susceptibility, even revealing significant relationships with yield. On the other hand, recent studies relating plant biochemicals with spectral reflectance open the door to a deep assessment of plant status which would have implications on plant breeding and ecosystem studies. In this work, we investigated in durum wheat the relationship between crop yield and the metabolite profiles of the flag leaf and ear tissues. To this aim, five durum wheat genotypes grown in four environments consisting in two high yielding environments and two rainfed trials in the field were examined. Spectral signature of leaves, ears and plot canopies were recorded with a FieldSpec4 spectroradiometer in the 400-2500nm range. LASSO regression models indicated a strong determination of yield by the metabolite profiles of either leaves, lemmas and glumes (Adjusted R<sup>2</sup>= 0.653; 0.655 and 0.564 for the validation sets respectively). Yield prediction accuracy was always enhanced when the metabolite profile at anthesis instead of grain-filling stage is used. Additionally, the models proved to be still robust when they are applied to high and low yielding datasets separately. Further results showed a promising performance of hyperspectral information for the calibration of those plant metabolites related with yield, such as proline, valine, fucose and succinate.

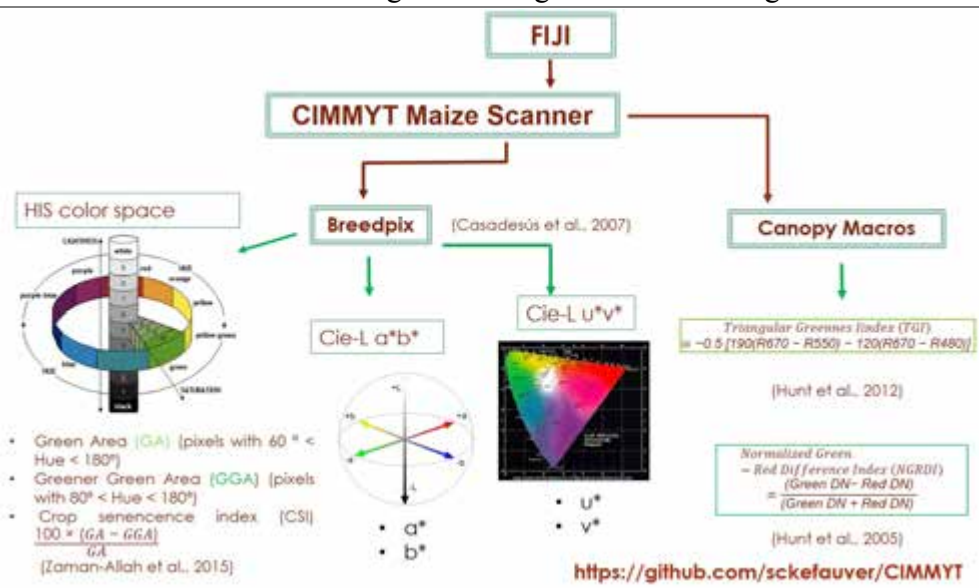
	Training set			Validation set			Metabolite data transformatin	Testing by separate environments	
	R <sup>2</sup>	Adj R <sup>2</sup>	RMSE	R <sup>2</sup>	Adj R <sup>2</sup>	RMSE		High Yielding	Low Yielding
<b>Anthesis</b>									
Leaf	0.845	0.775	0.691	0.685	0.653	0.861	Not transformed	R <sup>2</sup> = 0.37; p<0.001 Adj R <sup>2</sup> = 0.347	R <sup>2</sup> = 0.571; p<0.001 Adj R <sup>2</sup> = 0.555
Glume	0.813	0.742	0.737	0.605	0.564	0.956	log-transformed	R <sup>2</sup> = 0.196; p=0.016 Adj R <sup>2</sup> = 0.1657	R <sup>2</sup> = 0.406; p<0.001 Adj R <sup>2</sup> = 0.3843
Lema	0.898	0.833	0.593	0.686	0.655	0.855	log-transformed	R <sup>2</sup> = 0.441; p<0.001 Adj R <sup>2</sup> = 0.421	R <sup>2</sup> =0.606; p<0.001 Adj R <sup>2</sup> = 0.591
<b>Grainfilling</b>									
Leaf	0.774	0.707	0.792	0.651	0.615	0.874	Not transformed	R <sup>2</sup> = 0.491; p<0.001 Adj R <sup>2</sup> = 0.472	R <sup>2</sup> = 0.467; p<0.001 Adj R <sup>2</sup> = 0.447
Glume	0.743	0.637	0.902	0.504	0.454	1.081	log-transformed	R <sup>2</sup> = 0.078; p=0.135 Adj R <sup>2</sup> = 0.045	R <sup>2</sup> =0.473; p<0.001 Adj R <sup>2</sup> = 0.454
Lema	0.817	0.675	0.858	0.322	0.254	1.271	log-transformed	R <sup>2</sup> = 0.012; p=0.955 Adj R <sup>2</sup> = -0.035	R <sup>2</sup> = 0.262; p=0.0038 Adj R <sup>2</sup> = 0.237

**Legend** LASSO regression models predicting grain yield from leaf, glume and lemma metabolite profiles at anthesis and grain-filling stages. Statistics are provided for the training and validation sets and for the regressions obtained by applying the models for each yielding environment.

Title	UAV and Proximal Sensing for Phenotyping Maize in African Breeding Programs
Authors	S.C. Kefauver <sup>1</sup> , M.L. Buchailot <sup>1</sup> , A. Gracia-Romero <sup>1</sup> , O. Vergara-Díaz <sup>1</sup> , M.A. Zaman-Allah <sup>2</sup> , G. El-Haddad <sup>3</sup> , C. Thierfelder <sup>2</sup> , J.E. Cairns <sup>2</sup> , J.L. Araus <sup>1</sup> <sup>1</sup> University of Barcelona, B.E.E.C.A. Plant Physiology Section. Av. Diagonal, 643, 08028, Barcelona, SPAIN <sup>2</sup> International Maize and Wheat Improvement Center, CIMMYT Southern Africa Regional Office. Peg Mazowe Road, 12.5 km, MP 163, Harare, ZIMBABWE <sup>3</sup> Software Engineer, Floor 2, Nassim El Kayem Bldg.. Road, 7, Sector 8, Jeita, LEBANON
Keywords	maize, remote sensing, UAV, phenotyping, Africa

**Abstract**

Maize is the most commonly cultivated cereal in Sub-Saharan Africa (SSA) in terms of land area and production, where continued population growth, soil degradation, and climate change challenge food security. Low yields in this region are very often associated with low soil fertility and low fertilizer availability. On the other hand, Conservation Agriculture (CA) has been proposed to enhance soil health and productivity. In several parallel studies, proximal and remote sensing phenotyping measurements were conducted on maize plants from the ground “phenopole” and from a UAV (unmanned aerial vehicle) platform. For the studies on comparative maize performance under managed low nitrogen and phosphorous fertilizer conditions, we evaluated a set of indices derived from Red-Green-Blue (RGB) images compared to field-based NDVI and SPAD as phenotyping and crop monitoring tools. With regards to contrasting phosphorous fertilization conditions, we also evaluated remote sensing indices derived from multispectral (visible and infrared) UAV image data. In the combined management effects studies, RGB, multispectral, and thermal sensor performance was evaluated for assessing maize yield under different planting densities and tillage practices, including both CA and conventional ploughing. In general, RGB indices assessed at both ground and aerial levels correlated comparably with grain yield, with slight differences potentially related to the higher spatial resolution of ground imaging. Furthermore, RGB based indexes related to canopy vigor often performed better than multispectral data at assessing phenotypic yield differences, again potentially due to the greater resolution of the RGB data, although multispectral performance was improved by applying a NDVI threshold soil mask. These studies together reinforce the effectiveness of UAV remote sensing and its potential for high throughput plant phenotyping and crop management under different nutrient and management conditions, with a potential argument in favor of higher resolution and more affordable RGB indices for field or aerial image-based vegetation monitoring.

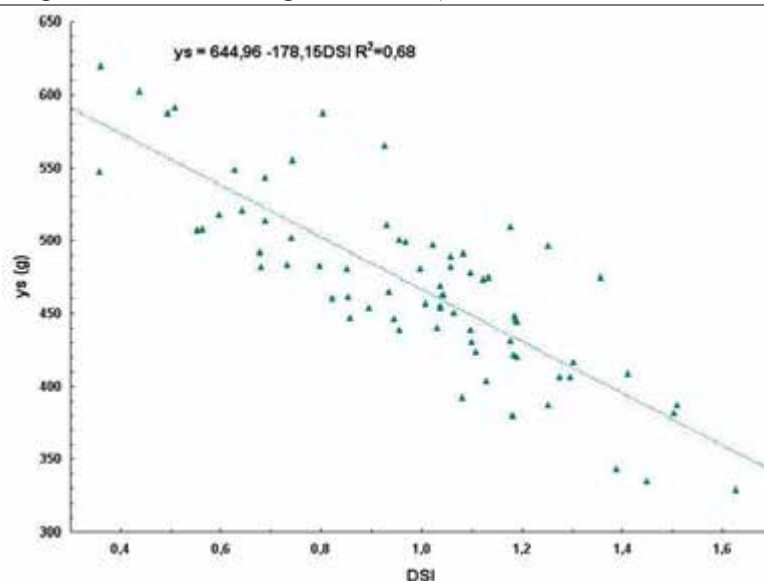


Legend	CIMMYT MaizeScanner RGB Processing Workflow
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Title	Potential Associations Between Grain Yield, Drought Indexes and some Agronomic Traits of a Durum Wheat Collection
Authors	I Zouari <sup>1</sup> , S Rezgui <sup>1</sup> , A Daaloul <sup>1</sup> <sup>1</sup> National Institute of Agronomy of Tunisia, Department of Horticultural Sciences. 43, Avenue Charles Nicole, 00216 96929973, 1082, Tunis, TUNISIA
Keywords	Durum wheat, Tolerance indices, Yield indices, Agronomic traits

**Abstract**

Twenty-three cultivars of Durum wheat provided by the International Center for Agricultural Research in the Dry Areas (ICARDA) and the national check cultivar Karim were evaluated in trials in Bou Salem region under rainfed conditions and in Kairouan region under irrigated conditions. Tolerance indices (DSI and TOL) and yield indices (MP, GMP and STI) have been evaluated on the basis of yields obtained in these two stations. The results showed that the best selection strategy for a high yield potential and for drought tolerance would be based on a selection for high geometric mean productivity (GMP) and then select among the most productive cultivars those having the lowest drought susceptibility index (DSI). The genotypes Lgt3//Bcr/Sbl5 and Arislahn-10, with a wide adaptation capacity, have been identified as the most adapted to rainfed and irrigated conditions. In the second part of the trial, agronomic traits (spikes number, plant height, spike length, number of spikelets per spike, number of kernels per spike, thousand kernels weight, biomass, grain yield and harvest index) have been evaluated under rainfed and irrigated conditions. Under rainfed conditions, water stress appeared mostly during heading and grain filling periods. Grain yield was the most affected trait by the water stress in the rainfed conditions and decreased by 34.4%; Thousand grain weight showed a Genotype × Environment interaction. Genotypic responses variability during grain filling may be attributed to tolerance or susceptibility to water drought during this period. Associations' analysis between the studied traits showed that under rainfed conditions, grain yield would be mostly favoured by high biomass and spikes number ( $r1_{rg, bm}=0.9^{**}$  and  $r1_{rg, ne}=0.45^{**}$ ). Under irrigated conditions, grain yield have been positively correlated with harvest index and to a lesser degree with biomass ( $r2_{rg, ir}=0.56^{**}$  et  $r2_{rg, bm}=0.27^*$ ).



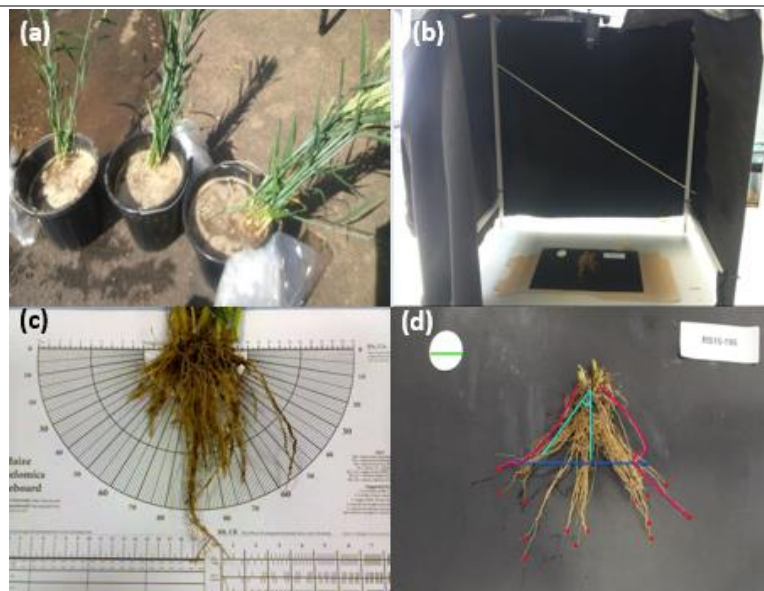
Legend	Relationship between yield under rainfed conditions and DSI Index
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## **Session 3: *Abiotic Stresses***

Title	Genetic diversity for rooting traits and tolerance of water and nutrient stresses in wheat
Authors	J FOULKES <sup>1</sup> , L YORK <sup>1</sup> , S SLACK <sup>1</sup> , M HAWKESFORD <sup>2</sup> , M BENNETT <sup>1</sup> <sup>1</sup> University of Nottingham. School Biosciences, University of Nottingham, Sutton Bonington Campus, LE125RD, Loughborough, UNITED KINGDOM <sup>2</sup> Rothamsted Research. Plant Sciences Department, Harpenden, AL5 2JQ, Hertfordshire, UNITED KINGDOM
Keywords	wheat, resource use efficiency, field root phenotyping

**Abstract**

Breeding root systems more efficient for water and nitrogen capture represents a promising avenue for accelerating yield gains in wheat. We quantified variation in grain yield, biomass and N-use efficiency (NUE) and associated traits in panels of diverse hexaploid wheat germplasm comprising landraces and synthetic-derived wheats under low and high N conditions. Intensive phenotyping has revealed novel diversity in senescence-related traits associated with improved biomass under both high and low N conditions. Mapping of SSD lines derived from landraces × UK cultivar Paragon crosses has revealed novel QTL for biomass and NUE and related traits. Yield variation was mainly explained by variation in N uptake under low N implying root traits were determining improved yield. Our recent work has developed high-throughput platforms for field phenotyping of root system architecture. Root crown phenotyping, or shovelomics, relies on excavation of the upper portions of root systems and measuring root properties such as numbers, angles, densities and lengths. We phenotyped root crowns in a Savannah × Rialto winter wheat population consisting of 94 doubled-haploid (DH) lines and the two parents. Substantial variation and heritability were observed for all shovelomics root traits. Trait validation was carried out through soil coring on a subset of 14 DH lines and the two parents. We observed that drought reduced grain yield per plant by 21.0%. Under rain-fed conditions, nodal root angle and roots/shoot were positively associated with root length density at 40-60 cm depth; and nodal root angle and roots/shoot were positively associated with canopy stay-green and yield. Genetic analysis has revealed novel QTL regions for nodal root traits. We conclude that shovelomics is a valuable technique for quantifying genetic variation in nodal root traits in wheat. The perspectives for future goals to raise yield potential and resource efficiency and the challenge to transfer traits into commercial varieties will be discussed.



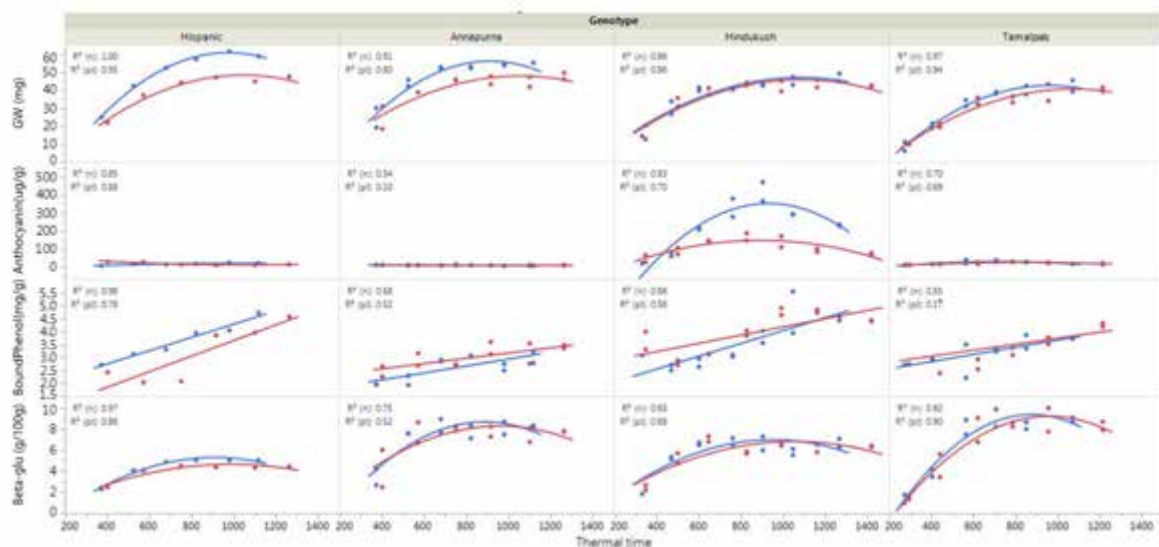
Legend	Fig. 1 (a) Root crowns soaking in the field, (b) root crown imaging station in the laboratory, (c) root crown analysed using visual scoring board and (d) root crown analysed using Image J software.
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Title	Optimizing winter wheat traits to improve resilience to a changing environment in rainfed crop systems of Turkey and Iran
Authors	M.S Lopes <sup>1</sup> , E. Ozer <sup>2</sup> , M. Karaman <sup>3</sup> , M. Roustaii <sup>4</sup> , J. Kamali <sup>5</sup> <sup>1</sup> CIMMYT, GWP. Sehit Cem Ersever Caddesi No: 9-11 Yenimahalle, , 9-11, 06810 , Ankara , TURKEY <sup>2</sup> Bahri Dagdas International Agricultural Research Institute. PK:125, Karatay, 125, 42020, Konya, TURKEY <sup>3</sup> Gap Uluslararası Tarımsal Araştırma ve Eğitim Merkezi . Silvan Yolu Üzeri , 9. Km PK.72 , 21110 , Diyarbakir, TURKEY <sup>4</sup> Cereal Department, Dryland Agricultural Research Institute (DARI). North Ring Road, PO BOV 119, , 5517643511 , Maragheh , IRAN <sup>5</sup> The International Maize and Wheat Improvement Center (CIMMYT). Seed and Plant Improvement Institute Campus (SPII), Mahdasht Avenue Shahid Fahmideh Blvd., P.O. Box 11194119, 31585, Karaj, IRAN
Keywords	heading, low rainfall, reproductive stage, vegetative stage, within species diversity
Abstract	<p>Erratic weather patterns associated with increased temperatures and decreasing rainfall pose unique challenges for wheat breeders playing a key part in the fight to ensure global food security. Within rain fed winter wheat areas of Turkey and Iran unusual weather patterns may prevent attaining maximum potential increases in winter wheat genetic gains. This is primarily related to the fact that the yield ranking of tested genotypes may change from one year to the next. Changing weather patterns may interfere with the decisions breeders make about the ideotype(s) they should aim for during selection. To inform breeding decisions, this study aimed to optimize major traits by modeling different combinations of environments and by defining a probabilistic range of trait variations that maximized grain yields (Fig. 1). Optimal phenology was highly related to the temperature and to rainfall at which winter wheat genotypes were exposed around heading time (20 days before and after heading). Specifically, later winter wheat genotypes were exposed to higher temperatures both before and after heading, increased rainfall at the vegetative stage, and reduced rainfall during grain filling compared to early genotypes. These variations in exposure to weather conditions resulted in shorter grain filling duration and lower grain yields in long-duration genotypes. This research tested if diversity within species may increase resilience to erratic weather patterns. Calculated production of a selection of five high yielding genotypes was tested against monoculture and revealed that a set of diverse genotypes with different phenology and plant height was not beneficial. New strategies of progeny selection are discussed: narrow range of variation for phenology in families may facilitate the discovery and selection of new drought resistant and avoidant wheat lines targeting specific environments. Finally, development of new tools for parental selection will be discussed.</p>
	<p>Figure 1 consists of two graphs. Graph A is a line graph showing Grain Yield (gm<sup>-2</sup>) on the y-axis (ranging from 180 to 340) versus Phenology Category on the x-axis (ranging from 1 to 7). Multiple lines represent different genotypes, showing varying yields across categories. Graph B is a scatter plot with a quadratic regression line. The y-axis is Grain Yield (gm<sup>-2</sup>) (200 to 280) and the x-axis is Phenology Means per category (days) (192 to 202). The regression equation is <math>y = -1.5306x^2 + 596.7x - 57875</math> with <math>R^2 = 0.9856</math>. A vertical line indicates the maximum yield (max GY) at 194.9 days to heading.</p>
Legend	Fig. 1- Grain yield (GY) of seven phenology categories in a winter wheat population of 250 varieties and breeding lines grown in Turkey and Iran (1, very early, 2, early, 3, early-medium, 4, medium, 5, medium late, 6 late and 7, very late). Twenty s

Title	Synthesis of bioactive compounds in barley during grain filling in response to late abiotic stress
Authors	M Martínez-Subirá <sup>1</sup> , MA Moralejo <sup>1</sup> , L Cistué <sup>2</sup> , MP Romero <sup>1</sup> , R Savin <sup>1</sup> , I Romagosa <sup>1</sup> <sup>1</sup> Universidad de Lleida, Agrotecnio Center. Alcalde Rovira Roure, 191, 25198, Lleida, SPAIN <sup>2</sup> Consejo Superior de Investigaciones Científicas, Estación Experimental de Aula Dei. Montañana, 1005, 50059, Zaragoza, SPAIN
Keywords	Barley grain, Phenolic compounds, Fiber, Terminal stress

**Abstract**

The response of barley genotypes to late abiotic stress, particularly high temperature during grain filling, was studied in a field experiment at Semillas Batlle, Bell-Lloc Lleida, Spain. Dynamics of bioactive compounds synthesis ( $\beta$ -glucan, arabinoxylans, free, including anthocyanins, and bound phenolic compounds) was determined for four barley genotypes throughout grain filling. Treatments consisted in the barley genotypes: Hispanic, (a two-rowed, hulled, non-waxy and yellow grain European commercial variety), Annapurna, (a recent Batlle and CSIC release which is a two-rowed, naked, waxy and yellow grain derived from a cross between a European and an American food barley), Hindukush, (an un-adapted two-rowed, naked, non-waxy and purple grain genotype of Himalayan origin) and Tamalpais, (an un-adapted six-rowed, naked, non-waxy and yellow genotype of Mexican origin) subjected to high post-anthesis temperatures. The high temperature was imposed by covering half of the plots with clear high-light transmission 500 gauge polythene film 15 days after anthesis. From anthesis, five main spikes of each genotype, marked at heading, were collected at weekly intervals during grain filling to maturity. Genotypes responded differentially to the abiotic stress. The two commercial varieties significantly reduced their grain weight under plastic, whereas the exotic genotypes were more resilient to high temperatures. A relative decrease of anthocyanin content in the coloured variety grown under plastic could be associated not just to high temperature but more likely to reduced radiation. Differential genotypic responses associated to abiotic stress were not that clearly observed for bound phenolic compounds and for  $\beta$ -glucan content throughout grain filling. Both compounds increased concentration in the endosperm through time but whereas the slope for bound phenolic compounds remained relatively constant through grain filling,  $\beta$ -glucan concentration reached a plateau just before physiological maturity.



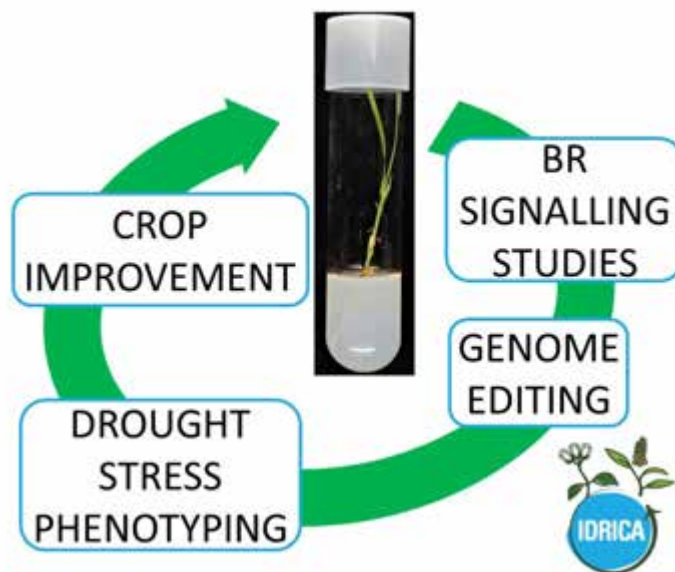
**Legend** Figure 1. Dynamic of dry weight and bioactive compounds synthesis in four genotype under normal (blue) and included abiotic stress (red) in Thermal time in Growing Degree Days after Anthesis.

Title	Carbon and nitrogen metabolism in laminar and non-laminar photosynthetic organs under contrasting water regimes in low- and high-yielding durum wheat varieties
Authors	R. Vicente <sup>1,2</sup> , O. Vergara-Díaz <sup>1</sup> , R. Morcuende <sup>3</sup> , S. C. Kefauver <sup>1</sup> , N. Aparicio <sup>4</sup> , J. L. Araus <sup>1</sup> <sup>1</sup> Faculty of Biology, University of Barcelona, Department of Evolutionary Biology, Ecology and Environmental Sciences. Av. Diagonal , 643, 08028, Barcelona, SPAIN <sup>2</sup> Max Planck Institute of Molecular Plant Physiology, System Regulation. Am Mühlenberg, 1, 14476, Potsdam, GERMANY <sup>3</sup> Institute of Natural Resources and Agrobiological of Salamanca, IRNASA-CSIC. Cordel de Merinas , 40-52, 37008, Salamanca, SPAIN <sup>4</sup> Agro-technological Institute of Castilla y León (ITACyL). Ctra. Burgos , km 119, 47071 , Valladolid, SPAIN
Keywords	Carbon metabolism, Nitrogen metabolism, Drought stress, Genotypic variability, Organs
Abstract	<p>There is a need to generate improved crop cultivars adapted to the future changing climate to satisfy the increasing food demand in the upcoming years. This is particularly relevant in durum wheat, which is subjected to water limitation in the Mediterranean basin, compromising grain yield. Our aim is to compare plant performance of low- and high-yielding cultivars to understand the mechanisms associated with high yield under contrasting water regimes. We used a multi-level approach covering agronomic components, physiological traits and metabolic switches, including a high throughput phenotyping platform at ground and aerial scale. Based on grain yield results from 24 elite cultivars grown under irrigated and rainfed field conditions during three crop seasons (2013-2016), we selected Don Sebastian (DS) and Pelayo (PE) as low- and high-yielding cultivars, respectively. Multivariate and univariate analyses of agronomic components and field measurements during the 2015/2016 crop season clearly showed that grain yield and harvest index was higher in PE due to an increment in grain (ear) dry weight, associated with lower canopy biomass and higher photosynthetic rate trend. Physiological and gene expression results suggested that C/N metabolisms were altered in laminar and non-laminar organs (flag leaf blade and sheath, peduncle, glume, lemma and awn) between cultivars under irrigated and rainfed conditions, particularly in the ear organs. Chlorophyll, glucose, fructose and protein contents were higher in PE compared to DS in several organs, and the photosynthetic and respiratory genes were upregulated. Although grain yield was higher in PE than in DS, grain N yield was similar, revealing that N assimilation and/or translocation were not promoted, even when N-metabolism genes were strongly induced. Our study provides new insights into the physiological understanding of low- and high-yielding cultivars at whole plant level that could improve the resilience of wheat under near-future climate change scenario conditions.</p>
	<p>The figure is a Principal Component Analysis (PCA) plot. The x-axis is labeled 'PC1 (25.1%)' and ranges from -10 to 10. The y-axis is labeled 'PC2 (16.7%)' and ranges from -10 to 10. The plot shows several distinct clusters of data points, each representing a different organ and cultivar combination under specific water regimes. A legend titled 'Groups' provides the key for these clusters:</p> <ul style="list-style-type: none"> <li>awn.DS.RF (yellow circle)</li> <li>awn.DS.SI (orange circle)</li> <li>awn.PE.RF (light blue circle)</li> <li>awn.PE.SI (dark blue circle)</li> <li>glume.DS.RF (pink circle)</li> <li>glume.DS.SI (light purple circle)</li> <li>glume.PE.RF (dark purple circle)</li> <li>glume.PE.SI (red circle)</li> <li>leaf.DS.RF (green circle)</li> <li>leaf.DS.SI (light green circle)</li> <li>leaf.PE.RF (dark green circle)</li> <li>leaf.PE.SI (black circle)</li> <li>lemma.DS.RF (light blue circle)</li> <li>lemma.DS.SI (dark blue circle)</li> <li>lemma.PE.RF (light blue circle)</li> <li>lemma.PE.SI (dark blue circle)</li> <li>peduncle.DS.RF (light blue circle)</li> <li>peduncle.DS.SI (dark blue circle)</li> <li>peduncle.PE.RF (light blue circle)</li> <li>peduncle.PE.SI (dark blue circle)</li> <li>sheath.DS.RF (red circle)</li> <li>sheath.DS.SI (dark red circle)</li> <li>sheath.PE.RF (red circle)</li> <li>sheath.PE.SI (dark red circle)</li> </ul>
Legend	Principal component analysis of the interaction organ × water regime × cultivar based on C/N metabolism-associated traits. DS, Don Sebastian; PE, Pelayo; SI, supplemental irrigation; RF, rainfed conditions.

Title	Genome editing in Sorghum: a vanguard cereal to study drought stress
Authors	D. Martignago <sup>1</sup> , D. Blasco <sup>1</sup> , M. Capellades <sup>1</sup> , A. I. Caño-Delgado <sup>1</sup> <sup>1</sup> CRAG. Campus UAB, Carrer de la Vall Moronta, S/N, 08193, Cerdanyola del Vallès, SPAIN
Keywords	Sorghum, drought, CRISPR, genome editing, brassinosteroid

**Abstract**

Sorghum (*Sorghum bicolor* [L.] Moench) is the 5th most cultivated cereal worldwide. Sorghum is a versatile crop adapted to hot and dry agroecologies and it is a staple food in many drought-threatened regions. In Europe, sorghum is used as animal feed and grown in regions in which the decreasing water availability is deterring maize farming. However, sorghum commercialization for human consumption is gaining interest because of its nutritional (high protein and antioxidants content, low glycaemic index, gluten-free) and agronomical (low input, high resilience) characteristics. Sorghum is widely considered the model species for C4 grasses for plant research. Its diploid genome (~730 Mbp) is highly repetitive, but more amenable to genomic studies than its close relative maize. Our team has recently started to work in cereals with the aim to translate knowledge and expertise from the *Arabidopsis* brassinosteroid signalling field into sorghum. Specifically, we would like to investigate the protective roles of brassinosteroids to drought stress. Genome editing technologies offer unprecedented opportunities for cereal science and crop improvement. However, limited plant transformation capability is hindering this approach in sorghum. Our research group is currently developing plant transformation and genome editing tools in sorghum that will allow us the production of mutants in sorghum brassinosteroid key genes. In parallel, we are setting up a high-throughput phenotyping platform in controlled condition to study the obtained mutants in normal conditions and under drought stress. This platform will also be used to perform a preliminary screening on drought performances using a collection of Iberian sorghum accessions, prior to further investigations ultimately leading to field trials. Overall, we aim to produce cereals better adapted to climate change and able to ensure food security and sustainability, the greatest challenges of the XXI century.



Legend	Graphical abstract of "Genome editing in Sorghum: a vanguard cereal to study drought stress"
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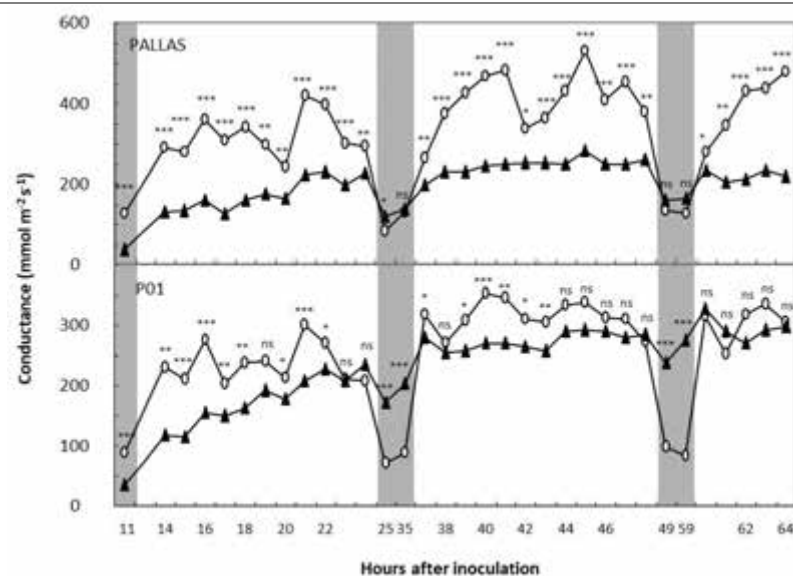
Title	Elevated CO2 effect on wheat grain quality evolution during grain filling period																																																					
Authors	D. Soba <sup>1</sup> , T. Fuertes-Mendizábal <sup>2</sup> , S. Ben Mariem <sup>1</sup> , F. Gilard <sup>3,4</sup> , C. González-Murua <sup>2</sup> , J.J. Irigoyen <sup>5</sup> , G. Tcherkez <sup>3,4,6</sup> , I. Aranjuelo <sup>1</sup> <sup>1</sup> Instituto de Agrobiotecnología, Agricultura Sostenible y Cambio Climático. Avenida Pamplona, 123, 31192, Mutilva, SPAIN <sup>2</sup> University of the Basque Country (UPV/EHU), Department of Plant Biology and Ecology. Barrio Sarriena, s/n, 48940, Leioa, SPAIN <sup>3</sup> Institut de Biologie des Plantes, Université Paris-Sud, Plateforme Métabolisme-Métabolome. Bâtiment, 630, 91405, Orsay cedex, FRANCE <sup>4</sup> INRA, UMR INRA/UCBN Institut de Biologie Fondamentale et Appliquée, Université de Caen Basse-Normandie, Ecophysiologie Végétale, Agronomie et Nutrition. Esplanade de la Paix, s/n, 14032, Caen, FRANCE <sup>5</sup> Universidad de Navarra, Grupo de Fisiología del Estrés en Plantas (Dpto. de Biología Ambiental), Unidad Asociada al CSIC, EEAD, Zaragoza e ICVV, Logroño, Facultad de Ciencias y Farmacia. Irunlarrea, 1, 31008, Pamplona, SPAIN <sup>6</sup> Australian National University, Research School of Biology, College of Medicine, Biology and Environment. -, -, 2601, Canberra ACT, AUSTRALIA																																																					
Keywords	CO2, Wheat, Grain quality, Grain filling																																																					
Abstract	<p>The increase in atmospheric CO2 concentration is predicted to influence wheat production and its nutritional and quality properties. In the present study, durum wheat (<i>Triticum durum</i> L. cv. Sula) was grown under two different CO2 (400 versus 700 ppm) concentrations in four greenhouses to examine effects on crop yield and grain quality in different phenological moments (ranging from grain filling to maturity). Exposure to elevated CO2 significantly increased aboveground biomass and grain yield components. However, elevated CO2 had a negative influence in parameters related to quality and nutritional properties. More specifically grain N concentration (15,5%; P=0.005) and gluten proteins (11.7%;P=0.044) decreased at maturity. Phenology had important changes in N metabolism, mostly linked with the conversion of free amino acids to proteins through the grain filling phase. Phenology also had a relevant effect in grain C concentration where it was observed an increase of 10% (P=0.000) at maturity. A non-significant 6% increase in starch content and a significant decrease in sucrose (-66%; P=0.000), the main C translocation form, were also observed between grain filling and maturity. Generally speaking, phenology caused a decrease in amino acids, carbohydrates, organic acids and lipids. Elevated CO2 is affecting grain properties through grain filling phase. These properties are important for consumer nutrition, health and industrial processing. Experimental evidence for these changes is still poor but deserves further attention.</p>																																																					
	<table border="1"> <thead> <tr> <th></th> <th>Wheat traits</th> <th>Ambient</th> <th>Elevated</th> <th>CO2 eff. %</th> <th>p-level</th> </tr> </thead> <tbody> <tr> <td rowspan="3">Grain fill.</td> <td>Grain DM</td> <td>1.14 ± 0.17</td> <td>1.19 ± 0.60</td> <td>4.10</td> <td>0.858</td> </tr> <tr> <td>Total DM</td> <td>13.36 ± 1.76</td> <td>15.04 ± 3.56</td> <td>12.60</td> <td>0.324</td> </tr> <tr> <td>Harvest Index</td> <td>0.086 ± 0.017</td> <td>0.079 ± 0.034</td> <td>-8,77</td> <td>0.638</td> </tr> <tr> <td rowspan="5">Maturity</td> <td>Grain DM</td> <td>7.15 ± 1.74</td> <td>14.59 ± 1.87</td> <td>104.11</td> <td>0.001</td> </tr> <tr> <td>Total DM</td> <td>15.94 ± 2.47</td> <td>27.30 ± 3.82</td> <td>71.29</td> <td>0.000</td> </tr> <tr> <td>Harvest Index</td> <td>44.57 ± 7.10</td> <td>53.56 ± 2.24</td> <td>20.17</td> <td>0.047</td> </tr> <tr> <td>TGW</td> <td>48.14 ± 7.84</td> <td>50.58 ± 13.50</td> <td>5.08</td> <td>0.742</td> </tr> <tr> <td>Tiller number</td> <td>6.67 ± 1.97</td> <td>9.00 ± 1.97</td> <td>34.93</td> <td>0.050</td> </tr> <tr> <td>Ear number</td> <td>5.67 ± 1.03</td> <td>6.33 ± 1.86</td> <td>11.64</td> <td>0.461</td> </tr> </tbody> </table>		Wheat traits	Ambient	Elevated	CO2 eff. %	p-level	Grain fill.	Grain DM	1.14 ± 0.17	1.19 ± 0.60	4.10	0.858	Total DM	13.36 ± 1.76	15.04 ± 3.56	12.60	0.324	Harvest Index	0.086 ± 0.017	0.079 ± 0.034	-8,77	0.638	Maturity	Grain DM	7.15 ± 1.74	14.59 ± 1.87	104.11	0.001	Total DM	15.94 ± 2.47	27.30 ± 3.82	71.29	0.000	Harvest Index	44.57 ± 7.10	53.56 ± 2.24	20.17	0.047	TGW	48.14 ± 7.84	50.58 ± 13.50	5.08	0.742	Tiller number	6.67 ± 1.97	9.00 ± 1.97	34.93	0.050	Ear number	5.67 ± 1.03	6.33 ± 1.86	11.64	0.461
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Legend	Growth and grain parameters of durum wheat (cv. Sula) cultivated under ambient and elevated CO2																																																					

## **Session 4: *Biotic Stresses***

Title	Plant physiological dysfunctions at the crossroad between disease resistance and resistance cost.
Authors	E. Prats <sup>1</sup> <sup>1</sup> CSIC-Institute for Sustainable Agriculture. Alameda del Obispo s/n, s/n, 14004, Cordoba, SPAIN
Keywords	Stomatal lock-up, Photosynthetic dysfunctions, resistance, pathogens, resistance cost

**Abstract**

Relation between pathogenesis and stomatal function is a field of plant pathology recognised relatively recently. Most studies have focused on the pathogen, i.e. how pathogen virulence factors modify stomatal aperture to facilitate host invasion. However, we have observed that pathogen challenge leads to stomatal closure more rapidly in resistant than in susceptible plants; this suggests that activation of stomatal closure enhances signalling pathways involved in resistance. In addition, in the mid- and long-term, resistance responses to powdery mildew pathogens in barley and oats, lead to stomata lock in an open configuration, displaying little or no closure in response to diurnal rhythms or abscisic acid. As a result, these plants exhibit compromised tolerance to drought. These stomatal dysfunctions have severe impacts on gas exchange, and causes photosynthetic disruption through the over-reduction of redox-active components and poorer cooling via the transpirational stream. Overall, these dysfunctions probably results in a yield cost of resistance particularly in locations with higher light levels and/or prone to drought, and it is therefore imperative to define their underlying mechanisms. At the beginning, and based on set of isogenic lines, these stomatal dysfunctions were associated with resistance responses mediated by R genes. However recent studies showed that dysfunctions were genotype but not response-type dependent since genotypes with similar resistance responses when assessed histologically showed very different locking patterns. Thus, the extent of the photosynthetic alterations is not directly related to the extent of HR. The latter studies on the possible link with oxidative stress occurring during defense and disruption of chlorophyll degradation pathway will be explained.

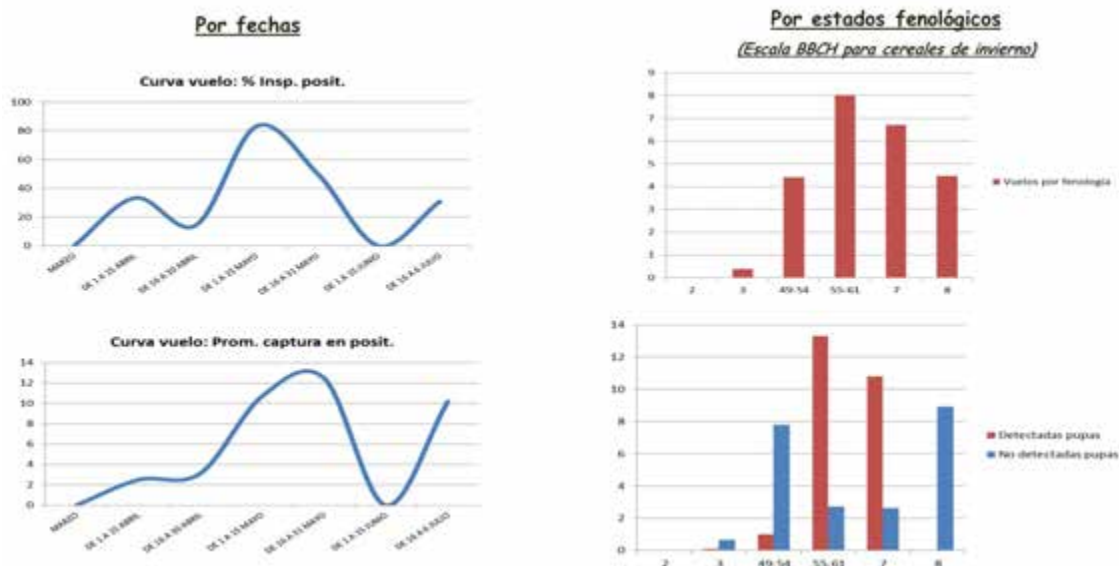


Legend	Leaf conductance in healthy (circle) and powdery mildew inoculated (triangle) Pallas and P01 barleys under a 12 h dark (shaded)/12h light (unshaded) photoperiod. *, ** and *** indicate significance at P < 0.05, 0.01 and 0.001. Figure from Prats et al 2006. J Exp Bot.
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Title	Incidence of <i>Oscinella frit</i> L (Diptera: Chloropidae) in Castilla y León.
Authors	F.J. Ciudad Bautista <sup>1</sup> , A. Santiago Pajón <sup>1</sup> , M.C. García Ariza <sup>1</sup> , M.R. González Barbero <sup>1</sup> , J.C. González Ruiz <sup>1</sup> , C. Caminero Saldaña <sup>1</sup> <sup>1</sup> Instituto Tecnológico Agrario de Castilla y León, Unidad de Cultivos Herbáceos. Carretera de Burgos km. 119, 119, 41070, Valladolid, SPAIN
Keywords	Barley, Wheat, Insect, Pest

**Abstract**

The frit fly, *Oscinella frit* L., is a migrating insect pest, which in Castilla y León is causing severe damage on barley. All grass species could be host. The flies oviposit on the young and tender shoots of grains and grasses, the larvae entering the shoot and feeding downward in the middle. Occasionally eggs are laid on or within the glumes just after heading, in which case the larvae eat out the soft kernel. Female flies of first generation, emerging from overwinter larvae, oviposit in younger secondary tillers, and these aren't very important in final crop yield. Flies of second generation find the barley kernels in grain filling period, and larvae eat the kernel. Pupae are formed inside the glumes, from which third-generation adults emerge. This type of damage was observed for the first time in 2011, and since then it has been increasing in recent years. From 2015 the presence of adults on cereals crops has been accounted in the Winter Cereal Pests and Diseases Surveillance Procedure of JCyL. Since then 716 barley fields and 790 wheat fields has been monitored. Adult flies were found in 18 and 15% of the barley and wheat fields respectively. Flies were present also in oats and rye fields. In 2017 number of flies captured by butterfly nets in a systematic approach was recorded. Two peaks of flies were observed, from middle March to middle April and from last days of April to middle June. Ears of wheat and barley were collected in fields with and without recorded flies. No kernel damage was observed in wheat. Kernel damage in barley was only observed in the fields in which the presence of adults was high during the period from BBCH 55 to BBCH70. In these fields, the yield lost was estimate in 20.18%.



**Legend** % of inspection in which adult flies are detected. N° of flies captured in butterfly nets. Number of flies captured in different barley development stages. Number of grains eaten in ears if adult flies are detected

Title	Aerial platforms as a new approach to select resistant lines for yellow rust in bread wheat breeding program.
Authors	Y. Pallavicini <sup>1</sup> , R. Martínez-Peña <sup>1</sup> , B. González <sup>1</sup> , S. C. Kefauver <sup>2</sup> , A. Gracia-Romero <sup>2</sup> , N. Aparicio <sup>1</sup> <sup>1</sup> Instituto Tecnológico Agrario de Castilla y León, Unidad de herbáceos. Carretera Burgos , km118, 47071, Valladolid, SPAIN <sup>2</sup> Integrative Crop Ecophysiology Group, Universitat de Barcelona, Section of Plant Physiology. Avenida Diagonal, 645, 08028, Barcelona, SPAIN
Keywords	Triticum aestivum, Fungal resistance, vegetation index, RGB images, phenotyping
Abstract	<p>During the last years wheat production in Europe has been seriously threatened by a new race of yellow rust (<i>Puccinia striiformis</i> f.sp.tritici). The cultivation of resistant wheat cultivars is the most effective and environmentally-friendly strategy. Therefore, developing new germplasm resistant to this disease has become a priority objective not only to increase production but also to stabilize it. Traditionally, field phenotyping for yellow rust has been performed using visual scales of canopy effects; however, this method is subjective in nature and not easy to standardize. Remote sensing has become an important methodology to improve precision and throughput in phenotyping. It allows to screen large numbers of genotypes at a lower cost and faster than the conventional method. Moreover, it provides to breeding programs the opportunity to assess genetic diversity under field conditions. The objective of this study was to assess the efficiency of a set of remote sensing indices (VIs) acquired by aerial platforms, as an alternative to visual assessment to increase the selection efficiency in a bread wheat breeding program for resistance to yellow rust. A field trial with 256 bread wheat breeding lines were field visually evaluated for yellow rust resistance and grain yield (GY) was also determined. Also, nine multispectral vegetation indices as well as ten derived from red, green, blue (RGB) images were calculated on different dates using an aerial platform. The breeding lines exhibited a wide range of resistance to yellow rust, and the GY was affected by the level of infestation. Results showed significant correlations between most of the remote sensing indices and the visual level of resistance to rust. Moreover, some of them detected rust symptoms at early stages of the disease. It suggests that VIs would be a potentially rapid and efficient approach to detect rust resistance in breeding programs.</p>
Legend	Evolution of the correlation coefficient between the levels of resistance to yellow rust estimated by visual assessment and RGB indices calculated on three dates. (n.s. not significant ( $p>0.05$ ); * significant ( $p<0.05$ ); ** highly significant ( $p<0.01$ ))

## **Posters of Sessions 1 and 2**

Title	Earliness per se x temperature interaction on wheat developmental traits
Authors	H Ochagavía <sup>1</sup> , P Prieto <sup>1</sup> , S Griffiths <sup>2</sup> , G.A Slafer <sup>1,3</sup> <sup>1</sup> University of Lleida, Department of Crop and Forest Science & Agrotecnio. Avenida Alcalde Rovira Roure, 191, 25198, Lleida, SPAIN <sup>2</sup> John Innes Centre. Norwich Research Park, Colney Ln, NR4 7UH, Norwich, UNITED KINGDOM <sup>3</sup> ICREA, Catalanian Institution for Research and Advanced Studies. Passeig de Lluís Companys, 23, 08010, Barcelona, SPAIN
Keywords	Eps, temperature, heading, developmental phases, cardinal temperatures
Abstract	<p>Differences in flowering time even when photoperiod and vernalisation responses are satisfied are regulated by earliness per se (Eps) genes. The name of the genes is based on the widespread assumption that these differences in development are “intrinsic” and independent of the environment. However, some theoretical ideas and few empiric evidences (with a ‘major’ Eps gene in <i>Triticum monococcum</i>) suggested that Eps might be “temperature-sensitivity” genes. No evidences have been reported on likely Eps x temperature interactions on time to anthesis for ‘minor’ Eps genes in hexaploid wheat; and even less on other developmental traits. We grew four near isogenic lines (NILs) derived from Spark x Rialto cross with contrasting Eps alleles (early vs late alleles) under seven temperature regimes under long days in growth chambers located at the University of Lleida (UdL, Spain) and John Innes Centre (JIC, UK). Lines carrying the Eps-late allele headed always later than those with Eps-early alleles. However, at low temperatures the effects of the Eps genes were more remarkable than at mild and warm temperatures, which revealed an Eps x temperature interaction. Variations of flowering time due to Eps x temperature was associated with an increase in sensitivity to temperature during late reproductive phase, which might be an avenue to improve the fertility of the spikes. Results also showed the interaction between Eps alleles and temperature on spikelet number per spike was not relevant, indicating these alleles were useful to fine-tuning heading time but without any effect on this yield component. Additionally, Eps alleles exhibited the ability to modify the cardinal temperatures.</p>
	<p>Figure A: Bar chart showing Time to heading (days) on the y-axis (0 to 200) and Temperature (°C) on the x-axis (6, 9, 12, 15, 18, 21). For each temperature, there are two bars: an open bar for Eps-early and a closed bar for Eps-late. The Eps-late bars are consistently higher than the Eps-early bars. Significance markers (***) are present above the bars at 6, 9, 15, and 18 °C, and (**) above the bar at 12 °C. An inset bar chart shows 'Delay by Eps-late (days)' on the y-axis (0 to 15) for temperatures 6, 9, 12, 15, and 18 °C, with values increasing from ~10 to ~12 days.</p> <p>Figure B: Line graph showing Rate of development towards heading (1/d) on the y-axis (0.000 to 0.020) and Temperature (°C) on the x-axis (0 to 30). Two lines are plotted: a solid line for Eps-early and a dashed line for Eps-late. Both lines show a peak rate of development around 18-20 °C. The Eps-late line peaks at a higher rate (~0.018) than the Eps-early line (~0.015). Cardinal temperatures (Tmax) are indicated: Tmax-early = 19 °C and Tmax-late = 17 °C. Other Tmax values are shown for different temperatures: Tmax-early = 2 °C, Tmax-late = 3 °C, Tmax-early = 24 °C, and Tmax-late = 23 °C.</p>
Legend	Days from the onset of the experiment to heading for lines carrying Eps- early (open bars) or Eps-late (closed bars) alleles grown under constant seven temperatures (A). Relationship between rate of development towards heading and thermal time (B).

Title	Genome Wide Association Analysis for Cell Wall Bound Hydroxycinnamates
Authors	A López-Malvar <sup>1</sup> , DJ Figueroa-Garrido <sup>1</sup> , LF Samayoa <sup>2</sup> , A Butrón <sup>3</sup> , RA Malvar <sup>3</sup> , R Santiago <sup>1</sup> <sup>1</sup> Facultad de Biología, Departamento de Biología Vegetal y Ciencias del Suelo. Agrobiología Ambiental, Calidad de Suelos y Plantas (UVIGO), Unidad Asociada a la MBG (CSIC). Universidad de Vigo, Ciudad universitaria de Vigo, Campus Universitario Lagoas-Marcosende, s/n, 36310, Vigo, Pontevedra, SPAIN <sup>2</sup> North Carolina University, Crop Science. Beryl Rd, s/n, 27695, Raleigh, North Carolina, USA <sup>3</sup> Misión Biológica de Galicia (CSIC), Mejora Genética Vegetal. Pazo de Salcedo, Carballeira, 8, 36143, Pontevedra, SPAIN
Keywords	Association mapping, hydroxycinnamic acid, diversity panel, cell-wall fortification, Zea mays

**Abstract**

The structural reinforcement of the cell walls by hydroxycinnamates plays a significant role as defense mechanism against pests and diseases and interferes with forage digestibility or biofuel production. The study of the genetic basis of the hydroxycinnamic acids biosynthesis and cross-linking would lead us to quantitative trait loci (QTL) and candidate genes identification, helping breeding strategies based on marker assisted, genomic and phenotypic selection. A Genome Wide Association Analysis (GWAS) was carried out to identify Single Nucleotide Polymorphism (SNPs) associated with cell wall hydroxycinnamates using a subset of inbred lines belonging to the maize 282-inbred diversity panel, through two years, using an  $\alpha$ -lattice design. Inbred lines were genotyped with more than 240000 SNPs and phenotyped by High Performance Liquid Chromatography protocols. Sixty-five SNPs were identified as significantly associated with cell wall bound hydroxycinnamates; seventeen with p-Coumaric acid, twelve with Ferulic acid, and seven with total diferulates. Attending to diferulates isomers individually, seven SNPs were related with isoform 8-o-4, eleven with 5-5-diferulate, three with 8-5 diferulate and eight with 8-5 linear diferulate. The regions associated with those markers co-localize with other cell wall traits and also with functions in pests' resistance, digestibility and bio-ethanol production as mentioned. Besides, we found new regions of interests that may be related to the genetic basis of hydroxycinnamic acids. A set of genes containing or physically close to these SNPs are proposed as candidate genes involved in phenylpropanoid and monolignol biosynthesis, transfer to the cell wall and polymerization, putatively ferulic acid biosynthesis, arabinoxylan chain biosynthesis and reorganization or genes involved in cellulose biosynthesis and deposition. This study supports the advantages of using a diversity panel in an association analysis in order to confirm regions and genes related to the phenylpropanoid pathway, and describe new regions particularly linked to hydroxycinnamates. Breeding approaches will be designed in the near future.

Associated Trait	SNP position (Mb)	QTL bin	Candidate Gene	Gene product	Gene position (Mb)	Function
p-CA	174.64	1.05	GRMZM2G117340	Homocysteine transferase	172.04	
p-CA	286.70	1.11	AC206399.3_1636	Cellulose synthase-5	280.60	Cellulose biosynthesis and deposition
DFA S-S, DFA 8-o-4	295.48	1.11	AC19825.3_10838	Cellulose synthase-8	296.25	Cellulose biosynthesis and deposition
DFA S-S, DFA 8-S, DFA 8-S-L, DFA 8, FA	297.49	1.11	GRMZM2G056702	Actin depolymerization factor	293.24	
DFA S-S, DFA 8-S, DFA 8-S-L, DFA 8, FA	297.49	1.11	AC19825.3_10834	Cellulose synthase-8	296.25	Cellulose biosynthesis and deposition
DFA S-S, DFA 8-S, DFA 8-S-L, DFA 8, FA	297.49	1.11	GRMZM2G167056 (bin2)	Methylmalatolaldehyde reductase	292.17	
DFA 8S1	161.13	3.05	GRMZM2G158496	Arabinosyl transferase GT47	160.07	Arabinosyl chain biosynthesis and reorganization
DFA S-S, DFA 8-o-4, DFA 8	184.63	3.06	GRMZM2G112718	Laccase	183.70	Monolignol export to the cell wall and polymerization
p-CA	175.60	3.05	GRMZM2G127363	Expressed protein	176.92	
p-CA	175.60	3.05	GRMZM2G094067	ZmKcsr1-like	172.96	
DFA S-S	85.42	6.01	GRMZM2G127948	Cellulose synthase-3	82.39	Cellulose biosynthesis and deposition
FA	129.44	6.05	AC198248.3_10841	Zmpx3 (peroxidase)	125.19	Monolignol and common phenylpropanoid compound biosynthesis
			GRMZM2G04356	BAHD-CoA-acyltransferase Clade II	127.90	Putatively ferulic acid biosynthesis
			GRMZM2G108714	BAHD-feruloyl-CoA acyltransferase FFD2658	128.24	Putatively ferulic acid biosynthesis
			AC218196.3_10832	Cellulose synthase-2	128.56	Cellulose biosynthesis and deposition
			GRMZM2G108714	Arabinosyl feruloyl transferase	128.24	Arabinosyl chain biosynthesis and reorganization
DFA S-S, DFA 8-S, DFA 8, FA	132.34	8.05	GRMZM2G0812874	R-3-L-xylosyltransferase or xylosyltransferase	131.22	Arabinosyl chain biosynthesis and reorganization
DFA S-S, DFA 8-S, DFA 8-S-b, DFA 8	22.52	10.03	GRMZM2G056270	Zinc Finger C3HC4-type MB1.1	25.31	

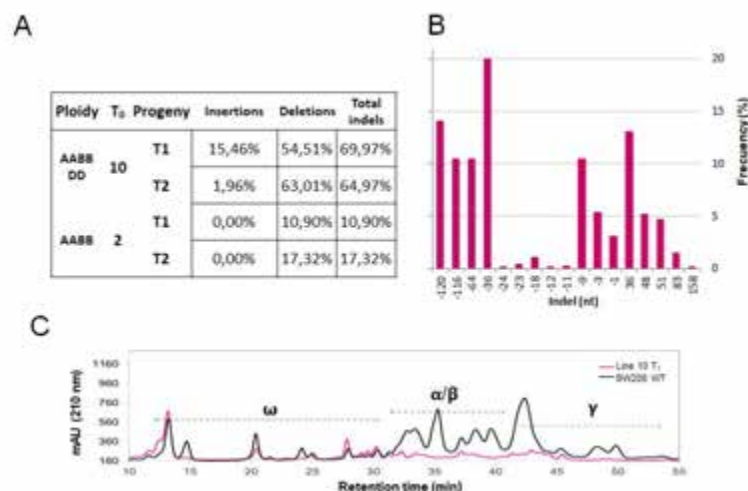
**Legend** Table 1: Candidate genes for each significantly SNP associated with hydroxycinnamates. SNP position, QTL bin, Gene product, gene position and function of the most remarkable candidate genes

Title	Variability for glutamine synthetase 1 homoeogenes and N dose response in Triticum spp.
Authors	A. Solé <sup>1</sup> , M. López-Fernández <sup>1</sup> , P. Giraldo <sup>1</sup> , J.M. Carrillo <sup>1</sup> , L. Pascual <sup>1</sup> , E. Benavente <sup>1</sup> <sup>1</sup> Universidad Politecnica de Madrid. Avda. Complutense, s/n, 28040, Madrid, SPAIN
Keywords	Bread wheat, Durum wheat, Nitrogen-use efficiency, Glutamine synthetase
Abstract	
<p>Glutamine synthetase (GS) is a key enzyme for the transformation of ammonium into glutamine, a main step for inorganic N assimilation in higher plants. In wheat, the cytosolic GS isoforms are coded by the homoeogenes GS1. Recent studies have demonstrated a role of allelic variability on yield components and quality traits. We have determined the haplotypes of GS1 genes in a group of 30 bread and durum wheat varieties including landraces, old commercial varieties and varieties released from the end of the XXth century. The study has revealed a high allelic diversity for the genes located on the A and B wheat genomes, though all allelic variants were mapped to non-coding regions. No polymorphism has been detected for the GS1 gene on the D bread wheat genome. Field trials have been conducted to assess the response to N dose of this set of varieties. Thousand-kernel weight (TKW), grain protein content (GPC) and SDS-sedimentation volume (SedV) have been evaluated. For TKW, the response has been variable among varieties. GPC and SedV have generally decreased with lower N fertilizing level, but the differences were not significant in some varieties. Deciphering the relation, if any, between the GS1 genes haplotypes characterized and the N dose responses observed is hampered by the great genetic variability found within this relatively small group of wheat varieties.</p>	
<p>The figure consists of six bar charts arranged in a 3x2 grid. The columns are labeled 'Bread wheat varieties' and 'Durum wheat varieties'. The rows are labeled 'TKW', 'GPC', and 'SedV'. Each chart shows the relative ratio of the trait under intermediate (light bars) and low (dark bars) N doses compared to standard N fertilizer levels. The y-axis for all charts ranges from 0.0 to 1.0. The x-axis lists 30 wheat varieties. In the TKW charts, light bars are generally higher than dark bars, indicating a positive response to intermediate N. In the GPC and SedV charts, light bars are generally higher than dark bars, indicating a decrease in these traits at lower N doses.</p>	
Legend	Relative ratio of thousand-kernel weight, grain protein content and SDS-sedimentation volume under intermediate (light bars) and low (dark bars) N doses compared to the values obtained with standard N fertilizer levels. Data used are from field trial

Title	Engineering the major coeliac disease immunogenic complex in wheat by CRISPR/Cas9
Authors	S. Sánchez-León <sup>1</sup> , J. Gil-Humanes <sup>2</sup> , C. V. Ozuna <sup>1</sup> , M. J. Giménez <sup>1</sup> , C. Sousa <sup>3</sup> , D. F. Voytas <sup>2</sup> , F. Barro <sup>1</sup> <sup>1</sup> Instituto de Agricultura Sostenible, Mejora Genética Vegetal. Avenida Menéndez Pidal s/n, Campus Alameda del Obispo, SN, 14004, Córdoba, SPAIN <sup>2</sup> University of Minnesota, Department of Genetics, Cell Biology, and Development. 1500 Gortner Avenue, Cargill Building, 55108, Saint Paul, USA <sup>3</sup> Universidad de Sevilla, Departamento de Microbiología y Parasitología, Facultad de Farmacia. Profesor García González, SN, 41012, Sevilla, SPAIN
Keywords	CRISPR/Cas9, coeliac disease, $\alpha$ -gliadins

#### Abstract

The gluten proteins from wheat, barley and rye are responsible for several gluten-related disorders affecting more than 7% of the Western population. Coeliac disease is an autoimmune disorder, triggered in genetically predisposed individuals by the ingestion of gluten proteins. The  $\alpha$ -gliadin family, a group of gluten proteins from wheat, contains three highly stimulatory peptides, of which the 33-mer is the main immunodominant peptide in coeliac patients. This is a protease-resistant, 33-amino acid peptide that contains six overlapping copies of three distinct, tandemly-organized epitopes. The  $\alpha$ -gliadin gene copy number has been estimated by different techniques between 25 to even 100 copies per haploid genome. This makes the  $\alpha$ -gliadin family especially challenging for genome editing. Applications of CRISPR/Cas9 to create new traits in crops with complex, polyploid genomes, such as wheat are still limited. We had produced mutant lines of three wheat cultivars using two sgRNAs targeting two conserved regions adjacent to the 33-mer. Up to 35 different genes of the 45 possible targets showed InDels, and all mutant lines showed strong reduction in  $\alpha$ -gliadins content. DNA analysis of progeny showed heritability of the mutations and no off-target. It was possible to obtain transgene-free lines by segregation. Monoclonal antibodies showed that Immunoreactivity was reduced in some lines up to 85% in comparison to that of the wild type. The results demonstrate that high mutation frequency and specificity can be achieved using CRISPR/Cas9 to modify complex genomic loci, providing lines with reduced immunoreactivity. Although these lines are not suitable for coeliac sufferers, they can be used to produce low gluten foodstuff for those who want to reduce the gluten intake. In addition, they can serve as source material in plant breeding programs to introgress this trait into elite wheat varieties.



Legend Figure 1. Gene editing and protein quantification of  $\alpha$ -gliadins in wheat edited lines with sgApha2. (A) Percentage of edited reads and their heritability from T1 plant to T2 plants of bread wheat (line 10), and durum wheat (line 2). (B) Frequency of


Title	“Combining Abilities for Cell Wall Components in Corn Hybrids”
Authors	DJ Figueroa-Garrido <sup>1</sup> , A López-Malvar <sup>1</sup> , RA Malvar <sup>2</sup> , A Butrón <sup>2</sup> , A Torres <sup>3</sup> , L Trindade <sup>3</sup> , R Santiago <sup>1</sup> <sup>1</sup> Facultad de Biología, Departamento de Biología Vegetal y Ciencias del Suelo. Agrobiología Ambiental, Calidad de Suelos y Plantas (UVIGO).Unidad Asociada a la MBG (CSIC). Universidad de Vigo. Campus As Lagoas Marcosende, SN, 36310, Vigo (Pontevedra), SPAIN <sup>2</sup> Misión Biológica de Galicia (CSIC), Genética y mejora de maíz. Pazo de Salcedo. Carballeira, 8, 36143, Salcedo. Pontevedra, SPAIN <sup>3</sup> Wageningen University, Wageningen UR Plant Breeding. Droeendaalsesteeg, 1, 6708, Wageningen, HOLLAND
Keywords	Diallel, General and specific combining abilities (GCA, SCA), hybrid, corn borer, Zea mays

**Abstract**

Corn cell wall composition has been directly related to pests defence, more precisely to corn borer resistance. The inbred lines EP39, EP42, EP47 and CM151 were crossed in a diallel mating design without reciprocals obtaining as a result a total of six hybrids which differ in cell wall composition and borer resistance. A randomized complete block design with three replicates was trialled in two different environments. General and specific combining abilities (GCA, SCA) were calculated for cell wall traits (fibers, lignins, polysaccharides and phenol cross-linking) and related with borer resistance. Hybrids significantly differed in fiber content, polysaccharides and phenols composition, and resistance to corn borers. The resistant hybrid EP39xCM151 showed higher concentrations for neutral detergent fiber (NDF), lignin from neutral detergent fiber (L-NDF) and xylose; whereas the susceptible hybrid EP42xEP47 showed higher ferulic acid monomers concentration. Regarding the GCA of the parental inbred lines, the combination with the inbred EP39 significantly decreased the ferulic acid concentration, while the inbred EP47 increases its concentration; on the other hand, EP42 decreased total diferulates content. For the polysaccharides composition the only significant effect was observed for xylose (GCA was positive for EP39 and negative for the EP47). And for fibers, EP47 differed from the other three showing negative effects for NDF and L-NDF, while the CM151 inbred differed significantly from the others increasing NDF. In all cases the GCA were more important than the SCA, meaning that for all traits the additive effects are the most important and, therefore, we would expect a good response to selection programs. In relation to the borer resistance, EP42 hybrids, could decrease total diferulates and increasing susceptibility; while the lower contents of fibers and lignin could be responsible for pest’s weakness of EP47 hybrids. Our results support the hypothesis that different cell wall biochemical mechanisms for borer resistance could be operating.



Legend	Combining Abilities for Cell Wall Components in Maize hybrids
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Title	Potential utilization of durum wheat landraces for breeding
Authors	S.G. Atienza <sup>2</sup> , A. Pérez de Luque <sup>1</sup> , J.C. Sillero <sup>1</sup> , C.M. Ávila <sup>1</sup> <sup>1</sup> IFAPA-Alameda del Obispo. Avda. Menéndez Pidal, s/n, 14080, Córdoba, SPAIN <sup>2</sup> CSIC, Plant Breeding. Avda. Menéndez Pidal, s/n, 14004, Córdoba, SPAIN
Keywords	durum wheat, landraces
Abstract	<p>Plant adaptation to environmental conditions is crucial for the success of crops. Landraces are a valuable resource for the improvement of crop adaptation. For instance, barley landraces outperform modern cultivars at low-productivity sites (Yahiaoui et al. 2014), likely due to a better ability to fill the grain under stressful conditions. Landraces usually show large genotype-by-environment interaction as a result of local adaptation. Besides they usually show a wide genetic diversity that is easily transferable to breeding programs. In this work we evaluated a collection of Spanish durum obtained from CRF-INIA to determinate their potential in breeding. In this work we performed a preliminary evaluation of a durum wheat collection kindly provided by CRF-INIA. This collection consisted of 159 genotypes and it included the durum wheat collection developed by Ruiz et al. (2013) along with durum wheat accessions originally collected from southern Spain. Preliminary assessment included heading date, plant height and yield in order to get a first evaluation of their potential for durum wheat breeding. Most accessions were outside the recommended heading date for our conditions. Spikes of the majority of accessions emerged later than the latest control with delays between 1 and 25 days. Only five accessions showed heading days values below 129 days after sowing. Similarly only 8 accessions were below 1m tall which resulted in a variable degree of lodging. The most promising accessions were selected for in the current growing season.</p> <p>Acknowledgements Research funded by Grant PP.AVA.AVA.201601.17 from IFAPA (Agricultural and Fishery Research and Training Institute), Junta de Andalucía, Spain including FEDER funding. All authors are members of FiRCMe Network, funded by MINECO (AGL2016-81855-REDT). We thank CRF-INIA for providing the seeds used in this work. References Ruiz M et al. (2013) Crop Sci 53: 2530-2537. Yahiaoui et al. (2014) Plant Breed 133: 218-226</p>
	
Legend	Partial view of the field trial.

Title	Impact of N fertilization in agronomic and flour nutritional traits.
Authors	S. Ben Mariem <sup>1</sup> , C. Collar <sup>2</sup> , F. Morales <sup>1,3</sup> , I. Aranjuelo <sup>1</sup> <sup>1</sup> Instituto de Agrobiotecnología, AGRICULTURA SOSTENIBLE Y CAMBIO CLIMATICO. AVDA DE PAMPLONA, 123, 31192, Pamplona, SPAIN <sup>2</sup> Instituto de Agroquímica y Tecnología de Alimentos, Ciencia de alimentos. Avda. Catedrático Agustín Escardino, 7, 46980, Valencia, SPAIN <sup>3</sup> Estación Experimental de Aula Dei, Nutrición Vegetal. Avda. Montañana, 1005, 50059, Zaragoza, SPAIN
Keywords	durum wheat, N use efficiency, yield, grain quality

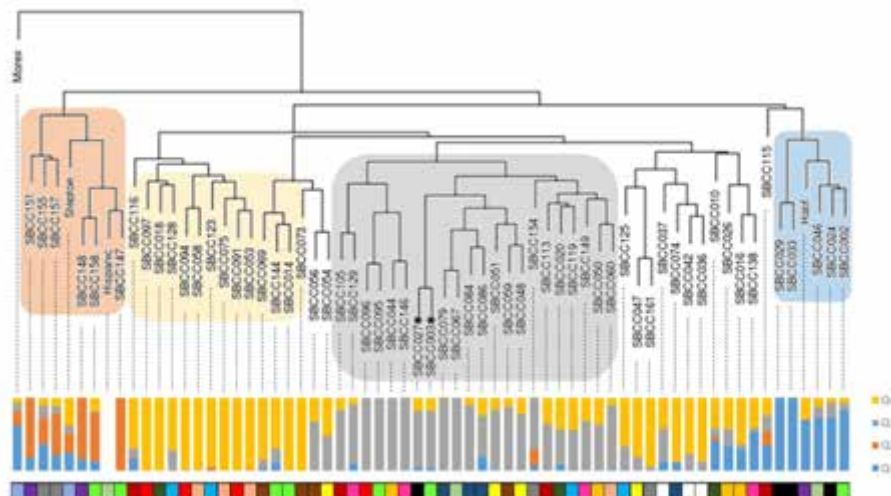
**Abstract**


The availability and management of N are major determinants of crop productivity and the associated environmental agro-ecosystems. Within this context, it is crucial to improve crop N use efficiency (NUE). The aim was to study the influence of N fertigation on yield and grain quality of 20 durum wheat cultivars. In a first stage, half of plants within each genotype were watered with high N (HN, ½ Hoagland nutrient solution), whereas the other half was watered with low N (LN, modified ½ Hoagland with one-third of N). Based on yield and NUE data, six genotypes were selected for a secondary study in which deep flour nutritional traits were characterized. More specifically, together with the agronomic characterization, grain quality analyses were assessed to characterize mineral composition, carbohydrate concentration (soluble sugars and starch), glutenin and gliadin concentration, polyphenol quantitative profile, antioxidant activity, and dough viscosity profile. Obtained data showed that crop yield increased in HN whereas no differences were detected among genotypes. Mineral composition was not affected by N but was genotype-dependent. In fact, low yielding genotypes showed higher Ca, Cu, Fe, Mn and Zn concentrations. LN fertigation increased grain carbohydrate concentrations, showing genotypes with high yield the highest amounts. Furthermore, the increase of starch concentration under LN increased dough viscosity. Nitrogen supply improved grain quality through increases in gliadin and glutenin concentration, although without differences among genotypes. Contrary to this, under LN, the low yielding genotypes had the highest values. Flour total phenol concentration was significantly higher and bioaccessible phenols lower under HN. Low yielding genotypes had the highest values of total and bioaccessible phenols, and antiradical activity. Overall, our data show that decreasing the amount of N to one-third ensures durum wheat agronomic and quality traits, showing genotype 3 an efficient response to low N availability.

Genotypes	Mean production (g/plant)		% grain N		NUE (g grain/g N)	
	Nitrogen rate					
	High	Low	High	Low	High	Low
6	8.68 <sup>b</sup>	7.85 <sup>b</sup>	2.9 <sup>cd</sup>	2.1 <sup>a</sup>	34.03 <sup>b</sup>	47.98 <sup>d</sup>
10	7.17 <sup>b</sup>	7.99 <sup>b</sup>	3.5 <sup>a</sup>	2.1 <sup>a</sup>	28.71 <sup>a</sup>	47.23 <sup>d</sup>
18	8.74 <sup>b</sup>	8.22 <sup>b</sup>	2.8 <sup>c</sup>	2.2 <sup>a</sup>	35.70 <sup>bc</sup>	45.55 <sup>d</sup>
3	5.92 <sup>ab</sup>	6.28 <sup>ab</sup>	3.2 <sup>d</sup>	2.6 <sup>b</sup>	31.77 <sup>ab</sup>	39.19 <sup>c</sup>
9	6.27 <sup>ab</sup>	5.40 <sup>a</sup>	3.4 <sup>de</sup>	2.7 <sup>bc</sup>	29.52 <sup>a</sup>	36.78 <sup>bc</sup>
16	5.97 <sup>ab</sup>	5.18 <sup>a</sup>	2.8 <sup>bc</sup>	2.7 <sup>bc</sup>	36.04 <sup>bc</sup>	38.40 <sup>c</sup>


Within samples mean values with different following letters do differ significantly from each other (p < 0.05).

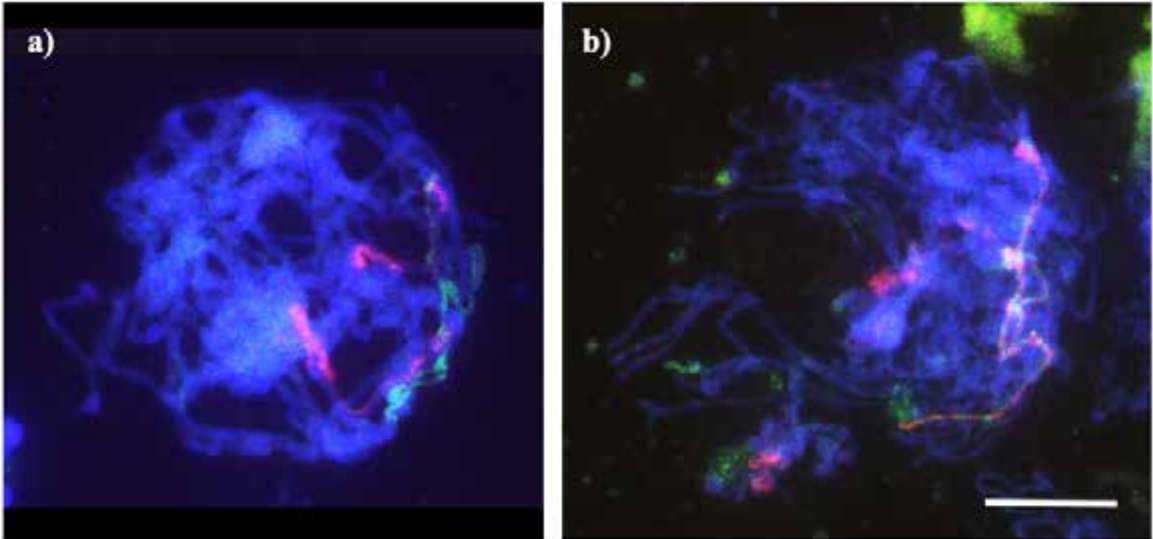
Legend	Nitrogen efficiency indices of durum wheat under high and low nitrogen treatments.
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Title	Copy-number variation through k-mer count analysis
Authors	C. P. Cantalapiedra <sup>1</sup> , E. Igartua <sup>1</sup> , A. M. Casas <sup>1</sup> , B. Contreras-Moreira <sup>1</sup> <sup>1</sup> Estación Experimental de Aula Dei - CSIC, Plant Genetics. Av. Montañana, 1005, 50059, Zaragoza, SPAIN
Keywords	genotyping, copy-number variation, presence-absence variation, genomics, genetics
Abstract	<p>Genetic studies often rely on the identification of polymorphisms in populations or collections of individuals from the same species. SNPs and indels are the most common kind of polymorphism used, since a huge amount of them can be obtained and the procedures to characterise them are well established. Other kinds of genomic variation, such as copy-number variation (CNV) or structural variation, are more rarely exploited despite literature reports linking them to phenotypic differences. In some loci, SNPs and small indels cannot be reliably identified, leaving those loci out for downstream analyses. For instance, closely related sequences (e.g. paralog genes) often produce noisy mappings, which have been called apparent heterozygous mappings (AHMs). These AHMs are produced due to CNV or presence-absence variation between the genotypes under comparison, and lead to the detection of abundant fake heterozygous SNPs. AHMs can be described as a kind of CNV which is specific to non-identical copies. Unmasking such variation could help to i) assess the completeness of a genome or pan-genome reference, ii) confirm results from other CNV genotyping methods, iii) provide hints about the history and behavior of duplicating DNA loci, and iv) reveal novel intra-species genetic diversity useful for genetic studies. We developed a software pipeline, kmeleon, available at <a href="https://github.com/ead-csic-compbio/kmeleon">https://github.com/ead-csic-compbio/kmeleon</a>, designed to identify regions harboring AHMs. kmeleon uses as input read mappings, which is a common resource used for most high-throughput sequencing analyses. It can be used for both homozygous and heterozygous samples. kmeleon identifies and counts sequences present on AHMs. These counts are extended to wider intervals, which can be used to detect polymorphic variation. This information allows including those troublesome loci in downstream analyses.</p>
	
Legend	We used exome capture data of a collection of Spanish barleys, along with a few other accessions including Morex, the genotype of the genome reference, to detect AHMs. We used k-mer count on those AHMs to infer a phylogenetic tree which is congruent

Title	Carotenoid accumulation patterns and lutein esterification process during grain development
Authors	M.G. Mattera <sup>1</sup> , D. Hornero-Méndez <sup>2</sup> , S.G. Atienza <sup>1</sup> <sup>1</sup> CSIC, Plant Breeding. Avda. Menéndez Pidal, s/n, 14004, Córdoba, SPAIN <sup>2</sup> CSIC, Department of Food Phytochemistry. Campus Universidad Pablo Olavide., Edificio 46, Ctra. de Utrera km 1, 41013, Seville, SPAIN
Keywords	Grain development
Abstract	<p>Hexaploid tritordeum (<math>\times</math>Tritordeum martini A. Pujadas (Pujadas 2016) is the amphiploid derived from the cross between <i>Hordeum chilense</i> and durum wheat (Martín and Sánchez-Monge 1982). This new crop has higher carotenoid content than durum wheat (Atienza et al. 2007) and a distinctive profile of lutein esterification with fatty acids. Carotenoid esters increase carotenoid retention during storage of grains (Mellado-Ortega and Hornero-Méndez 2016; Mellado-Ortega et al. 2015) and flour (Mellado-Ortega and Hornero-Méndez 2017) and thus it is a trait of interest for cereal breeding. Lutein esters can be synthesized during storage (Ahmad et al. 2015) but they have been found after harvesting in tritordeum seeds which may indicate that carotenoids esters are produced earlier by <i>H. chilense</i> genes. Recent advances have shown that chromosomes 7D and 7Hch are important for the synthesis of lutein esters (Mattera et al. 2015; Ahmad et al. 2015). In this work the pattern of accumulation of carotenoid and derived esters was studied during grain filling in a set of wheat-<i>H. chilense</i> chromosome substitution lines comparatively to tritordeum, durum and common wheat. To do this spikes were marked at anthesis and grains were collected at specific times (Figure 1). Acknowledgements Research funded by Grant AGL2014-53195R, from Ministerio de Economía y Competitividad, Spain (MINECO) including FEDER funding. M.G.M. was recipient of FPI (BES-2012-055961). D.H.-H. is a member of CaRed Network, funded by MINECO (BIO2015-71703-REDT). S.G.A. is a member of FiRCMe Network, funded by MINECO (AGL2016-81855-REDT) References Ahmad FT et al (2015) <i>J Cereal Sci</i> 64, 109-115. Atienza SG et al. (2007) <i>J Agric Food Chem</i> 55, 4244-4251. Martín A, Sánchez-Monge E (1982) <i>Euphytica</i> 31, 261-267. Mattera MG et al. (2015) <i>Crop Pasture Sci</i> 66, 912-921. Mellado-Ortega, Hornero-Méndez (2016) <i>Food Chem</i> 192, 714-723. Mellado-Ortega, Hornero-Méndez (2017) <i>Foods</i> 6, 111. Pujadas A (2016) <i>Acta Botanica Malacitana</i> 41, 325-338</p>
	
Legend	Figure 1. Spikes marked at anthesis for grain sampling.

Title	High nitrate supply alters root and shoot metabolism and overall growth of maize plants
Authors	I. Saiz-Fernández <sup>2,3</sup> , A. del Canto <sup>2</sup> , A. Yoldi-Achalandabaso <sup>1</sup> , N. De Diego <sup>2,4</sup> , A. Mena-Petite <sup>1</sup> , A. Muñoz-Rueda <sup>1</sup> , U. Pérez-López <sup>1</sup> , M. Lacuesta <sup>2</sup> <sup>1</sup> Universidad del País Vasco/Euskal Herriko Unibertsitatea, UPV/EHU, Biología Vegetal y Ecología. B° Sarriena, s/n, 48940, Leioa, SPAIN <sup>2</sup> Universidad del País Vasco/Euskal Herriko Unibertsitatea, UPV/EHU, Biología Vegetal y Ecología. P° de la Universidad, 7, E-01006, Vitoria-Gasteiz, SPAIN <sup>3</sup> Institute of Biophysics AS CR and CEITEC–Central European Institute of Technology, Mendel University in Brno, Laboratory of Plant Molecular Biology. Zemědělská, 1, CZ-61300, Brno, CZECH REPUBLIC <sup>4</sup> Centre of the Region Haná for Biotechnological and Agricultural Research, Palacký University, Department of Chemical Biology and Genetics. Šlechtitelů, 11, CZ-78371, Olomouc, CZECH REPUBLIC
Keywords	maize, nitrogen, phytohormone, root, shoot
Abstract	<p>Nitrogen is one of the main factors that condition crop production, affecting plant growth and development. Thus, the amount of N fertilizer applied to crops has increased every year, especially in cereal production. However, in recent years, some studies have indicated that, in some growing conditions and growing areas, the influence of N supply on plant growth may be less than expected, especially in C4 plants. Moreover, in previous works we have shown that high NO<sub>3</sub><sup>-</sup> doses over 5 mM decreased biomass production of maize. This reduction was perceptible in shoots prior to roots, where phytomer expansion was reduced. Therefore, it is essential to adjust the optimal nitrogen supply that guarantees the highest crop yield being, in addition, economically and environmentally sustainable. Nitrogen (N) is an important regulator of photosynthetic carbon (C) flux. N enrichment increases the flow of newly fixed C into Krebs cycle intermediates and amino acids, while decreasing the flux into starch and sucrose. Thus, an adequate balance between N and C metabolism is necessary for the correct plant development. In this regard, an excessive N supply can alter this balance and cause alteration in some metabolites, including phytohormones, which lead to a decrease in leaf expansion and overall biomass production. In this work we analyze the impact of nitrate in N and C metabolism and the role of phytohormonal signaling mainly in maize roots, as the main organ implicated in its absorption. High nitrate concentration (over 5 mM) altered maize root development and modified nitrogen and carbon metabolism, by activating stress responses. Accumulation of Mn<sup>2+</sup> and Ca<sup>2+</sup>, and the non-proteinogenic amino acid <math>\gamma</math>-aminobutyric acid (GABA), was related to high nitrate supply. Acknowledgments This research was supported by MEC-INIA (grant RTA2010-00041-CO2-02). Research group of Basque Government (GV-IT1022-16). Iñigo Saiz Fernández had a fellowship from the UPV/EHU.</p>
	<p>Figure 1 consists of two bar charts, A and B. Chart A shows the Relative Weight Rate (RWR) of maize roots at four time points: 15, 22, 30, and 45 days. The y-axis ranges from 0.00 to 0.18. Four nitrate concentrations are compared: 2.5 mM (white bars), 5 mM (black bars), 15 mM (grey bars), and 30 mM (hatched bars). At 15 days, RWR is low and similar across concentrations. At 22 days, RWR increases, with 5 mM showing the highest value (~0.16). At 30 days, RWR decreases significantly for 15 mM and 30 mM compared to 2.5 mM. At 45 days, RWR is highest for 5 mM (~0.11) and lowest for 30 mM (~0.06). Chart B shows Root Dry Weight (DW) in grams at 30 days. The y-axis ranges from 0.0 to 2.5. The four concentrations are compared. 5 mM shows the highest DW (~1.9 g), followed by 2.5 mM (~1.3 g), 15 mM (~1.0 g), and 30 mM (~1.1 g). Letters 'a' and 'b' indicate statistical significance groups.</p>
Legend	Figure 1. (A) Relative weight rate (RWR, g g <sup>-1</sup> day <sup>-1</sup> ) of maize roots grown with different nitrate concentrations and (B) dry weight (DW, g) of maize roots grown at 30 days after germination.

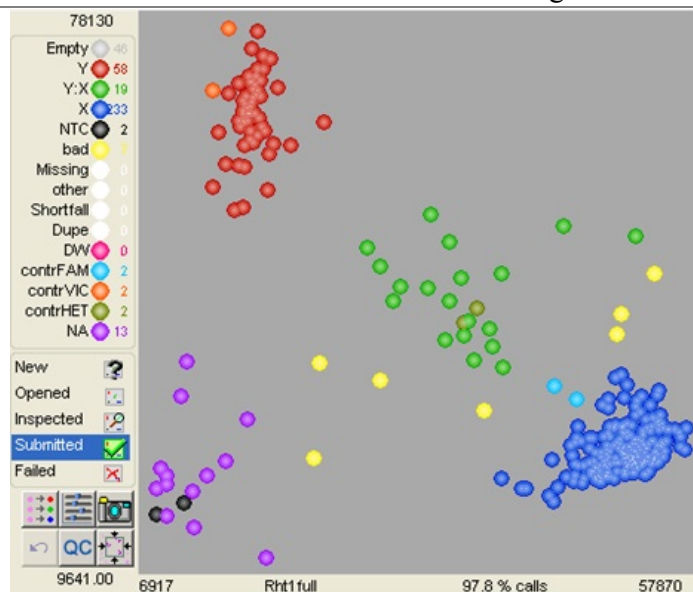
Title	Exploring synteny relationships of <i>Hordeum chilense</i> genome for tritordeum breeding
Authors	C.M. Avila <sup>3</sup> , M.G. Mattera <sup>1</sup> , C. Rodríguez-Suárez <sup>1</sup> , C. Palomino <sup>1</sup> , M.C. Ramírez <sup>1</sup> , A. Kilian <sup>4</sup> , D. Hornero-Méndez <sup>2</sup> , S.G. Atienza <sup>1</sup> <sup>1</sup> CSIC, Plant Breeding. Avda. Menéndez Pidal, s/n, 14004, Córdoba, SPAIN <sup>2</sup> CSIC, Chemistry and Biochemistry of Pigments, Food Phytochemistry Department. Campus Universidad Pablo Olavide, Ctra. de Utrera km 1, 41013, Seville, SPAIN <sup>3</sup> IFAPA-Centro Alameda del Obispo, Área de Mejora y Biotecnología. Avda. Menéndez Pidal s/n, s/n, 14080, Córdoba, SPAIN <sup>4</sup> Diversity Arrays Technology Pty Ltd. Kirinari st., Bruce, Bldg 3, Lv D, University of Canberra, ACT 2617, Canberra, AUSTRALIA
Keywords	<i>Hordeum chilense</i> , synteny, development
Abstract	<p>Hexaploid tritordeum (<math>\times</math>Tritordeum martini A. Pujadas (Pujadas 2016) has become a new crop due to its functional characteristics. The most important one is the golden colour of its flour which is caused by the presence of carotenoids (Atienza et al. 2007a). This new amphiploid was obtained after chromosome doubling of the hybrid between <i>Hordeum chilense</i> (Figure 1) and durum wheat (Martín &amp; Sánchez-Monge 1982). <i>H. chilense</i> genes are responsible for the high carotenoid content (Atienza et al. 2007b; Rodríguez-Suárez et al. 2014) and the distinctive esterification profile of carotenoids (Mellado-Ortega and Hornero-Méndez 2015). The conservation of the carotenoid pathway has allowed the identification of the main genes responsible for the high carotenoid content in tritordeum (Atienza et al. 2007b; Mattera et al. 2015, Rodríguez-Suárez et al. 2014). However, this approach is not possible for processes where the pathway is not fully understood. Alternative strategies such as synteny-based candidate gene identification could be very useful in tritordeum breeding and related projects using barley genome as reference. In this work we aimed to investigate synteny relationships between <i>H. chilense</i> and barley through the development using DArTSeq markers. A good degree of collinearity was observed between both species with the exception of the pair 7H-7Hch where significant reorganization was observed. Acknowledgements Research funded by Grant AGL2014-53195R, from Ministerio de Economía y Competitividad, Spain (MINECO) including FEDER funding. M.G.M. was recipient of FPI (BES-2012-055961). D.H.-H. is a member of CaRed Network, funded by MINECO (BIO2015-71703-REDT). S.G.A. is a member of FiRCMe Network, funded by MINECO (AGL2016-81855-REDT) References Atienza SG et al. (2007b) Austr J Agric Res 58, 767-773. Atienza SG et al. (2007a) J Agric Food Chem 55, 4244-4251. Martín A, Sánchez-Monge E (1982) Euphytica 31, 261-267. Mattera MG et al. (2015a) Crop Pasture Sci 66, 912-921. Mellado-Ortega, Hornero-Méndez (2015) J Cereal Sci 62, 15-21. Pujadas A (2016) Acta Botanica Malacitana 41, 325-338 Rodríguez-Suárez C et al. (2014) Plant Mol Biol 84, 659-673.</p>
	
Legend	Figure 1. Detail of <i>Hordeum chilense</i> at field conditions.

Title	Unzipping how homologous chromosomes can recognise and associate in pairs in wheat
Authors	M.C. Calderón <sup>1</sup> , M.D. Rey <sup>2</sup> , A. Martín <sup>1</sup> , P. Prieto <sup>1</sup> <sup>1</sup> Instituto de Agricultura Sostenible (CSIC), Plant Breeding. Avenida Menéndez Pidal , s/n, 14004, Córdoba, SPAIN <sup>2</sup> John Innes Centre. Norwich Research Park, s/n, NR47UH, Norwich, UNITED KINGDOM
Keywords	Hordeum, Triticum aestivum, meiosis, chromosome-recognition, subtelomeres
Abstract	<p>Wheat is one of the most important crops in the world and it is crucial to understand its genome organization for plant breeding purposes. Chromosomes associate regularly in pairs in wheat during meiosis, the cellular process to produce gametes in sexually reproducing organisms. Thus, shed light on the system of a basic eukaryotic cellular mechanism such as meiosis is of fundamental importance in plant breeding since understanding the bases of chromosome specificity/pairing during meiosis will allow its manipulation to introduce genetic variability from related species into a crop. The success of meiosis in a polyploid like wheat depends on regular pairing of homologous chromosomes and recombination, processes mainly controlled by the Ph1 locus. This means that pairing and recombination of related chromosomes rarely occur in the presence of this locus, making difficult wheat breeding through the incorporation of genetic variability from related species. Using genomic in situ hybridisation (GISH) performed in double monosomic H. vulgare-H. chilense addition lines we have showed that homoeologous cultivated and wild barley chromosomes can associate in the wheat background, even in the presence of the Ph1 locus. Our results suggest that the Ph1 locus does not prevent chromosome recognition and pairing but recombination between homoeologous chromosomes. The role of subtelomeres (the telomere associated sequences in the terminal region of the chromosomes) in homologous chromosome recognition is also discussed here.</p>
	
Legend	Homoeologous <i>Hordeum chilense</i> and <i>Hordeum vulgare</i> chromosomes can associate in early meiosis in the wheat background. a) non-homoeologous 7Hch5Hv and b) homoeologous 5Hch5Hv chromosomes. Scale bar represents 10 micr

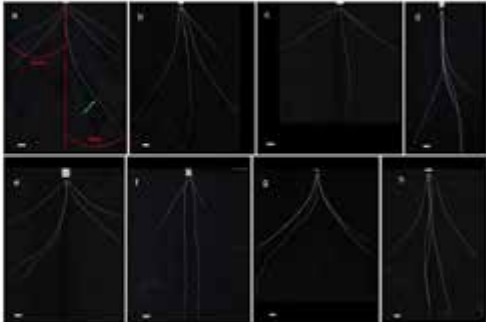
Title	Allelic variation of Rht, Vrn and Ppd genes in a set of bread wheat ( <i>Triticum aestivum</i> L.) lines cultivated in eastern Algeria
Authors	Z. Fellahi <sup>1</sup> , A. Hannachi <sup>2</sup> , S. Dreisigacker <sup>3</sup> , D. Sehgal <sup>3</sup> , A. Yahyaoui <sup>3</sup> , H. Bouzerzour <sup>4</sup> <sup>1</sup> University of Mohamed El Bachir El Ibrahim, Faculty of Life and Natural Sciences and Earth Sciences and the Universe. Department of Agronomy, El-Anasser, 34030, Bordj Bou Arréridj, ALGERIA <sup>2</sup> National Agronomic Research Institute of Algeria, Division des agro-systèmes Est. Route des fermes, BP 08, 19000, Setif, ALGERIA <sup>3</sup> International Maize and Wheat Improvement Center . km. 45 Carretera Mexico-Veracruz El Batan, Texcoco, Estado de Mexico, CP 56130, MEXICO <sup>4</sup> University of Ferhat Abbas, Faculty of Life and Natural Sciences. Ecology and Plant Biology Department, VRBN Lab, 19000, Setif, ALGERIA
Keywords	Rht, Vrn, Ppd, Haplotype, Adaptation

**Abstract**

An experiment was carried out at the bioscience laboratory of the International Maize and Wheat Improvement Center, CIMMYT (Mexico), with the aim to characterize 600 F4 bread wheat (*Triticum aestivum* L.) lines along with their 9 parents for Rht, Vrn, and Ppd, genes. The molecular screening indicates that the distribution of the target dominant alleles is depending on the locus and the line/population. Among parents, except Mahon-Demias, a tall cultivar, the other parents are semi-dwarf and carry one dominant allele at Rht-1 or Rht-2 loci. Regarding the growth habit, all parents are of spring type and possess at least one dominant allele at Vrn-A1, Exon7\_C / T\_Vrn-A1, Vrn-B1, Vrn-D1, Ppd-B1 and Ppd-D1 loci. Among the F4 lines, the dwarfing alleles Rht-B1b and Rht-D1b are contained, respectively, in 66% and 8% of the lines evaluated. Compared to Rht-D1b, the effect of Rht-B1b on plant height is more pronounced. The vernalization insensitive alleles Vrn-A1a, Claire-type, Vrn-B1b and Vrn-D1a are present, respectively, in 19%, 46%, 45% and 49% of the lines tested. Similarly, 87% of the lines contain the photoperiod insensitive allele Ppd-D1a, whereas no line carries the Ppd-B1a allele. The results indicate also that the Ppd-B1 and Vrn-D1 genes have the most pronounced effects on the flowering initiation compared to the other genes tested. The study of the allelic combinations indicates a wide diversity of haplotypes. There are 4 for plant height and 25 divided into 4 groups for the duration of the vegetative growth phase. The F4 evaluated lines follow approximately the same development patterns of late genotypes in favorable environments. Indeed, those with of medium stature and late flowering time are the most productive.



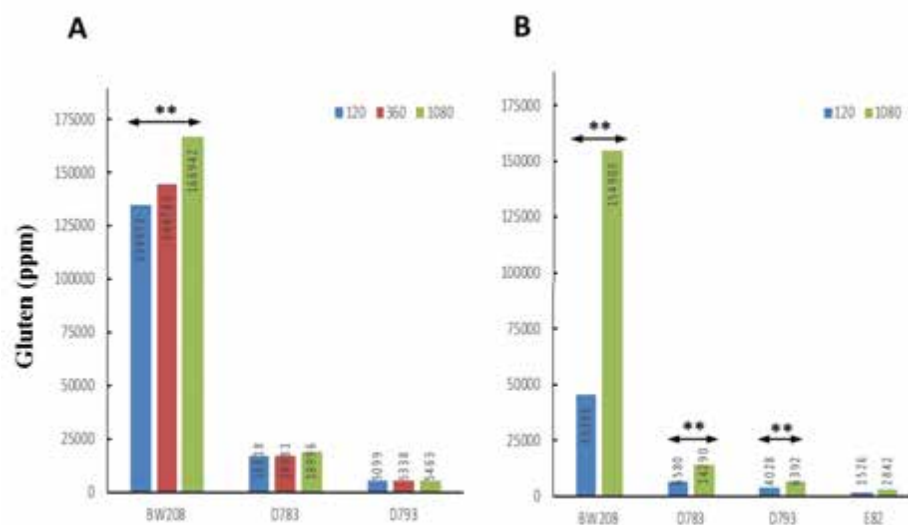
**Legend** Rht-B1\_SNP

Title	Variation for root architecture in a core collection of durum wheat and their relation with eco-geographical and agronomic traits
Authors	M Ruiz <sup>1</sup> , P Giraldo <sup>2</sup> , JM González <sup>3</sup> <sup>1</sup> Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Centro Nacional de Recursos Fitogenéticos. Autovía de Aragón, km 36, 28800, Alcalá de Henares, SPAIN <sup>2</sup> Universidad Politécnica de Madrid, Dpto. Biotecnología y Biología Vegetal. Ciudad Universitaria, s/n, 28040, Madrid, SPAIN <sup>3</sup> Universidad de Alcalá, Dpto. Biomedicina y Biotecnología. Campus Universitario. Edificio de Biología Celular y Genética, s/n, 28805, Alcalá de Henares, SPAIN
Keywords	root, durum wheat, landraces
Abstract	
<p>To obtain varieties with root systems adapted to abiotic stress-prone environments, it is necessary to search for new genotypes in genetically diverse materials, such as landraces, more likely to carry novel alleles for different root features. A core collection of 94 Spanish landraces of durum wheat, including three subspecies (dicoccon, turgidum and durum), was evaluated for nine root traits and the weight of the shoots at the seminal stage. Distinctive rooting phenotypes were characterized within each subspecies, mainly in subsp. durum. Contrasting rooting types, including large roots with shallow distribution or those with a high number of roots, were identified. Correlations with climatic traits showed that root shape is more relevant in the adaptation to eco-geographical zones in the subsp. dicoccon, whereas in the subsp. turgidum and durum, which come from warmer and drier zones, both the size and shape of root characteristics could have an adaptive role. The root traits with the largest positive effects on some yield components under water limitations included root diameter in subsp. dicoccon, root size in turgidum, and number of roots in durum. Twenty-eight marker–trait associations (MTAs), previously identified in this collection for agronomic or quality traits, were associated with some root seminal traits.</p>	
	
Legend	Examples of root architecture in accessions of the three subspecies: dicoccon (a, b), turgidum (c, d) and durum (e-h). The white bar at the end of each image represents 1 cm long. Figure (a) shows how Minimum and Maximum angle with respect to vertical

Title	Gluten proteins in low-gliadin wheats: effects of different nitrogen levels during fertilisation
Authors	M.D. García-Molina <sup>1</sup> , F. Barro <sup>1</sup> <sup>1</sup> Institute for Sustainable Agriculture (IAS-CSIC), Molecular breeding. Alameda del Obispo, S/N, 14004, Córdoba, SPAIN
Keywords	Transgenic wheat, Gliadins, Coeliac disease, Nitrogen, Competitive R5 ELISA

**Abstract**

Gluten proteins are major determinants of the bread-making quality of wheat but also are related to human disorders such as coeliac disease. The protein accumulation during grain filling is strongly influenced by nitrogen fertilisation (Wieser and Seilmeier, 1998) and it can produce modification on the grain protein composition (López-Bellido et al., 1998; Wieser et al., 2004; Garrido-Lestache et al., 2005). Thus, using different wheat lines with the gliadin fractions strongly down-regulated by RNAi, and nitrogen supplied in different levels, we studied shifts in grain protein balance. The final goal is to design new field experiments keeping low the gliadins and good yield. We have characterised the gluten proteins in low-gliadin wheat lines as influenced by nitrogen treatments in two greenhouse experiments. In Experiment 1 we used three nitrogen fertiliser rates (120, 360 and 1080 mg N) added at sowing stage; Experiment 2 included two nitrogen levels (120 and 1080 mg N) added according to the greatest demand per plant, that would correspond to the germination stage (growth stage 07) and pseudo stem erection (growth stage 30), according to the Zadoks scale (Zadoks et al., 1974) using split applications. The protein quantification was accomplished by RP-HPLC and gluten content (ppm) determined using Competitive R5 ELISA. Lines D793 and E82 showed a greater reduction in gliadins content and an increment in glutenins content with increasing nitrogen. Competitive R5 ELISA showed a significant decrease in gluten content of transgenic lines using split applications of nitrogen (Experiment 2) with 120 mg N compared to Experiment 1 (Figure); however, gluten content of line E82 was not affected by variations in N fertilisation.

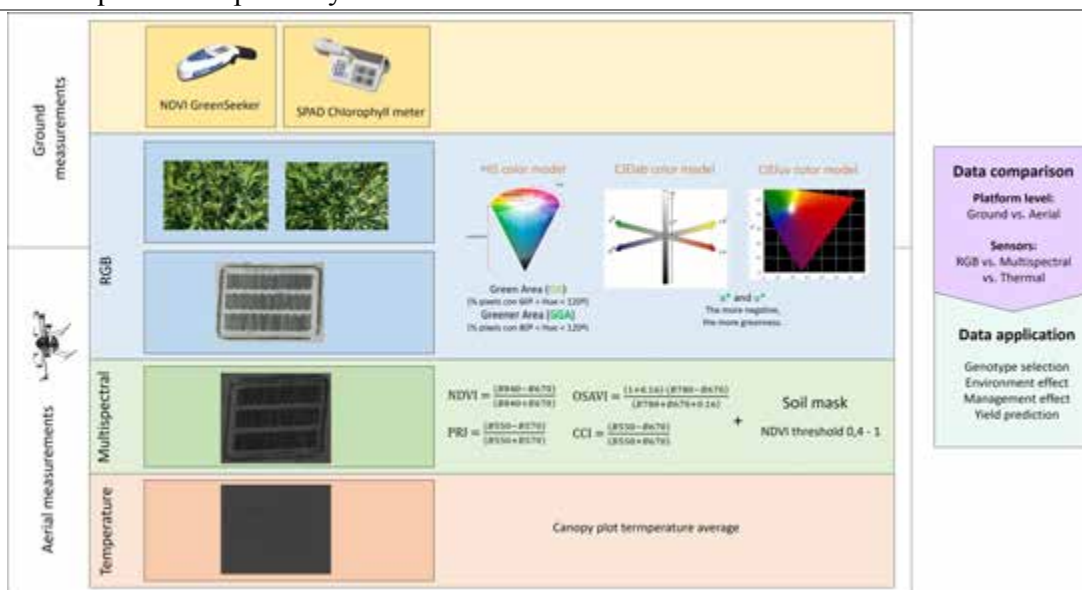


**Legend** Gluten content (ppm) by ELISA R5 of wild-type and low-gliadin wheats with different nitrogen levels (mg N) from experiments 1(A) and 2(B)

Title	REMOTE SENSING PHENOTYPING FOR ESTIMATING GENOTYPIC VARIABILITY IN GRAIN YIELD OF DURUM WHEAT UNDER DIFFERENT WATER AND TEMPERATURE CONDITIONS
Authors	A. Gracia-Romero <sup>1</sup> , J.A. Fernández Gallego <sup>1</sup> , O. Vergara-Diaz <sup>1</sup> , R. Vicente <sup>1</sup> , F. Chairi <sup>1</sup> , M.D. Serret <sup>1</sup> , J. Bort <sup>1</sup> , M.T. Nieto-Taladriz <sup>2</sup> , J. Mérida Silva <sup>3</sup> , N. Aparicio <sup>4</sup> , S.C. Kefauver <sup>1</sup> , J.L. Araus <sup>1</sup> <sup>1</sup> Universitat de Barcelona, Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals. Avinguda Diagonal, 643, 08028, Barcelona, SPAIN <sup>2</sup> Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA). Ctra. de La Coruña, Km. 7,5, 28040, Madrid, SPAIN <sup>3</sup> Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA). Plaza de España, Sector 3, 41013, Sevilla, SPAIN <sup>4</sup> Instituto Tecnológico Agrario de Castilla y León (ITACyL). Ctra. Burgos, Km. 119, 47071, Valladolid, SPAIN
Keywords	wheat, remote sensing, phenotyping, UAV

**Abstract**

Climate change is one of the primary culprits for the standstill of genetic progress of cereal crops at the Mediterranean region. Thus, efforts in phenotyping programs should be focused on understanding the relationships between the genotypes, the environment and the agricultural management (GxExM). Here we present an evaluation study of a set of remote sensing indexes derived from RGB (Red, Green and Blue), multispectral and thermal images, measured from the ground and from the air using a UAV platform, for the assessment of genotypic differences in yield of 24 durum wheat varieties (*Triticum turgidum* L. var. durum). The panel was grown under supplementary irrigation, rainfed and late-planting conditions at three different sites located on a wide range of latitudes in Spain (Coria del Rio, Aranjuez and Valladolid). At early stages, indexes that performed better were the ones related with the initial vigor of the plants as the RGB index Green Area (GA) and the multispectral Normalized Difference Vegetation Index (NDVI). During the grain filling, RGB indexes related with the greenness of the canopy as  $a^*$  or the Chlorophyll Content Index, correlated with yield. Finally, during maturity, the correlations were much lower and the only indexes that worked well were those capable of detecting the varieties that stayed green (i.e. photosynthetically active), such as the Triangular Greenness Index (TGI). Our results showed that to detect the correct establishment of the crop, assess the amount of green biomass contributing to the grain filling and identify the senescence could be critical traits useful for variety selection criteria and for the prediction of yield. Furthermore, RGB images are presented as a powerful and low-cost alternative for assessing crop performance. Moreover, combination of specific indexes measured at a given growing stage may allow to build up robust equations to predict yield.

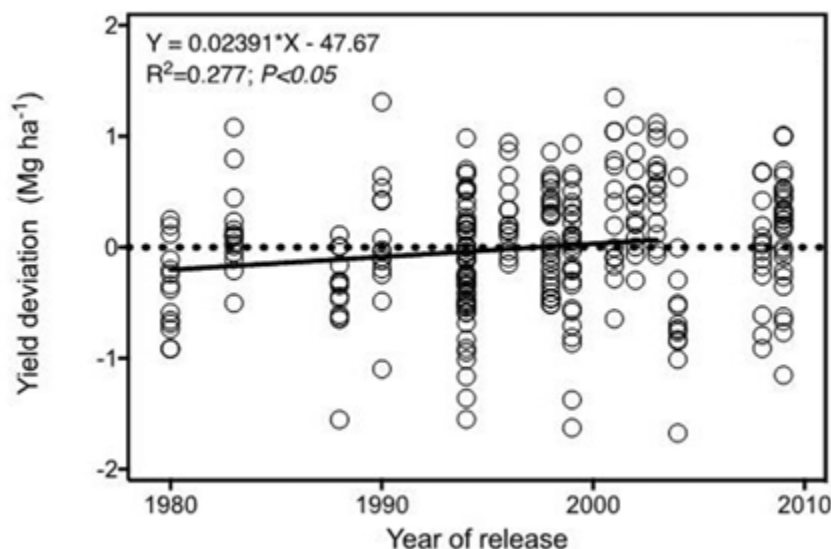


**Legend** Work flow of the data collection and the data processing.

Title	Post-Gr een Revolution genetic advance in durum wheat: the case of Spain
Authors	F. Chairi <sup>1</sup> , O. Vergara Diaz <sup>1</sup> , T. Vatter <sup>1</sup> , N. Aparicio <sup>2</sup> , M.T. Nieto <sup>3</sup> , S.C. Kefauver <sup>1</sup> , J. Bort <sup>1</sup> , M.D. Serret <sup>1</sup> , J.L. Araus <sup>1</sup> <sup>1</sup> University of Barcelona. Av. Diagonal, 643, 08028, Barcelona, SPAIN <sup>2</sup> Instituto de Tecnología Agraria de Castilla y León (ITACyL). Ctra. de Burgos , Km. 117, 47071, Valladolid, SPAIN <sup>3</sup> Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA). Crta. de la Coruña, Km. 7,5, 28040, Madrid, SPAIN
Keywords	Agronomical yield components, grain nitrogen, carbon isotope composition, durum wheat, genetic gain

Abstract

Durum wheat is the 10th most important crop worldwide. Approximately 80% of the world's crop area of this species is concentrated in the Mediterranean, with Spain being one of the largest producers. Literature indicates that the genetic advance in yield, resulting from the Green Revolution, seems to have declined or even ceased. To addresses the question of whether there has been any genetic gain in yield for durum wheat released in Spain after the Green Revolution field experiments were carried out with a wide range of durum wheat cultivars (released in Spain from 1980 to 2010). Trials were conducted in sites embracing a wide range of growing temperatures and water regimes at Aranjuez (Madrid) and Zamadueñas (Valladolid) during three consecutive growing seasons under rainfed and supplemental irrigation, and at Coria (Sevilla) for two consecutive seasons under rainfed conditions alone. Statistical analysis revealed grain yield to increase with the year of release of cultivars at a rate of 24 kg ha<sup>-1</sup> y<sup>-1</sup> from 1980 to 2003, with no clear additional improvements thereafter. On the other hand, the number of kernels m<sup>-2</sup> and number of kernels per spike together with aerial biomass at harvest and grain nitrogen yield increased with the year of release of cultivars. However, no differences were found for thousand kernel weight, number of spikes m<sup>-2</sup>, days to heading, plant height, harvest index, canopy temperature depression, carbon isotope discrimination, or grain nitrogen concentration. The moderate grain yield improvement from 1980 to 2003 was associated with kernels m<sup>-2</sup> and kernels spike<sup>-1</sup>, with an increase of 117 kernels m<sup>-2</sup> y<sup>-1</sup> and 0.24 kernels spike<sup>-1</sup> y<sup>-1</sup>, respectively. Overall, these results indicated the rate of genetic progress in yield of durum wheat in Spain after the Green Revolution has been low and even stopped during the last decade.

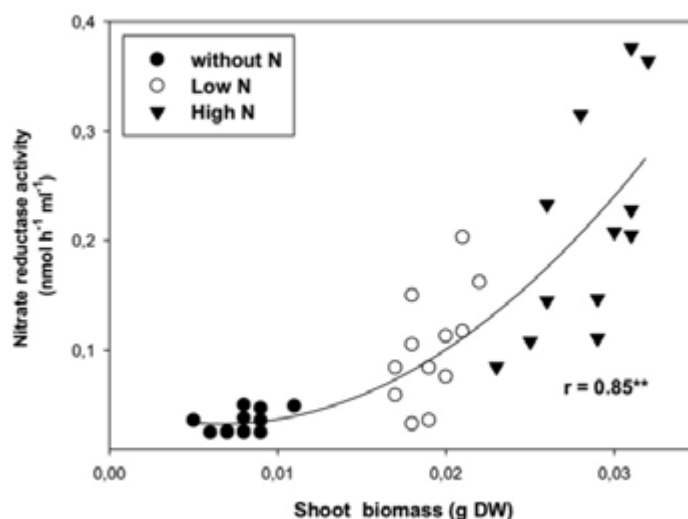


Legend Fig 1: Yield deviation of durum wheat varieties released between 1980 and 2009. The deviation is the difference between the yield of a given variety in a given environment and the mean of all varieties in each of the environments.

Title	Comparative response of Nitrate Reductase activity, Nitrogen Utilisation Efficiency (NutE) and Nitrogen Physiologic Efficiency (NPE) in Tunisian durum wheat cultivars
Authors	S. Ayadi <sup>1</sup> , Z. Chamekh <sup>1</sup> , C. Karmous <sup>1</sup> , Z. Hammami <sup>1</sup> , S. Jallouli <sup>1</sup> , I. Zouari <sup>1</sup> , N. Ahmed <sup>1</sup> , F. Ben Azaiz <sup>1</sup> , Y. Trifa <sup>1</sup> <sup>1</sup> National institute of agronomy of Tunisia (INAT), Agronomy and crop biotechnology. Cité Mahrajène, 43 Manzah 1, 1082, Tunis, TUNISIA
Keywords	Nitrate reductase, nitrogen utilization efficiency, landrace and improved genotype

**Abstract**

Nitrogen (N) limitation in the environment, and its consequences for plant growth have long been of interest to agronomists and plant physiologists. Thereby, genotypic variation in nitrogen utilization efficiency (NutE) could be related to the differences in N uptake and in the effectiveness of a genotype to utilize this nutrient. A hydroponic culture experiment was conducted to evaluate growth response and NutE of four Tunisian durum wheat cultivars, two landrace genotypes (Bidi and Azizi) and two improved ones (Om Rabia and Khiar) under two concentrations of potassium nitrate (1mM and 10mM). Results showed that cultivars significantly differed in their plant shoot height (SH) and shoot dry weight (SDW). There was also a significant difference in NutEshoot which could be explained by the genotypic variation in N uptake. Results also showed a significant interaction effect ( $p \leq 0.001$ ) genotypes  $\times$  N treatments for total chlorophyll content (ChlT), N uptake (Nup), N concentration (Nc) and nitrogen utilization efficiency for shoot (NutEshoot). Nitrate reductase activities (NR) were the most affected trait by nitrogen showing an increase of 250% under high N treatments (10mM) compared to control media (1mM). A significant exponentially relationship exists between NR activity (NR) and shoot biomass (SDW) for the different N levels ( $R^2 = 0.85$ ;  $p < 0.001$ ). Nitrogen treatment effect was highly significant for all traits studied other than NPEshoot. SH and (NutEshoot) traits increased by 1.77% and 6.25% respectively for landrace genotypes compared to the improved genotypes. In conclusion, the higher NutE in the landrace wheat genotype appears mainly to be due to the lower shoot N uptake of landraces compared to the improved genotypes. NutEshoot is very important trait because improvement in NutEshoot would result directly in more plant biomass.



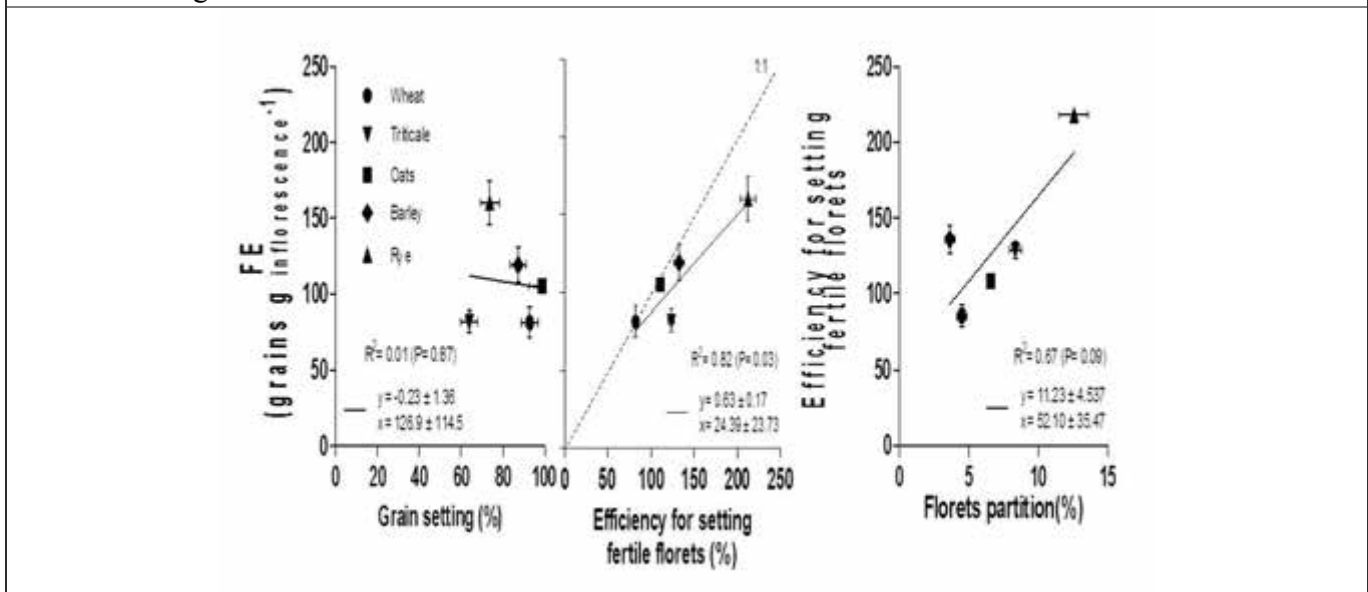
**Legend** Relationship between NR activity and shoot biomass across the four genotypes within each of the three nitrogen treatments. Each point represents the individual value for a given replication and genotype within a nitrogen treatments. Variables mentio

Title	FRUITING EFFICIENCY DIFFERENCES BETWEEN WINTER CEREALS
Authors	A. L. Garcia <sup>1</sup> , R. Savin <sup>1</sup> , G. A. Slafer <sup>2</sup> <sup>1</sup> University of Lleida, Department of Crop and Forest Science & Agrotecnio. Rovira Roure, 191, 25198, Lleida, SPAIN <sup>2</sup> Catalonian Institution for Research and Advanced Studies (ICREA). Passeig de Lluís Companys, 23, 08010, Barcelona, SPAIN

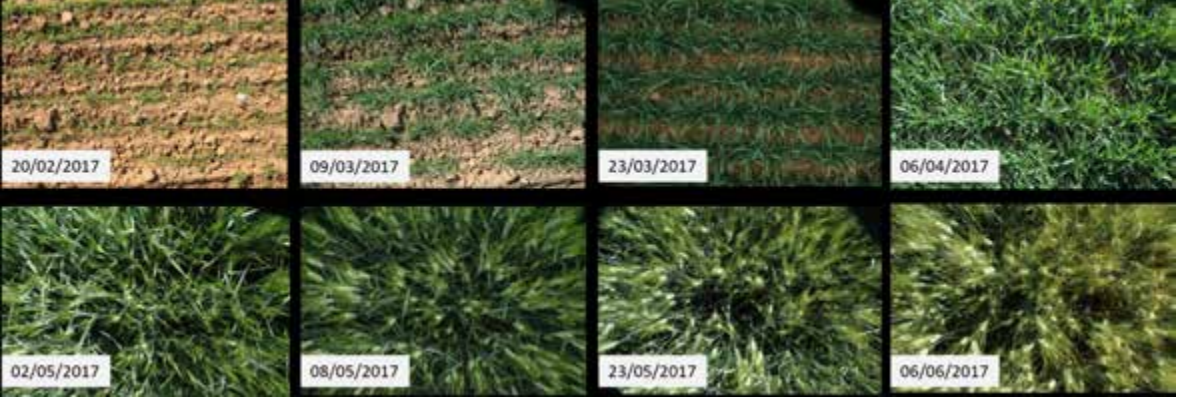
Keywords Grain number, fruiting efficiency, spike dry weight at anthesis, cereals

Abstract

Grain number (GN) is critical for yield determination, and understanding its physiology may be instrumental to further improving yield. Studying similarities and differences in yield physiology among cereals may highlight physiological traits which might become critical and/or help understanding some constitutive differences between them. Even though the main component explaining past gains in wheat yield has been increases in spike dry weight at anthesis (SDWa), some authors have discussed the idea of focusing on fruiting efficiency (FE). In this research we reported for the first time a comparison of GN determination due to inflorescence DWa and/or FE between five winter cereals crops (wheat, rye, barley, oats and triticale), analysing likely physiological bases for them and possible trade-offs. Firstly in a literature search, we found limited papers on FE, mostly in wheat with some few data available for barley and triticale and nothing on oats and rye. Then, we run four experiments comparing them directly and found that in triticale, barley and oats differences in GN has been positively related with SDWa, while in wheat and rye, relationships were more clear related with FE. A wide range of FE variation was evidenced among cereals: triticale and wheat showed the lowest, rye exhibited the highest and barley and oats had intermediate values. Regarding to physiological causes of differences in FE we found no relationship with grain set percentage: differences in FE were mainly due to those in the efficiency for setting fertile florets during pre-flowering inflorescence growth. Results also evidenced that this efficiency for setting fertile florets was related to the proportion of inflorescence resources partitioned to the growth of floret primordia. We found a negative relationship between individual grain weight and FE, which might explain constitutive differences in grain size.



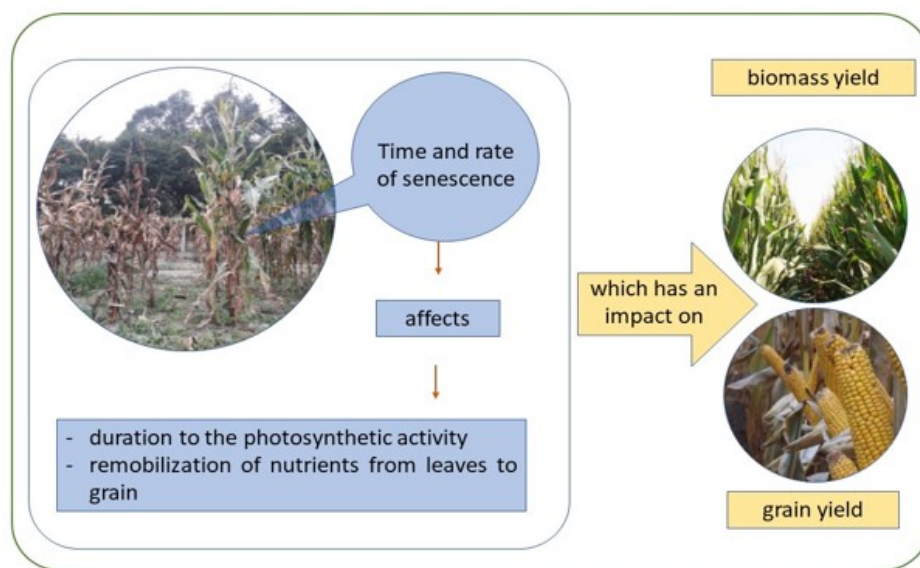
Legend Fig. 1. Relationship between fruiting efficiency and grain setting (left panel), fruiting efficiency and efficiency for setting fertile florets (central panel) and efficiency for setting fertile florets and florets partition (right panel).

Title	Canopy Vegetation Indices to assess yield in durum wheat.
Authors	Raquel Martínez-Peña <sup>1</sup> , Yésica Pallavicini <sup>1</sup> , Shawn C. Kefauver <sup>2</sup> , Adrián Gracia-Romero <sup>2</sup> , Ismael Araus-González <sup>1</sup> , Nieves Aparicio <sup>1</sup>  <sup>1</sup> Instituto Tecnológico Agrario Castilla y León. Carretera de Burgos, Km. 119, 47071, Valladolid, SPAIN  <sup>2</sup> Integrative Crop Ecophysiology Group, Section of Plant Physiology, Faculty of Biology, Universitat de Barcelona . Diagonal, 645, 08028, Barcelona, SPAIN
Keywords	NDVI, Triticum turgidum var. durum, Spectral indices, RGB indices
Abstract	Vegetation indices (VIs), obtained from remote sensing and those derived from RGB conventional digital images, based on canopies are quite simple and effective algorithms for quantitative and qualitative evaluations of vegetation cover, vigor, and yield among other applications. In the study, we compared ground vs aerial assessed RGB and multispectral indices capacity to assess yield in durum wheat ( <i>Triticum turgidum</i> L. var. durum) trial. Twenty-one genotypes were grown under irrigated conditions in northeastern Spain, in a field trial with three repetitions. During the cycle, zenithal RGB images were acquired in eight moments. Then RGB and multispectral aerial images were acquired, using an unmanned aerial vehicle flying under remote control at around 50m height, in two dates after anthesis. Vegetation indices derived from RGB and multispectral images were calculated for each plot. At harvest, grain yield were determined per plot. Pearson correlation coefficients were calculated between VIs indices and grain yield of each plot. Regarding the indices measured on ground, they showed the greatest correlations. The best indices showing correlation coefficients higher than 0.75 were the spectral index “Normalized Difference Vegetation Index (NDVI)” followed by the RGB indices “Green area” and “Greener area”; all of them at anthesis. Regarding aerial measurements, thermal index an NDVI showed correlations coefficients above 0.75, both of them in grain filling. Other indices also showed correlations between 0.7 and 0.74. Before heading none index was significant. The results suggests that several indices could be used as potential grain yield predictors. Especially those related with biomass production, plant water content or temperature. The phenological moment of the crop at which the VIs are taken is important, since aerial VIs predicted yield more strongly at grain filling while the VIs on ground at anthesis.
	
Legend	RGB images showing the evolution of the crop from February to June.

Title	Maize breeding for delayed senescence “STAY GREEN”
Authors	M. Caicedo <sup>1,2</sup> , R. A. Malvar <sup>1</sup> , G. Padilla <sup>3</sup> , M. Lema <sup>1</sup> , P. Revilla <sup>1</sup> , M. La Fuente <sup>1</sup> , J. Jiménez <sup>1</sup> , B. Ordás <sup>1</sup> <sup>1</sup> Misión Biológica de Galicia, Pontevedra. Carballeira, 8, 36143 , Salcedo, Pontevedra, SPAIN <sup>2</sup> Instituto Nacional de Investigaciones Agropecuarias (INIAP), Pichincha. Av. Eloy Alfaro y Amazonas, N30-350, 170315, Quito, ECUADOR <sup>3</sup> Servicio de Bioinformática y Bioestadística, Centro de Investigaciones Biológicas (CIB), Madrid. Calle Ramiro de Maeztu, 9, 28040, Madrid, SPAIN
Keywords	Stay green, senescence, gene expression

**Abstract**

Delayed senescence or “Stay-green” (SG) is a desirable trait for crop yield associated with the biomass production, lodging resistance, and yield. Previous publications have reported both physiological and genetic studies about senescence on a small number of genotypes, resulting in partial conclusions. Our research deepens on the genetic and physiological mechanisms related to maize senescence. We 1) evaluated the functional SG of a wide sample of temperate inbred lines, 2) identified QTL related to the trait in a MAGIC population and 3) carried out an analysis of the changes in gene expression during leaf senescence. The results confirmed the presence of the functional SG trait in most lines originally classified as such. The group of lines with late photosynthesis had on average the highest grain yield and biomass yield but also the highest grain filling duration and grain moisture. We conclude that functional stay-green is favorable for grain yield but at the cost of increase grain moisture. Association mapping identified 11 important QTLs associated with the chlorophyll index, the maximum quantum yield of photosystem II and plant visual aspect, and two candidate genes associated with the chlorophyll index were proposed. Finally, we identified 1083 and 588 genes that were up and down regulated, respectively, during the senescence in all seven lines. The genes that were down regulated were mainly involved in photosynthesis, while the genes up regulated were related to catabolic processes. A subset of 196 differentially expressed genes codified for transcription factors; some of them are homologous to transcription factors found in Arabidopsis in different signaling pathways.

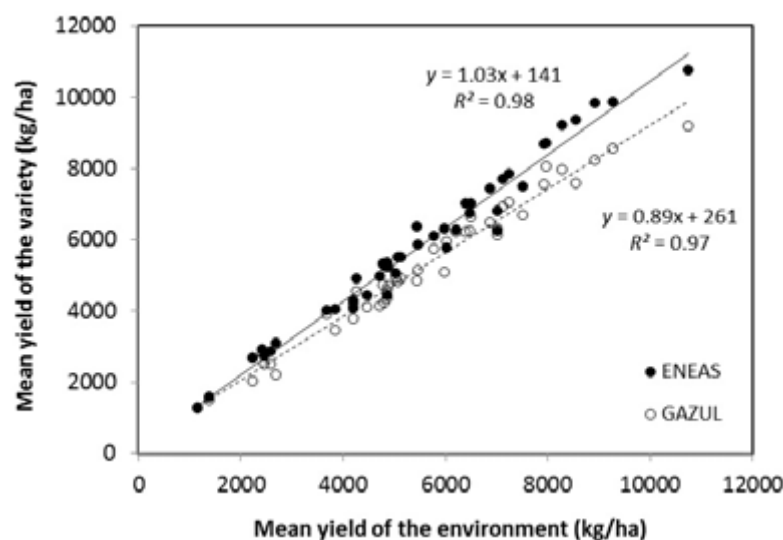


Legend	Impact of stay green trait on grain and biomass yield
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Title	Bread wheat improvement to meet the requirements of the Spanish agricultural sector
Authors	F Álvaro <sup>1</sup> , JC Sillero <sup>2</sup> , N Aparicio <sup>3</sup> <sup>1</sup> IRTA, CULTIUS EXTENSUS. Av. ROVIRA ROURE, 191, 25198, LLEIDA, SPAIN <sup>2</sup> IFAPA, Centro Alameda del Obispo. Av. Menéndez Pidal, SN, 14004, Córdoba, SPAIN <sup>3</sup> ITACyL, Unidad Cultivos Herbáceos. Ctra. Burgos, km 119, 47071, Valladolid, SPAIN
Keywords	Wheat, Breeding, Yield potential, Adaptation, Quality

**Abstract**

The Spanish bread wheat seed market is mostly based in the introduction of varieties developed in other countries that may not express their potential under Mediterranean conditions, predominant in the main growing areas of the country. With the aim of developing new varieties adapted to the agricultural, environmental and qualitative Spanish requirements, a public wheat breeding program has been conducted during the last 13 years in coordination between IRTA, IFAPA, ITACyL and ITAP (the last, until 2012), and funded under four INIA projects. The main breeding goals pursued are: high productivity, resilience to abiotic stresses, resistance to main diseases and bread-making quality. A multidisciplinary approach is followed. Crosses are conducted between elite lines of diverse origin carrying desired traits. The advance of generations follows a modified pedigree scheme. For the most promising crosses, the advance of generations is accelerated by following the Single Seed Descent method under controlled conditions, at a pace of two generations by year. Selection for disease resistance, quality and agronomic type starts at F2. Advanced lines are tested in multi-environment trials to identify specific and wide adaptation. New technologies based on digital images have been introduced as selection tools for traits related to environmental adaptation. Due to the increased impact of yellow rust epidemics in Spain in the last years, a marker-assisted backcross scheme is implemented to introduce sources of adult plant resistance, and pyramid effective race-specific resistance genes. As a result, two high-yielding varieties with good bread-making quality and rust resistance, have been released and transferred to seed companies: ENEAS (2012) and 08THES2162 (2014). Another line is running its first year of the official trials of the OEVV (Spanish Office of Plant Varieties) and two more are ready to be submitted to evaluation by the same office by the end of this field season.

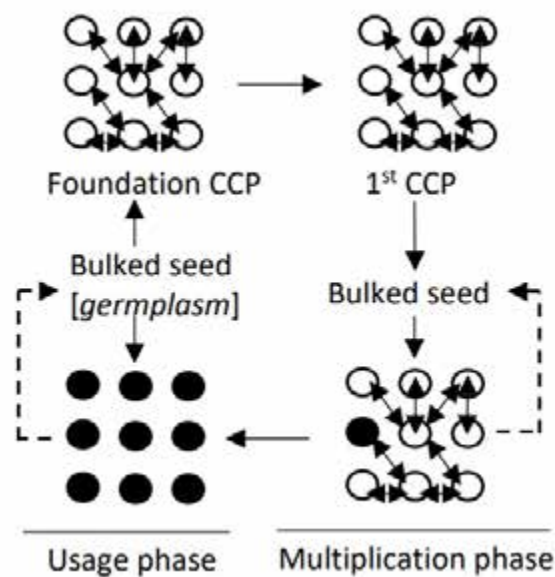


**Legend** Mean yield of the variety ENEAS and the check GAZUL in 44 experiments conducted by official agencies in Spain (2010-2012)

Title	Composite cross populations (CCPs) of wheat: The intensive use of genetic variation in the future wheat breeding
Authors	J. KIM <sup>1</sup> <sup>1</sup> University of Lleida , the Department of Crop and Forest Science & Agrotecnio . Av. Rovira Roure, 191, 25198, Lleida, SPAIN
Keywords	Wheat, CCPs, Genetic diversity, Evolutionary breeding, Adaptability

**Abstract**

The winter wheat Composite Cross Populations (CCPs) were originally created in 2002 at the Organic Research Centre, Elm Farm in England and since then, the cycling of CCPs wheat was conducted in various geographical locations of Europe. During one growing season (2015/16), nine different CCPs wheat which have different growing backgrounds and two commercial wheat varieties were grown in the Netherlands (Wageningen) to evaluate physiological traits of CCPs wheat. Phenotypic performances of 15 different traits were phenologically observed. Basically, CCPs wheat maintains genetically diverse population and in terms of genetic diversity, the concept of CCPs (Fig. 1) presented various future perspectives in wheat breeding. For example, CCPs wheat exhibited more resilience and buffering capacity against environmental variability than commercial varieties. Therefore, for CCPs wheat, it was suggested that adaptation or stability of genotypes across a wide range of environments are more crucial elements. For adaptability, Finlay-Wilkinson regression model was suggested as  $VP = VG + \beta E + e$ . If the regression coefficient ( $\beta$ ) is high, it was considered as showing a higher adaptation across a wider range of environments. Stability was calculated as a deviation ( $s_2d$ ) from the regression and therefore, high stability was suggested as little variations over environments and/or years. In this research, CCPs wheat exhibited higher adaptability and stability over years compared with commercial varieties. This result indicates genetically diverse populations could change its genetic makeup over years by natural selection and gradually increase resilience in environmental changes, and the most efficient way to increase diversification at the genetic levels in populations could be Composite Cross Populations (CCPs) as an example of evolutionary breeding. Therefore, in wheat production, CCPs wheat can be presented as a new paradigm; ‘Relying on the intensive use of genetic variation, not intensive selection’ in the future wheat breeding.



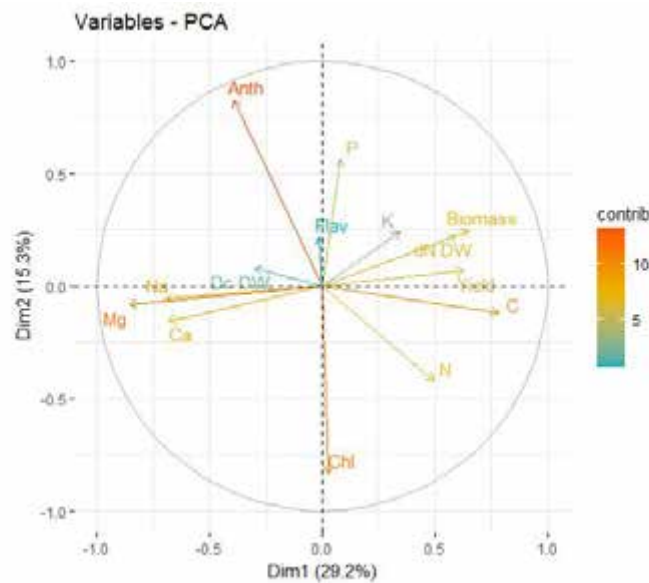
**Legend** Fig 1. The stage of CCPs. Composite Cross Populations (CCPs) wheat breeding basically focuses on varietal mixtures without artificial selection of individual plants.

## **Posters of Sessions 3 and 4**

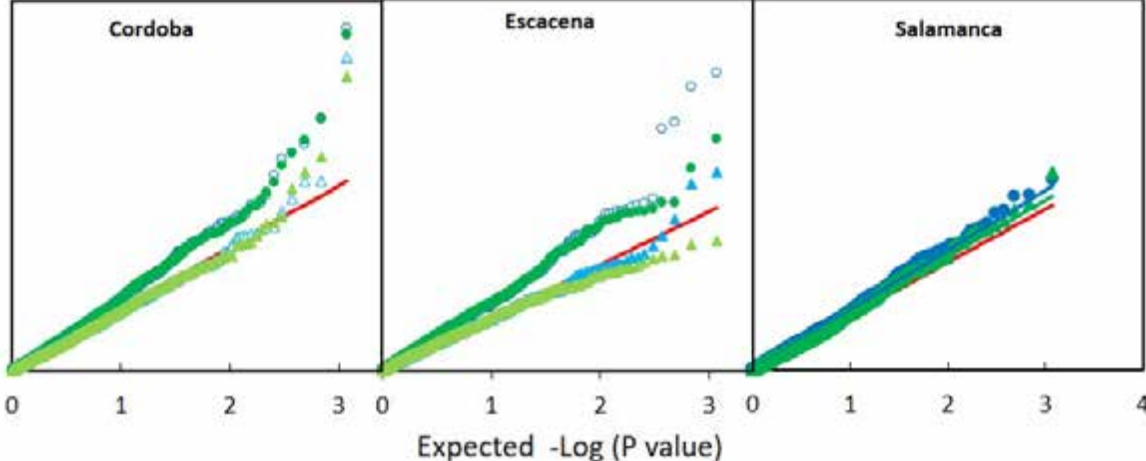
Title	Early assessment of the effect of irrigating with saline water in the agronomical performance of the pseudocereal <i>Chenopodium quinoa</i> : comparing different approaches
Authors	F.Z. Rezzouk <sup>1</sup> , M.A. Shahid <sup>2</sup> , S. Yousfi <sup>1</sup> , M.D. Serret <sup>1</sup> , J.L. Araus <sup>1</sup> <sup>1</sup> University of Barcelona, Plant physiology. avinguda Diagonal, 643, 08028, BARCELONA, SPAIN <sup>2</sup> International Center for Biosaline Agriculture (ICBA). Al Ain Road Al Ruwayyah, 2, 14660, Dubai, UNITED ARAB EMIRATES
Keywords	Quinoa, Salinity, Stable isotope compositions, ions concentration, Pigments

**Abstract**

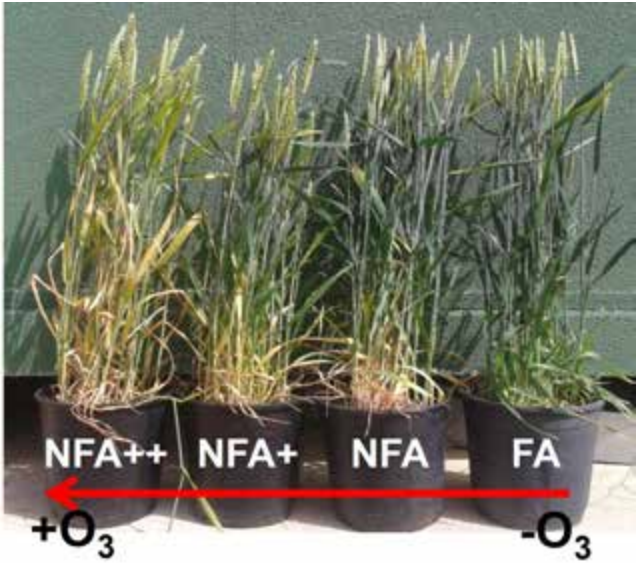
Quinoa is a very versatile crop, amenable for the hot agronomical conditions of Middle East, where it is cultivated under irrigation, frequently using brackish water. This study aims to compare different approaches to early detect the effect of salinity in the agronomical performance of this crop. A set of 20 accessions were grown under drip irrigation in a sandy soil at ICBA (UAE). Plants were grown up to one week after emergence using good quality water (0.4 dS m<sup>-1</sup>). Then, half of the trial was submitted to irrigation with brackish water (15 dS m<sup>-1</sup>) and continued for the rest of the growing unit maturity. After one week of applying brackish water chlorophyll, anthocyanin and flavonoid contents were evaluated in fully expanded leaves of both control (fresh water) and brackish water irrigated plants using a portable meter (Dualex). The same leaves were then harvested, dried and the stable carbon and nitrogen isotope compositions ( $\delta^{13}C$  and  $\delta^{15}N$ ) and the total N content of the dry matter analyzed (by EA-IRMS), together with the total content of K, Na, P, K and Mg ions (ICPES). Grain yield and biomass decreased by 27.2% and 14.7% as a response to the brackish water. Genotypic and treatment effects existed for yield and biomass, as well as the analytic traits above. Regardless of the irrigation conditions the best traits in terms of correlation with biomass and yield were the Mg and K contents and  $\delta^{15}N$ . A stepwise model using different traits (mainly Mg, K and  $\delta^{15}N$ ) explained 33.1% of variability in biomass and 56.0% in grain yield, under brackish irrigation, 52.4% and 34.9% under control, and 42.4% and 38.6% under the combination of both regimes, respectively. The combined analysis of ion concentration and stable isotope signature allow an early evaluation of the effect of irrigation salinity and to identify the best performing genotypes within each irrigation condition.



Legend	Principal component analysis (PCA) of 20 quinoa genotypes growing under two different irrigation conditions (good quality water and brackish water), using as variables 14 different analytic traits of leaves collected one week after treatments
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Title	Genetic plasticity of oat agronomic traits associated with climate variable changes
Authors	N Rispail <sup>1</sup> , G Montilla-Bascón <sup>1</sup> , J Sánchez-Martín <sup>1</sup> , F Flores <sup>2</sup> , C Howarth <sup>3</sup> , T Langdon <sup>3</sup> , D Rubiales <sup>1</sup> , E Prats <sup>1</sup> <sup>1</sup> CSIC-Institute for Sustainable Agriculture. Alameda del Obispo s/n, s/n, 14004, Cordoba, SPAIN <sup>2</sup> E.T.S.I. La Rábida. Universidad de Huelva, s/n, 21819, Palos de la Frontera, SPAIN <sup>3</sup> Institute of Biological, Environmental and Rural Sciences, University of Aberystwyth, UK. Penglais Hill, s/n, SY23 FL, Aberystwyth, UNITED KINGDOM
Keywords	Association analysis, oat, Resilience, Adaptation
Abstract	<p>Although oat cultivation in Mediterranean region is steadily increasing, its yield in these regions lacks far behind oat yield obtained in Northern regions. This is mainly rooted to the low adaptation of current oat cultivars to Mediterranean environments. Increasing yield in Southern regions through improvement of oat crop resilience is therefore urgently needed. Better-adapted landraces, known as good reservoirs of favourable traits including disease resistance and abiotic stress tolerance, could contribute to increase oat resilience. To drive the selection of agro-climate adapted genotypes we integrated genome wide association approaches with analysis of the phenotypes of genetic variants and the weight of associated markers across different environmental variables. Association models, taking into account oat population structure, were applied on either arithmetic means or best linear unbiased prediction (BLUPs) for the five agronomic traits evaluated to ensure robust identification of associations. The meta-analysis of the six joint environments (mega-environment) identified 5 markers associated with yield, 3 with biomass, 4 with HI, 5 with flowering date and 7 associated with rust severity. Four of these associated markers were located within expressed genes. These associations were only mildly influenced by climatic variables indicating that these markers are good candidates to improve the genetic potential of oat under Mediterranean conditions. In turn, models highlighted several marker-trait associations, strongly affected by particular climatic variables including high rain pre- or post-flowering and high temperatures, revealing a high genetic plasticity of oat. These results will contribute to increase oat resilience for particular climatic conditions and the strength of breeding programmes for plant adaptation to a wider range of climatic conditions in the current scenario of climate change. This research was financially supported by the Project AGL2016-78965-R (Spanish Ministry of Economy and Competitiveness) and the European Regional Development Funds (ERDF).</p>
	
Legend	Distribution of p values for the different models used in this study for the association between markers and rust resistance in three different locations.

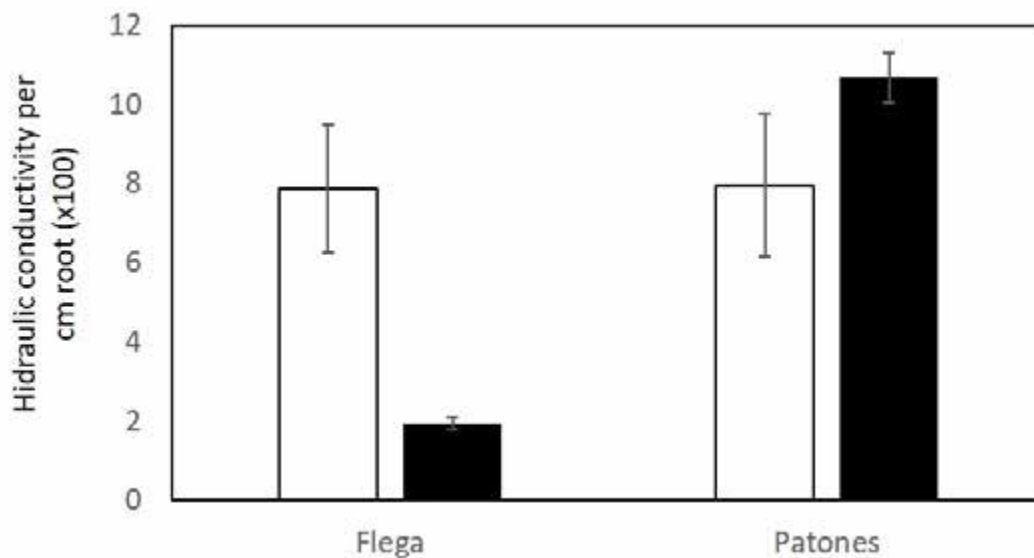
Title	Characterization of antioxidant enzymatic response of five barley genotypes under drought stress																		
Authors	A THAMEUR <sup>1</sup> , L.L MARTINS <sup>2</sup> , M.P MOURATO <sup>2</sup> , A FERCHICHI <sup>3</sup> , M LOPEZ-CARBONELL <sup>4</sup> <sup>1</sup> CRRA SIDI BOUZID. Road Gafsa Km 6, 357, 9100, SIDI BOUZID, TUNISIA <sup>2</sup> LEAF, Instituto Superior de Agronomia, Universidade de Lisboa.. Tapada da Ajuda , 1349, -017 , Lisboa, PORTUGAL <sup>3</sup> National Institute of Agronomy of Tunis . Avenue Charles Nicolle, 43 , 1082, Tunis, TUNISIA <sup>4</sup> Faculty of Biology, University of Barcelona.. Av Diagonal, 643, 08028, Barcelona , SPAIN																		
Keywords	barley, oxidative stress, hydrogen peroxide, antioxidant enzymes, gas exchange.																		
Abstract	Barley ( <i>Hordeum vulgare</i> L.), one of the world's most extensively cultivated crops, is regarded as drought tolerant compared with other Triticale members. There are also differences in drought tolerance between barley species. Genotype Ardhaoui, inhabiting arid areas of the South of Tunisia, is regarded as being markedly more salt tolerant than other genotypes. The objective of this research is to define the role of antioxidant defense system in drought tolerance of five barley genotypes: (1) Ardhaoui (A), (2) Pakistan (P), (3) Rihane (R), (4) Manel (M) and (5) Roho (RO). Therefore, in the present study, we investigated the plant water status, gas exchanges parameters, changes in the concentration of hydrogen peroxide (H <sub>2</sub> O <sub>2</sub> ) and the activities of antioxidant enzymes [superoxide dismutase (SOD), catalase (CAT), peroxidase (POX), ascorbate peroxidase (APX) and glutathione reductase (GR)]. The genotypes were subjected to water stress by withholding irrigation during 23 days. Results showed that stomatal conductance (gs) was reduced in all genotypes by drought treatment, but it was less pronounced in genotype Ardhaoui. An increase in H <sub>2</sub> O <sub>2</sub> was observed. The SOD activity seems to be involved in the response to water stress for genotypes Ardhaoui, Pakistan and Rihane. Similarly, the activity of CAT was significantly increased in all studied genotypes.																		
	<table border="1"> <caption>Data for Figure 1: Variation of the specific activity of catalase (CAT)</caption> <thead> <tr> <th>Genotype</th> <th>Control (μmoles min<sup>-1</sup> mg<sup>-1</sup>)</th> <th>Stressed (μmoles min<sup>-1</sup> mg<sup>-1</sup>)</th> </tr> </thead> <tbody> <tr> <td>A</td> <td>~1.2 (c)</td> <td>~3.2 (d)</td> </tr> <tr> <td>P</td> <td>~1.5 (b)</td> <td>~7.5 (a)</td> </tr> <tr> <td>R</td> <td>~1.3 (c)</td> <td>~5.5 (b)</td> </tr> <tr> <td>M</td> <td>~2.0 (a)</td> <td>~5.5 (b)</td> </tr> <tr> <td>RO</td> <td>~1.5 (b)</td> <td>~3.8 (c)</td> </tr> </tbody> </table>	Genotype	Control (μmoles min <sup>-1</sup> mg <sup>-1</sup> )	Stressed (μmoles min <sup>-1</sup> mg <sup>-1</sup> )	A	~1.2 (c)	~3.2 (d)	P	~1.5 (b)	~7.5 (a)	R	~1.3 (c)	~5.5 (b)	M	~2.0 (a)	~5.5 (b)	RO	~1.5 (b)	~3.8 (c)
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M	~2.0 (a)	~5.5 (b)																	
RO	~1.5 (b)	~3.8 (c)																	
Legend	Figure 1. Variation of the specific activity of catalase (CAT).																		

Title	An assessment of O <sub>3</sub> -sensitivity of Spanish bread wheat ( <i>Triticum aestivum</i> L.) varieties
Authors	V. Bermejo-Bermejo <sup>1</sup> , I. González-Fernández <sup>1</sup> , A. Solé <sup>2</sup> , S. Elvira <sup>1</sup> , J. Sanz <sup>1</sup> , J. M. Carrillo <sup>2</sup> , E. Benavente <sup>2</sup> , R. Alonso <sup>1</sup> <sup>1</sup> CIEMAT (Centro de Investigaciones Energéticas, Medioambientales y Tecnológicas), Ecotoxicology of Air Pollution. Avda. Complutense, 40, 28040, Madrid, SPAIN <sup>2</sup> Universidad Politécnica de Madrid, Biotechnology and Plant Biology. Avda. Complutense, s/n, 28040, Madrid, SPAIN
Keywords	Bread wheat, O <sub>3</sub> -sensitivity, Yield, Grain protein, Water use efficiency
Abstract	<p>Wheat is currently considered the most sensitive cereal to the increasing levels of surface ozone. Accordingly, the exposure and dose-response functions developed for this crop are currently used for assessing the risk of O<sub>3</sub> effects on agricultural production at European scale. However, these functions are based on Central and Northern European cultivars and climate. A study was carried out in an Open-Top chambers facility to assess the relative O<sub>3</sub>-sensitivity of 12 bread wheat varieties representing different degrees of breeding selection. Four O<sub>3</sub> treatments that reproduced from pre-industrial O<sub>3</sub> levels to atmospheres reaching the highest hourly values registered currently in the agronomic areas of Spain were used. Their effects on grain yield and grain protein yield were determined. Physiological parameters related with gas exchange like photosynthesis, stomatal conductance, water use efficiency (WUE), chlorophyll content and relative water content (RWC) were also measured to study the physiological mechanisms involved in the response. Grain yield of none of the local landraces was influenced by the O<sub>3</sub> treatment whereas increasing O<sub>3</sub> levels negatively affected yield of most of the commercial varieties. Despite grain protein concentration of modern varieties increased under elevated O<sub>3</sub>, the resulting grain protein yield per hectare was lower compared to the control filtered-air treatment. However, no effect of O<sub>3</sub> treatments was detected on the local varieties. RWC and the chlorophyll content was significantly reduced by O<sub>3</sub>, especially in modern varieties; similarly, modern varieties exposed to the pollutant reduced their WUE compromising their availability for supporting water deficit. The study suggests that: i) bread wheat varieties derived from breeding activity can be more affected than local landraces in future scenarios of Global Change, where increased levels of tropospheric O<sub>3</sub> are expected; ii) ozone effects can be higher than expected when the indirect consequences like reduction on WUE are considered.</p>
	
Legend	Plants of bread wheat cv. Berdún cultivated under filtered air (FA; reproduces pre-industrial levels), non-filtered air (NFA) and non-filtered air supplemented with 20 nl/l O <sub>3</sub> (NFA+) or 40 nl/l O <sub>3</sub> (NFA++)

Title	Encourage spending or saving water? A strategy for coping with drought in oats involve abscisic acid mediated modulation of transpiration coupled with improved root hydraulics
Authors	FJ Canales <sup>1</sup> , N Rispaíl <sup>1</sup> , O García-Tejera <sup>2</sup> , E Prats <sup>1</sup> <sup>1</sup> CSIC-Institute for Sustainable Agriculture. Alameda del Obispo s/n, s/n, 14004, Cordoba, SPAIN <sup>2</sup> IRTA-Institute of Agrifood Research and Technology. Torre Marimon, s/n, 08140 , Caldes de Montbui , SPAIN
Keywords	Drought, Oat, Hydraulic conductivity, Root, Abscisic acid

**Abstract**

It is widely recognised that an early reduction of transpiration under drought stress conditions “save water” for the plant. Thus, early and tight closure of stomata under drought conditions has been traditionally accepted as a drought resistance mechanism. However, stomata closure uncouple the electron flux from CO<sub>2</sub> reduction promoting oxidative stress and decreasing carbon fixation and plant growth. As an alternative to cope with drought, some plants species follow a “water spending” model according to which, plants exhibit higher stomata control showing lower sensitivity to evaporative demand and soil moisture, and allowing larger fluctuations in leaf potential maintaining photosynthesis and avoiding oxidative stress. Yet, they may exhibit a higher risk of xylem embolism. In this work, we studied the drought tolerance strategy of a drought resistance and a drought susceptible oat genotype over an imposed water deficit time course of 20 days. We observed that the susceptible genotype increased dramatically the abscisic acid, at a relative soil water content as high as 60% resulting in a reduction of stomatal conductance. Despite this, leaf water potential decreased concomitantly due to a decrease in root hydraulic conductivity (conductivity per root length) in this genotype that showed early drought symptoms. By contrast, the resistance genotype, showed a mild and slow increase in abscisic acid that allowed maintaining transpiration longer. This was associated with an increase in root hydraulic conductivity together with an increase in total root length and in the length of the thinnest roots. This strategy allowed the resistance genotype to maintain higher water potential reducing drought symptoms and promoting growth under water deficit conditions. This research was financially supported by the Project AGL2016-78965-R (Spanish Ministry of Economy and Competitiveness) and the European Regional Development Funds (ERDF).

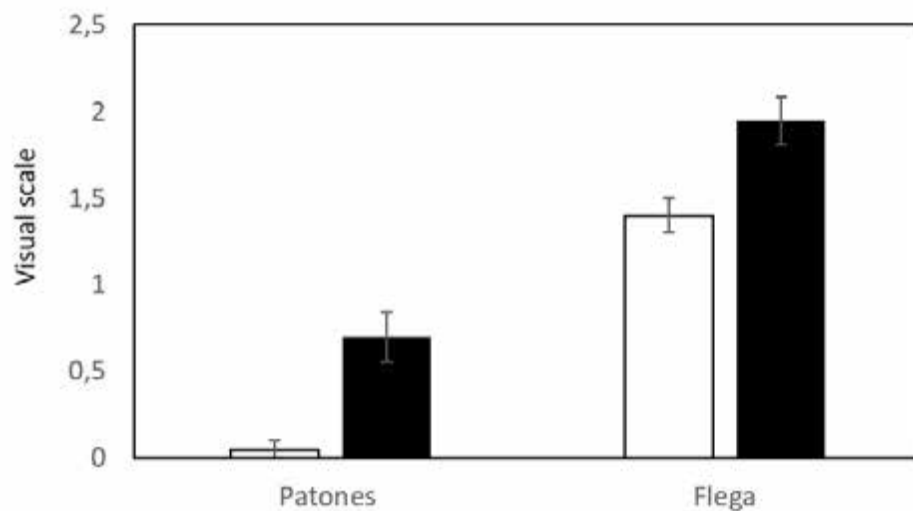


**Legend** Effect of drought in root hydraulic conductivity in Flega (susceptible) and Patones (resistant) oat genotypes. White bar= control treatment; solid bars= drought treatment . Data are mean of 5 replicates + standard error.

Title	A novel role for OPDA (12-oxo Phytodienoic Acid) for coping with drought in oat by modulating root growth
Authors	F Canales <sup>1</sup> , V Arbona <sup>2</sup> , A Gómez-Cadenas <sup>2</sup> , LAJ Mur <sup>3</sup> , E Prats <sup>1</sup> <sup>1</sup> CSIC-Institute for Sustainable Agriculture. Alameda del Obispo s/n, s/n, 14004, Cordoba, SPAIN <sup>2</sup> Ecofisiologia i Biotecnologia Dpt. Ciències Agràries i del Medi Natural. Universitat Jaume I. Campus Riu Sec., s/n, 12071, Castelló de la Plana, SPAIN <sup>3</sup> Institute of Biological, Environmental and Rural Sciences, University of Aberystwyth, UK.. Penglais Hill, s/n, SY23 FL, Aberystwyth, UNITED KINGDOM
Keywords	Drought, Oat, Jasmonates, 12-oxo Phytodienoic Acid

**Abstract**

Jasmonates (JA), include a diverse group of jasmonic acid derivatives, such as Ile-jasmonic or dihydrojasmonic acid and its biosynthetic intermediate, 12-oxo phytodienoic acid (OPDA). Although recent data indicate an involvement of JA in drought tolerance responses, there is still controversy around this. We investigated dynamic changes in JA profile of oat plants, including roots and leaves of two well-characterized genotypes for drought resistance, over a 20 day time-course. We observed clear differences regarding the pattern of the hormones during the drought time course between leaves and roots. Jasmonic acid and Ile-jasmonic followed a similar trend. However, this was very different from the observed pattern for OPDA. Whereas no differences were observed in leaves between the tolerant and susceptible genotype, a completely different behavior was observed regarding roots. The tolerant genotype showed a dramatic reduction of this metabolite from the earliest sampling times while the susceptible genotype only showed a slight reduction in earlier time-points and even increases of OPDA in intermediate sampling-times. Exogenous application of OPDA through injection in the neck of the plants increased drought symptoms in the tolerant genotype, reduced the relative water content of the leaves and reduced the length of the roots. The reduction of the root length was coupled with an overall increase in the average diameter of the roots. This suggests that the susceptible genotype reduced root OPDA as a way to promote the growth of new roots, favoring the proportion of small diameter roots, which are crucial players for water up-take. This research was financially supported by the Project AGL2016-78965-R (Spanish Ministry of Economy and Competitiveness) and the European Regional Development Funds (ERDF).

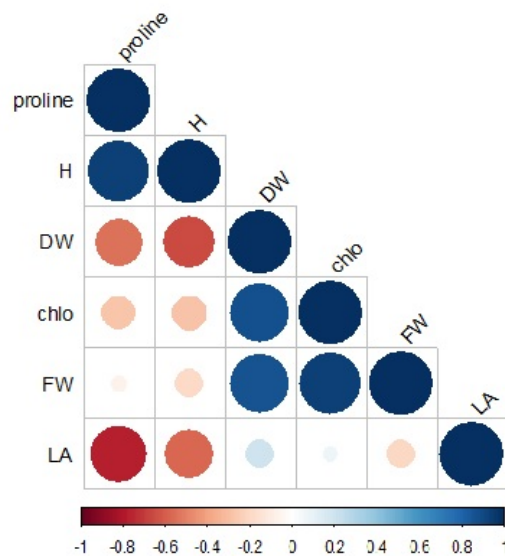


**Legend** Effect of OPDA on drought symptoms in Flega (susceptible) and Patones (resistant) oat genotypes. Symptoms were measured according to a 0-5 visual scale in which 5 indicate the most severe symptoms. White bar= control treatment; solid bars= OPDA treat

Title	Screening for drought tolerance in durum wheat genotypes in seedling stages
Authors	S. Jallouli <sup>1</sup> , S. Ayadi <sup>1</sup> , Z. Hammami <sup>1</sup> , M. Rabii, Y. Trifa <sup>1</sup> <sup>1</sup> Tunisian National Institute of Agronomy. Charles Nicole Avenue Cité Mahrajène, 43, 1082, Tunis, TUNISIA
Keywords	durum wheat, drought tolerance, screening

**Abstract**

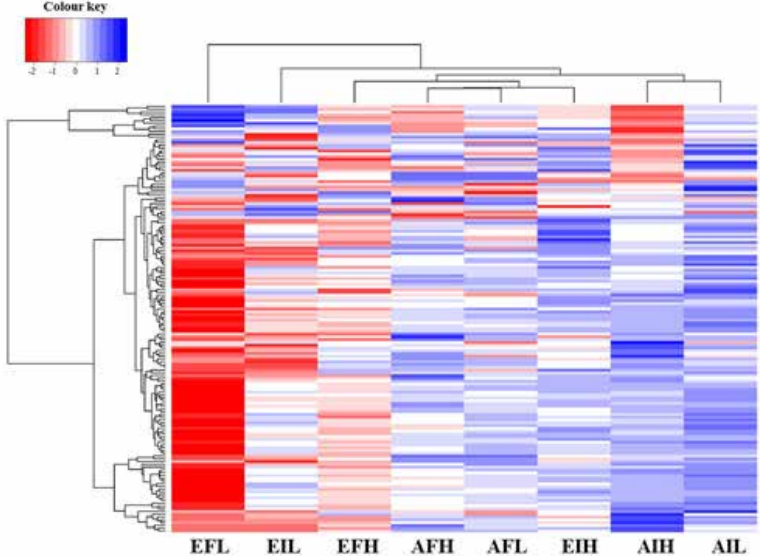
Durum wheat plays a considerable role in ensuring food security in the Mediterranean region. Drought is the abiotic stress that affects the most wheat biomass and grain yield. Drought stress tolerance was evaluated in 5 Tunisian durum wheat improved genotypes (Maali (known as drought tolerant), Khiar, Omrabia, Nasr and Razzek) in seedling stages. The genotypes were grown under controlled conditions with two treatments (control and osmotic stress). The osmotic stress was applied by the addition of polyethylene glycol (PEG) to the hydroponic medium. Considerable differences in the evaluated traits (fresh and dry weight (FW, dryW), hydration rate (H), leaf area (LA), proline content (proline) and chlorophylls content (chlo)) were found among the control and drought-stressed plants. Drought stress generally caused a marked reduction in plant growth. For all genotypes, the dryW in stressed plants increased with the rate of 33% compared to control plants. According to the different measured parameters, on average Maali proved to be the most tolerant to drought than the other genotypes with the lowest dryW reduction rate (3%). The correlation test between all parameters showed a negative correlation ( $R=-0.54$ ) between the dry weight and proline content but a positive correlation ( $R=0.87$ ) between dry weight and total chlorophylls content. As Maali is known as drought tolerant, rapid screening for drought tolerance in seedling stages in hydropony is a reliable and efficient method.




Legend	correlation test for tested parameters
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Title	Acclimation to elevated CO <sub>2</sub> is improved by low Rubisco and carbohydrate content, and enhanced Rubisco transcripts in the G132 barley mutant												
Authors	J. Córdoba <sup>1</sup> , P. Pérez <sup>1</sup> , R. Morcuende <sup>1</sup> , F. Valeros <sup>1</sup> , J.L. Molina-Cano <sup>2</sup> , R. Martínez-Carrasco <sup>1</sup> <sup>1</sup> Institute of Natural Resources and Agrobiology of Salamanca, IRNASA-CSIC, Abiotic Stress. Cordel de Merinas, 40-52, 37008, Salamanca, SPAIN <sup>2</sup> IRTA (Institute for Food and Agricultural Research and Technology), Field Crops. Av. Alcalde Rovira i Roure, 191, 25198, Lérida, SPAIN												
Keywords	Elevated CO <sub>2</sub> , Mutagenesis, Photosynthesis, Gene expression, Rubisco												
Abstract	Variations induced by mutagenesis may identify targets for adapting to rising atmospheric CO <sub>2</sub> concentrations. G132 is a barley ( <i>Hordeum vulgare</i> L.) mutant with strong decreases in photosynthesis, Rubisco and carbohydrate content, but increased Rubisco transcripts. We tested the hypothesis that G132 will record a greater stimulation of photosynthesis and dry mass gain than the wild-type (WT) in response to CO <sub>2</sub> enrichment. A growth chamber experiment compared the mutant G132 and the Graphic WT developed in ambient (390 μmol mol <sup>-1</sup> ) and elevated (1200 μmol mol <sup>-1</sup> ) CO <sub>2</sub> . Photosynthesis, protein and carbohydrate contents, plant dry matter and leaf area were determined. The transcriptome responses to elevated CO <sub>2</sub> were investigated using microarrays and qRT-PCR. CO <sub>2</sub> enrichment increased leaf area in G132 but not in WT, and induced greater dry mass increases in the mutant, attributable to increases in total green area in the former. Growth in elevated CO <sub>2</sub> stimulated photosynthesis more in G132 than in WT, in association with a lack of Rubisco down-regulation and lower carbohydrate levels in G132. Elevated CO <sub>2</sub> induced more changes in gene expression in WT than G132. Clustering of the corresponding transcripts showed that the expression of genes involved in carbohydrate synthesis, in G132, cell wall synthesis and modification, in WT, nitrate reductase, significantly more in G132 than WT, and jasmonate metabolism in G132 was enhanced, while that for stress-related genes was repressed in both genotypes by elevated CO <sub>2</sub> . Rising atmospheric CO <sub>2</sub> decreased the transcript levels for a greater number of transcription factors in WT than in G132. The low Rubisco and carbohydrate content and enhanced Rubisco transcripts recorded in G132 are traits that may improve adaptation to elevated CO <sub>2</sub> . Acknowledgements Funding was received from grants RTA2009-00006-C04-01, CSI148A11-2 and CSI250U13. J. Córdoba had an INIA pre-doctoral research contract. A.L. Verdejo and M.A. Boyero contributed to the experimental work.												
	<table border="1"> <caption>Photosynthesis-CO<sub>2</sub> responses</caption> <thead> <tr> <th>Category</th> <th>G132</th> <th>WT</th> </tr> </thead> <tbody> <tr> <td>Direct</td> <td>~2.3</td> <td>~1.9</td> </tr> <tr> <td>Acclimatory</td> <td>~1.2</td> <td>~0.9</td> </tr> <tr> <td>Net</td> <td>~2.9</td> <td>~1.8</td> </tr> </tbody> </table>	Category	G132	WT	Direct	~2.3	~1.9	Acclimatory	~1.2	~0.9	Net	~2.9	~1.8
Category	G132	WT											
Direct	~2.3	~1.9											
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Legend	CO <sub>2</sub> responses of photosynthesis (A). Direct: Ratio of A at 1200/A at 390 μmol mol <sup>-1</sup> CO <sub>2</sub> , plants grown at ambient CO <sub>2</sub> . Acclimatory: A for plants grown at elevated CO <sub>2</sub> /grown at ambient CO <sub>2</sub> , measured at 1200 μmol mol <sup>-1</sup> CO <sub>2</sub> Net: Direct x Acclimatory												

Title	Genetic analysis of F2 diallel crosses in durum wheat ( <i>Triticum durum</i> Desf.) under semi arid conditions
Authors	A. Hannachi <sup>1</sup> , Z. Fellahi, H. Bouzerzour <sup>1</sup> INRAA. 2, avenue des Frères OUDEK. BP 200 Hassen BADI. El Harrach , BP 200 Hassen BADI. El Harrach , 16200, Alger, ALGERIA
Keywords	wheat, Diallel analysis, Drought, Gene action, Hayman analysis.
Abstract	
<p>The present study was carried out to investigate the genetic system controlling yield and its component traits of 15 hybrids generated by crossing 6 diverse durum wheat varieties in a half diallel fashion. Analysis of F2 data indicated high significant differences among parents and hybrids for all studied traits indicating a wide diversity among parental genotypes. Estimates values of variances components due to dominance (H1) and additive (D) effects of genes in F2 revealed that non-additive genetic effects was more pronounced in the inheritance of CC,HD,NS, NGS and GY. On the other hand, additive type of gene action was evident for plant height (PH) and thousand kernels weight (TKW). Ratio of dominant and recessive alleles <math>[4DH1]0.5 + F / [4DH1]0.5 - F</math> was less than unit only for NS, indicating higher proportions of recessive genes against the dominant genes for this trait. The distribution of positive and negative genes in parents, estimated by the ratio <math>H2/4H1</math>, deviated from 0.25 for the traits viz., PH, DH, NS, TKW and GY. The heritability in narrow sense was higher for DH, PH, TKW, moderate for NGS and CC, lower for NS and GY. Wr-Vr graphical analysis indicated the involvement of partial dominance genes action for CC, PH, DH, NS, NGS and TKW while GY exhibited an over-dominance gene action. For Chlorophyll content, parents Mexicali, Waha and Ofanto possessed an excess of dominant genes, while Zenati Bouteille/Flamingo, Gaviota durum and Guemgoum Rkhem, possessed more recessives genes. For PH, Gaviota durum possessed more dominant genes contrarily Waha, Mexicali75 and Zenati Bouteille contained maximum recessive genes. For DH, Ofanto contained alleles that are more dominant while Guemgoum Rkhem contained more recessive. Altogether, the obtained results indicated that most of traits were controlled by both additive and non-additive gene action. The preponderance of non-additive gene action suggested delaying selection for the targeted traits to later generation.</p>	
	
Legend	Experimental dispositif

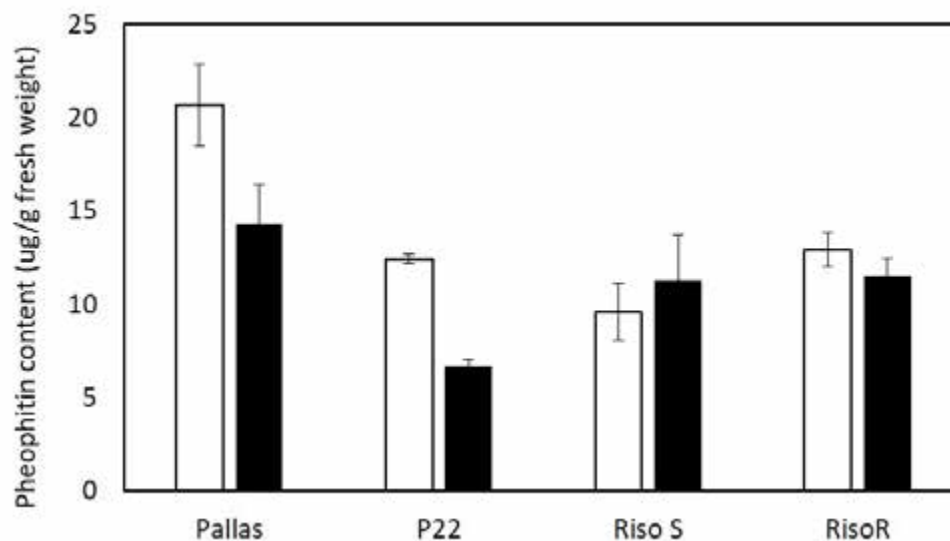
Title	Characterization of the transcript and metabolite responses of durum wheat to elevated CO <sub>2</sub> and high temperature at two nitrogen supplies using a qRT-PCR platform for central metabolism-related genes
Authors	<p>R. Vicente<sup>1,2</sup>, P. Pérez<sup>1</sup>, R. Martínez-Carrasco<sup>1</sup>, B. Usadel<sup>3</sup>, S. Kostadinova<sup>4</sup>, E. Marcos-Barbero<sup>1</sup>, R. Morcuende<sup>1</sup></p> <p><sup>1</sup>Institute of Natural Resources and Agrobiology of Salamanca, IRNASA-CSIC, Abiotic Stress. Cordel de Merinas, 40-52, 37008, Salamanca, SPAIN</p> <p><sup>2</sup>Max Planck Institute of Molecular Plant Physiology. Am Mühlenberg, 1, 14476, Potsdam-Golm, GERMANY</p> <p><sup>3</sup>RWTH Aachen University, Institute for Biology 1. Worringer Weg, 3, 52074, Aachen, GERMANY</p> <p><sup>4</sup>Agricultural University, Agrochemistry and Soil Science. Mendeleev, 12, 4004, Plovdiv, BULGARIA</p>
Keywords	Elevated CO <sub>2</sub> , High temperature, Nitrogen, Central metabolism, Gene expression
Abstract	
<p>Global climate is being significantly altered due to anthropogenic activities. As a consequence the concentration of CO<sub>2</sub> in the atmosphere is increasing and the earth's mean surface temperature is also rising. Hence, global climate change could substantially undermine future global security because of its potential impact on agricultural crop productivity. Durum wheat accounts for more than 50% of total wheat production area in the Mediterranean, one of the most vulnerable to climate change, and it is important understanding the mechanisms of crop responses to future environmental conditions. To achieve this goal, we developed a qRT-PCR platform for the expression analysis of more than a hundred C and N metabolism genes in durum wheat, based on available bread wheat genes and the identification of orthologs of known genes in other plant species. Additionally, we investigated the effect of elevated CO<sub>2</sub> and temperature on primary metabolism of durum wheat grown in field chambers at two levels of N supply by combining transcript profile analysis, using the qRT-PCR platform, with biochemical and physiological parameters in flag leaves at anthesis. Long-term exposure to elevated CO<sub>2</sub> led to a decline of photosynthetic capacity and nitrogen compounds, particularly Rubisco, associated with a downregulation of both N metabolism and photosynthetic related genes. These effects were significantly more pronounced in plants grown at low N supply. High temperatures triggered a similar pattern of changes to those described for elevated CO<sub>2</sub>, although photosynthesis was improved by a higher stomatal conductance. Thus, the extent to which C and N assimilation can be reduced depends upon N availability. This PCR platform can also be used to investigate wheat responses to other abiotic stresses. Acknowledgments Funding was received from grants AGL2009-11987, AGL2013-41363-R (ERDF). R. Vicente and E. Marcos-Barbero had an FPI and JCyL fellowship, respectively. M.A. Boyero and A.L. Verdejo for technical assistance.</p>	
	
Legend	Hierarchically clustered heat map of parameters at ambient or elevated (A 370; E 700 ppm) [CO <sub>2</sub> ], ambient or 4°C higher (I; F) temperature, and low or high (L; H) N supply in flag leaves. Data represent log <sub>2</sub> transformed fold changes relative to AIH.

Title	Resistance to leaf rust in a core collection of ancient Spanish tetraploid wheats
Authors	F Martínez-Moreno <sup>1</sup> , M Ruiz <sup>2</sup> , MI Blandón <sup>1</sup> , P Giraldo <sup>3</sup> <sup>1</sup> Universidad de Sevilla, Dpto. Ciencias Agroforestales. Ctra. Utrera, km 1, 41013, Sevilla, SPAIN <sup>2</sup> Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Centro Nacional de Recursos Fitogenéticos. Autovía de Aragón, km 36, 28800, Alcalá de Henares, SPAIN <sup>3</sup> Universidad Politécnica de Madrid, Dpto. Biotecnología y Biología Vegetal. Ciudad Universitaria, s/n, 28040, Madrid, SPAIN
Keywords	durum wheat, leaf rust, landraces
Abstract	<p>Leaf rust (caused by the fungus <i>Puccinia triticina</i>) is an important foliar wheat disease worldwide and in Spain. In this work a core collection of 91 genotypes of ancient Spanish tetraploid wheat (51 durum, 31 rivet and 9 emmer) from the CRF (Plant Genetic Resources Center) were inoculated with two durum wheat isolates: Conil Don Jaime and Jerez Don José. Four primary leaves per genotype were inoculated at about 14 days after sowing, performed in a greenhouse with trays filled and peat moss soil and sand. Durum cultivar Don Rafael was included in the tests as susceptible check. For each isolate 24 mg of spores were mixed with 1g of talcum powder and the mixture was blown over the plants. Then plants were incubated in a compartment at 100% humidity, 17-20°C, and darkness during 15 hours. At 12 days after inoculation, infection type (IT) was assessed according to the McNeal scale (0-9). Susceptible reaction was frequent. Only 16 genotypes (17.6%) were resistant to isolate Conil Don Jaime and 14 genotypes (15.4%) to isolate Jerez Don José. Both isolates displayed a similar virulence when tested on the collection. In durum wheats, 13.7% and 11.7% of genotypes were resistant to the two isolates, respectively, whereas 19.4 and 16.1% were in rivet wheats and 33% in emmer wheats. Despite the high susceptibility, there are resistant genotypes that might be used in breeding programs in durum wheat (Morisco de Tenerife, Tremén duro), rivet wheat (Gigante velloso de Najera, Blanco de Vegadeo), and emmer wheat (Poveda).</p>
	
Legend	Figure 1. Different reactions to leaf rust in the genotypes of the tetraploid core collection. Top leaf shows the reaction (infection type) of susceptible check Don Rafael (IT 9). The other two leaves show a resistant reaction, IT 4 and IT 1, respect

Title	New players in the cost of resistance: chlorophyll degradation pathway and photosynthetic dysfunctions in mlo resistant barleys
Authors	G Montilla-Bascón <sup>1</sup> , M Roca <sup>2</sup> , LAJ Mur <sup>3</sup> , E Prats <sup>1</sup> <sup>1</sup> CSIC-Institute for Sustainable Agriculture. Alameda del Obispo s/n, s/n, 14004, Cordoba, SPAIN <sup>2</sup> Food Phytochemistry Department, Instituto de la Grasa, Consejo Superior de Investigaciones Científicas (CSIC), . University Campus Pablo de Olavide, , Building 46, 41013, Sevilla, SPAIN <sup>3</sup> Institute of Biological, Environmental and Rural Sciences, University of Aberystwyth, UK. Penglais Hill, s/n, SY23 FL, Aberystwyth, UNITED KINGDOM
Keywords	Resistance cost, mlo, Powdery mildew, barley

#### Abstract

*Blumeria graminis* DC (Speer) ff. spp., causes cereal powdery mildew constraining cereal production in temperate regions. Barley genotypes carrying the *mlo* gene display highly effective papilla-based penetration resistance to powdery mildew that has proved durable for over 30 years. Penetration resistance through papilla, localized cell wall appositions at attack sites, is a durable resistance mechanism that prevents powdery mildew cell penetration and provide a race non-specific broad-spectrum resistance. However, the *mlo* barleys shows adverse pleiotropic effects such as large necrotic/chlorotic flecks on leaves, accelerated leaf senescence and reduced grain yield. These adverse effects are particularly dramatic under stress conditions and for this reason, *mlo* cannot be used in winter barleys. Despite its importance for crop production, the mechanism(s) leading to these pleiotropic effects are still not understood nor are its molecular and cellular bases. In previous work, we observed that the damages were associated with particular genetic backgrounds and were linked to stomatal and photosynthetic dysfunctions. In this work we studied the role of xanthophyll cycle metabolites and chlorophyll degradation pathway in two sets of *mlo*-isogenic lines with different genetic background. Data showed a decrease in chlorophyll a and b and in pheophitin in the resistant isolate characterized by necrotic flecking. Overall, xanthophyll metabolites increased following pathogen inoculation in the resistant *mlo* line lacking lesions. Furthermore, anteroxanthin increased in all genotypes following pathogen challenge but with higher increases in the resistant *mlo* genotype lacking lesions. This research was financially supported by the Project AGL2016-78965-R (Spanish Ministry of Economy and Competitiveness) and the European Regional Development Funds (ERDF).

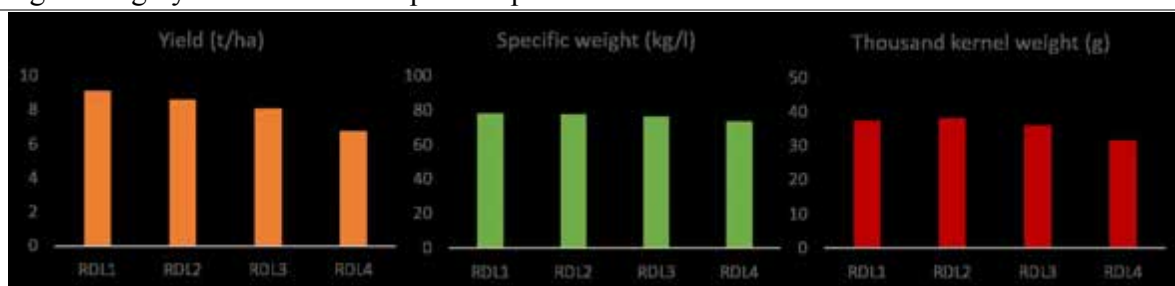


Legend	Pheophitin content in healthy barley isogenic lines of two different backgrounds (Pallas and Riso; white bars) or after challenge with powdery mildew (black bars). Data are mean of 5 replicates + standard error.
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Title	Effect of yellow rust on agronomical traits in bread wheat
Authors	Y. Pallavicini <sup>1</sup> , R Martínez-Peña <sup>1</sup> , B González-Jiménez <sup>1</sup> , M C Díez-Fraile <sup>1</sup> , N Aparicio <sup>1</sup> <sup>1</sup> Instituto Tecnológico Agrario. Carretera Burgos, km118, 47071, Valladolid, SPAIN
Keywords	wheat diseases, disease management strategies, <i>Puccinia striiformis</i> f. sp. tritici, wheat yield, wheat specific weight

#### Abstract

Yellow rust (*Puccinia striiformis* f.sp.tritici), especially the “Warrior race” has been responsible for a dramatic wheat yield loss across Europe during the last five years. The fungus proliferation is favoured by cool and humid conditions. The symptoms of this disease consists of yellow-oranges pustules arranged in stripes running along the leaves and less commonly on leaf sheaths, awns, and spikes; causing shrivelling and reduction of grain yield. Quantifying the damage caused by a disease is important to set priorities in the disease management strategies. The aim of this study was to assess which agronomical traits related with yield are affected by yellow rust. A field trial with 256 bread wheat breeding lines were evaluated in June of 2017 for yellow rust disease. In each plot, the percentage damage of yellow rust was visually estimated. Yield was measured at harvest and then specific weight, thousand kernel weight and plant height was determined. Correlations were performed to detect associations between the agronomical traits and rust damage. Results showed that yield was starkly reduced; there was a difference of almost 30% (2.1 tons) of yield between plots with less than 20% and more than 70% yellow rust damage. Thousand kernel weight was reduced a 16% and specific weight an 8%. The correlations showed that yellow rust affected grain yield ( $r=-0.64$ ,  $p<0.01$ ), specific weight ( $r= -0.45$ ,  $P<0.01$ ) and thousand kernel weight ( $r=-0.4$ ,  $P<0.01$ ). However, plant height was not affected. Our results suggests that the reduction in grain yield in disease conditions was probably due to a reduction in the amount of photoassimilates intended for grain filling, explaining the reductions in specific weight and thousand kernel weight. Further studies should include more yield components and grain quality parameters. Cultivating resistant lines or controlling the disease at early stages is highly recommended to prevent production loss



Legend Figure 1. Mean values of yield, specific weight and thousand kernel weight at different damage levels: RDL1 < 20% damage, RDL2= 20-40 % damage, RDL3= 40-70% damage and RDL4 >70% damage.