

# Barley adaptation. Lessons learned from landraces will help to cope with climate change

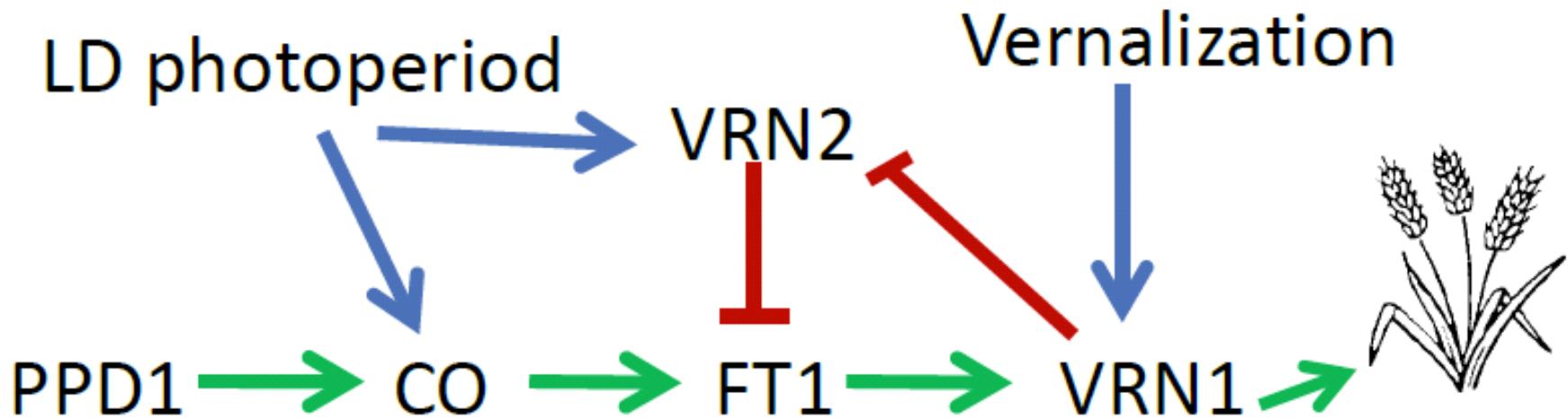
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**After domestication, crop expansion until current situation required adaptation to:**

- **TEMPERATURE, especially cold in temperate climates**
  - **DAYLENGTH**
- 
- **What do we know about the genes driving this adaptation process?**
  - **Have we explored in full the genetic diversity of these genes?**
  - **What are their agronomic effects?**
  - **Can we apply this knowledge to improve plant breeding for climate change scenarios?**



Simplified flowering time pathway in wheat, Nitcher, Distelfeld and Dubcovsky, 2012

# Three genes control variation in requirement for vernalization

**VRNH1**

- 5HL, MADS box transcription factor, *HvBM5A*.
- High similarity to *Arabidopsis* meristem identity genes *APETALA1*, *CAULIFLOWER*, and *FRUITFULL*.
- Dominant alleles reduce vernalization requirement.

**VRNH2**

- 4HL, Putative zinc finger and CCT domain, HvZCCTa,b.
- No clear homologous in *Arabidopsis*.
- Recessive allele reduce vernalization requirement.

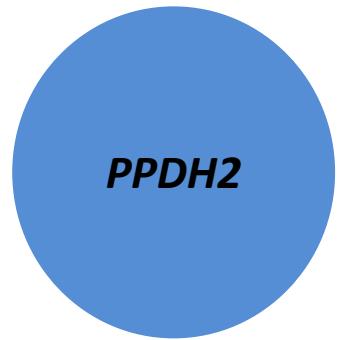
**VRNH3**

- 7HS, RAF kinase inhibitor-like protein, *HvFT1*.
- Homologous to *FLOWERING LOCUS T (FT)* gene of *Arabidopsis*.
- Dominant allele reduce vernalization requirement.

# Two genes control response to photoperiod



- 2HS, Pseudo-response regulator, *HvPRR7*
- Dominant allele, sensitive to long photoperiod, accelerates flowering.

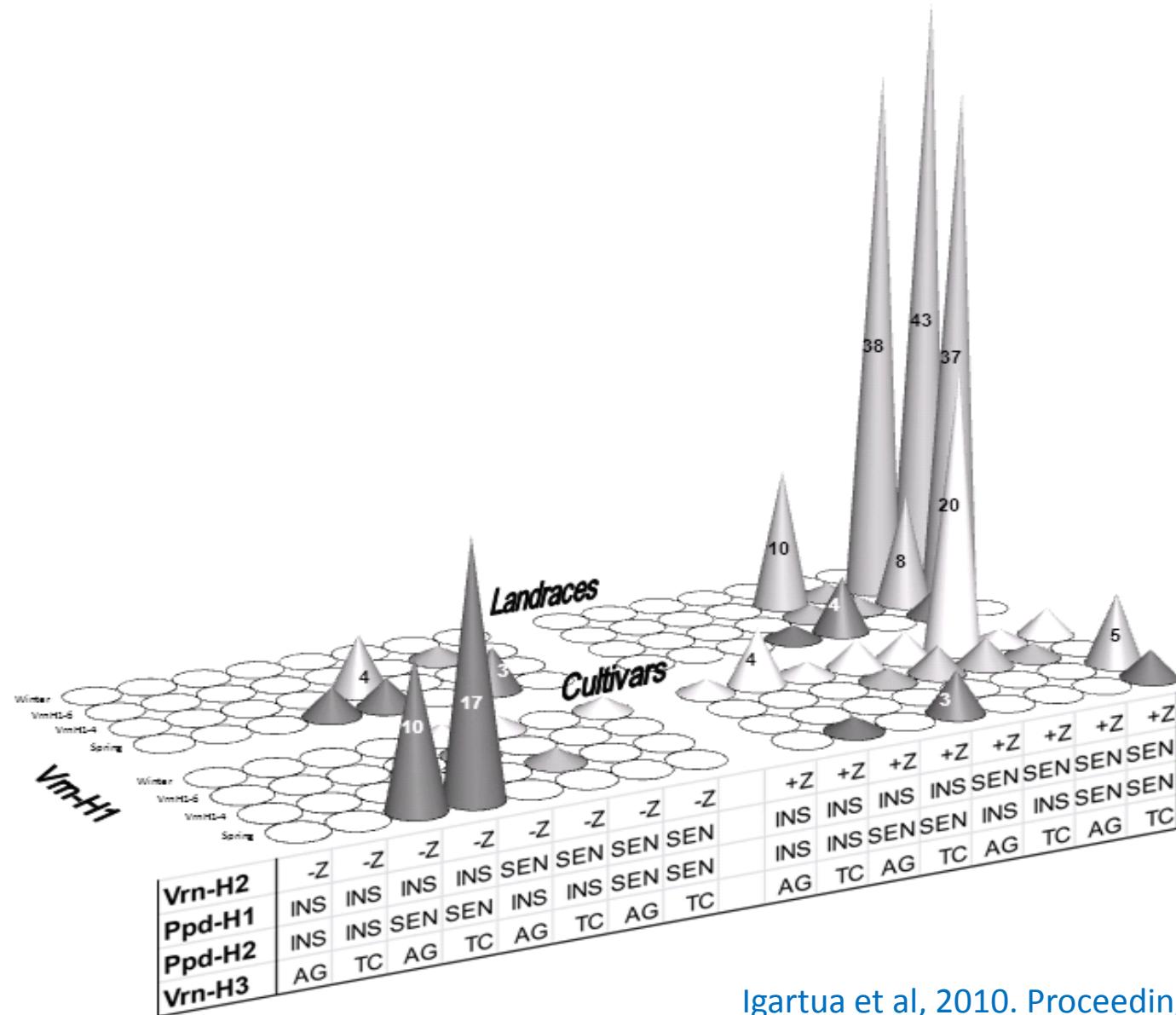


- 1HL, Candidate Phosphatidylethanolamine binding protein, *HvFT3*
- Dominant allele, presence of the gene, affects flowering under short photoperiod.



<http://www.eead.csic.es/EEAD/barley/index.php>

# Frequencies of loci in SBCC and reference European cultivars



Igartua et al, 2010. Proceedings 10th IBGS

# Frequencies of loci in SBCC and reference European cultivars

Locus, allele	6-row landraces	2-row landraces	Winter cultivars	Spring cultivars	Facultative cultivars
PpdH1	148	8	36	2	6
ppdH1	0	3	12	31	0
PpdH2	127	9	13	32	2
ppdH2	21	2	35	1	4
VrnH2	144	3	48	6	0
vrnH2	4	8	0	27	6
vrnH1	0	0	33	0	3
VrnH1-4	50	1	5	0	1
VrnH1-6	93	1	7	0	1
Others	0	0	3	0	1
VrnH1	5	9	0	33	0

Modified from Igartua et al, 2010. Proceedings 10th IBGS

# Population structure in the SBCC. Four populations:



– 2-row



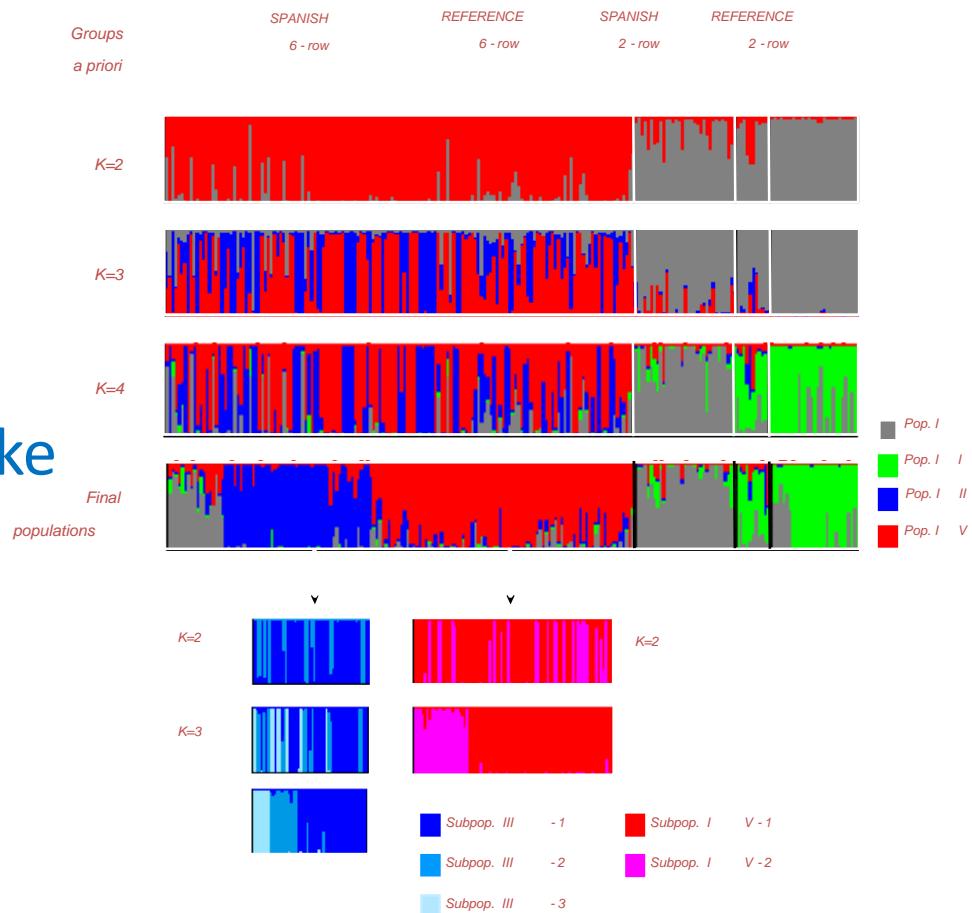
– 6-row European-like



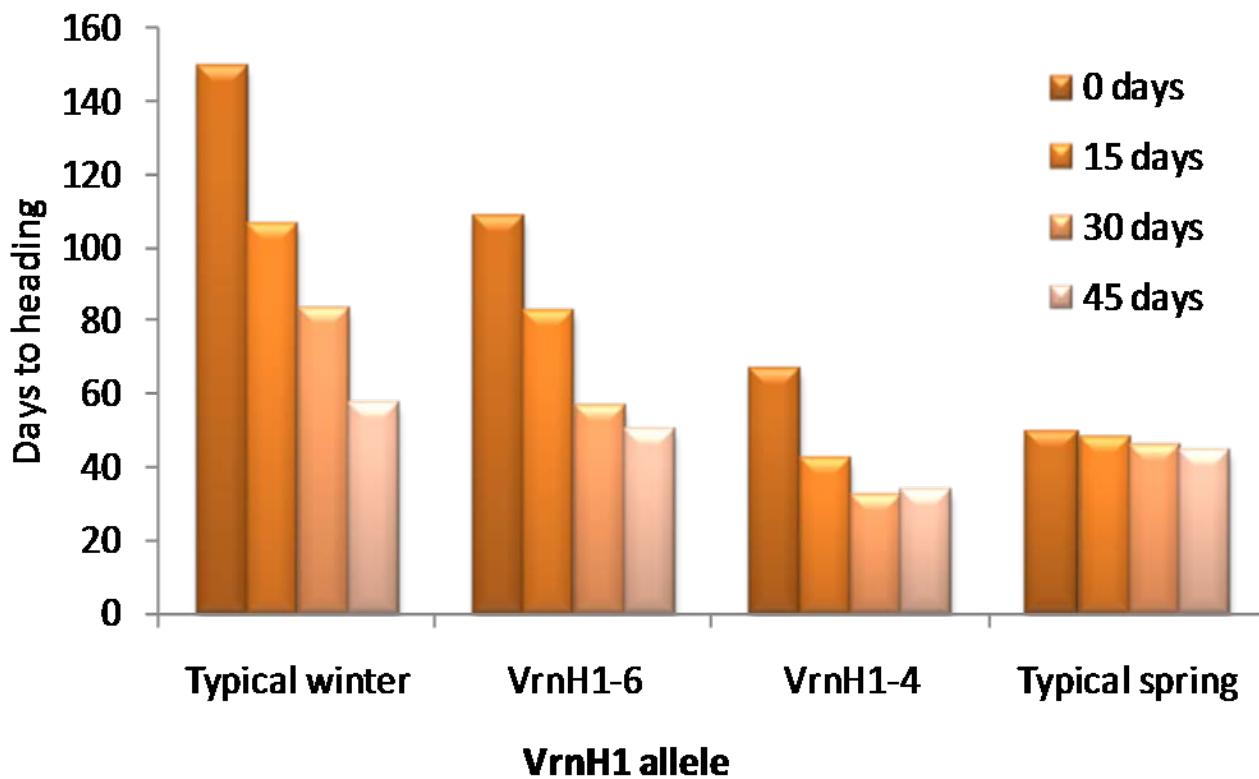
– 6-row Spanish



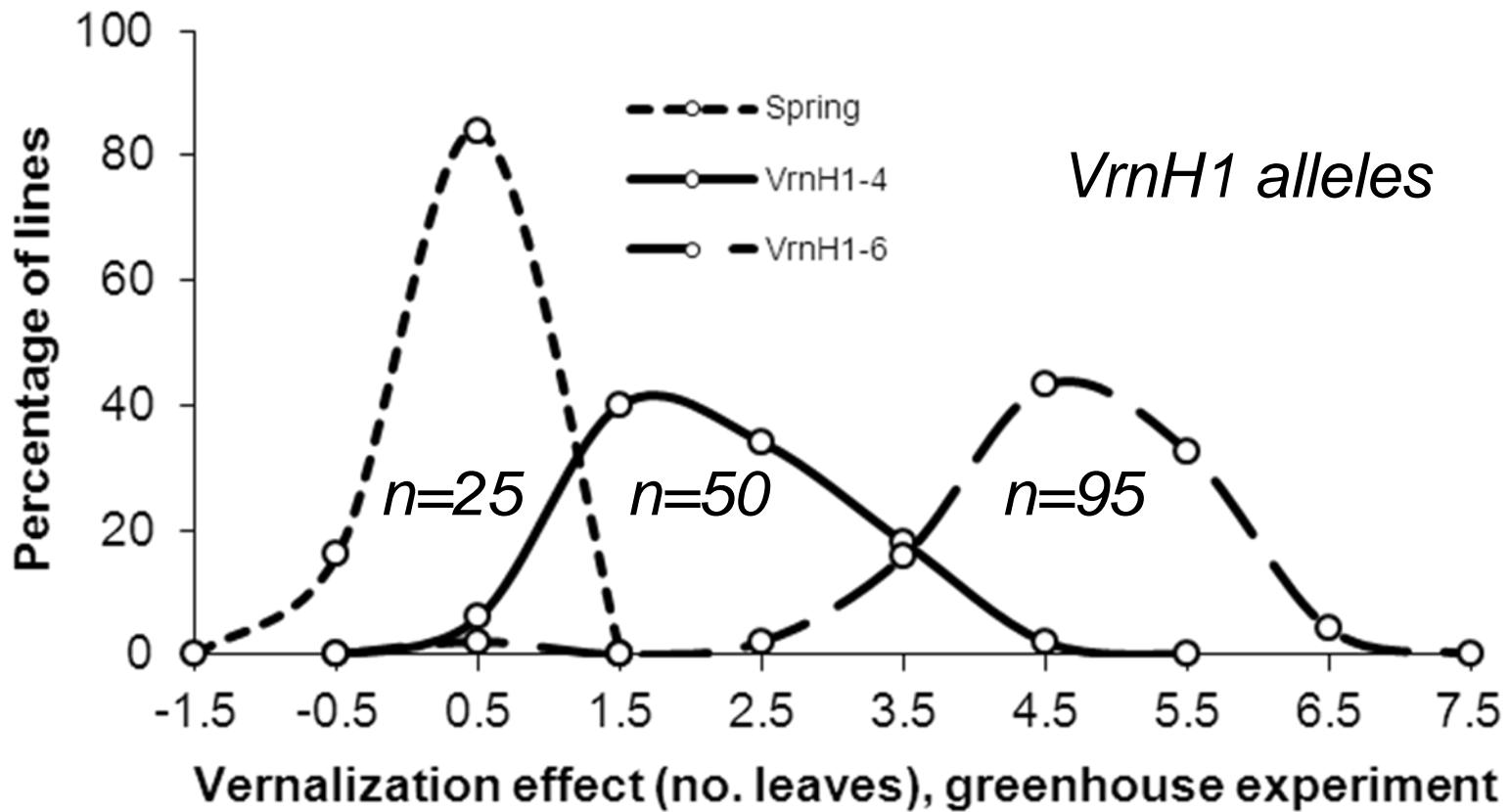
– 6-row Spanish



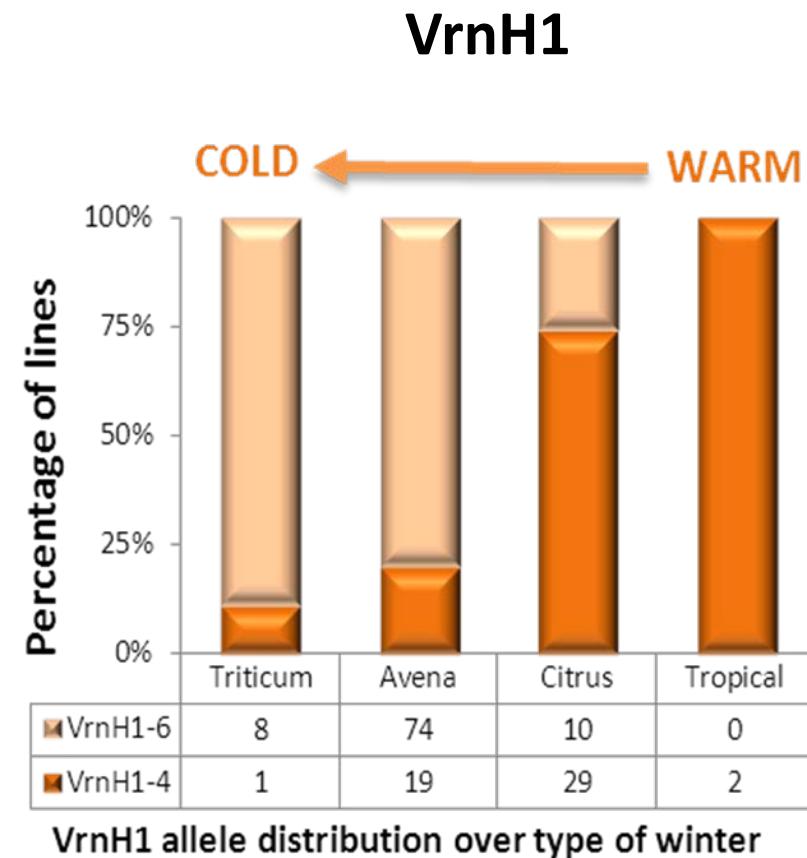
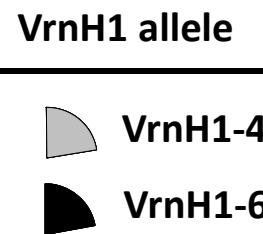
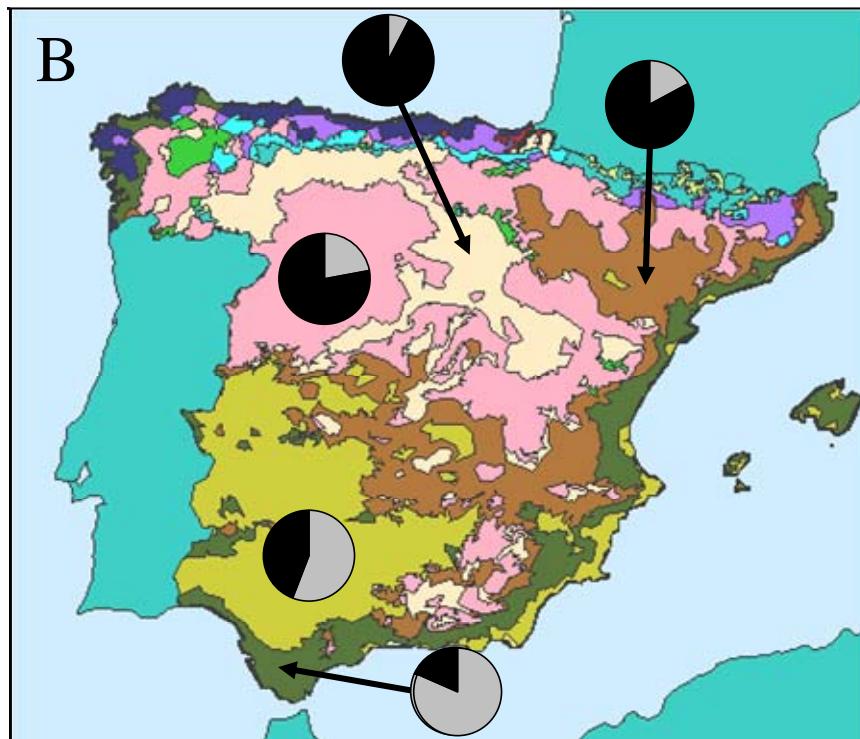
## *Allelic series in VrnH1. Vernalization effect*



## *Allelic series in VrnH1. Vernalization effect*



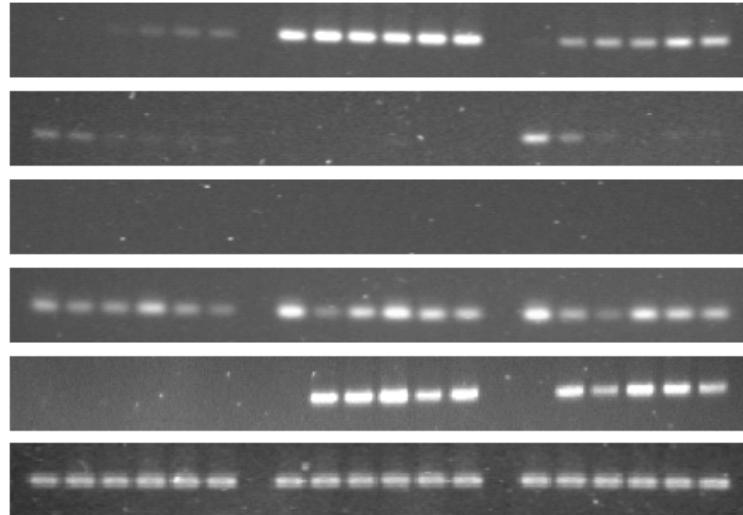
# *VrnH1* distribution associated with geographical features



# *VrnH1*, expression pattern

**Short-day, vernalization**

0 7 14 21 28 35 0 7 14 21 28 35 0 7 14 21 28 35



Plaisant

**vrnH1,  
winter**

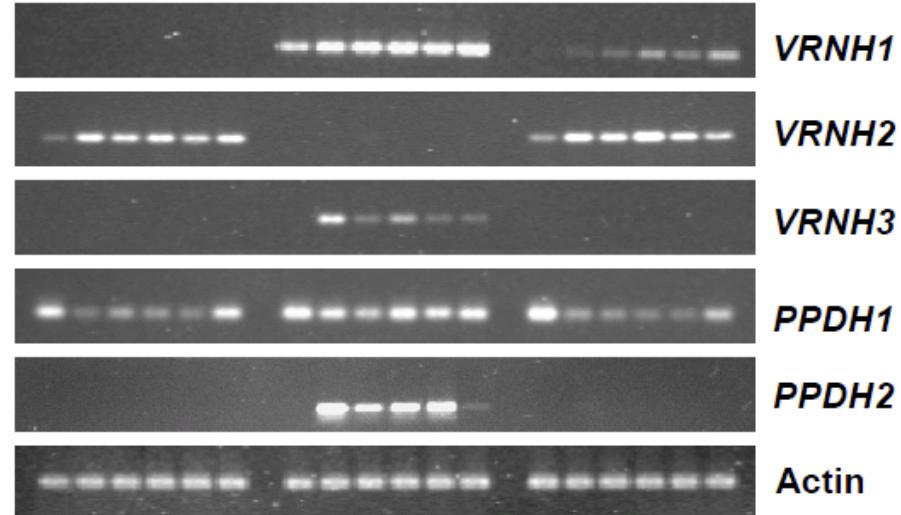
Alexis

**VrnH1,  
spring**    **VrnH1-4,  
intermediate**

SBCC058

**Long-day, unvernalized**

0 7 14 21 28 35 0 7 14 21 28 35 0 7 14 21 28 35



Plaisant

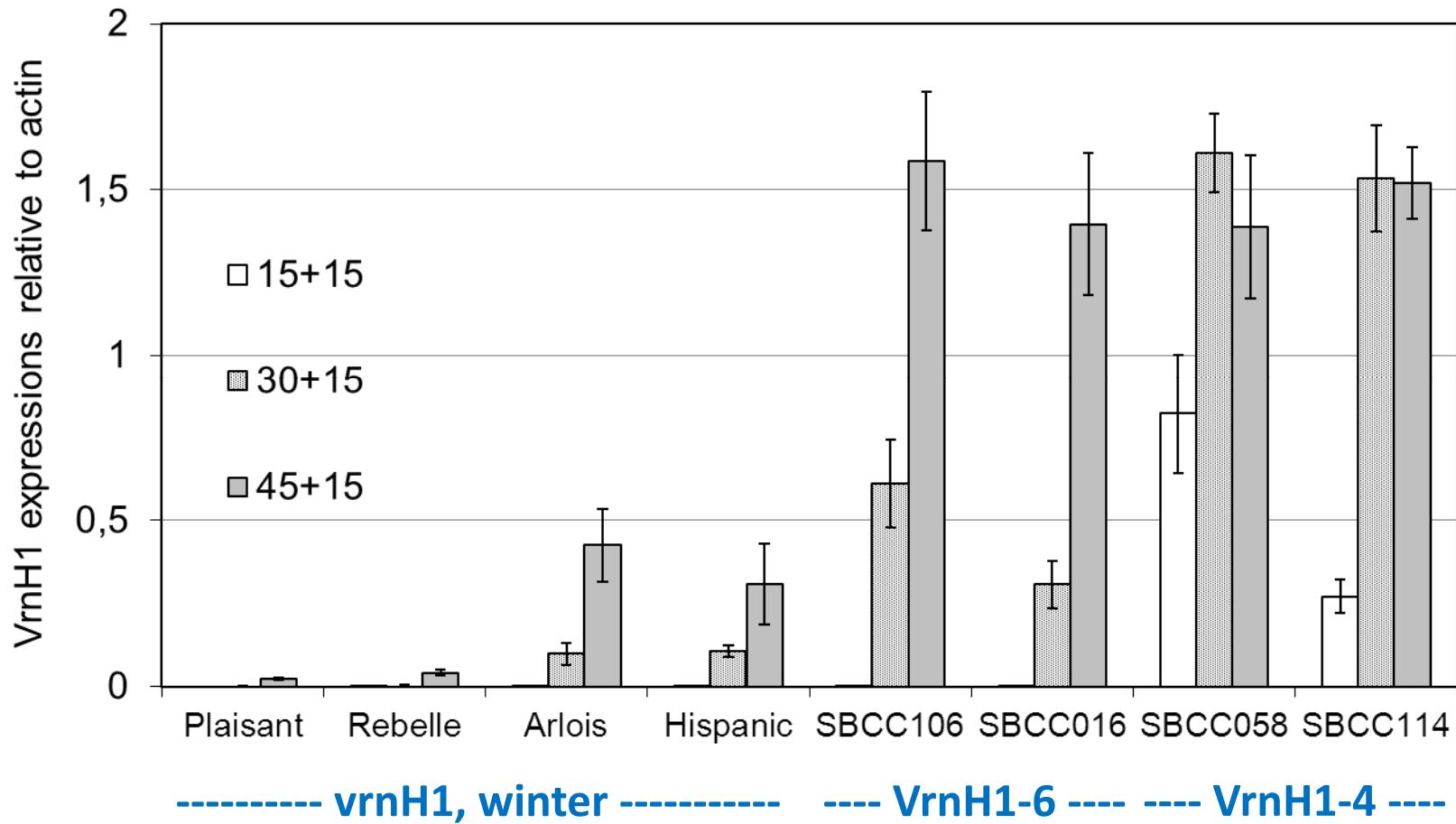
**vrnH1,  
winter**

Alexis

**VrnH1,  
spring**    **VrnH1-4,  
intermediate**

SBCC058

# *VrnH1*, expression pattern

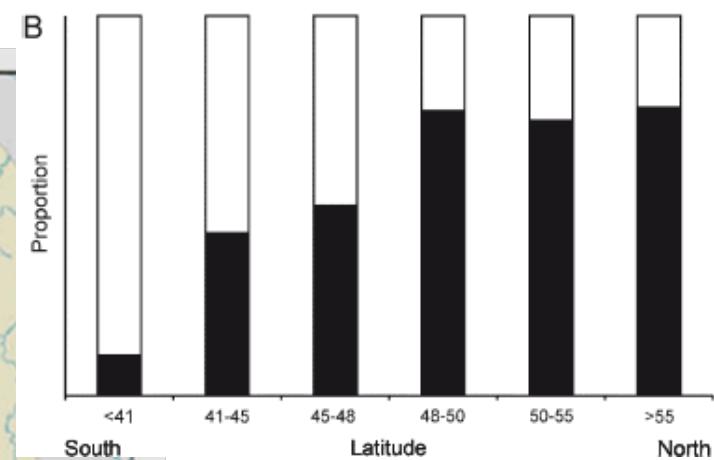
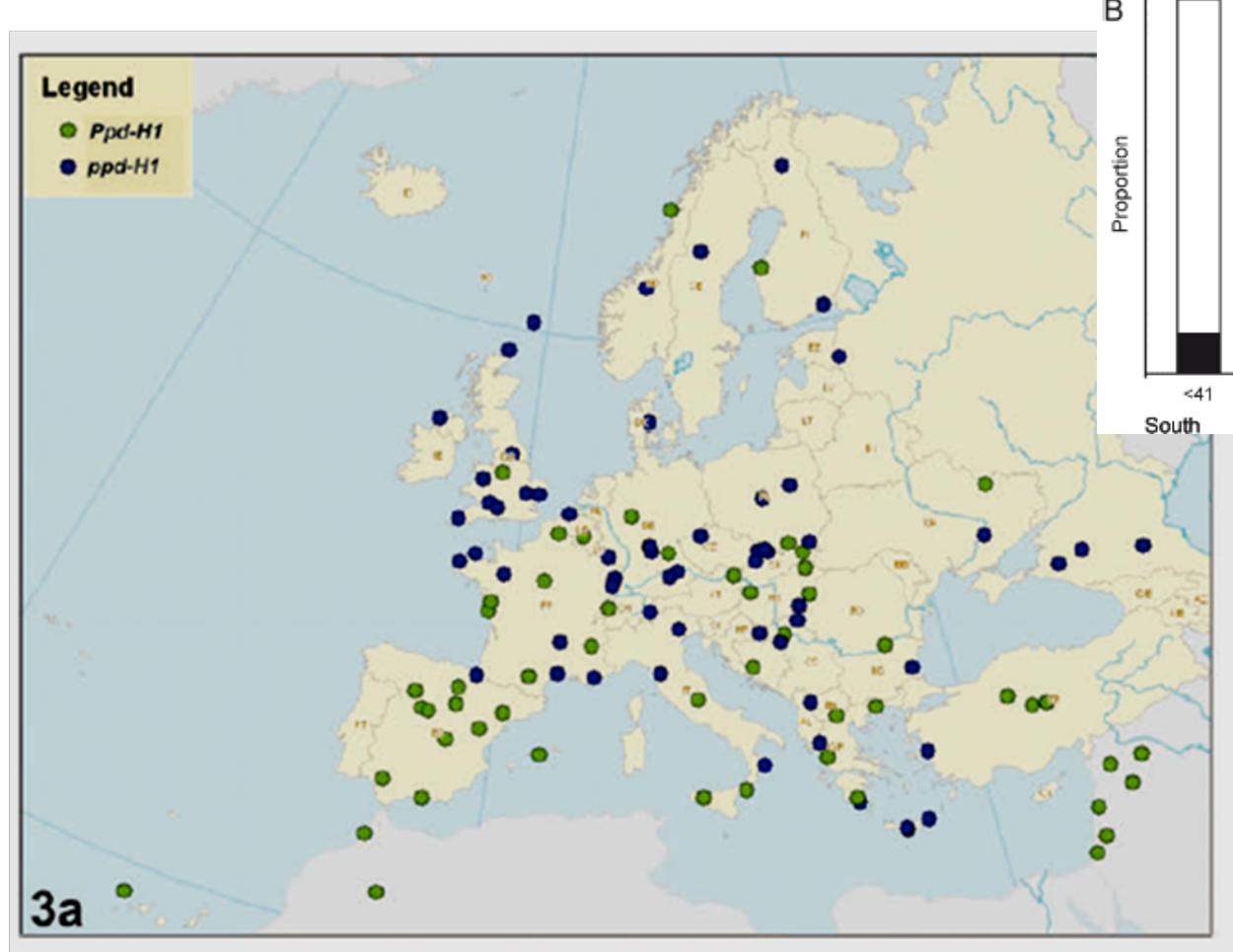


Modified from Casao, Karsai et al. 2011, BMC Plant Biol

## *Frequencies of loci in SBCC and reference European cultivars*

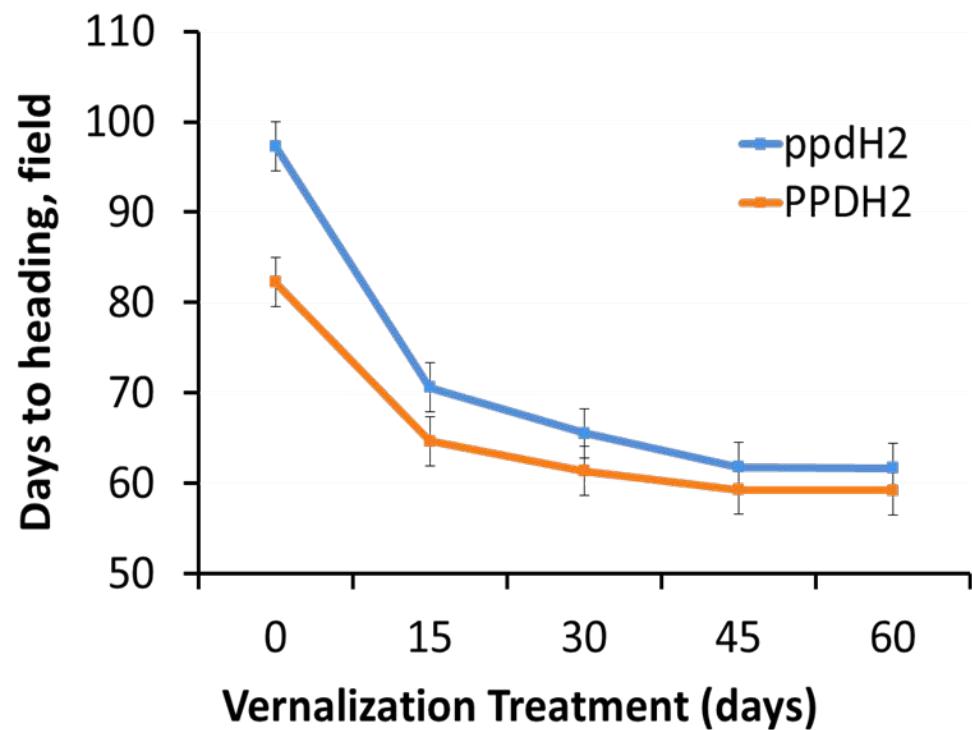
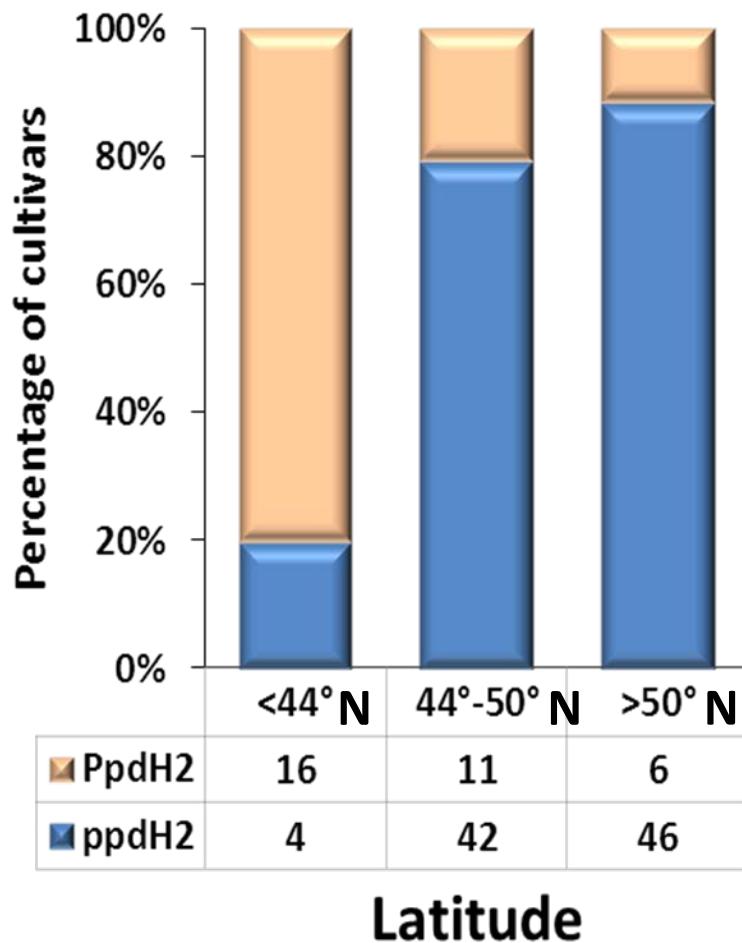
Locus, allele	6-row landraces	2-row landraces	Winter cultivars	Spring cultivars	Facultative cultivars
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ppdH1	0	3	12	31	0
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# *PpdH1* distribution associated with geographical features



# *PpdH2* distribution associated with latitude. Phenotypic effect

## *PpdH2*, winter barleys

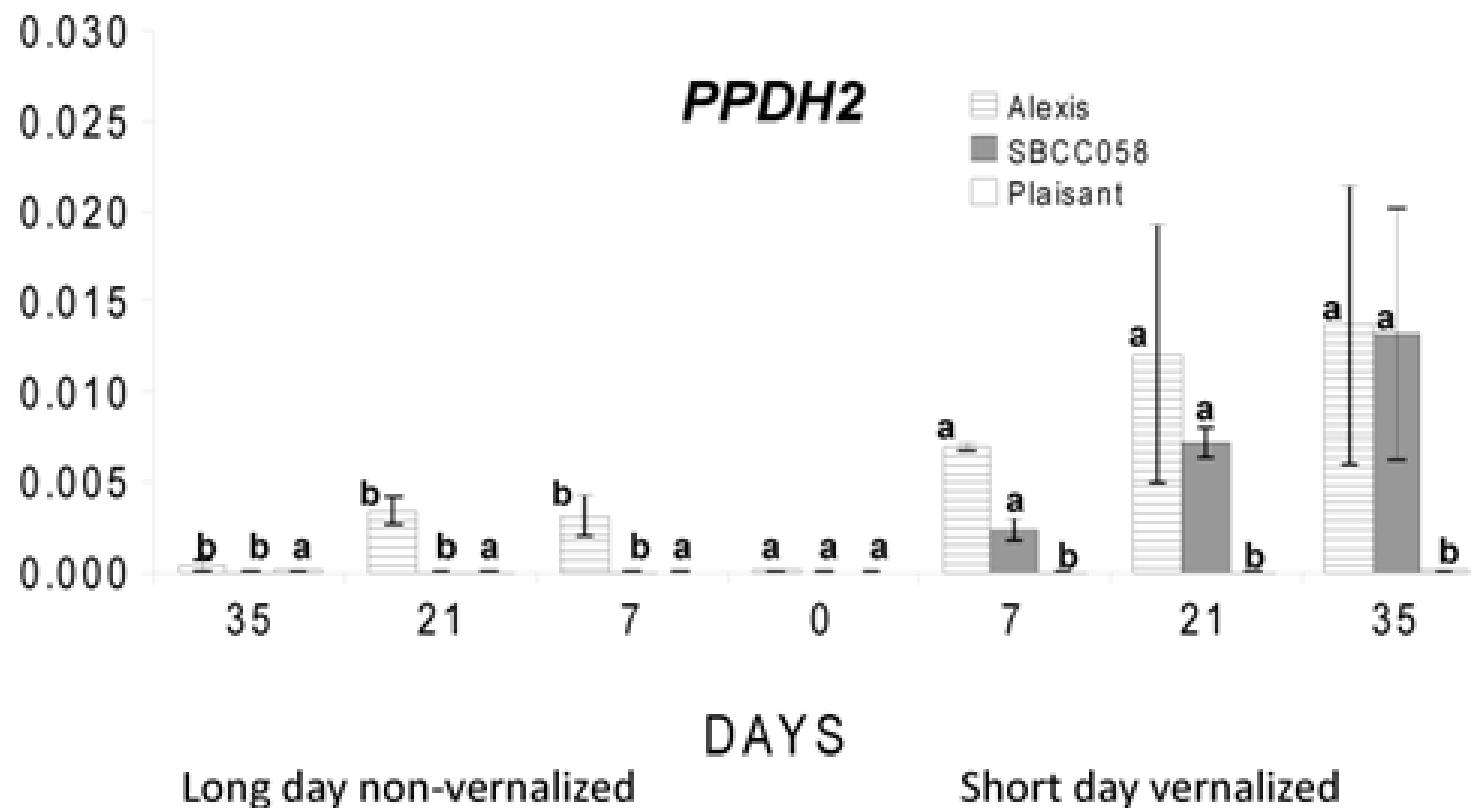


# *PpdH2*, expression pattern in SD and LD

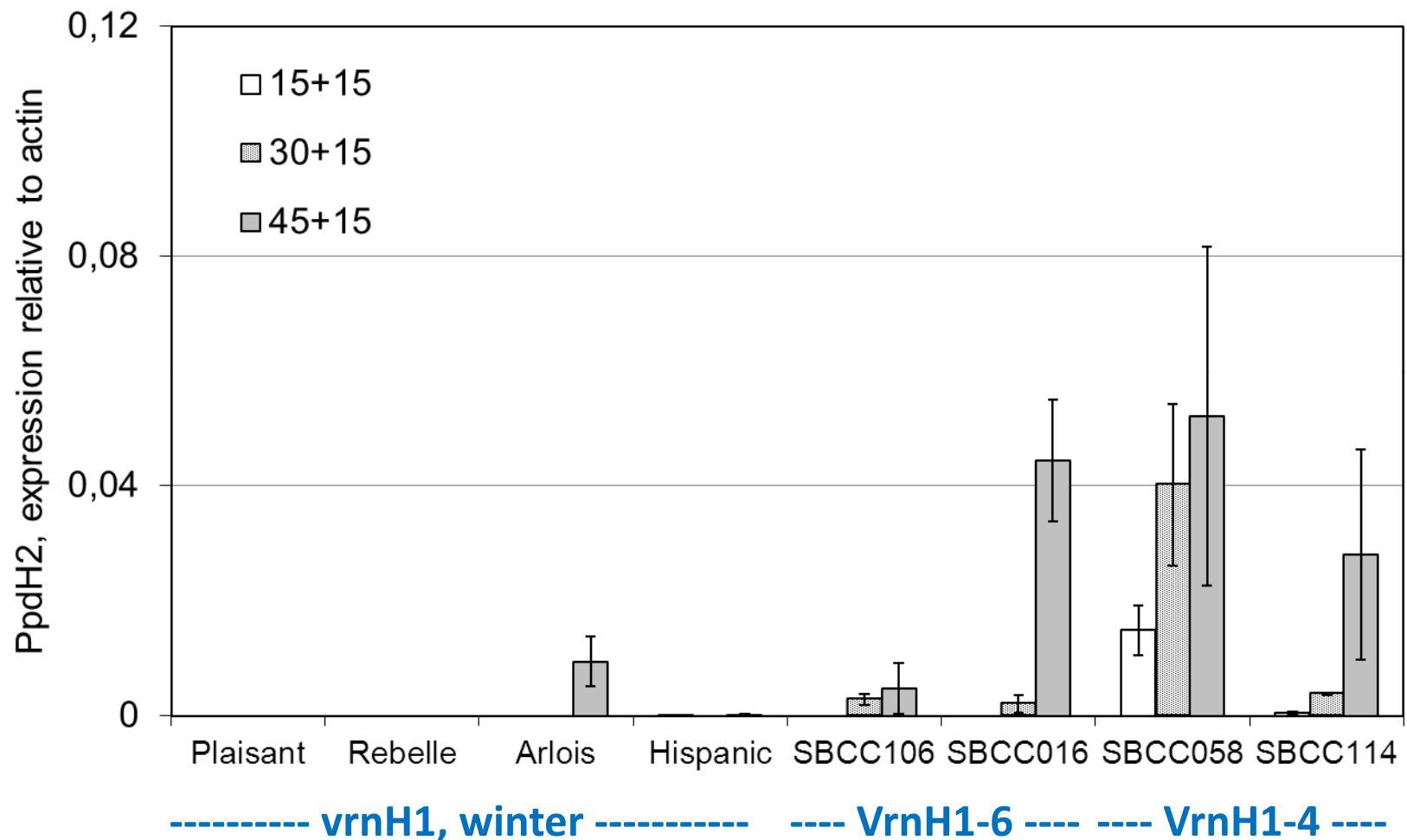
Alexis: VrnH1, spring, PpdH2

SBCC058: VrnH1-4, PpdH2

Plaisant: vrnH1, ppdH2

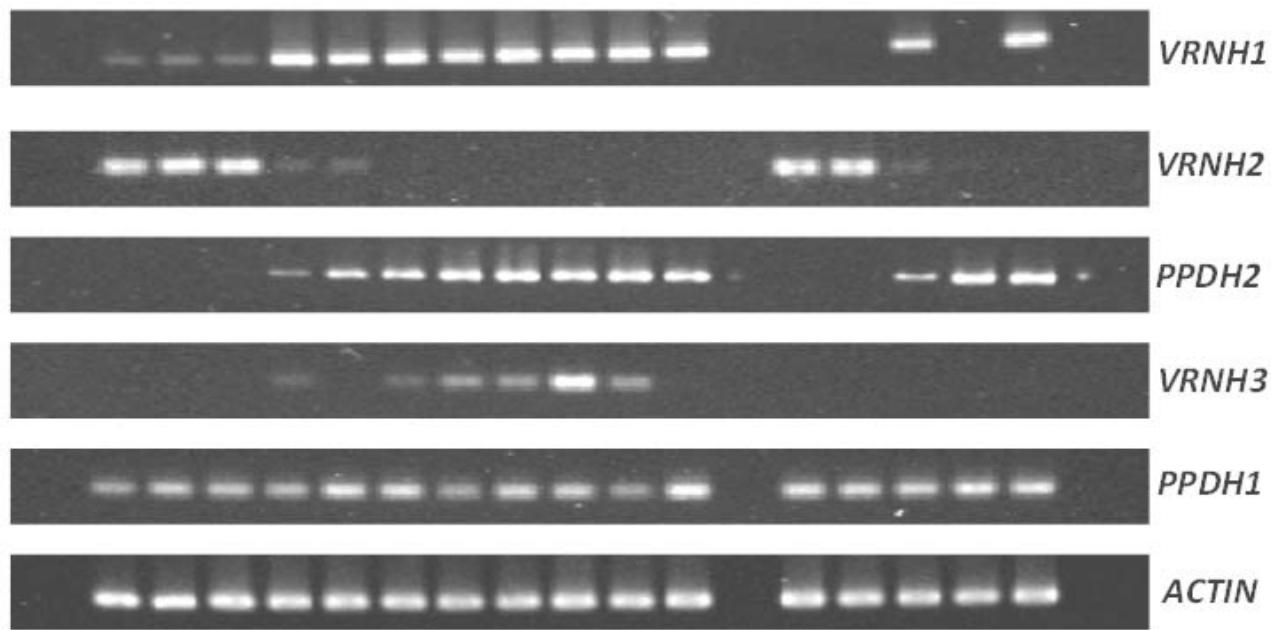


# *PpdH2*, expression pattern across *VrnH1* allelic series



Modified from Casao, Karsai et al. 2011, BMC Plant Biol

# *PpdH2, expression pattern*

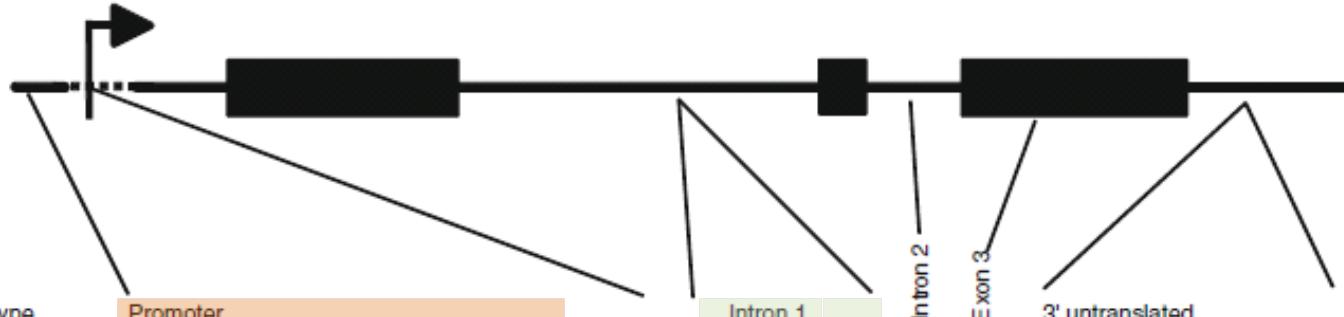


<i>VRNH1</i>	P	P	P	A	A	A	P	A	A	A	A	M	M	B	M	B
<i>VRNH2</i>	P	P	P	P	P	P	A	A	A	A	A	M	M	M	B	B
<i>PPDH2</i> <sup>1</sup>	-	-	-	-	-	-	-	-	-	-	-	M	B	B	B	B
<i>VRNH3</i> <sup>2</sup>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<i>PPDH1</i> <sup>3</sup>	P	P	A	P	A	P	P	P	A	P	A	-	-	-	-	-

Pané DH385 DH426 DH412 DH414 DH364 DH416 DH424 DH427 DH429 Alexis  
Mogador DH1855 DH1829 DH1819 Beka

# *VrnH3*, polymorphisms

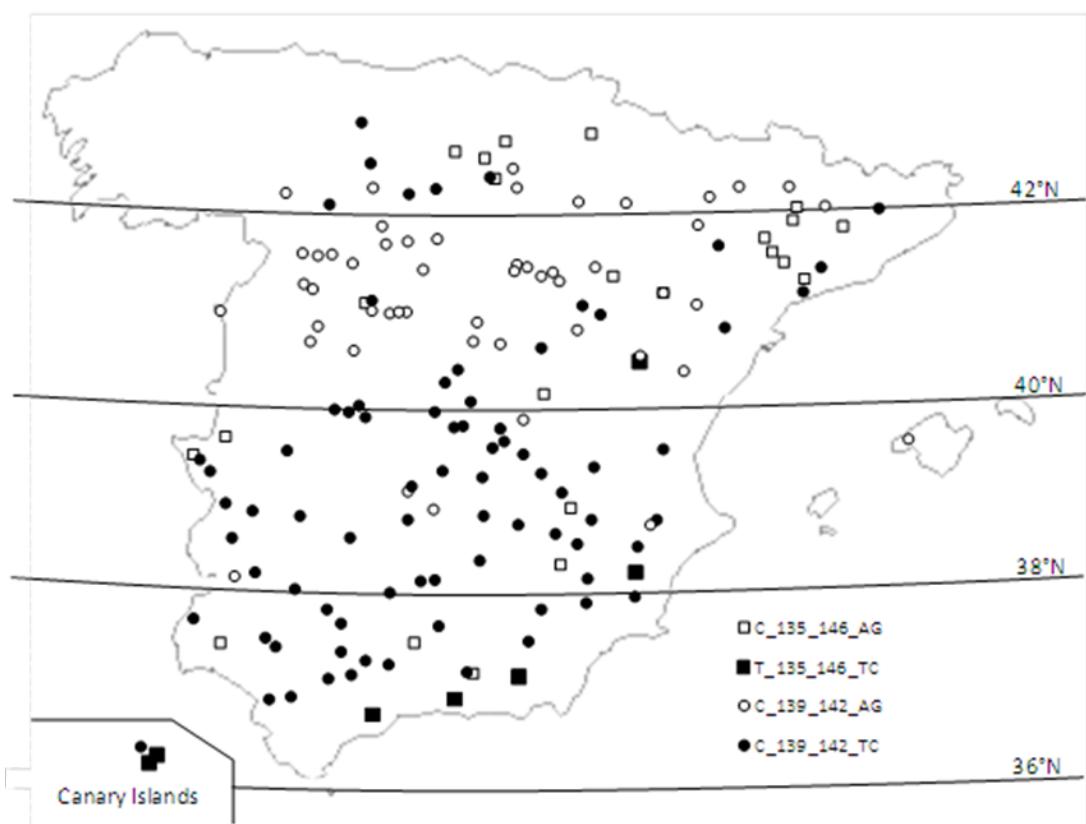
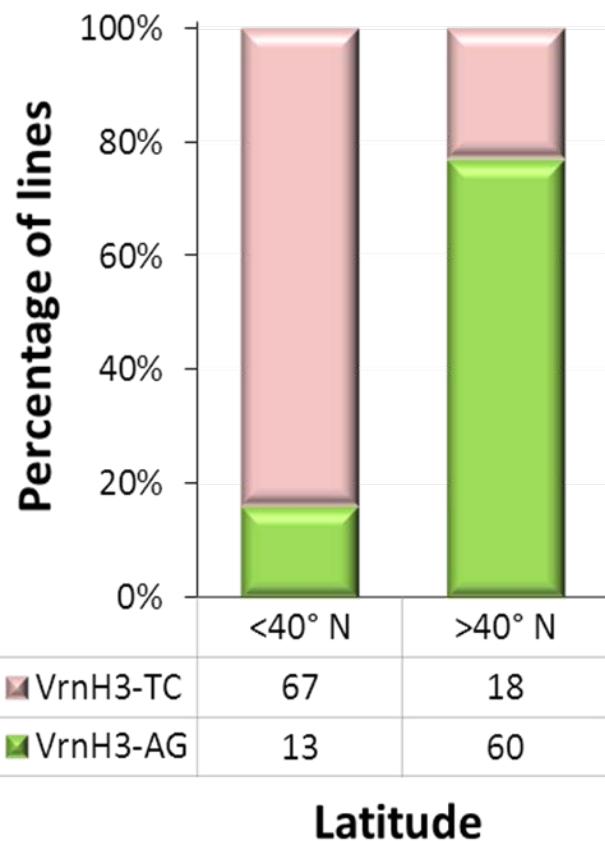
## **VrnH3**



The diagram illustrates the gene structure of *VrnH3*. It features a promoter region at the top left, followed by three exons represented as black rectangles. Between the first and second exons is an intron labeled 'Intron 1' with a length of 3328 bp. Between the second and third exons is an intron labeled 'Intron 2' with a length of 4078 bp, which contains a (GT)n repeat. The third exon is labeled 'Exon 3'. Below the gene structure is a table showing the genotype for each of these regions across various wheat accessions.

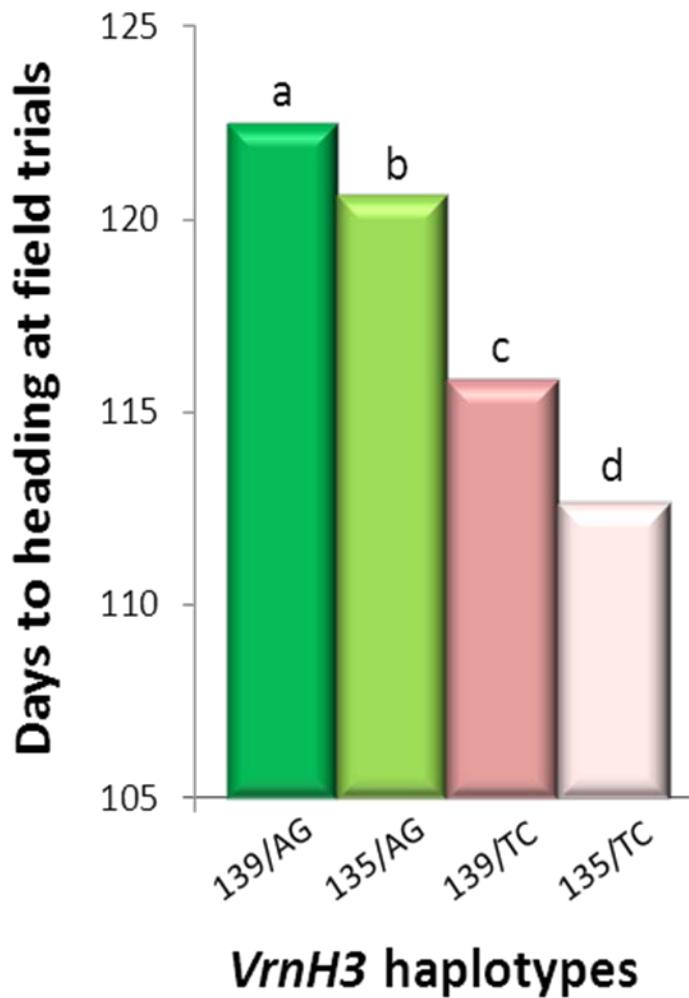
Genotype	Promoter	Intron 1	Intron 2	Exon 3	3' untranslated
	2349 2355 2468 2526 2584 2628 2686 2685 2736 2747 2824 2908 2927 2985 2940	3328 3340 3343 3467 3547 3661	(GT) 4078		
<b>W Lari</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	G	T C C G T C A A A
<b>W H.spontaneum</b>	C C G G ind A T G G G G C - C G T	G C C G T C	8	G	C T A A G T A C G
<b>W Calicuchima-sib</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	G	T C C G T C A A A
<b>W Kompolti korai</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	G	T C C G T C A A A
<b>F Dicktoo</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	A	T C C G T C A A A
<b>W SBCC106</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	G	
<b>W Esterel</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	G	
<b>W SBCC016</b>	T C C C ind A C G G - C C - C G T	A T C A A G	8	G	
<b>W Dairokkaku</b>	C C G G - G C A C G G T ind T C C	A C C A T C	8	G	C T A A T T A C G
<b>W SBCC145</b>	C C G G - G C A C G G T ind T C C	A C C A T C	8	G	
<b>W Strider</b>	C C G G - G C A C G G T ind T C C	A C T A A G	8	G	T T C A T T G A A
<b>S BGS213</b>	C C G G - G C A C G G T ind T C C	A C C A A G	8	G	T T C A T T G A A
<b>S SBCC154</b>	T C C C ind A C G G - C C - C G T	A T C A A G	8	G	
<b>S Beatrix</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	G	
<b>S Triumph</b>	T C C C ind A C G G - C C - C G T	A T C A T C	11	G	T C C G T C A A A
<b>S Tammi</b>	C C G G - G C A C G G T ind T C C	A C C A A G	8	G	T T C A T T G A A
<b>S Morex</b>	C C G G - G C A C G G T ind T C C	A C C A A G	8	G	
<b>S Stander</b>	C G G G - G C A C G G T ind T C C	A C C A A G	8	G	T T C A T T G A A

# *VrnH3* distribution associated with latitude



Adapted from Casas et al. 2011, Theor Appl Genet

# *VrnH3*, phenotypic effect



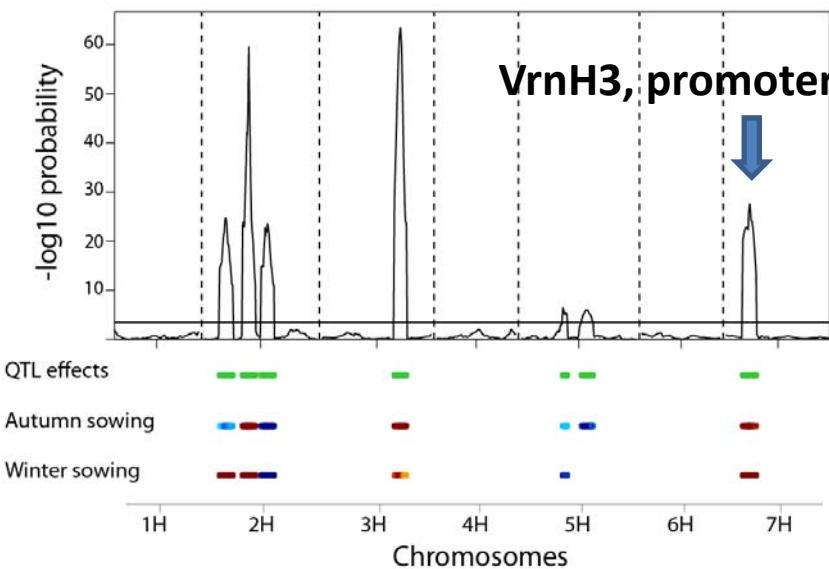
Association study, effect of *VrnH3* (*HvFT1*) alleles on flowering date in field trials of the Spanish Barley Core Collection

135-139: polymorphism at the promoter  
AG-TC: polymorphism at the first intron

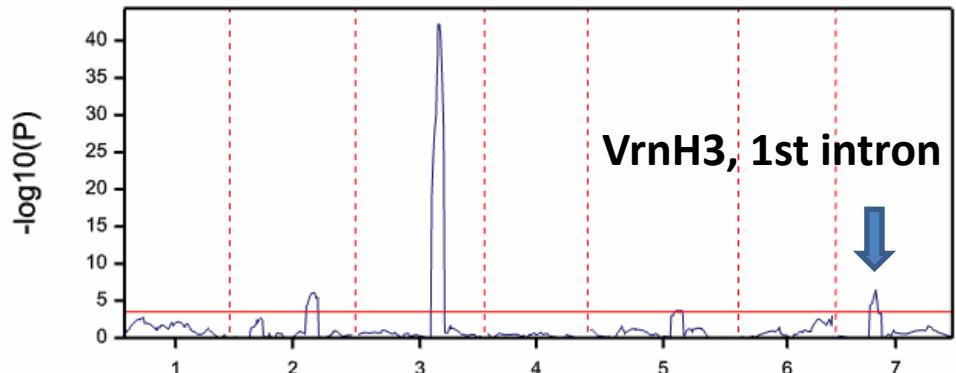
Adapted from Casas et al. 2011, Theor Appl Genet

# *VrnH3 validation, QTL search in biparental populations*

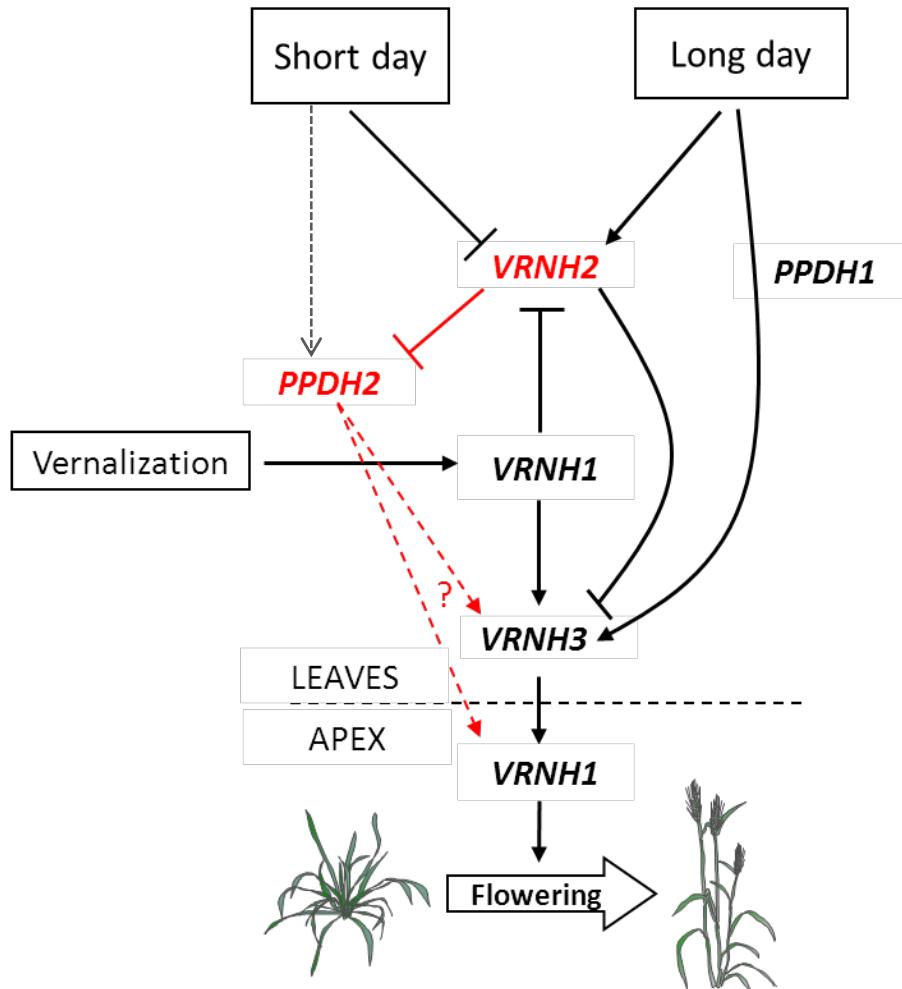
**SBCC145 x Beatrix**



**SBCC154 x Beatrix**



VrnH3. Three alleles confronted in two populations with one common parent. Effect of the polymorphisms at the promoter and first intron apparently confirmed with markers developed within the gene.



Based on Trevaskis et al. (2007) and Higgins et al. (2010), including findings in Casao et al J Exp Bot, 2011 and BMC Plant Biol, 2011

## Conclusions

- Most Spanish barley landraces are winter types with reduced vernalization requirement to match crop growth to the most favorable seasonal conditions. We propose that, under Mediterranean conditions, there are three safety mechanisms in place to secure that flowering occurs at an appropriate time, and to avoid early summer heat:
- first, intermediate *VrnH1* alleles, adapted to the prevalent winter temperature conditions;
- then, the presence of a functional *PPDH2* allele accelerates the promotion to flowering of winter cultivars under field conditions, especially when the vernalization requirement has not been fulfilled
- finally, the presence of long day sensitivity (provided by the sensitive *PPDH1* allele) gives a final boost towards flowering before temperatures rise too high.
- Other genes such as *VrnH3* or *Eam6* allow fine tuning to local temperatures

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