

10.1071/CP18102_AC

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Supplementary Material: *Crop & Pasture Science*, 2018, **69**, 1061–1075.

Ability of alleles of *PPD1* and *VRN1* genes to predict flowering time in diverse Australian wheat (*Triticum aestivum*) cultivars in controlled environments

Maxwell T. Bloomfield^{A,D}, *James R. Hunt*^A, *Ben Trevaskis*^B, *Kerrie Ramm*^B and *Jessica Hyles*^{B,C}

^AAgriBio Centre for Agribiosciences, La Trobe University, 5 Ring Road, Bundoora, Vic. 3083, Australia.

^BCSIRO Agriculture and Food, GPO Box 1700, Canberra, ACT 2601, Australia.

^CThe Plant Breeding Institute, University of Sydney, 107 Cobbitty Road, Cobbitty, NSW 2570, Australia.

^DCorresponding author. Email: M.Bloomfield@latrobe.edu.au

Supplementary materials

Supplementary Table S1. Mean thermal time to flowering (TTF; °Cd) for 13 near-isogenic lines (NILs) and 13 elite cultivars in different controlled environments.

LN=long day, not vernalised; LV=long day, vernalised; SN=short day, not vernalised; SV=short day, vernalised. P-value and LSD are for the two way interaction between environment and genotype.

Pair number	Multi-locus genotype	Cultivar (NIL, elite)	Environment			
			SN	SV	LN	LV
1	<i>aaaaa</i>	CSIROW077	1209	1182	669	682
		Young	1609	1412	794	846
2	<i>aaaav</i>	CSIROW105	1161	1179	700	702
		Axe	1090	1094	718	759
3	<i>aaavv</i>	CSIROW029	1241	1226	687	710
		Gauntlet	2064	2041	838	970
4	<i>aavaa</i>	Sunstate A	1711	1461	875	877
		Spitfire	1806	1883	952	1075
5	<i>aavav</i>	CSIROW005	2120	1602	993	938
		Mace	1882	1608	1039	998
6	<i>aavvv</i>	CSIROW007	2829	1357	1659	947
		Longsword	3374	2280	2102	1793
7	<i>abvaa</i>	CSIROW018	2305	2025	853	776
		Ellison	2680	2570	1116	1140
8	<i>acavv</i>	CSIROW087	1988	1821	741	756
		Sunbri	3445	3223	995	1216
9	<i>acvaa</i>	CSIROW002	2432	2096	832	782
		Trojan	2471	2323	992	992
10	<i>advvv</i>	CSIROW021	3404	2606	1874	1856
		Rosella	*	3105	2391	1348
11	<i>bavaa</i>	Sunstate B	1826	1512	876	877
		Scout	2626	2424	1100	1231
12	<i>bavva</i>	CSIROW003	1947	1541	899	854
		EGA Gregory	2533	2235	1038	1195
13	<i>bavvv</i>	CSIROW073	3027	2617	1910	1778
		EGA Wedgetail	3361	2629	2189	2140

P-value = <0.001

LSD = 178.5

*No value for elite cultivar Rosella in SN environment as no replicates reached anthesis in the experiment's duration.

Supplementary Table S2. VRN1 and PPD1 KASP™ markers utilised in this study.

Gene	Marker name	Allele	Forward Allele 1	Forward Allele 2	Reverse Primer 1	Reverse Primer 2	Sequence Reference	Marker Reference
<i>Vrn-A1</i>	CSIRO_wK001*	<i>a</i>	TCAAACGCGCCATACTTCG	TCAAACGCGCCATACTTCA	CCCACCACTGCCATTGATA		Wang <i>et al.</i> (2014)	Sukumaran <i>et al.</i> (2016)
<i>Vrn-B1</i>	CSIRO_wK002	<i>a</i>	GCAGCTAATGTGGGGTAGTCA	GCAGCTAATGTGGGGTAGTCT	CGCAAGCGGGAGTTACAT	TCCTATCATTCGTATTGCTAGCTC	Fu <i>et al.</i> (2005)	This study, causal for Triple Dirk B deletion
<i>Vrn-D1</i>	CSIRO_wK003	<i>a</i>	AATGGTGCCTAGGCGGAT	AATGGTGCCTAGGCGGAG	CGTCGCCTAGGTGTCAGG	GTGCTTGCTGCTTGAACAAA	Fu <i>et al.</i> (2005)	This study, causal for Triple Dirk E deletion
<i>Ppd-B1</i>	TaPpdBJ003	<i>a</i>	CGTGAAGAGCTAGCGATGAACA		TGGGCACGTTAACACACCTTT		Díaz <i>et al.</i> (2012)	Grogan <i>et al.</i> (2016)
<i>Ppd-B1</i>	CSIRO_wK004**	<i>b</i>	TGTACATACGTGATGCCTTCTAT	TGTACATACGTGATGCCTTCTAC	ACATATACAACCGTACACTCCG		Wang <i>et al.</i> (2014)	This study, linked to 90K SNP marker
<i>Ppd-B1</i>	CSIRO_wK005	<i>c</i>	CCAGTGATGTCGTCGCACA	CCAGTGATGTCGTCGCACG	CAGCAGCACCATTGACAGG		Beales <i>et al.</i> (2007)	This study, causal for Chinese Spring copy number allele
<i>Ppd-B1</i>	CSIRO_wK006	<i>d</i>	AGGGTGGTTCATGATGATGACC	AGGGTGGTTCATGATGATGACT	GCTTCCAACCTCAAGGACGA		IWGSC RefSeq assembly v1.0	This study, linked to <i>Ppd-B1</i> sequence
<i>Ppd-D1</i>	wMAS000024	<i>a</i>	CAAGGAAGTATGAGCAGCGGTT	AAGAGGAAACATGTTGGGGTCC	GCCTCCCACTACACTGGGC		Beales <i>et al.</i> (2007)	Grogan <i>et al.</i> (2016)
<i>Ppd-D1</i>	wMAS000025	<i>c</i>	TGACTTATACACCCGGACGGAG	GAACATGACACACAACCAACGC	TGTTAATTAATTTGACTGGCTCGGTA		Beales <i>et al.</i> (2007)	Dreisigacker <i>et al.</i> (2016)
<i>Ppd-D1</i>	wMAS000026	<i>d</i>	CGAGCAGCTCCCGACG	GGGCGAGCAGCTCCAAC	GGTCTCAATCAAGGCGGT		Beales <i>et al.</i> (2007)	Dreisigacker <i>et al.</i> (2016)

*Based on Excalibur_c7729_144, different reverse primer to published sequence.

**Based on Tdurum_contig54704_176. Use once 'c' allele has been eliminated.

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