**Wheat Durable Disease Resistance Gene Complex**

**Gene Name:** *Lr34/Yr18/Pm38*

**Chromosome**: 7DS

**Linkage**: Co-segregating with *Lr34/Yr18/Pm38*

**Marker Haplotype Rating**: 5

**Assay type**: Co-dominant

**Assay Reproducibility**: Very High

**Background:**

A large number of genes that confer race specific form of resistance to leaf rust, stripe (yellow) rust and powdery mildew have been identified in wheat. In addition, a small number of genes that confer partial or durable resistance to these have also been identified (Sing et al., 2003). Due to the rapidly evolving nature of the pathogens, the resistance conferred by race specific genes may be short term in nature compared to the resistance conferred by genes with partial/durable resistance. Availability of molecular markers would enable wheat breeders deploy the durable resistance genes in combination with race specific genes making wheat cultivars more sustainable under high disease pressure.

**Genetic Information:**

The gene complex that confer durable resistance to leaf rust (*Lr34*), yellow rust (*Yr18*), and powdery mildew (*Pm38*), located on the short arm of wheat chromosome 7D (7DS), has been recently characterized with functional co-dominant SNP markers (Krattinger et al., 2009: Lagudah et al., 2009). The broad-spectrum resistance complex of *Lr34/Yr18/Pm38* has been reported to be controlled by a single gene which encodes a putative ATP-binding cassette transporter (Krattinger et al., 2009). The KASP assay interrogates a three-base deletion (TCC) in exon 11 that is associated with the *Lr34/Yr18/Pm38* gene complex (Krattinger et al., 2009; Lagudah et al., 2009).

SNP Name: Lr34\_TCCIND

SNP ID: CIMwMAS0001

Intertek SNP ID: snpTA0023

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KASP Primer | Sequence | Haplotype | Phenotype | Controls |
| FAM | GGTATGCCATTTAACATAATCATGAA | Ins | *Lr34/Yr18/Pm38***-**  Susceptible | Pavon76\*, Pastor\* |
| VIC | GGTATGCCATTTAACATAATCATGAT | -:- | *Lr34/Yr18/Pm38***+**  Durable Resistance | Parula\*, Tonichi\* |
| Common | TACTATATGGGAGCATTATTTTTTTCC |  |  |  |

\* CIMMYT Spring wheat cultivars

**Consensus sequence:**

TACTATATGGGAGCATTATTTTTTTCCATC[TTC]ATGATTATGTTAAATGGCATACCAG

**Supporting figures:**

The genomic region containing *Lr34/Yr18/Pm38* gene complex is indicated in Fig 1 and Fig 2.

SNP viewer image of the assay with the two main genotypic allele classes – FAM (blue), VIC (red) and the heterozygotes (green) is in Fig. 3.

**NOTE: References and Figures are to be included as hyper links only.**

**References:**

Singh, R.P. and Huerta-Espino, J. 2003. Effect of leaf rust resistance gene *Lr34* on components of slow rusting at seven growth stages in wheat. Euphytica, 2003: 129: 371-376. (<https://link.springer.com/article/10.1023/A:1022216327934>)

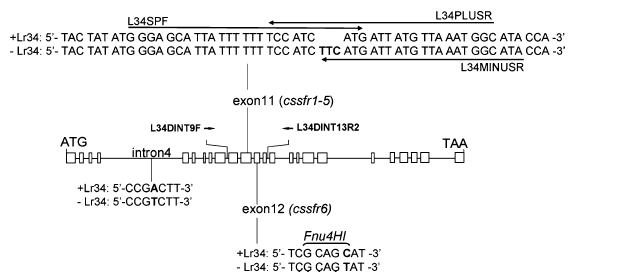
Krattinger, S. G., Lagudah, E.S. Spielmeyer, W., Singh, R.P., Huerta-Espino, J., McFadden, H., Bossolini E., Selter, L.L., Keller, B. 2009. A putative ABC transporter confers durable resistance to multiple fungal pathogens in wheat. Science 323: 1360-1363. DOI: 10.1126/science.1166453

(<http://science.sciencemag.org/content/early/2009/02/19/science.1166453>)

Lagudah, E.S., Krattinger, S.G., Herrera-Foessel, S., Singh, R.P., Huerta-Espino, J., Spielmeyer, W., Brown-Guedira, G., Selter, L.L., Keller, B. 2009. Gene-specific markers for the wheat gene *Lr34/Yr18/Pm38* which confers resistance to multiple fungal pathogens. Theor. Appl. Genet. 119: 889-898. DOI 10.1007/s00122-009-1097-z

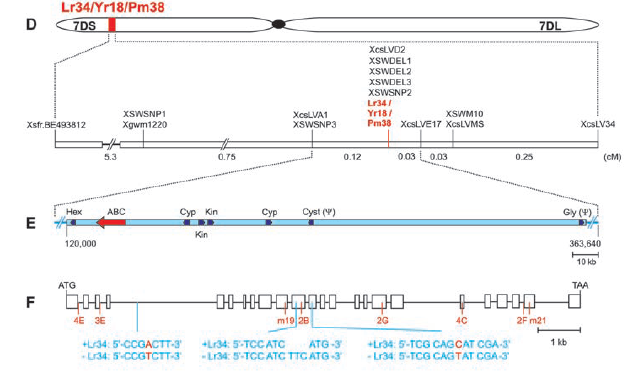
(<https://www.researchgate.net/publication/225395994_Gene-specific_markers_for_the_wheat_gene_Lr34Yr18Pm38_which_confers_resistance_to_multiple_fungal_pathogens>)

Fig. 1



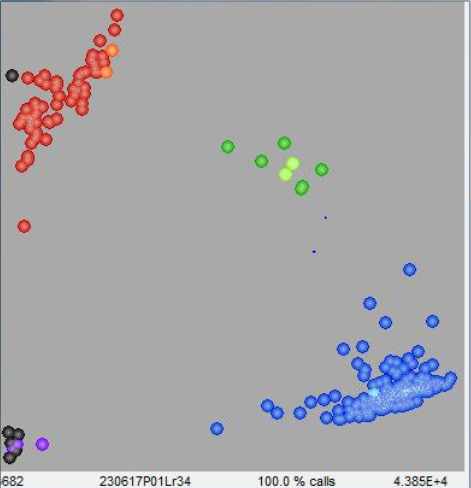
Source: Lagudah et al., 2009

Fig. 2



Source: Krattinger et al., 2009

**Fig. 3**



**Wheat Fusarium Head Blight Resistance**

**Gene Name:** *Fhb1*

**Chromosome**: 3BS

**Linkage**: Tight linkage with *Fhb1*

**Marker Haplotype Rating**: 4

**Assay type**: Co-dominant

**Assay Reproducibility**: Very High

**Background:**

Fusarium head blight (FHB) caused mainly by *Fusarium graminarum* is an important disease that affects wheat in warm and humid wheat growing regions that reduces grain yield and quality resulting in mycotoxin accumulation in the grain. Mycotoxins such as deoxynivalenol (DON), accumulated in grains affected by *F. granminarum*,can be harmful to human and animal health. Resistance to FHB is quantitatively inherited and different methods of resistance such as a) Resistance to initial infection (Type I) and b) Resistance to spread of infection (Type II) have been described. Using markers associated with large effect FHB QTLs can be used to improve FHB resistance in bread and durum wheats (Zhou et al., 2002; Miedaner et al., 2017).

**Genetic Information:**

The Chinese variety Sumai3 and its derivatives have demonstrated a high level of Type II resistance to FHB that has been deployed as a source of FHB resistance in numerous wheat breeding programs (Wilcoxson et al., 1992). A QTL with large effects, *Fhb1*, identified in Sumai 3 and its derivatives has been mapped to the short arm of wheat chromosome 3 (3BS). Although there are differences in the effects associated with *Fhb1* based on genetic backgrounds, *Fhb1* associated QTL can explain up to 50% of the phenotypic variation for Type II FHB resistance that also resulted in low DON accumulation in infected kernels (Bai et al., 1999; Zhou et al., 2002).

SNP markers have been developed that can be used to identify Sumai 3 based *Fhb1* resistance QTL (Bernado et al., 2012).

SNP Name: snp3BS-8

SNP ID: wMAS000008

Intertek SNP ID: snpTA0037

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KASP Primers | Sequence | Haplotype | Phenotype | Controls |
| FAM | CACATGCATTTGCAAGGTTGTTATCC | C | *Fhb1****-***(susceptible) | Chinese Spring, Pastor\* |
| VIC | CACATGCATTTGCAAGGTTGTTATCG | G | *Fhb1***+** (partial resistance) | Sumai 3, Ning 7840 |
| Common | CAAAGCAGCCTTAGGTCAATAGTTTGAAA |  |  |  |

\* CIMMYT origin

**Consensus sequence:** AACTCTGAAACAAAGCAGCCTTAGGTCAATAGTTTGAAATTTTCATATCAACACAA[G/C]GATAACAACCTTGCAAATGCATGTGCATTATAATGGCAGACTACAATCTTGGGCAACTAAAATTGAGTCGACTCGCTTGTCCCGGTGGGCCGATGGTGACAGCTCTCTTGACCCAATTTTCTTATGAAGCCAACCCAGAAGACCCATCGGCCTTGAAATTATGGGCTGGACCAATGTCCCAATGGGTAACATCGGCCCATTCCCATCGGGACTCTCACACGATCTAGCTTCCACCACCTCCCTCATATGCCACTTTGGACAGAAACGTGAAGAACCGAAGGAAACCAAGATTTCAATTGTTCAGTTTTGGATGAAAAATTGAAGAACCGTANGTAACTTTTTTTGTAATTATTGATGAACCTTTTGTCCTCTCTTGGAAGTTGGAACCTTTTCTATTTAGGGTGATAACTGGGGCACCTCTCTATGTATGGAATTGATCAACATGAATTTTTTATATATCTGGATTGAACTTCTCACCTCTGTAC

**Supporting figures:**

The genomic region representing *Fhb1* QTL is indicated in Fig 1.

SNP viewer image of the KASP assay is given in Fig. 2.

**NOTE: References and Figures are to be included as hyper links only.**

**References:**

1. Bai, G., Kolb, F., Shaner, G., Domier, L. 1999. Amplified fragment length polymorphism markers linked to a major quantitative trait locus controlling scab resistance in wheat. Phytopathology 89: 343–348.

(<https://apsjournals.apsnet.org/doi/pdfplus/10.1094/PHYTO.1999.89.4.343>)

1. Bernardo, A.N., Ma, H., Zhang, D., Bai, G. 2012. Single nucleotide polymorphism in wheat chromosome region harboring *Fhb1* for Fusarium head blight resistance.  Molecular Breeding 29: 477-488.

(<https://link.springer.com/article/10.1007%2Fs11032-011-9565-y>)

1. Miedaner, T., Kalih, R., Grobmann, M.S., Maurer, H.P. 2017. Correlation between Fusarium head blight severity and DON content in triticale as revealed by phenotypic and molecular data. Plant Breeding 135: 31-37.

(<https://onlinelibrary.wiley.com/doi/10.1111/pbr.12327>)

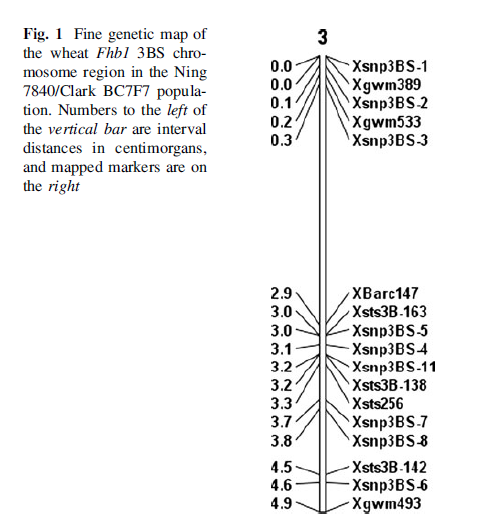
1. Wilcoxson, R.D., Busch, R.H., Ozmon, E.A. 1992. Fusarium head blight resistance in spring wheat cultivars. Plant Dis 76: 658–661.

(<https://www.apsnet.org/publications/PlantDisease/BackIssues/Documents/1992Articles/PlantDisease76n07_658.PDF>)

1. Zhou, W., Kolb, F.L., Bai, G., Domier, L.L., Yao, J.B. 2002. Effect of individual Sumai 3 chromosomes on resistance to scab spread within spikes and deoxynivalenol accumulation within kernels in wheat. Hereditas 137:81–89.

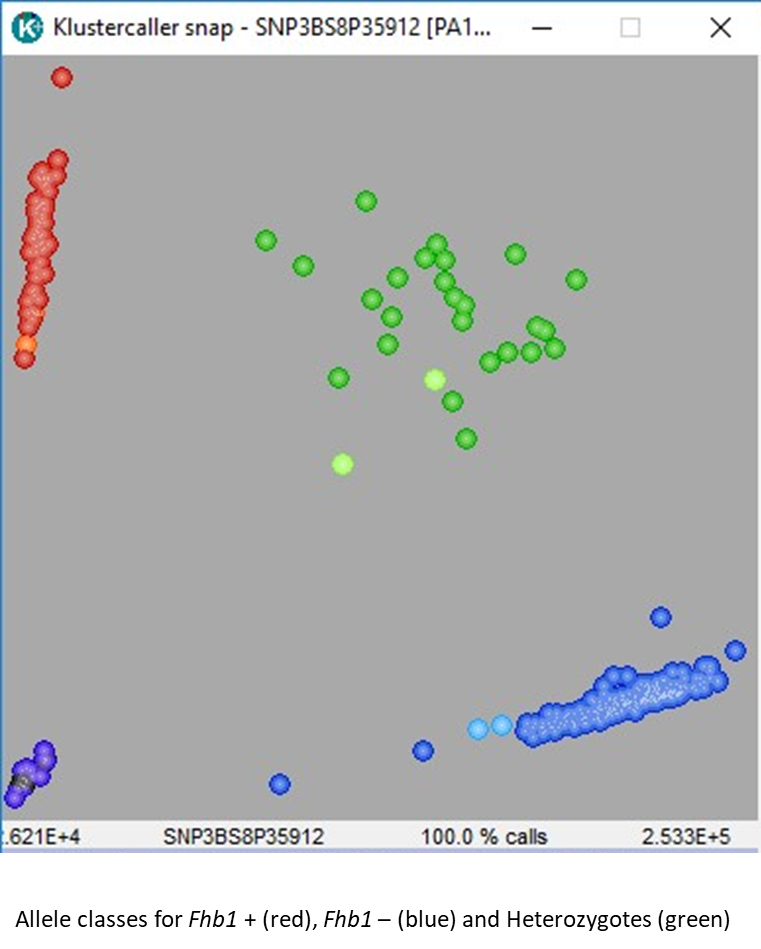
(<https://onlinelibrary.wiley.com/doi/pdf/10.1034/j.1601-5223.2002.01674.x>)

Fig. 1



**Source:** Bernado et al., 2012

Fig. 2

****

**Wheat Gene Cluster with Multiple Rust Resistance Genes**

**Gene Name:** *Lr37-Yr17-Sr38*

**Chromosome**: 2AS

**Linkage**: Co-segregating with *Lr37/Yr17/Sr38*

**Marker Haplotype Rating**: 5

**Assay type**: Co-dominant

**Assay Reproducibility**: High

**Background:**

The gene cluster known as VPM1 containing *Yr17, Lr37* and *Sr39* rust resistance genes that confer resistances to leaf rust, yellow (stripe) rust and stem rust respectively has been introgressed from *Triticum ventricosum*into cultivated wheat (Seah et al., 2000). The introgressed chromosome segment is located in the *T. ventricosum*translocation known as 2NS/2AS. Although rust races that have developed virulence to *Yr17*and *Lr37*have been reported (Robert et al., 1999), this gene cluster is known to provide resistance to a wide range of races and is useful in breeding in combination with other rust resistance genes (Helguera et al., 2003).

**Genetic Information:**

The gene complex present in the translocated chromosome segment from *Triticum ventricosum* into the short arm of wheat chromosome 2A (2AS) is inherited as a block of genes with little chance of recombination. Wheat breeders would be able to deploy the gene cluster into multiple wheat backgrounds using the SNP markers presented.

SNP Name: VPM\_SNP

SNP ID: CIMwMAS0004

Intertek SNP ID: snpTA0025

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KASP Primers | Sequence | Haplotype | Phenotype | Controls |
| FAM | CGCCGTTCCGAAYACGAGA | T | *Lr37/Yr17/Sr38***+**  (resistant) | Milan, Reedling |
| VIC | CGCCGTTCCGAAYACGAGG | C | *Lr37/Yr17/Sr38****-***  (susceptible) | Parula\*, Pavon76\* |
| Common | CCCTGGCTTGCACCTTCGACAA |  |  |  |
|  |  |  |  |  |

\* CIMMYT origin

**Note:** Some false positives among CIMMYT synthetic wheats have been observed.

**Consensus Sequence:** GGTCGCCCTGGCTTGCACCTTCGACAAGGGGCTACTGACCAARGC[C/T]CTCGTRTTCGGAACGGCGAGAAGGTTTGCAGGACCAGGAAGRAGATAGGAACCAAACATCNNNNNNNNNNNNNNNATGCCAYGCRCATTYRTTCCGATGCACAACCGAGCGAC

**Supporting figures:**

The genomic region containing the *T. ventricosum* chromosome segment in 2NS/2AS translocation is indicated in Fig 1.

SNP viewer image of the assay is in Fig. 2.

**NOTE: References and Figures are to be included as hyper links only.**

**References:**

Helguera, M., Khan, I.A., Kolmer, J., Lijavetzky, D., Zhong-qi, L., Dubcovsky, J. 2003. PCR assays for the *Lr37-Yr17-Sr38* cluster of rust resistance genes and their use to develop isogenic hard red spring wheat lines. Crop Sci. 43: 1839-1847.

(<https://dl.sciencesocieties.org/publications/cs/abstracts/43/5/1839>)

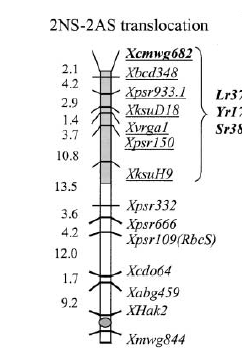
Robert, O., Abelard, C., Dedryver, F.1999. Identification of molecular markers for the detection of the yellow rust resistance gene *Yr17* in wheat. Molecular Breeding: 5:167-175.

(<https://link.springer.com/article/10.1023/A:1009672021411>)

Seah, S., Spielmeyer, W., Jahier, J., Sivasithamparam, K., Lagudah, E.S. 2000. Resistance gene analogs within an introgressed chromosomal segment derived from Triticum ventricosum that confers resistance to nematode and rust pathogens in wheat. Molecular and Plant Microbe Interactions 13: 334-341.

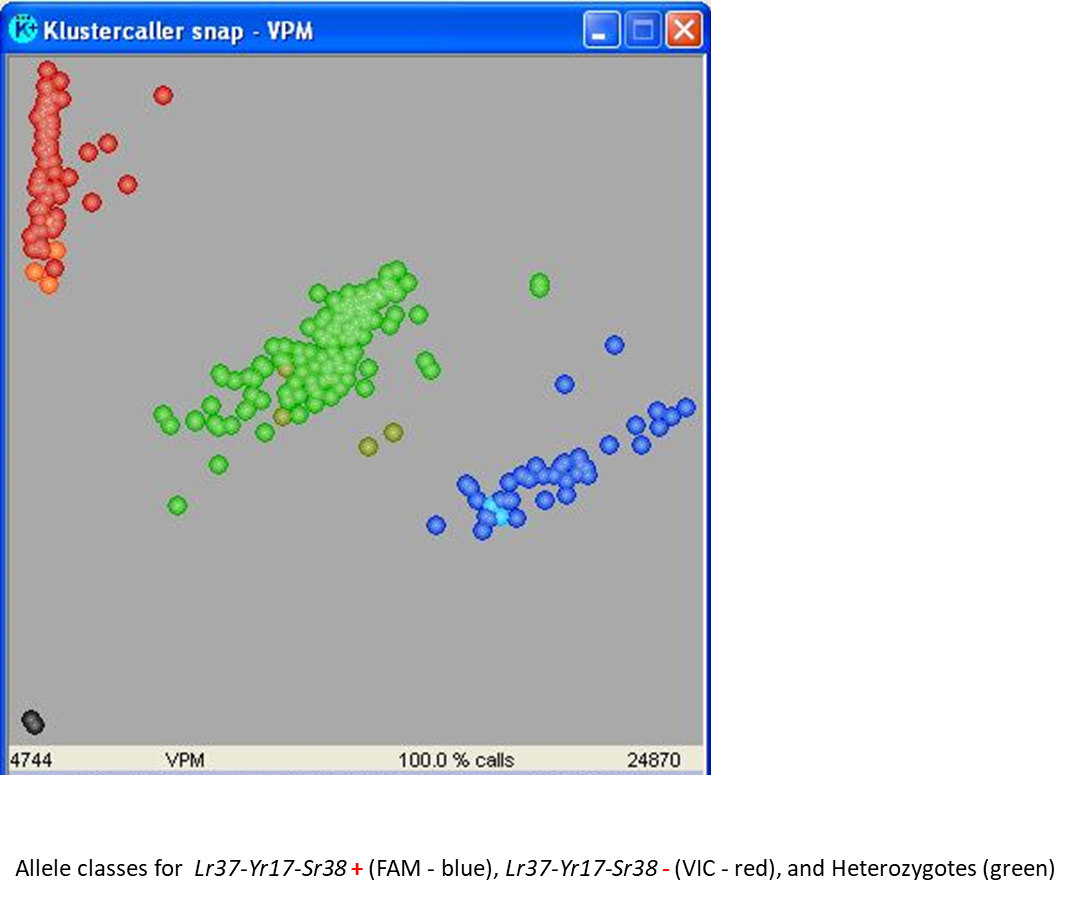
(<https://apsjournals.apsnet.org/doi/pdf/10.1094/MPMI.2000.13.3.334>)

**Fig. 1**



Source: Helguera et al., 2003

**Fig. 2**



**Wheat Dwarfing Genes**

**Gene Name:** *Rht-B1* and *Rht-D1*

**Chromosome**: 4BS (*Rht-B1*); 4DS (*Rht-D1*)

**Linkage**: Functional markers – Co-segregation with *Rht-B1* and *Rht-D1*

**Marker Haplotype Rating**: 5

**Assay type**: Co-dominant

**Assay Reproducibility**: Very High

**Background:**

High yielding wheat cultivars introduced during Green Revolution contained dwarfing genes for reduced height (Rht) (Hedden, 2003). Wheat cultivars with reduced height were less prone for lodging and facilitated better partitioning of photosynthate to the grain, resulting in increase of grains per spikelet. The widely used dwarfing genes are the mutants of *Rht-1* locus, designated *Rht-B1* and *Rht-D1* that are known to be present over 70% of current wheat cultivars (Evans, 1998). Genes *Rht-B1* and *Rht-D1* have origin from a Japanese wheat variety Norin10 (Hedden 2003).

**Genetic Information:**

Wheat dwarfing genes which are important in breeding for plant type with shorter stature are classified according to their sensitivity to externally applied gibberellins (GA).  Genes *Rht-B1* and *Rht-D1* are GA-insensitive, whereas *Rht8*is GA-sensitive. For *Rht-B1* and *Rht-D1*, alleles conferring the dwarf phenotype are *Rht-B1b* and *Rht-D1b* and the wild type alleles are *Rht-B1a* and *Rht-D1a* that result in tall plant types.  Semi-dwarf plant types are attained by a combination of *Rht-B1b* + *Rht-D1a*or *Rht-B1a* + *Rht-D1b.*  The genes *Rht-B1*and *Rht-D1*are located on the short arm of wheat chromosomes 4B and 4D respectively.  Diagnostic markers for *Rht-B1*and *Rht-D1*for the detection of point mutations responsible for the *Rht-B1b* and *Rht-D1b* have been developed (Ellis et al., 2002; Peng et al., 1999).

Gene: *Rht-B1*

Chromosome: 4BS

SNP Name – Rht-B1\_SNP

SNP ID - wMAS000001

Intertek Assay ID - snpTA0001

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KASP Primers | Sequence | Haplotype | Phenotype | Controls |
| FAM | CCCATGGCCATCTCSAGCTG | C | *Rht-B1a –* Wild type (Tall) | Sonora64\*, Wyalkatchem, Pavon76\*, Chinese Spring |
| VIC | CCCATGGCCATCTCSAGCTA | T | *Rht-B1b –* Dwarf | Pastor\*, Krichauff, Attilla\*, Seri M82\* |
| Common | TCGGGTACAAGGTGCGGGCG |  |  |  |

\* CIMMYT origin

Gene: *Rht-D1*

Chromosome: 4DS

SNP Name – Rht-D1\_SNP

SNP ID - wMAS000002

Intertek Assay ID - snpTA0002

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KASP Primers | Sequence | Haplotype | Phenotype | Controls |
| FAM | CATGGCCATCTCGAGCTRCTC | G | *Rht-D1a –* Wild type | Pastor\*, Krichauff, Attilla\*, Seri M82\* |
| VIC | CATGGCCATCTCGAGCTRCTA | T | *Rht-D1b –* Dwarf | Sonora64\*, Pavon76\*, Parula\*, Sonalika\* |
| Common | CGGGTACAAGGTGCGCGCC |  |  |  |

\* CIMMYT origin

**Consensus sequence:**

***Rht-B1:***

GAGAGGCGAGGTAGGGAGGCGAGAGGCGAGATCATGAAGCGCGAGTACCAGGACGCCGGAGGGAGCGGCGGTGGCGGGGGAGGCATGGGCTCGTCCGAGGACAAGATGATGGTGTCGGGGTCGGCGGCGGCGGGGGAGGGGGAGGAGGTGGACGAGCTGCTGGCGGCGCTCGGGTACAAGGTGCGGGCGTCCGACATGGCGGACGTGGCGCAGAAGCTGGAG[C/T]AGCTCGAGATGGCCATGGGGATGGGCGGCGTGGGCGCCGGCGCCGCGCCCGACGACAGCTTCGCCACCCACCTCGCCACGGACACCGTGCACTACAACCCCACCGACCTCTCCTCCTGGGTCGAGAGCATGCTGTCGGAGCTCAACGCGCCGCCGCCGCCCCTCCCGCCCGCCCCGCAGCTCAACGCCTCCACCTCCTC

***Rht-D1*:**

GGGAGTACCAGGACGCCGGAGGGAGCGGCGGCGGCGGTGGCGGCATGGGCTCGTCCGAGGACAAGATGATGGTGTCGGCGGCGGCGGGGGAGGGGGAGGAGGTGGACGAGCTGCTGGCGGCGCTCGGGTACAAGGTGCGCGCCTCCGACATGGCGGACGTGGCGCAGAAGCTG[G/T]AGCAGCTCGAGATGGCCATGGGGATGGGCGGCGTGGGCGCCGGCGCCGCCCCCGACGACAGCTTCGCCACCCACCTCGCCACGGACACCGTGCACTACAACCCCACCGACCTGTCGTCTTGGGTCGAGAGCATGCTGTCGGAGCTCAACGCGCCGCCGCCGCCCCTCCCGCCCGCCCCGCAGCTCAACGCCTCCAC

**Supporting figures:**

The linkage map location of *Rht-B1* and *Rht-D1* are in Fig. 1.

SNP viewer images of assay of *Rht-B1* and *Rht-D1* are in Fig. 2 and 3 respectively.

**NOTE: References and Figures are to be included as hyper links only.**

**References:**

1. Ellis, M.H., Spielmeyer, W., Gale, K.R., Rebetzke, G.J., Richards, R.A. 2002. 'Perfect' markers for the *Rht-B1b* and *Rht-D1b* dwarfing genes in wheat. Theor. Appl. Genet. 105: 1038-1042.

(<https://www.researchgate.net/publication/10903748_Perfect_markers_for_the_Rht-B1b_and_Rht-D1b_dwarfing_genes_in_wheat>)

1. Evans L.T. 1998. Feeding the ten billion: plants and population growth. Cambridge University Press.
2. Hedden. P. 2003. The genes of the Green Revolution. Trends in Genetics 19: 5-9.

(<https://doi.org/10.1016/S0168-9525(02)00009-4>)

1. Peng, J., Richards, D.E., Hartley, N.M., Murphy, G.P., Devos, K.M., Flintham, J.E., Beales, J., Fish, L.J., Worland, A.J., Pelica, F., Sudhakar, D., Christou, P., Snape, J.W., Gale, M.D., Harberd, N.P. 1999. ‘Green revolution’ genes encode mutant gibberellin response modulators. Nature 400: 256–261.

(<https://www.nature.com/articles/22307>)

Fig. 1

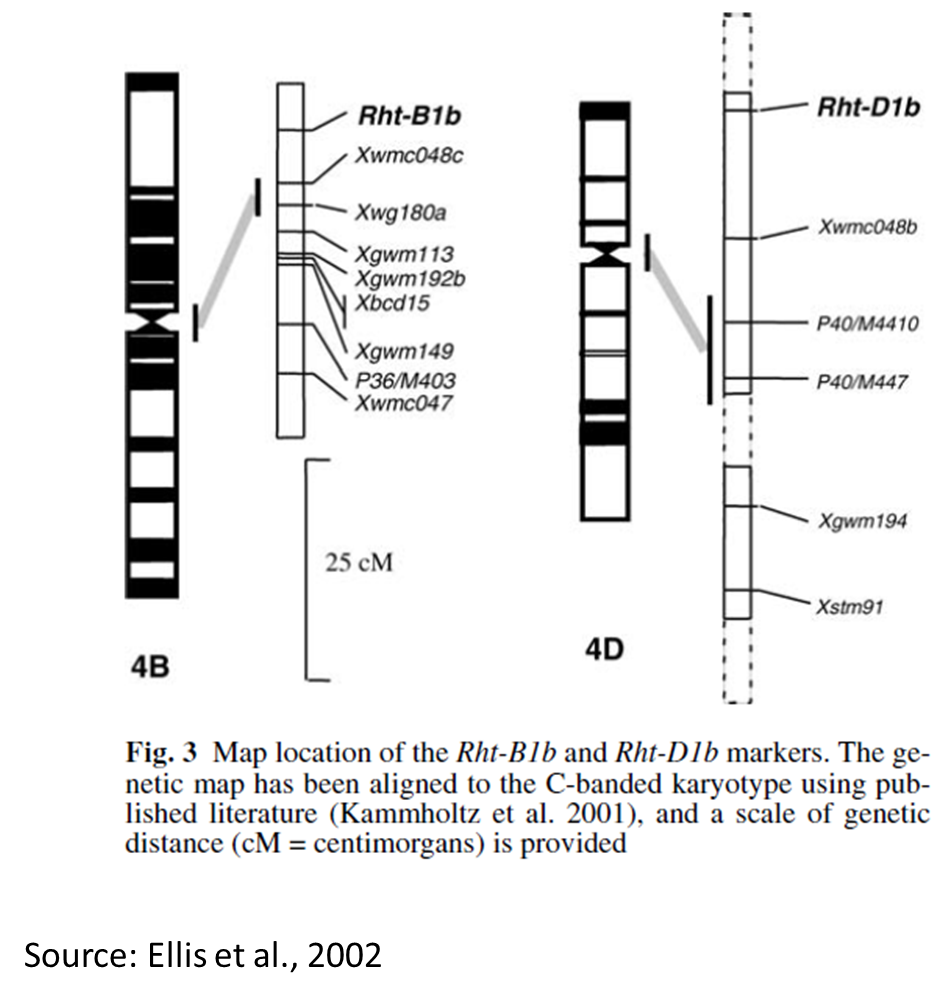


Fig.2

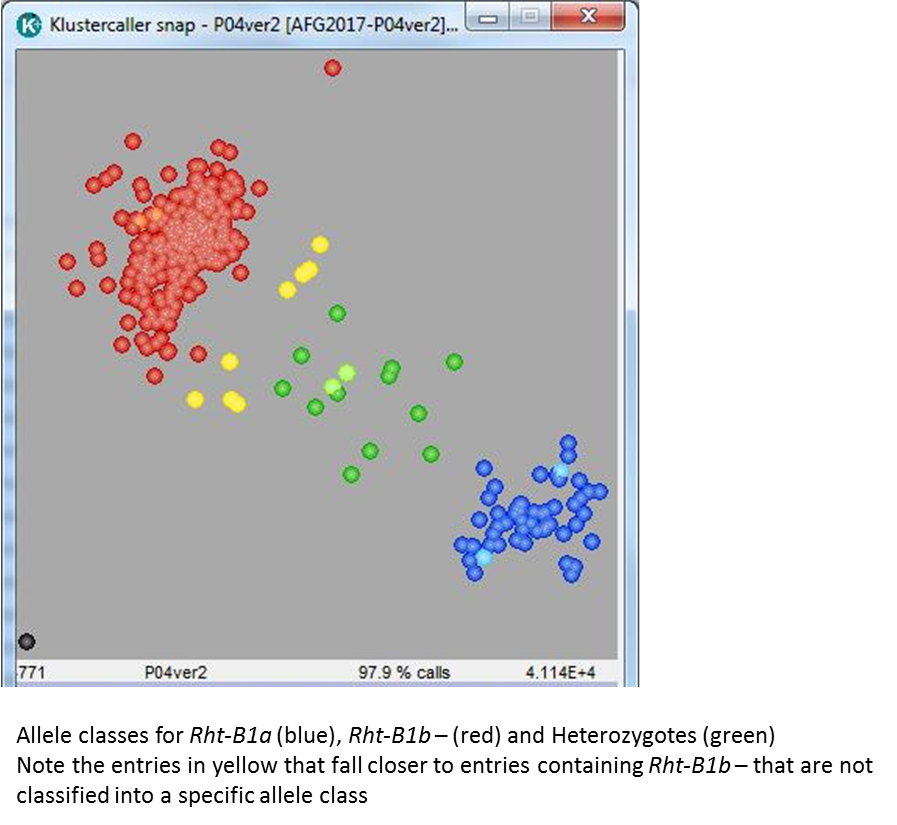
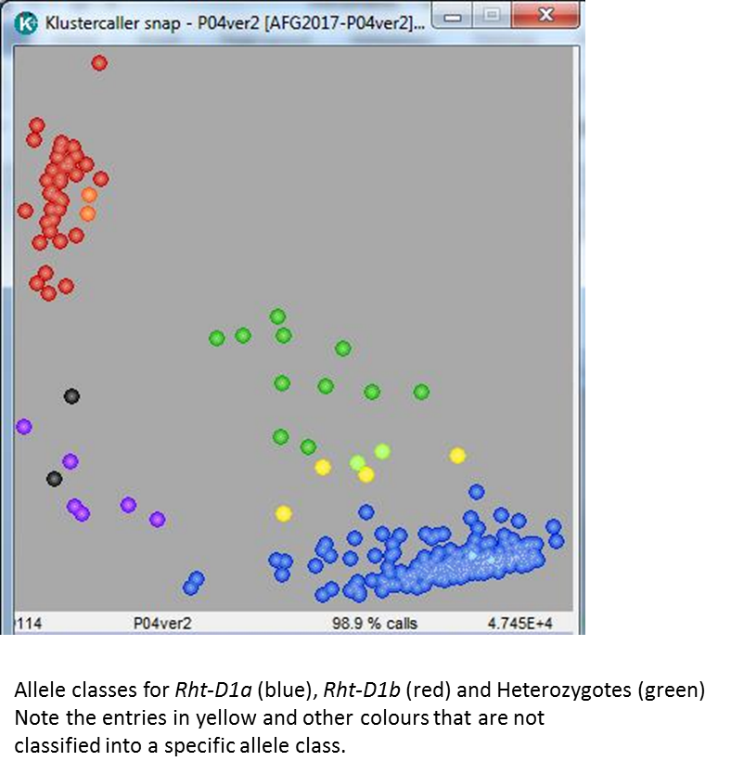


Fig.3



**Wheat Grain Protein Content**

**Gene Name –** *Gpc-B1*

**Chromosome:** 6BS

**Linkage**: Tightly linked marker

**Marker Haplotype Rating**: 4

**Assay type**: Co-dominant  
**Assay Reproducibility**: High

**Background:**

Grain protein content (GPC) is an important quality trait in pasta and bread wheats that is important for human nutrition. A promising source of GPC is wild emmer, *Triticum turgidum* L. ssp *dicoccoides* (Joppa and Cantrell, 1990). The high grain protein content gene (*Gpc-B1*), transferred from *T. turgidum* ssp. *dicoccoides* into durum wheat is a valuable source for increasing the grain protein content (GPC) in durum and bread wheat (Deckard et al., 1996).

**Genetic Information:**

The *Gpc-B1* gene has also been introgressed into hexaploid wheat backgrounds and is located on the short arm of chromosome 6B (6BS) (Joppa et al., 1997). Markers have been developed from a physical map of approx. 250 kb of the *Gpc-B1* region using a tetraploid wheat bacterial artificial chromosome library (Distelfeld et al., 2006). Stripe rust resistance gene *Yr36* is also closely linked to the *Gpc-B1* gene enabling breeders to use the same markers developed for *Gpc-B1* to manipulate *Yr36.*

SNP Name – GCP\_DUP

SNP ID - wMAS000017

Intertek Assay ID - snpTA0044

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KASP Primers | Sequence | Haplotype | Phenotype | Controls |
| FAM | CAAGAGGGGAGAGACATGTTACTT A | A | *Gpc-B1***-**normal GPC | Pastor\*, Chinese Spring |
| VIC | CAAGAGGGGAGAGACATGTTACTTT | T | *Gpc-B1***+**high GPC | Glupro, Anza-*Gpc-B1* |
| Common | GATTATGGGAGTAGGTTGGTGAGATAAAA |  |  |  |

\* CIMMYT origin

**Consensus Sequence:**

CTTAAAGAGATTCACATCAAAAGCTTATCATATTTTAAGCTCTTCTAAGAAAGGGAGAGAGAGATGCACTATTATAAGAGGAGATAATTCACATGTCTCCAAGAGGGGAGAGACATGTTACTT[/ACTT]TATTTGAGTCTATGTTACTCTAATCTTATTTTGCACTGATTTTATCTCACCAACCTACTCCCATAATCCAATGCTAGATTCATGGGTAGAGGAA

**Supporting figures:**

Genetic and physical maps of the *Gpc-B1* region is in Fig. 1

SNP viewer image of the assay is given in Fig. 2 (Uauy et al., 2006).

**NOTE: References and Figures are to be included as hyper links only.**

**References:**

1. Deckard, E.L., Joppa, L.R., Hammond, J.J,, Hareland, G.A. 1996. Grain protein determinants of the Langdon durum-dicoccoides chromosome substitution lines. Crop Sci. 36: 1513-1516.

(<https://dl.sciencesocieties.org/publications/cs/abstracts/36/6/CS0360061513?access=0&view=article>)

1. Distelfeld, A., Uauy, C., Fahima, T., Dubcovsky J. 2006. Physical map of the wheat high-grain protein content gene *Gpc-B1* and development of a high-throughput molecular marker. New Phytologist 169: 753-763.

(<https://nph.onlinelibrary.wiley.com/doi/abs/10.1111/j.1469-8137.2005.01627.x>)

1. Joppa, L.R., Cantrell, R.G. 1990. Chromosomal location of genes for grain protein content in wild tetraploid wheat. Crop Science 30: 1059–1064.

(<https://dl.sciencesocieties.org/publications/cs/abstracts/30/5/CS0300051059>)

1. Joppa, L.R., Du, C., Hart, G.E., Hareland, G.A. 1997. Mapping gene(s) for grain protein in tetraploid wheat (*Triticum turgidum* L.) using a population of recombinant inbred chromosome lines. Crop Sci. 37: 1586-1589.

(<https://dl.sciencesocieties.org/publications/cs/abstracts/37/5/CS0370051586>)

1. Uauy, C., Brevis, J.C. Dubcovsky, J. 2006. The high grain protein content gene Gpc-B1 accelerates senescence and has pleiotropic effects on protein content in wheat. J. Exp. Bot. 57: 2785-2794.

(<https://academic.oup.com/jxb/article/57/11/2785/681978>)

Fig. 1

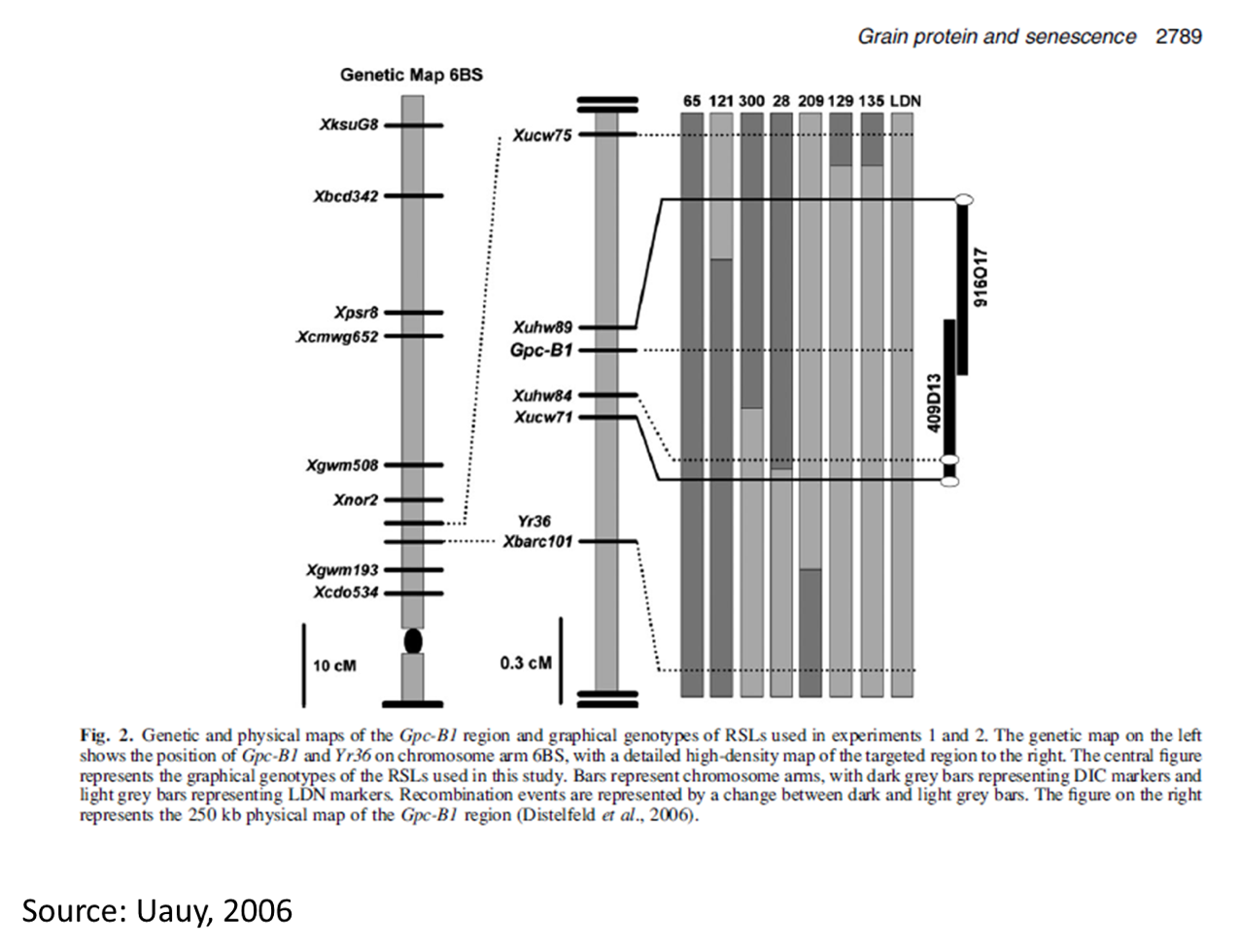


Fig. 2

