

## 1 **Supplementary Materials and Methods**

### 2 ***Reverse transcription and PCR***

3 Reverse transcription was performed using Invitrogen reagents and essentially following the  
4 Malmstrom and Shu (2004) protocol. Initially, 2  $\mu\text{L}$  Yan-R (10  $\mu\text{M}$ ) reverse primer and 3  $\mu\text{L}$   
5 of TNAE were mixed with 8  $\mu\text{L}$  RNase-free water, heated at 80°C for 10 min, and the reaction  
6 then cooled on ice followed by brief centrifugation. The following reagents were then added:  
7 4  $\mu\text{L}$  of 5  $\times$  First-Strand buffer, 2  $\mu\text{L}$  of 0.1 M DTT, 0.5  $\mu\text{L}$  of 0.6  $\mu\text{g}/\mu\text{L}$  BSA and 0.5  $\mu\text{L}$  of  
8 SuperScript III (200 U/ $\mu\text{L}$ ). The reaction was incubated at 55°C for 45 min, then 70°C for 10  
9 min, chilled on ice and then centrifuged briefly.

10 PCR reactions were also performed using Invitrogen reagents following either of two protocols.  
11 The first protocol was the basic multiplex RT-PCR system essentially as described by  
12 Malmstrom and Shu (2004) except that the total reaction volume was 25  $\mu\text{L}$  and included  
13 1.5  $\mu\text{L}$  of cDNA and 1 U of *Taq* DNA polymerase (Cat. No. 10-342-020). The thermocycling  
14 conditions were 95°C for 1 min, then 35 cycles of 95°C for 20 s, 60°C or 55°C for 20 s and  
15 72°C for 30 s, followed by 72°C for 5 min. The second protocol was based on that described  
16 by Chomic et al. (2010) using primers C1F1 and C1R2. The total reaction volume was 20  $\mu\text{L}$   
17 and consisted of 1  $\times$  PCR buffer, 1 mM  $\text{MgCl}_2$ , 200  $\mu\text{M}$  dNTPs, 490  $\mu\text{M}$  primer C1F1 and  
18 400  $\mu\text{M}$  primer C1R2, 1 U *Taq* DNA polymerase, and 1  $\mu\text{L}$  of cDNA. The thermocycling  
19 conditions were 95°C for 1 min, then 40 cycles of 95°C for 20 s, 50°C for 30 s and 72°C for  
20 30 s, followed by 72°C for 7 min.

21 To amplify viral sequence across the ORF2-ORF3 junction for isolates positive by ELISA for  
22 BYDV-MAV with PCR primers 2484F (5'-CGTACCTTCAAGGAAACGCC-3') and 2951R  
23 (5'-TGGCCTTCCTCGAGTTGTTC-3'), reverse transcription was conducted with the  
24 following modifications to the above method: 0.25  $\mu\text{L}$  of RNaseOUT (40 U/ $\mu\text{L}$ ) was used in  
25 place of BSA, SuperScript III (200 U/ $\mu\text{L}$ ) was reduced to 0.25  $\mu\text{L}$  and reactions were incubated  
26 at 50°C instead of 55°C. For PCR, the reactions consisted of 1  $\times$  PCR buffer, 2 mM  $\text{MgCl}_2$ ,  
27 200  $\mu\text{M}$  dNTPs, 400  $\mu\text{M}$  each primer, 1.5 U *Taq* DNA polymerase and 2  $\mu\text{L}$  of cDNA, and  
28 thermocycling conditions were 94°C for 1 min, then 35 cycles of 94°C for 10 s, 57°C for 10 s  
29 and 72°C for 30 s, followed by 72°C for 3 min.

30 All PCR products were analysed by electrophoresis on a 1% or 1.5% agarose gel in 0.5  $\times$  TBE  
31 buffer by comparison with 200 ng of a DNA marker (Fermentas GeneRuler DNA ladder, Cat.

32 No. SM0331), post-stained with ethidium bromide and visualized using a Bio-Rad gel  
33 documentation system under UV illumination.

#### 34 ***Sanger sequencing***

35 For purification prior to sequencing, PCR products from the reactions with Malmstrom and  
36 Shu (2004) and Chomic et al. (2010) primers were electrophoresed using an E-gel Clone Well  
37 0.8% SYBR Safe gel (Invitrogen) on an iBase (Ethrong Biotechnologies Ltd) according to the  
38 manufacturer's instructions and were then extracted in water. Excised target amplicons of  
39 electrophoretically separated PCR products generated using the primers designed in this study  
40 were purified using the ISOLATE II PCR and Gel Kit (Meridian Bioscience). PCR products  
41 were then sent to the Australian Genome Research Facility (AGRF, Brisbane Qld, Australia)  
42 for direct sequencing using the Sanger method using single primers from the reaction that  
43 generated that amplicon.

#### 44 ***Virus acronyms and GenBank accession reference sequences***

45 BVG, NC\_029906 barley virus G; BYDV-GAV, NC\_004666 barley yellow dwarf virus-GAV;  
46 BYDV-Ker-II, NC\_021481 barley yellow dwarf virus Ker-II; BYDV-Ker III, NC\_043123  
47 barley yellow dwarf virus Ker-III; BYDV-MAV, NC\_003680 barley yellow dwarf virus-MAV;  
48 BYDV-OYV, MK012645 BYDV-OYV (oat yellowing virus); BYDV-PAS, NC\_002160 barley  
49 yellow dwarf virus-PAS; BYDV-PAV, NC\_004750 barley yellow dwarf virus PAV; BYDV-  
50 SGV, NC\_043124 barley yellow dwarf virus-SGV; CYDV-RPS, NC\_002198 cereal yellow  
51 dwarf virus-RPS; CYDV-RPV, LC765997 cereal yellow dwarf virus RPV; CYDV-RPV,  
52 NC\_004751 cereal yellow dwarf virus-RPV; MYDV-RMV, NC\_021484 maize yellow dwarf  
53 virus-RMV; MYDV-RMV2, NC\_029990 maize yellow dwarf virus-RMV2; PEMV-1,  
54 NC\_003629 pea enation mosaic virus-1; MYFV, MT520166 miscanthus yellow fleck virus;  
55 SCYLV, NC\_000874 sugarcane yellow leaf virus; TYSV, OM829809 triticum yellow stripe  
56 virus; WYDV-GPV, NC\_012931 wheat yellow dwarf virus-GPV; and WLYaV, NC\_035451  
57 wheat leaf yellowing associated virus.

58 **Supplementary Table 1.** Reaction of survey samples in DAS-ELISA against antisera to  
 59 BYDV-PAV, BYDV-MAV and CYDV-RPV.

Isolate	BYDV-PAV <sup>A</sup>	BYDV-MAV <sup>A</sup>	CYDV-RPV <sup>A</sup>
2851	<b>0.686 / 0.006</b>	0.030 / 0.079	0.008 / 0.002
2852	<b>0.820 / 0.006</b>	0.039 / 0.044	0.003 / 0.004
2854	0.009 / 0.006	0.036 / 0.044	0.003 / 0.004
2855	0.008 / 0.006	0.039 / 0.044	<b>0.616 / 0.004</b>
2856	0.008 / 0.006	0.039 / 0.044	<b>1.628 / 0.004</b>
2868	0.011 / 0.006	0.066 / 0.044	<b>1.277 / 0.004</b>
2869	0.010 / 0.006	0.044 / 0.044	<b>0.199 / 0.004</b>
2870	0.008 / 0.006	0.037 / 0.044	<b>2.222 / 0.004</b>
2871	0.006 / 0.006	<b>0.300 / 0.044</b>	0.013 / 0.004
2872	0.009 / 0.006	<b>0.244 / 0.044</b>	0.003 / 0.004
2876	0.017 / 0.021	<b>0.209 / 0.023</b>	0.022 / 0.013
2877	0.014 / 0.021	<b>0.239 / 0.023</b>	0.012 / 0.013
2884	0.009 / 0.010	0.041 / 0.035	0.036 / 0.028
3001	0.010 / 0.011	<b>0.054 / 0.013</b>	<b>2.325 / 0.023</b>
3002	0.018 / 0.011	<b>0.055 / 0.013</b>	0.041 / 0.023
3003	<b>0.264 / 0.011</b>	0.009 / 0.013	0.031 / 0.023
3004	<b>0.355 / 0.021</b>	0.016 / 0.013	0.010 / 0.007

60 <sup>A</sup> Mean A<sub>404nm</sub> test sample / appropriate healthy control

61

62 **Supplementary Table 2.** Aphid transmission tests with selected YDV isolates.

Isolate	YDV species <sup>A</sup>	Test plant	Aphid species	Total number of plants/total number of aphids	Virus species indicated by ELISA in test plants		
					PAV	MAV	RPV
2851	BYDV-PAV	wheat cv. Crusader	<i>M. dirhodum</i>	1/20	-	-	-
2851	BYDV-PAV	oat cv. Culgoa	<i>R. maidis</i>	8/20	-	-	-
2851	BYDV-PAV	oat cv. Genie	<i>R. padi</i>	8/20	-	-	-
2852	BYDV-PAV	wheat cv. Crusader	<i>M. dirhodum</i>	1/20	-	-	-
2854 <sup>B</sup>	BVG + CrRLV	oat cv. Genie and Culgoa	<i>R. maidis</i>	4/20	-	-	-
2854 <sup>B</sup>	BVG + CrRLV	oat cv. Genie	<i>R. padi</i>	8/20	-	-	-
2856	CYDV-RPS	wheat cv. Crusader	<i>R. padi</i>	1/8	-	-	+
2868	CYDV-RPV	oat cv. Culgoa	<i>M. dirhodum</i>	8/20	-	-	-
2868	CYDV-RPV	oat cv. Genie	<i>R. maidis</i>	8/20	-	-	-
2868	CYDV-RPV	oat cv. Genie and Culgoa	<i>R. padi</i>	5/25	-	-	+
2869	CYDV-RPV	oat cv. Genie and Culgoa	<i>R. padi</i>	8/40	-	-	+
2870 <sup>C</sup>	BYDV-PAV + CYDV-RPV	oat cv. Culgoa	<i>M. dirhodum</i>	8/20	-	-	-
2870 <sup>C</sup>	BYDV-PAV + CYDV-RPV	oat	<i>R. maidis</i>	8/20	-	-	-
2870 <sup>C</sup>	BYDV-PAV + CYDV-RPV	oat cv. Genie and Culgoa	<i>R. padi</i>	4/20	-	-	+
2871	CrRLV	oats	<i>R. maidis</i>	8/20	-	-	-
2871	CrRLV	oat cv. Genie and Culgoa	<i>R. padi</i>	4/22	-	+	-
2877	CrRLV	oat cv. Genie	<i>M. dirhodum</i>	8/20	-	-	-
2877	CrRLV	oat cv. Genie	<i>R. maidis</i>	8/20	-	-	-
2877	CrRLV	oat cv. Genie and Culgoa	<i>R. padi</i>	5/28	-	+	-

63 <sup>A</sup>Virus species determined by sequencing of PCR amplicons except for CYDV-RPV in isolate  
64 2870 which was determined by ELISA only.

65 <sup>B</sup> This isolate was negative in ELISA and thus may not have been infectious for the  
66 transmission tests.

67 <sup>C</sup> This isolate was negative for BYDV-PAV by ELISA and thus may not have been infectious  
68 for the transmission tests.

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70 **Supplementary Table 3.** Percentage nucleotide identities derived from complete genome alignments (Geneious/Muscle) of CrRLV isolate 2871  
 71 and selected isolates of other yellow dwarf viruses.

	CrRLV	BYDV-GAV	BYDV-PAS	BYDV-PAV	BYDV-OYL	BYDV-MAV	BYDV-Ker II	BYDV-Ker III	WYDV-GPV	CYDV-RPV	CYDV-RPS	TYSV	WYLaV	SCYLV	MYFV	BVG	MYDV-RMV2	MYDV-RMV	PEMV-1
CrRLV		63.8	63.3	62.7	62.1	60.1	59.8	53.2	27.9	27.7	27.5	26.9	26.5	25.9	25.6	25.6	25.6	25.3	20.1
BYDV-GAV	63.8		71.2	79.4	70.1	84.3	61.4	52.0	29.8	28.9	29.3	28.7	26.8	26.3	26.7	27.1	27.3	26.9	20.6
BYDV-PAS	63.3	71.2		79.1	82.7	66.2	60.2	52.5	30.0	29.6	29.7	28.7	27.3	26.8	26.7	27.0	27.0	26.9	21.1
BYDV-PAV	62.7	79.4	79.1		76.0	74.3	60.6	52.8	30.7	29.8	30.2	29.7	27.5	27.3	27.5	27.3	27.6	27.6	21.1
BYDV-OYV	62.1	70.1	82.7	76.0		65.5	60.2	52.7	29.3	29.1	29.6	28.7	27.4	26.5	26.7	26.8	27.0	26.8	21.3
BYDV-MAV	60.1	84.3	66.2	74.3	65.5		58.3	56.4	30.4	29.4	29.8	29.4	27.2	26.6	26.8	27.6	27.8	27.4	20.9
BYDV-Ker II	59.8	61.4	60.2	60.6	60.2	58.3		54.2	27.0	26.7	27.0	26.2	25.7	25.6	25.6	24.9	25.3	25.2	19.9
BYDV-Ker III	53.2	52	52.5	52.8	52.7	56.4	54.2		28.1	27.9	27.3	27.9	26.0	25.8	25.4	26.4	26.4	26.7	20.9
WYDV-GPV	27.9	29.8	30.0	30.7	29.3	30.4	27.0	28.1		71.1	74.9	67.0	42.5	40.8	41.0	43.4	42.9	42.4	37.1
CYDV-RPV	27.7	28.9	29.6	29.8	29.1	29.4	26.7	27.9	71.1		72.9	68.1	42.7	41.6	41.0	43.8	43.4	42.9	36.7
CYDV-RPS	27.5	29.3	29.7	30.2	29.6	29.8	27.0	27.3	74.9	72.9		65.8	42.6	41.0	41.1	43.2	43.2	42.6	37.4
TYSV	26.9	28.7	28.7	29.7	28.7	29.4	26.2	27.9	67.0	68.1	65.8		42.1	41.0	40.0	42.5	42.4	41.9	35.4
WYLaV	26.5	26.8	27.3	27.5	27.4	27.2	25.7	26.0	42.5	42.7	42.6	42.1		64.9	60.6	47.1	47.8	46.8	33.1
SCYLV	25.9	26.3	26.8	27.3	26.5	26.6	25.6	25.8	40.8	41.6	41.0	41.0	64.9		62.3	45.9	45.9	45.4	31.5
MYFV166	25.6	26.7	26.7	27.5	26.7	26.8	25.6	25.4	41.0	41.0	41.1	40.0	60.6	62.3		45.8	45.9	44.7	31.2
BVG	25.6	27.1	27.0	27.3	26.8	27.6	24.9	26.4	43.4	43.8	43.2	42.5	47.1	45.9	45.8		76.0	69.9	33.1
MYDV-RMV2	25.6	27.3	27.0	27.6	27.0	27.8	25.3	26.4	42.9	43.4	43.2	42.4	47.8	45.9	45.9	76.0		69.7	33.4
MYDV-RMV	25.3	26.9	26.9	27.6	26.8	27.4	25.2	26.7	42.4	42.9	42.6	41.9	46.8	45.4	44.7	69.9	69.7		33.6
PEMV-1	20.1	20.6	21.1	21.1	21.3	20.9	19.9	20.9	37.1	36.7	37.4	35.4	33.1	31.5	31.2	33.1	33.4	33.6	

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73 See Supplementary Materials and Methods section for virus acronyms.

## Supplementary Data

Amplicon sequence data too short for GenBank lodgement.

>isolate\_2109 [organism=Luteovirus pavhordei] [collector=M. Aftab] coat protein gene, partial cds

ACGGATACTCAAGTCCTACCATCGTTACAAGATCACAAGTATCCGAGTTGAGTTTA  
AGTCACACGCGTCCGCCACTACGGCA

>isolate\_2689 [organism=Luteovirus pavhordei] [collector= G. Nixon] coat protein gene, partial cds

ATACTTAAGTCCTACCACCGTTACAAGATCACAAGTATCCGTGTTGAGTTTAAGTC  
ACACGCGTCCGCAACCACGGCCGGCGCTATCTTTATTGAAC

>isolate\_2871 [organism=Cereal red leaf virus] [collector=G. Platz] coat protein gene, partial cds

CTGCGGTATCAAACGGAGTACTTAAGTCCTACCACCGTTACAAGATCACAAGTATT  
ACGGTCGAGTTTAAGTCCCACGCCTCAGCAACCACAACC

>isolate\_2872 [organism=Cereal red leaf virus] [collector=G. Platz] coat protein gene, partial cds

AACGGAGTACTTAAGTCCTACCACCGTTACAAGATCACAAGTATTACGGTCGAGTT  
TAAGTCCCACGCCTCAGCAACCACAACC

>isolate\_2876 [organism=Cereal red leaf virus] [collector= M. Sharman] coat protein gene, partial cds

AACGGAGTACTTAAGTCCTACCACCGTTACAAGATCACAAGTATTACGGTCGAGTT  
TAAGTCCCACGCCTCAGCAACCACAACC