**Accessory Publication**

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 25 June 2007 | 19 Aug. 2007 3-leaf stage | 20 Aug. 2007 3-leaf stage | 21 Aug. 2007 0-leaf stage | 7 Sept. 2007 1-leaf stage | 21 Sept. 2007 2-leaf stage | 4 Oct. 2007 3-leaf stage | 5 Oct. 2007 3-leaf stage |

**Temporal Group One**

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 28 June 2007 | 22 Aug. 2007 3-leaf stage | 23 Aug. 2007 3-leaf stage | 24 Aug. 2007 0-leaf stage | 11 Sept. 2007 1-leaf stage | 25 Sept. 2007 2-leaf stage | 8 Oct. 2007 3-leaf stage | 9 Oct. 2007 3-leaf stage |

**Temporal Group Two**

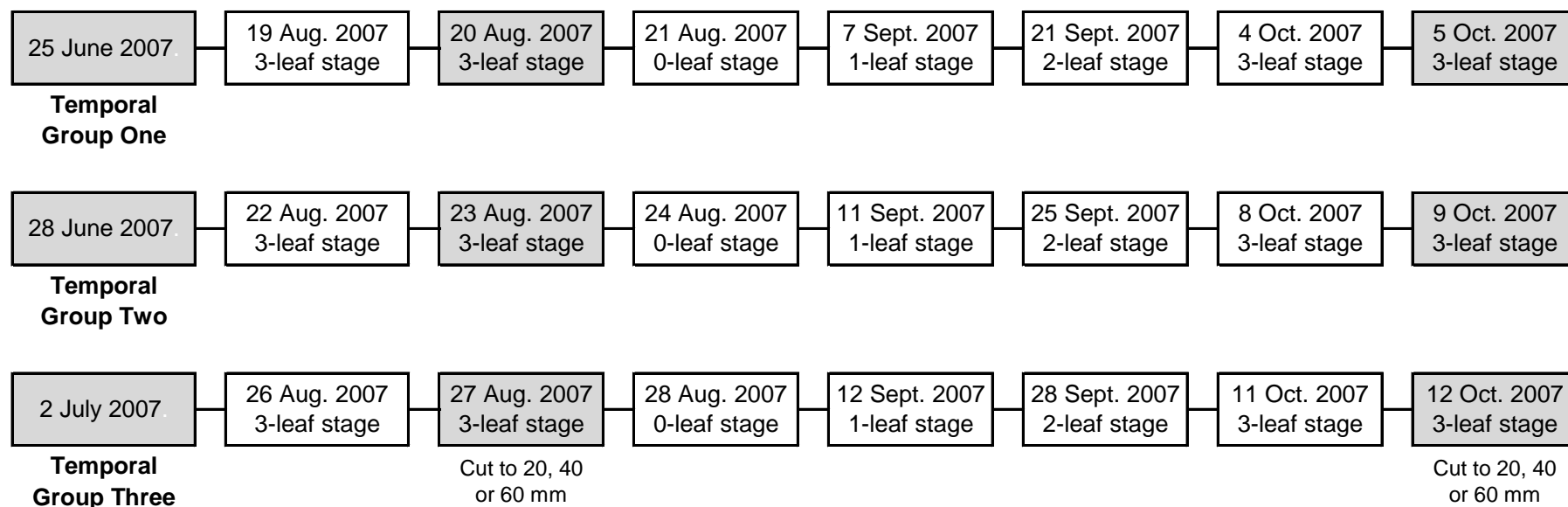| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 2 July 2007 | 26 Aug. 2007 3-leaf stage | 27 Aug. 2007 3-leaf stage | 28 Aug. 2007 0-leaf stage | 12 Sept. 2007 1-leaf stage | 28 Sept. 2007 2-leaf stage | 11 Oct. 2007 3-leaf stage | 12 Oct. 2007 3-leaf stage |

**Temporal Group Three**

Cut to 20, 40 or 60 mm

Cut to 20, 40 or 60 mm

**Fig. S1.** Diagrammatical representation of defoliation events. Perennial ryegrass-dominant plots were defoliated to 20, 40 or 60 mm residual height (grey boxes) and samples of perennial ryegrass lamina and stubble tissue were harvested from plants for reverse transcription quantitative polymerase chain reaction (RT-qPCR) analyses (white boxes). The lamina and stubble samples for RT-qPCR collected at the 3-leaf stage on the 19, 22 and 26 August were used as calibrator/control samples in the LightCycler software.

**Table S1. Meteorological data during the current study and averages from the past 30 years**

|  | Current study | | | | | Monthly averages (1976–2006) | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Jun. | Jul. | Aug. | Sept. | Oct. | Jun. | Jul. | Aug. | Sept. | Oct. |
| Maximum air temperature ($^o$C) | 14.6 | 14.7 | 15.1 | 17.0 | 17.6 | 14.3 | 13.7 | 14.6 | 16.2 | 17.9 |
| Minimum air temperature ($^o$C) | 4.7 | 5.7 | 6.1 | 6.4 | 8.2 | 5.0 | 4.0 | 4.8 | 6.6 | 8.4 |
| Radiation (MJ m$^{-2}$) | 6.5 | 6.3 | 9.3 | 12.9 | 17.5 | 6.1 | 6.8 | 9.2 | 12.8 | 16.2 |
| Total rainfall (mm) | 94 | 174 | 113 | 59 | 95 | 114 | 124 | 106 | 93 | 95 |

**Table S2. PCR primer sequences, amplicon sizes and amplification efficiency**

bp, base pairs; 3′UTR, three prime untranslated region; *rbcS1* and *rbcS2,* ribulose 1,5-bisphosphate carboxylase/oxygenase (Rubisco) small subunits; *rca*, Rubisco activase; *lhcb1* and *lhcb2*, Light harvesting chlorophyll *a*/*b* binding proteins; *fba*, fructose bisphosphate aldolase; *fbp*, fructose 1,6-bisphosphatase; *fnr*, ferredoxin-nicotinamide adenine dinucleotide phosphate oxidoreductase; *ugp,* uridine diphosphate glucose pyrophosphorylase; *sps*, sucrose phosphate synthase; *sus*, sucrose synthase; *ninv*, neutral/alkaline invertase; *hxk*, hexokinase; *hxt*, hexose transporter; *sut*, sucrose transporter; *1-sst*, sucrose:sucrose 1-fructosyltransferase; *feh*, fructan exohydrolase

| Gene | GenBank accession no. | Primer sequences (5′→3′) | Region primer in | Amplicon size (bp) | Amplicon in 3′UTR (%) | Efficiency |
|---|---|---|---|---|---|---|
| *rbcS1* | DX922407 | (F) ATA TCA CCT GGG TCG AGG AA | 3′UTR | 134 | 100 | 1.904 |
| | | (R) CCA ACG GCG AAT AAA GAA AC | 3′UTR | | | (±0.013) |
| *rbcS2* | EC778436 | (F) GAG GAG TCC GGC AAG GCA TAA | Coding | 74 | 72 | 1.950 |
| | | (R) TAT GCT TTT ACA TGT AGC CGG TTC | 3′UTR | | | (±0.039) |
| *rca* | GO924784 | (F) CCA AGA ACT TCG ACC CAA CTG | Coding | 142 | 58 | 1.937 |
| | | (R) AAC TTT CAT GCC CAG CCA TC | 3′UTR | | | (±0.026) |
| *lhcb1* | GO924759,     GO924785, | (F) GCC GAC AAC TTC ATT TCT | 3′UTR | 129 | 100 | 1.933 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | GO924789 | GA | | | | |
| | | (R) TGA GAA ATA ACC ACA AAC AGC A | 3′UTR | | | (±0.013) |
| *lhcb2* | GO924771, GO924781, GO924800 | (F) GCT GAC CCA GTC AAC AAC AA | Coding | 138 | 57 | 1.955 |
| | | (R) GTG CAG CTA CAC GTT GAT CC | 3′UTR | | | (±0.005) |
| *fba* | GO924786 | (F) CAC GTG TCG GGG TAC AAG T | Coding | 127 | 81 | 1.886 |
| | | (R) AGT ACA CCG CAG GAA GGA AG | 3′UTR | | | (±0.008) |
| *fbp* | GS923007 | (F) TGA TGC AAA TCC ATT TTG AAG | 3′UTR | 130 | 100 | 1.763 |
| | | (R) TGC TCC TCT TGG TGT CTT TG | 3′UTR | | | (±0.005) |
| *fnr* | GO924778, GO924792, | (F) GCA AAT GTT TCT TCC CAC CT | 3′UTR | 122 | 100 | 1.998 |
| | | (R) AAC AGC TTA TCG CGC TCT TT | 3′UTR | | | (±0.073) |
| *ugp* | GO924802, GO924803 | (F) TCC AGT TCT CCT TCC CTG AG | 3′UTR | 122 | 100 | 1.955 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | (R) GAA GTG CAG ATG GAC AGA GG | 3′UTR | | | (±0.035) |
| *sps* | GR510765 | (F) AGA CGT TAT CGC GCT TGA TT | Coding | 110 | 6 | 1.907 |
| | | (R) ACT GGT GTC ATT TTG TCG GTA | Coding/3′UTR | | | (±0.036) |
| *sus* | GR516033 | (F) CAT GAA GAG GTG CCT TCA GA | 3′UTR | 126 | 100 | 1.834 |
| | | (R) CCA AAA CCT CAC ACA AGT GC | 3′UTR | | | (±0.049) |
| *ninv* | AM489692 | (F) TGA GTT CTC GGC ACT GTT AAG | 3′UTR | 146 | 100 | 1.827 |
| | | (R) AGG AAT GCT CAA GCA AGT GA | 3′UTR | | | (±0.007) |
| *hxk* | GO924754 | (F) ACC TTC CTT CGG CTA TTC TG | 3′UTR | 129 | 100 | 1.877 |
| | | (R) CCT CCA TCT CCA TTG TTC CT | 3′UTR | | | (±0.033) |
| *hxt* | GS923006 | (F) TCG CTG GTG GTA ATT TTG TG | 3′UTR | 134 | 100 | 1.953 |
| | | (R) CCA GGA TTA CAG CCT CAC | 3′UTR | | | (±0.077) |

| | | G | | | | |
|---|---|---|---|---|---|---|
| *sut* | GO924755 | (F) GCC TCA AGA CTC CGT AGA GC | 3′UTR | 123 | 100 | 1.977 |
| | | (R) CAG ACC ACC TAG CCG GTA AT | 3′UTR | | | (±0.028) |
| *feh* | DQ016297, DQ073968 | (F) CCT CTG ACA ACA TGG AGG AG | Coding | 139 | 0 | 1.982 |
| | | (R) AAG CCT CCA TAK GCT GGT GT | Coding | | | (±0.004) |
| *1-sst* | AB288056 | (F) CCA AGT TTA GCT CGT GTT GC | 3′UTR | 116 | 100 | 1.923 |
| | | (R) TAT TGT ACG ATC CCC ATC CA | 3′UTR | | | (±0.040) |