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Author(s)	Shinozuka, H.; Hisano, H.; Yoneyama, S.; Shimamoto, Y.; Jones, ES; Forster, JW; Yamada, T.; Kanazawa, Akira
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Gene expression and genetic mapping analyses of a perennial ryegrass glycine-rich RNA-binding protein gene suggest a role in cold adaptation

H. Shinozuka, H. Hisano, S. Yoneyama, Y. Shimamoto, E. S. Jones, J. W. Forster, T. Yamada, A. Kanazawa

H. Shinozuka, H. Hisano, S. Yoneyama, Y. Shimamoto, A. Kanazawa (corresponding author)

Graduate School of Agriculture, Hokkaido University, Sapporo 060-8589, Japan

E-mail: kanazawa@res.agr.hokudai.ac.jp

Tel: +81-11-706-3873

Fax: +81-11-706-4933

E. S. Jones, J. W. Forster

Primary Industries Research Victoria, Victorian AgriBiosciences Centre, La Trobe University, Bundoora, Victoria 3083, Australia; and Molecular Plant Breeding Cooperative Research Centre, Australia

T. Yamada

Field Science Center for Northern Biosphere, Hokkaido University, Sapporo 060-0811, Japan

Present address:

Y. Shimamoto

Faculty of Bioindustry, Tokyo University of Agriculture, Abashiri, 099-2493, Japan

E. S. Jones

Present address: Crop Genetics Research and Development, Pioneer Hi-Bred International, 7300 NW 62nd Avenue, Johnston, Iowa 50131-1004, United States of America

Abstract A perennial ryegrass cDNA clone encoding a putative glycine-rich RNA binding protein (*LpGRP1*) was isolated from a cDNA library constructed from crown tissues of cold-treated plants. The deduced polypeptide sequence consists of 107 amino acids with a single N-terminal RNA recognition motif (RRM) and a single C-terminal glycine-rich domain. The sequence showed extensive homology to glycine-rich RNA binding proteins previously identified in other plant species. *LpGRP1*-specific genomic DNA sequence was isolated by inverse PCR amplification. A single intron which shows conserved locations in plant genes was detected between the sequence motifs encoding RNP-1 and RNP-2 consensus protein domains. Significant increase in the mRNA level of *LpGRP1* was detected in root, crown and leaf tissues during the treatment of plants at 4°C, through which freezing tolerance is attained. The increase in the mRNA level was prominent at least 2 hr after commencement of the cold treatment, and persisted for at least one week. Changes in mRNA level induced by cold treatment were more obvious than those due to treatments with abscisic acid (ABA) and drought. The *LpGRP1* protein was found to localize in the nucleus in onion epidermal cells, suggesting that it may be involved in pre-mRNA processing. The *LpGRP1* gene locus was mapped to linkage group 2. Possible roles for the *LpGRP1* protein in adaptation to cold environments are discussed.

Keywords: freezing tolerance; glycine-rich RNA-binding protein; *Lolium perenne*; post-transcriptional control; stress response

Introduction

Post-transcriptional mechanisms for regulation of gene expression involve control of pre-mRNA processing, transportation to cytoplasm and mRNA stability. These regulatory mechanisms are mediated by specific interaction between RNA-binding proteins and RNA molecules. An increasing number of proteins containing conserved RNA-binding motifs have been identified (for a review, see Alba and Pages 1998). These motifs include the RNA-recognition motif (RRM), the arginine-rich motif, the RGG box, the hnRNP K homology motif, the Zn-finger motif and the double-stranded RNA binding motif. The best-characterized motif, RRM, contains two short sub-motifs designated RNP-1 and RNP-2. There is a family of proteins that contain a glycine-rich sequence (for a review, see Sachetto-Martins et al. 2000). Proteins that contain both an RRM and a glycine-rich region at the C-terminus (glycine-rich RNA-binding proteins) belong to protein families characteristic of each structural class. This class of proteins was identified first in plants (Gomez et al., 1988), and more recently, in mammals (Derry et al. 1995; Nishiyama et al. 1997) and cyanobacteria (Sato 1994; Sugita and Sugiura 1994). Maruyama et al. (1999) showed that the cyanobacterial RNA-binding proteins and eukaryotic glycine-rich proteins are similar to each other in both structure and regulation, and that this similarity has resulted from convergent evolution.

The glycine-rich RNA-binding proteins are widely distributed in plants, including both angiosperms and gymnosperms (Sachetto-Martins et al. 2000). An increase in gene expression in response to environmental stresses such as cold, drought or wounding is one of the typical features of plant glycine-rich RNA-binding proteins (Alba and Pages 1998; Sachetto-Martins et al. 2000). Ribohomopolymer-binding assays showed that glycine-rich RNA-binding proteins such as those from maize (MA16, Ludevid et al. 1992), *Nicotiana sylvestris* (GRP-1b, Hirose et al. 1993; RGP-3, Moriguchi et al. 1997), and barley (BLT801, Dunn et al. 1996) have high affinity for poly(G) and poly(U).

Analyses of sub-cellular localization demonstrated that glycine-rich RNA-binding proteins from maize (MA16, Alba et al. 1994), *N. sylvestris* (RZ-1, Hanano et al. 1996; RGP-1b and RGP-3, Moriguchi et al. 1997), and *Sinapis alba* (SaGRP-1a, Heintzen et al. 1994) are located in nuclei. Recently, the MA16 protein was found to interact with RNA helicase (Gendra et al. 2004). Both the MA16 and RGP-1b proteins accumulate predominantly in the nucleolus, while the RGP-3 protein accumulates in nucleoplasm (Alba et al. 1994; Moriguchi et al. 1997). Because of these features, participation of the MA16 and RGP-1b proteins in pre-ribosomal RNA processing and/or rRNA transport to the cytoplasm, as well as participation of the RGP-3 protein in pre-mRNA processing, have been suggested (Alba et al. 1994; Moriguchi et al. 1997). It is also known that the expression of a glycine-rich RNA-binding protein in *Arabidopsis thaliana* (AtGRP1) is regulated according to a circadian clock through alternative pre-mRNA splicing (Staiger et al. 2003). The overall function of glycine-rich RNA-binding proteins is still unknown. However, these observations suggest that they are involved in the control of RNA processing and/or mRNA stability in response to environmental stimuli.

Like many other plants growing in global temperate regions, the agronomically important pasture grass species perennial ryegrass (*Lolium perenne* L.) can acquire freezing tolerance through exposure to low, non-lethal temperatures, a phenomenon known as cold acclimation. In addition to numerous physiological and biochemical changes, changes in gene expression at low temperatures have been detected for a large number of genes in plants, although limited information is available on the relationship between changes in gene expression and tolerance to low temperature (for a review, see Pearce 1999). To understand the mechanisms of freezing tolerance in perennial ryegrass, we have analyzed the process of adaptation to freezing in terms of changes in gene expression (Tominaga et al. 2001), alteration of cellular structural properties (Tominaga et al. 2004), and detection of quantitative trait loci (QTLs) for electrical conductivity of cell extracts that correlate with frost tolerance (Yamada et al. 2004). In the present study,

we describe the isolation of the gene for a glycine-rich RNA-binding protein, and describe changes in gene expression during cold acclimation in perennial ryegrass. The cDNA and genomic DNA structure of the gene, subcellular localization of the protein, and location on the reference genetic map were also established.

Materials and methods

Plant materials

Plants from *Lolium perenne* cv. Aberystwyth S23 were used for gene isolation and analysis of gene expression. In order to assign the *LpGRP1* gene to the reference genetic map, 164 individuals from the p150/112 mapping population, derived from the cross between a multiple heterozygous parent of complex descent as pollinator and a doubled haploid as female parent (Jones et al. 2002a, 2002b), were analyzed.

Construction and screening of cDNA library

For construction of a cDNA library, total RNA was isolated from cold-treated perennial ryegrass plants. After germination of seeds in soil, plants were grown under conditions of 16 hr light at 22°C and 8 hr dark at 18°C each day in a plant growth room over a period of 30 days. These plants were used for cold treatment. For cold treatment, plants were kept under light for 8 hr at 6°C and then in the dark for 16 hr at 2°C each day in a cold acclimation room. Plants were maintained in this condition for 14 days. Total RNA was isolated from crown tissues of 30 individual plants using TRIzol reagent (GIBCO BRL). Poly(A)⁺ RNA was purified using Dynabeads Oligo (dT)25 (Dyna). The cDNA was synthesized from the poly(A)⁺ RNA and then ligated to lambda phage vector using the lambda ZAP Express cDNA Synthesis Kit (Stratagene) according to the

manufacturer's instructions. In vitro packaging was carried out using Gigapack Gold III Packaging Extract (Stratagene). A partial glycine-rich RNA-binding protein cDNA sequence was amplified by PCR from the perennial ryegrass cDNA using a combination of the oligo(dT) primer and a gene-specific primer (5'-TGCTTCGTGGGCGGCCTC-3'). The latter was designed based on a glycine-rich RNA-binding protein cDNA isolated from wheat (Guiltinan and Niu 1996; Imai, unpublished data). The amplified fragment was cloned into the pGEM-T Easy vector (Clontech) and was used as a probe to screen the cDNA library (total titre = 6×10^6 pfu) by plaque hybridisation using the ECL Direct gene detection system (Amersham Pharmacia Biotech) in order to obtain a full-length cDNA clone.

Inverse PCR

Genomic DNA from an individual plant of cultivar Aberystwyth S23 was digested with *EcoRV* or *SacI*, and circularized by self-ligation using the Ligation high system (TOYOBO). Two rounds of PCR were carried out for amplification. The first round of the PCR was carried out in a total volume of 50 μ l using self-ligated DNAs as a template with KOD-plus DNA polymerase (TOYOBO). The second round of the PCR was carried out using a 0.1 μ l aliquot of the reaction mixture from the first round of PCR. To amplify target sequences, primers Inv.PCR-lpgrp1-F1 (5'-GTTTAGCGGCAAGAATGGCG-3') and Inv.PCR-lpgrp1-R1 (5'-CCTACTAGACGAACCGGAAC-3') were used for the first round PCR, and primers Inv.PCR-lpgrp1-F2 (5'-AGAGTACCGTTGCTTCGTCG-3') and Inv.PCR-lpgrp1-R2 (5'-AACCGGGAACGAGGACTAGT-3') were used for the second round of PCR. The PCR cycling conditions were: 96°C for 30 sec, 53°C for 30 sec, 72°C for 3 min for the first round PCR; and 96°C for 30 sec, 56°C for 30 sec, and 72°C for 3 min for the second round PCR. These cycles were repeated 28 times, and the

reaction mixture was then further incubated at 72°C for 5 min. The PCR products were cloned into the pGEM-T Easy vector (Clontech) and were subjected to sequence analysis.

DNA sequence analysis

DNA sequencing was performed with a DNA sequencing kit and a DNA sequencer (ABI373; PERKIN ELMER Applied Biosystems) according to the manufacturer's instruction. Alignment of DNA sequence was carried out using CLUSTAL W Multiple Sequence Alignment Program version 1.8 (<http://clustalw.genome.jp>) (Thompson et al. 1994). The aligned sequences were displayed using BIOEDIT (Hall 1999). Regulatory DNA elements present in the 5' upstream sequence of the gene were identified using Plant Cis-Acting Regulatory DNA Elements (PLACE) database (<http://www.dna.affrc.go.jp/PLACE/>) (Higo et al. 1999).

Treatment of plants

Plants were grown in hydroponic culture in 1/4 MS medium (Murashige and Skoog 1962), pH 5.5 under 24 hr lighting conditions at 22°C for 4 weeks. The culture medium was renewed every 10 days. The apparatus of hydroponic culture consisted of two parts. The upper part was a draining tray on which seeds were laid such that the roots elongated from the seeds could absorb water as well as nutrients from the liquid medium in the bottom tray. Cold treatment was carried out by transferring a draining tray (upper tray) on which plants were grown onto another bottom tray that had been kept at 4°C in a cold room. RNA was isolated from plants before and (2 hr and 6 hr) after transfer to the cold room. Abscisic acid (ABA) treatment was carried out by the same method: the upper tray was transferred onto another bottom tray in which 1/4 MS

medium was supplemented with 100 μ M ABA. RNA was isolated from plants 4 hr after the ABA treatment. Drought stress was applied to plants by lifting up the upper tray and placing it onto paper towels to eliminate water. RNA was isolated from plants kept in a growth chamber for 2 hr after this drought treatment. For cold treatments longer than 24 hr, soil-grown plants in a growth room were transferred to a cold acclimation room as described previously. RNA was isolated from plants cold-treated for 1, 3, 7, and 14 days after commencement of this treatment. The deacclimation treatment was performed by transferring the plants that had been cold-treated for 14 days to the plant growth room (22°C). RNA was extracted from plants 14 days after they were transferred to the plant growth room.

Isolation of nucleic acids and gel blot analysis

Total DNA was isolated from an individual plant as described by Doyle and Doyle (1987). DNA (30 μ g) was digested with restriction enzymes and fractionated by electrophoresis on a 0.8% (w/v) agarose gel. Total RNA was isolated from plants as described by Napoli et al. (1990). Total RNA (10 μ g) was fractionated by electrophoresis on a 1% agarose gel. After electrophoresis, nucleic acids were transferred to nylon membranes (Hybond N+, Amersham Pharmacia Biotech) and allowed to hybridise with labelled probes. Labelling of probes, hybridisation, washing of membranes, and detection of signals were carried out using the Alkphos Direct nucleic acid labelling and detection system (Amersham Pharmacia Biotech). The full-length *LpGRP1* cDNA sequence was labelled for use as a hybridisation probe.

Subcellular localization of LpGRP1 with enhanced green fluorescent protein (EGFP) fusion

A DNA fragment containing the entire *LpGRP1* coding region was amplified from a cDNA clone using primers “lpgrp1-For-*Bam*HI” (5'-GGATCCATGGCGGAAGAGTACCGTTG-3') and “lpgrp1-Rev-G-*Nco*I” (5'-CCATGGCACCTCCACCTCCACCTCCGTTCCCTCCAGTTGCCGGCAG-3'). The first six nucleotides of these primers provide restriction endonuclease sites that were used in subsequent plasmid construction. After cloning the PCR products into the pGEM-T Easy vector (Clontech), the *Bam*HI-*Nco*I fragment of the plasmid containing the *LpGRP1* gene was force-cloned across the *Bam*HI and *Nco*I sites of a plasmid vector that contains the *EGFP* gene (Clontech) in place of the GUS gene of plasmid pBI221 (Clontech) in the downstream of the cauliflower mosaic virus 35S promoter (Fujino, unpublished). This permitted the synthesis of an LpGRP1-EGFP fusion protein with a stretch of 7 amino acids between the fusion partners. The *LpGRP1-EGFP* plasmid was introduced into the epidermal cells of onion (*Allium cepa*) by the particle bombardment method essentially as described previously (Hisano et al. 2004). Tissues were examined after overnight incubation on 1/2 MS medium at 27°C in the dark using a fluorescence microscope (Olympus BX-51).

Genetic mapping of *LpGRP1* locus

Southern hybridisation analysis of DNA isolated from each individual of the mapping population was performed as described above. The scored genotypes were compared with segregation data of molecular markers (predominantly heterologous restriction fragment length polymorphisms [RFLPs] and amplified fragment length polymorphisms [AFLPs]) as described by Jones et al. (2002a) using MAPMAKER 3.0 (Lander et al. 1987) with a threshold confidence value of LOD>2.0. Genetic map distances were estimated from recombination values by application of the Kosambi function (Kosambi 1944). Comparative genomics analysis was performed using the TBLASTX function in

GrainGenes (<http://wheat.pw.usda.gov/cgi-bin/blast>) restricted to wheat expressed sequence tags (ESTs) assigned to mapped deletion bins (Qi et al. 2003). The locations of highest matching sequences were determined using the wEST SQL query function in GrainGenes (<http://wheat.pw.usda.gov/wEST/>).

Nucleotide sequence accession number

The *LpGRP1* genomic DNA sequence has been submitted to DDBJ with the accession number AB207971.

Results

Cloning of *LpGRP1* cDNA

Five clones were isolated from the perennial ryegrass cDNA library by hybridisation screening with a truncated putative glycine-rich RNA-binding protein cDNA. Partial sequencing analysis of these 5 clones revealed almost identical sequences. The longest putative full-length cDNA was 609 nucleotides long, discounting the poly(A)-tail, and encodes an open reading frame (ORF) from nucleotides 81 to 404. The deduced polypeptide sequence consists of 107 amino acids with a predicted molecular weight of 11.3 kDa. The alignment of the amino acid sequence with those of cognate proteins from other plants indicated that the N-terminal region containing an RRM domain is highly conserved (Fig. 1). The RRM contained perfect RNP-1 and RNP-2 sub-domain consensus sequences. The C-terminal region of the protein contained a glycine-rich sequence consisting of 22 amino acids. Because of these apparent structural characteristics, we designated the gene *LpGRP1* (*Lolium perenne* glycine-rich RNA-binding protein 1).

Isolation and analysis of the *LpGRP1* genomic DNA region

Genomic DNA for the *LpGRP1* gene was isolated using the method of inverse PCR (I-PCR). Sequence analysis of the amplified DNA fragment revealed the presence of single intron within the coding sequence of the gene (Fig. 2), between the sequences that encode RNP-2 and RNP-1 within the RRM domain.

The 5' upstream sequence was examined for the presence of transcriptional regulatory sequences. Data base searches revealed various elements known to be responsible for transcriptional activation by cold and/or other environmental stresses, such as: a low-temperature-responsive element (LTRE; Dunn et al. 1998), an ABA-responsive element (ABRE; Marcotte et al. 1989), and a dehydration-responsive element/C-repeat (DRE/CRT; Dubouzet et al. 2003) as well as a circadian clock element (Harmer et al. 2000) (see Fig. 2). Although the actual roles of these regulatory elements in *LpGRP1* transcription are yet to be determined, the presence of such elements suggests that the *LpGRP1* expression may be inducible by low temperature.

Southern hybridisation analysis of perennial ryegrass genomic DNA with a *LpGRP1* cDNA probe was performed and hybridisation signals of approximately 1.6 kb and 2.6 kb were detected for *EcoRV*- and *SacI*-digested DNA, respectively (data not shown). The sizes of these fragments corresponded with those anticipated from sequence analysis of amplified DNA, suggesting that the genomic sequence was not derived from artefactual amplification events, such as PCR-mediated recombination (Cronn et al. 2002).

Expression of *LpGRP1* gene in response to environmental stresses

Changes in the mRNA level of the gene during the process of cold treatment at 4°C

were analyzed. Previous crown freezing tests using crown tissue have shown that cold treatment confers a significant freezing tolerance to various perennial ryegrass accessions. For instance, the survival rate of cultivar Riikka under freezing conditions at -6°C for 16 hr increased from 0% to 62% by virtue of the cold treatment (Yamashita et al. 1993). Northern blot analysis clearly indicated that the mRNA level of *LpGRP1* increased during the cold treatment (Fig. 3A). The increase in the mRNA level was detectable for at least as early as 2 hr after commencement of the cold treatment (Fig. 3B), and the increase continued over the next 1 week of cold treatment (Fig. 3A). The increased level of *LpGRP1* mRNA remained unchanged during further cold treatment and reverted to pre-induction levels following transfer of plants to more normal conditions, leading to deacclimation of freezing tolerance (Fig. 3A). Expression of the *LpGRP1* gene was consequently demonstrated to be clearly associated with cold stress. The increase in the mRNA level by the cold treatment was detected in leaf, root and crown tissues (Fig. 3C). The mRNA level was also increased in response to ABA and drought treatments (Fig. 3B). No changes in the plant appearance were observed following cold or ABA treatments, but drought treatment was associated with crinkled leaves and roots (data not shown).

Subcellular localization of the LpGRP1 protein

In order to determine the subcellular localization of the LpGRP1 protein, a transient expression assay was performed using a LpGRP1-EGFP reporter fusion protein. The *LpGRP1-EGFP* gene construct was introduced into epidermal cells of onion by particle bombardment, and fluorescence was observed under microscope. When the *EGFP* gene alone was introduced into cells as a control, EGFP-derived fluorescence was observed in both the cytoplasm and the nucleus (Fig. 4E) as reported previously (see, for examples, Genda et al. 2004; Sano and Tanaka 2005; Wang et al. 2005). In contrast,

when EGFP was fused to the LpGRP1 protein, fluorescence of EGFP was detected only in the nucleus (Figs. 4A, 4B, 4C and 4D). In about 30% of observed nuclei, the fluorescence was missing from nucleoli and was detected only in nucleoplasm. It seems likely that LpGRP1 protein is capable of localization in both nucleoplasm and nucleoli.

Genetic map location of the *LpGRP1* gene

The *LpGRP1* gene was assigned to the reference genetic linkage map of perennial ryegrass through RFLP detected by Southern-hybridisation analysis of *DraI*-digested genomic DNA from the p150/112 population (Jones et al. 2002a, 2002b). In the F₁ progeny set of this one-way pseudo-testcross population, 3.3-kb and 3.6-kb DNA fragments detected by the *LpGRP1* cDNA probe displayed exclusive allelic Mendelian segregation compatible with an AB x BB genetic structure (data not shown). The corresponding RFLP locus (designated as xlpgrp1) was located within the interval between the AFLP e40t49173 and the rice cDNA-detected heterologous RFLP marker xc472 in the distal part of linkage group (LG) 2 (data not shown), in a region of conserved synteny with the long arms of the wheat homoeologous group 2 chromosomes and rice chromosome 4 (Jones et al., 2002a). The estimated map distance between the xlpgrp1 and xc472 loci was 4.1 cM. It is possible that the *LpGRP1* gene may be located close to genes for antifreeze proteins (AFPs; Sidebottom et al. 2000) on LG2, as AFP gene loci have been identified on the corresponding chromosome in meadow fescue (*Festuca pratensis* Huds.), (Humphreys et al. 2004), which is closely related to the *Lolium* species and shows a high level of conserved synteny and colinearity (Alm et al. 2003).

The *LpGRP1* gene sequence exhibited sequence similarity with a number of wheat ESTs that have been physically mapped based on deletion bins spanning defined regions of the genetic map (Endo and Gill 1996; Qi et al. 2003). The highest matches were

obtained with ESTs assigned to homoeologous groups 5AL, 5BL and 5DL (BE406557: $E = 2 \times 10^{-26}$), 3BL (BE485118: $E = 1 \times 10^{-22}$), and 2AS and 2BS (BM140613: $E = 4 \times 10^{-16}$), respectively. The highest-matching EST was also detected with high confidence by the wheat *whGRP1* gene that was used to obtain the perennial ryegrass clone ($E = 2 \times 10^{-30}$).

Discussion

The cDNA sequences for glycine-rich RNA-binding proteins have been isolated from a number of plant species. The N-terminal RRM domain of such proteins are highly conserved, but the C-terminal glycine-rich region shows substantial diversity (see for example, Stephen et al. 2003). The LpGRP1 protein described here contained motifs typical of this protein family: the RNP-1 and RNP-2 sub-domain motifs, as well as glycine-rich sequence. The glycine-rich portion of this protein was relatively short (22 amino acids following Gly 86). The length of the glycine-rich sequence in the LpGRP1 protein is apparently one of the shortest reported, only a glycine-rich RNA-binding protein from a *Medicago* species is shorter (AF191305; Potenza et al. 2001). Sachetto-Martins et al. (2000) have suggested that diversity in the length of the glycine-rich region may be attributable to enhanced genetic recombination in regions of high GC content such as observed in the mammalian keratin family. In addition, the structure of the *LpGRP1* gene glycine-rich region constitutes a simple sequence repeat (SSR) array with the structure $(GGC)_5N_9(GGC)_5$, and may consequently undergo expansions or contractions based on DNA polymerase-mediated replication slippage, as is typical of this sequence class (Weber and May 1989).

Through analysis of the *LpGRP1* genomic DNA sequence, a single intron was identified within the coding region of the gene. The intron was located to a position between the RNP-2 and RNP-1 sub-domain motifs. Intron location was compared

between reported genomic DNA sequences of plant glycine-rich RNA binding proteins, namely, maize (MA16, Gomez et al. 1988), *Euphorbia esula* (GRBP1 and GRBP2, Horvath and Olson 1998), *Brassica napus* (BnGRP10, for intron position, see Horvath and Olson 1998), *Nicotiana sylvestris* (RGP-3, Moriguchi et al. 1997), and *Arabidopsis thaliana* (Ccr1, for intron position, see Horvath and Olson 1998). The intron position between the RNP-2 and RNP-1 motifs is highly conserved between *LpGRP1* and these genes (for the position of intron, see Fig. 1). This location is the sole intron type in both the *LpGRP1* gene and all others apart from RGP-3, which contained in total 3 introns (within RNP-2, between RNP-2 and RNP-1, and downstream from RNP-1) (see Fig. 1; Moriguchi et al. 1997). This observation suggests that intron sequence was present between the sequences that encode the RNP-2 and RNP-1 sub-domains early in plant evolution, and that two more introns arose in other locations within the ancestral gene to RGP-3, subsequent to divergence from the other genes of this family.

In this study, changes in *LpGRP1* mRNA level in response to environmental stresses were analyzed, revealing clear increases during cold treatment of plants. The increase started within 2 hr after commencement of the cold treatment, continued for up to one week, and returned to pre-induction levels when plants were returned to normal temperature conditions. In general, the freezing tolerance of plants increases in proportion to the extent of increase in the period of cold acclimation. More than 7 days of cold treatment are required for achievement of the maximum level of freezing tolerance in perennial ryegrass (Lorenzetti et al. 1971). As a consequence, changes in *LpGRP1* mRNA levels during cold treatment parallel the acquisition of freezing tolerance through cold acclimation, suggesting that the *LpGRP1* protein may be closely associated with the transition to enhanced freezing tolerance. Electron microscopic analyses have revealed both enlargement of chloroplasts (potentially permitting increased accumulation of carbohydrates) and a proportionate decrease in the size of vacuoles (possibly permitting the removal of freezeable water from cells) during cold

treatment of perennial ryegrass (Tominaga et al. 2004). The gradual changes in *LpGRP1* mRNA level observed during cold treatment consequently occur in parallel to changes in the organellar structural properties, although these phenomena may be non-causally correlated rather than directly functionally associated. The results of Northern hybridisation analysis also demonstrated that induction of *LpGRP1* expression occurs in response to ABA treatment and drought stress, in addition to cold treatment.

The cellular localization of the LpGRP1 protein was investigated by fusion with an EGFP reporter protein, revealing predominant localization in the nucleus. Studies of both gene expression in response to environmental stimuli and cellular protein localization suggest that the LpGRP1 protein has functions comparable to those of SaGRP-1a of *S. alba* (Heintzen et al. 1994) and/or RGP-3 of *N. sylvestris* (Moriguchi et al. 1997), which are also localized in the nucleus and have been inferred to be involved in pre-mRNA processing.

It is known that the mRNA levels of a large number of genes change during cold treatment in plants growing in temperate regions (see Pearce 1999). It is tempting to speculate that glycine-rich RNA binding proteins may function as RNA chaperones that stabilize various gene transcripts in cold environments. Due to their broad distribution and cold-inducible gene expression in a wide range of organisms, glycine-rich RNA-binding protein may play fundamental roles in the adaptation of organisms to cold environments. In this context, a role for post-transcriptional control of a number of genes by glycine-rich RNA-binding proteins would not be unexpected.

The *LpGRP1* gene was mapped as an RFLP locus (*xlpgrp1*) to the lower distal region of perennial ryegrass LG2. QTLs for winter hardiness in the field have been identified on LGs 2, 4, 6 and 7 in preliminary studies based on evaluation of the F₂ (Aurora x Perma) population (Yamada and Forster 2005), which has been aligned with the p150/112 population-derived reference map (Armstead et al. 2002). The winter hardiness QTL on LG2 was closely linked to the extrapolated location of *xlpgrp1*. In the

related species *Festuca pratensis*, major QTLs for frost tolerance/winter survival have been mapped on LGs 1, 2, 5, and 6 (Alm et al. 2005). Co-location of stress-related genes with QTLs for stress tolerance has been previously reported in other members of the Poaceae family, especially the Triticeae cereals (reviewed by Cattivelli et al. 2002). The cold-regulated transcriptional activator, C-repeat binding factor (CBF) 3, was linked to the frost-tolerance locus *Fr-A2* on wheat chromosome 5A (Vagujfalvi et al. 2003). The genes of the CBF family were also co-incident with a QTL for cold tolerance in barley (Francia et al. 2004). However, the long arms of the homoeologous group 2 chromosomes of the Triticeae (2A, 2B and 2D of wheat, as well as 2H of barley) have not to date been identified as major sites for QTLs associated with cold tolerance. Recently, analysis of genomic introgression between winter susceptible *Lolium multiflorum* and the winter tolerant species *Festuca pratensis* revealed that a derived freezing-tolerant genotype contained a *Festuca* introgression segment in a terminal region of *Lolium* chromosome 2 (Kosmala et al. 2005). As LG2 of perennial ryegrass is the syntentic counterpart of the Triticeae group 2 chromosomes, the observation of QTL-candidate gene co-location on LG2, as well as associated functional data reported in this study, may indicate that some of the genes commonly showing allelic variation for winter hardiness differ between the pasture grasses and the cereals. However, it is very likely, on the basis of comparative genetics and genomics studies, that the basic repertoire of genes involved in cold tolerance mechanisms is highly conserved between the two groups.

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Legends of figures

Fig. 1 Multiple alignment of plant glycine-rich RNA-binding protein sequences. The RNP-1 and RNP-2 motifs are indicated above the sequence. The conserved amino acids are shown in shading. Amino acids common to all the aligned sequences are shown by asterisks below the sequence. The aligned sequences are *A. thaliana* AtGRP7 (Z14987; van Nocker and Vierstra, 1993), *S. alba* SaGRP1a (L31374; Heintzen et al., 1994), *L. perenne* LpGRP1 (AB207971; this study), *Hordeum vulgare* Blt801 (U49482; Dunn et al., 1996), *N. sylvestris* NsRGP1b (D16205; Hirose et al., 1993), *Zea mays* MA16 (X12564; Gomez et al. 1988), and *N. sylvestris* NsRGP3 (D67086; Moriguchi et al. 1997). The filled triangle and open triangles indicate positions of intron in *LpGRP1* and *NsRGP3*, respectively. Numbers on the right refer to amino acid position from the N-terminal methionine.

Fig. 2 Nucleotide and predicted amino acid sequences of the *LpGRP1* gene. The RNP-2 and RNP-1 motifs are boxed. Nucleotide sequences present in the cDNA are shown by uppercase letters. The predicted amino acid sequence is shown under the nucleotide sequence. Numbers on the right refer to the nucleotide position of this region as well as amino acid position from the N-terminal methionine. The putative TATA box and regulatory elements as well as restriction sites are indicated below the sequence.

Fig. 3 Changes in the mRNA levels of the *LpGRP1* gene in the crown tissues of plants depending on the environmental conditions. (A) Northern hybridisation analysis of RNA extracted from crown tissues of plants treated at 4°C for 1 day, 3 days, 7 days, and 14 days, treated at normal temperature (22°C) after 14 days of the 4°C treatment (deacclimation), and of control plants (0 day). (B) Northern hybridisation analysis of RNA extracted from crown tissues of plants treated at 4°C for 2 hr and 6 hr, treated with

0.1 mM ABA for 4 hr, and treated with drought for 2 hr, and of control plants. (C) Northern hybridisation analysis of RNA extracted from roots, crown and leaf tissues of plants treated at 4°C for 6 hr (6h LT), and of control plants. RNA (10 µg) was separated on a 1% (w/v) agarose gel, transferred to membrane and hybridised with labelled *LpGRP1* cDNA. The EtBr-stained rRNA bands indicate that equal amount of RNA was loaded in each lane. Corresponding positions of rRNA bands on the hybridised membranes are shown on the left side of the panels A and B.

Fig. 4 Subcellular localization of the LpGRP1 protein, shown by representative images of nuclei from transiently transformed onion epidermal cells expressing an EGFP fusion to the LpGRP1 protein. Images of DAPI staining (A), EGFP fluorescence (B), and lighting (C), and EGFP fluorescence signal overlaid with lighting image (D) are shown. The *EGFP* gene alone was introduced into cells as a control (E). Bar = 50 µm.

AtGRP7	-----	-----	-----	MASGDVEYRC	FVGGLAWATD	20
SaGRP1a	-----	-----	-----	MASPDVEYRC	FVGGLAWATD	20
LpGRP1	-----	-----	-----	MA---EYRC	FVGGLAWATN	17
Blt801	-----	-----	-----	MA--DVEYRC	FVGGLRWATD	18
NsRGP1b	-----	-----	-----	MA--EVEYSC	FVGGLAWATT	18
MA16	-----	-----	-----	MAAADVEYRC	FVGGLAWATS	20
NsRGP3	MAFYNKLGLL	LRQSI SGNV	SATSPMPSML	DAVRCMSTKL	FVGGLSWGTD	50
Consensus				*	*****	*
AtGRP7	DRAL [△] ETAF [△] AQ	YGDV [△] IDS [△] K [△] II	NDRETGRSRG	FGFVTFKDEK	AMKDAIEGMN	70
SaGRP1a	DRAL [△] ETAF [△] SQ	YGEVL [△] DSK [△] II	NDRETGRSRG	FGFVTFKDEK	SMKDAIEGMN	70
LpGRP1	DQSL [△] EQAF [△] SQ	FGEIT [△] DCK [△] II	NDRETGRSRG	FGFVTFSSSE	SMKNAIEGMN	67
Blt801	DQSL [△] QNAF [△] SK	YGDV [△] IDS [△] K [△] II	TDRETGRSRG	FGFVTFASDE	AMRQAI [△] EAMN	68
NsRGP1b	DRTL [△] LADAF [△] GT	YGEVL [△] DSK [△] II	NDRETGRSRG	FGFVTFKDEK	CMRDAIEGMN	68
MA16	NESL [△] ENAF [△] AS	YGEIL [△] DSK [△] VI	TDRETGRSRG	FGFVTFSSSE	SMLDAIE [△] NMN	70
NsRGP3	DQSL [△] LRDAF [△] AT	FGDVV [△] DARV [△] I	VDRDSGRSRG	FGFVNF [△] SDDE	CANEAI [△] KAMD	100
Consensus	*	*	*	*	*	*
AtGRP7	GQDL [△] DGRS [△] IT	VNEAQS [△] RGSSG	GGGGH [△] RG [△] GG	GGYRS [△] GG [△] GGG	YSGGG [△] GSYGG	120
SaGRP1a	GQDL [△] DGRS [△] IT	VNEAQS [△] RGSSG	GGGGGR [△] GGG	G-YRS [△] GG [△] GGG	YGGGG [△] GYGG	119
LpGRP1	GQDL [△] DGRN [△] IT	VNEAQS [△] R-SG	GGGGGY [△] SGG	GGGDS [△] AGNWR	N-----	107
Blt801	GQDL [△] DGRN [△] IT	VNEAQS [△] RRSD	GGG- [△] -GF [△] GG	GGGGY [△] GGQRR	EGGG [△] GYGGG	115
NsRGP1b	GQEL [△] DGRS [△] IT	VNEAQA [△] RGS-	- [△] - [△] - [△] - [△] GG	GGGGY [△] GGRR	EGGG [△] GYGGG	109
MA16	GKEL [△] DGRN [△] IT	VNQAQS [△] RGGG	GGGGGY [△] GGRR	GGGGY [△] GGRR	DGGY [△] GGGGGY	120
NsRGP3	GQEL [△] QGRN [△] IR	VSI [△] AQER [△] APR	SGGF [△] GGSG [△] GG	FGGGY [△] GQARD	NDG [△] Y-----	144
Consensus	*	*	*	*	*	40
AtGRP7	GGGRREGGGG	YSGGGGGYSS	RGGGGGSYGG	GRREGGGGYG	GGEGGGYGG	170
SaGRP1a	GGRE- [△] - [△] - [△] - [△] GG	YSGGGGGYSS	RGGGGGGYGG	GGRR- [△] - [△] - [△] - [△] D	GGEGGGYGG	160
LpGRP1	-----	-----	-----	-----	-----	107
Blt801	GGGYGGGRSG	GGGG- [△] - [△] - [△] YGS	RDGGGGGYGG	GGGGYGGSRG	GSGGGNWRE-	161
NsRGP1b	GGGYGGGRRE	GGGGGYGGGR	REGGGGGYGG	GGYGGGGRY-	-----	148
MA16	GGRREGGGGG	YGGGGGYGGR	REGGGGGYGG	GGGGWRD- [△] - [△] - [△] - [△]	-----	157
NsRGP3	-----	-----	-----	-----	-----	144
Consensus						
AtGRP7	GGGGGW	176				
SaGRP1a	GGGGGW	166				
LpGRP1	-----	107				
Blt801	-----	161				
NsRGP1b	-----	148				
MA16	-----	157				
NsRGP3	-----	144				
Consensus						

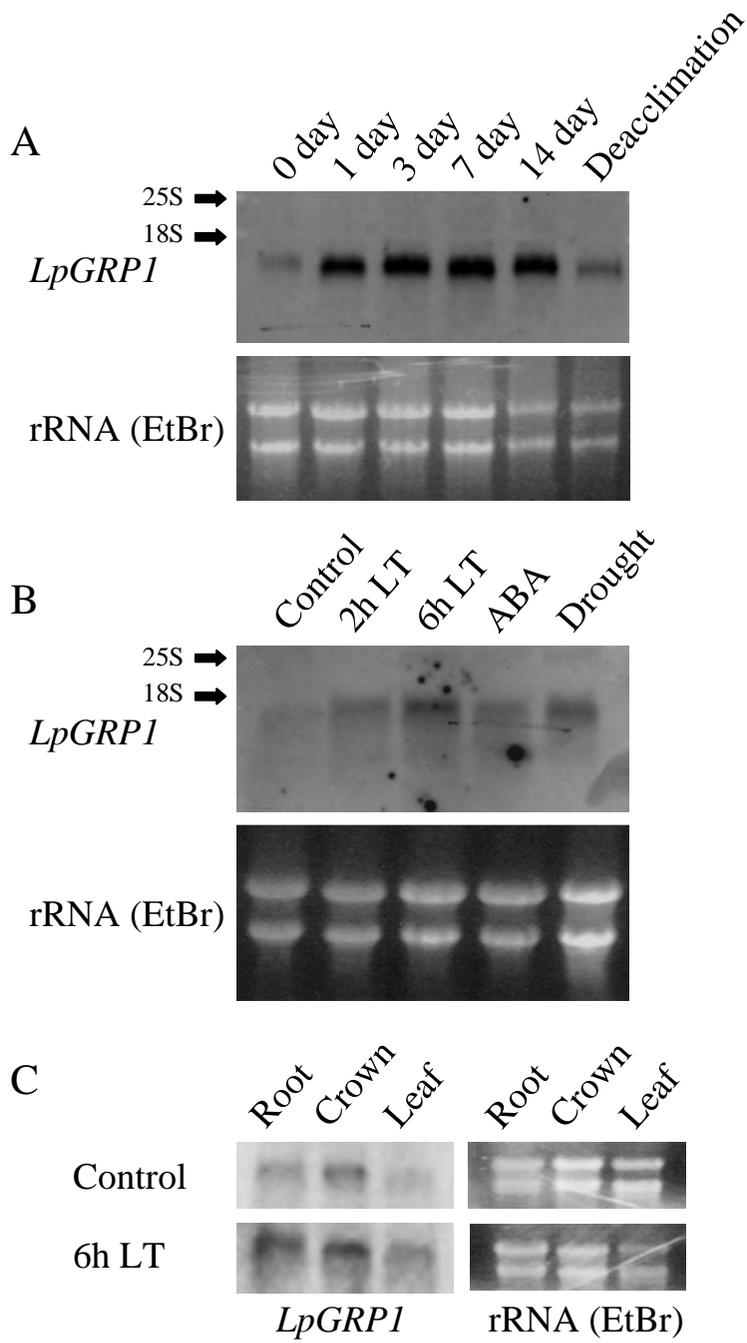


Fig. 4

