Two Novel Mitogen-Activated Protein Signaling Components, OsMEK1 and OsMAP1, Are Involved in a Moderate Low-Temperature Signaling Pathway in Rice

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Rice (Oryza sativa) anther development is easily damaged by moderately low temperatures above 12°C. Subtractive screening of cDNA that accumulated in 12°C-treated anthers identified a cDNA clone, OsMEK1, encoding a protein with features characteristic of a mitogen-activated protein (MAP) kinase kinase. The putative OsMEK1 protein shows 92% identity to the maize (Zea mays) MEK homolog, ZmMEK1. OsMEK1 transcript levels were induced in rice anthers by 12°C treatment for 48 h. Similar OsMEK1 induction was observed in shoots and roots of seedlings that were treated at 12°C for up to 24 h. It is interesting that no induction of OsMEK1 transcripts was observed in 4°C-treated seedlings. In contrast, rice lip19, encoding a bZIP protein possibly involved in low temperature signal transduction, was not induced by 12°C treatment but was induced by 4°C treatment. Among the three MAP kinase homologs cloned, only OsMAP1 displayed similar 12°C-specific induction pattern as OsMEK1. A yeast two-hybrid system revealed that OsMEK1 interacts with OsMAP1, but not with OsMAP2 and OsMAP3, suggesting that OsMEK1 and OsMAP1 probably function in the same signaling pathway. An in-gel assay of protein kinase activity revealed that a protein kinase (approximately 43 kD), which preferentially uses myelin basic protein as a substrate, was activated by 12°C treatment but not by 4°C treatment. Taken together, these results lead us to conclude that at least two signaling pathways for low temperature stress exist in rice, and that a MAP kinase pathway with OsMEK1 and OsMAP1 components is possibly involved in the signaling for the higher range low-temperature stress.

Rice (Oryza sativa) is widely cultivated in a large number of different natural environments (Nishiyama, 1984). Compared with other cereal crops such as wheat (Triticum aestivum) and barley (Hordeum vulgare), rice is much more sensitive to low temperature as a result of its tropical origin. Male sterility is the most severe consequence among the many chilling-induced agronomic damages in rice production. The developmental stages from pollen formation to fertilization are the most vulnerable to low temperature throughout the life cycle of rice plants (Nishiyama, 1984). It has been reported that the young microspore stage in pollen development was the most sensitive to low temperature (Satake and Hayase, 1970). Exposure of rice plants at the tetrad stage to a moderately low temperature (12°C) for 4 d resulted in male sterility in 80% of spikelets (Satake and Hayase, 1970; Nishiyama, 1984). Microscopic observation of developing rice anthers suggested that one possible reason for the male sterility after low-temperature treatment was the failure of anther development. The observed abnormalities included the cessation of anther development, the arrest of pollen development, anthers remaining within the flowers after anthesis, and partial or no dehiscence (Satake, 1976). Cytological observation revealed a dilatation of tapetal layers in chilling-treated rice anthers (Nishiyama, 1976, 1984). The dilatation of tapetal layer was accompanied by a vigorous augmentation of cytoplasmic organelles such as mitochondria, proplastids, Golgi bodies, and endoplasmic reticula (Nishiyama, 1976, 1984). Chilling temperature treatment also affects the physiological status of anthers. Non-reducing sugar content was found to increase rapidly, whereas the acid phosphatase activity decreased in the moderately temperature-treated rice anthers (Nishiyama, 1984). Possible involvement of phytohormones such as gibberellin and auxin in the chilling-induced male sterility has been reported (Nishiyama, 1975; Yoshioka and Suge, 1996). However, it is still largely unknown how chilling temperature induces molecular events that result in male sterility in rice plants.

Signal transduction networks enable cells to perceive the variations in the extracellular environments and to mount an appropriate response. The mitogen-
activated protein (MAP) kinase cascade pathway is among the most well-characterized signal transduction systems in animals, yeast, and plants (Jonak et al., 1994; Hirt, 1997; Mizoguchi et al., 1997; Robinson and Cobb, 1997; Schaeffer and Weber, 1999). The core of the MAP kinase cascade is constituted by MAP kinase (MAPK), MAPK kinase (MAPKK, also known as MEK) and MAPKK kinase (MAPKKK, also known as MEKK). Recently, MAPKKK kinases were identified in animal, yeast, and plant systems. The MAPK cascade was primarily found to be involved in regulating cell division, development, and differentiation, and in coordinating responses to stress stimuli in animals and yeast (Herskowitz, 1995; Robinson and Cobb, 1997; Schaeffer and Weber, 1999). In recent years, a variety of genes encoding MAPKs, MAPKKs, and MAPKKKs have been cloned from different plant species (Hirt, 1997; Mizoguchi et al., 1997; Ligatorink, 2000; Calderini et al., 2001). An increasing body of evidence has shown that MAPKs play important roles in signal transduction in response to drought, reactive oxygen species, pathogen defense, wounding, and/or low temperature in plants (Seo et al., 1995; Jonak et al., 1996; Mizoguchi et al., 1996; Shinozaki and Yamaguchi-Shinozaki, 1996; He et al., 1999; Romeis, 2001; Ren et al., 2002). In alfalfa (Medicago sativa), an MAPK homolog, MMK4, has been linked with touch, drought, and salinity stresses (Bögø et al., 1996; Jonak et al., 1996). It has also been demonstrated that SIPK (an MAPK homolog) is activated by salicylic acid within 5 min in tobacco (Nicotiana tabacum) suspension cultures (Zhang and Klessig, 1997). In a similar manner, transcripts of WIPK, an MAPK homolog in tobacco, accumulate 1 min after mechanical wounding (Seo et al., 1995). In addition, WIPK is involved in jasmonate-based wound signal transduction pathway (Seo et al., 1999).

In this study, we cloned two novel components of an MAPK pathway, OsMEK1 and OsMAP1, that are induced by 12°C treatment to elucidate the molecular responses of rice to a range of moderately low temperatures that eventually cause abnormal development of pollen. We characterized temperature dependence of OsMEK1 and OsMAP1 expression and a myelin basic protein (MBP) kinase activity. We conclude that there is a novel signal transduction pathway, distinct from the existing Lip19-involved pathway, for low-temperature responses in rice.

RESULTS
cDNA Subtraction, Cloning, and Sequence Analysis of Rice OsMEK1

A PCR-based cDNA subtraction was used to isolate cDNA clones that are induced during 12°C treatment in rice anther. The cDNA synthesized from 12°C-treated rice anther poly(A)^+ RNA and the cDNA from nontreated anther poly(A)^+ RNA was used as the “tester” and “driver” of the subtraction, respectively. A cDNA fragment (550 bp) showing high homology to ZmMEK1 (Hardin and Wolniak, 1998) was isolated after subtraction. The 550-bp fragment was used as a probe to screen a cDNA library for isolation of a full-length cDNA, designated OsMEK1. A 1.4-kb cDNA was identified and found to contain a 1,064-bp open reading frame. The putative protein encoded by OsMEK1 cDNA has 355 amino acids with features characteristic of MAPKK. OsMEK1 is predicted to have an estimated molecular mass of 40 kD and a pI of 5.47. The putative OsMEK1 protein contains the 11 conserved catalytic subdomains that are typical of Ser/Thr protein kinases (Fig. 1A). A plant MEK-specific S/TXXXXS/T motif was identified between subdomains VII and VIII in OsMEK1 (Fig. 1A). This motif differs from that of animal and yeast MEKs (SXXXX/T; Ichimura et al., 1998b). The putative OsMEK1 protein is closely related to the maize ZmMEK1 (overall 92% identity and 97% similarity at the amino acid sequence level; Hardin and Wolniak, 1998). The deduced amino acid sequence of OsMEK1 also exhibits extensive homology to other plant MEKs (Fig. 1A). Phylogenetic analysis of the amino acid sequences of the reported plant PEK homologs revealed that OsMEK1 and ZmMEK1 are grouped together with two dicot MEKs, AtMEKh (accession no. AB013392) and tobacco NQK1 (accession no. AB05514; Fig. 1B). They branched out of the subgroup 2 of plant MEKs (Mizoguchi et al., 1997) to form a novel subgroup, subgroup 4 (Fig. 1B).

Expression of OsMEK1 Is Responsive to 12°C Treatment But Not to 4°C Treatment

The full-length OsMEK1 cDNA hybridized to a single transcript of approximate 1.5-kb by northern-blot analysis of rice anther total RNA (Fig. 2A). The OsMEK1 mRNA was detected in anthers of non-stressed plants, however, 12°C treatment was found to dramatically increase the level of the OsMEK1 mRNA. In a similar manner, the OsMEK1 mRNA was also detected in nonstressed flowers, sheaths, stems, and nodes from 8-week-old rice plants. Lower levels were detected in 8-week-old leaf blades and mature seed endosperm (Fig. 2B). In 7-d-old seedlings, the level of the OsMEK1 mRNA was higher in roots than that in shoots (Fig. 2B).

To examine the expression of OsMEK1 in response to low temperature in detail, we used roots and shoots of 7-d-old rice seedlings. Northern-blot analyses revealed that the accumulation of the OsMEK1 mRNA was steadily induced in roots and shoots during a 24-h treatment at 12°C (Fig. 2C). The induction of OsMEK1 in roots and shoots was initiated within 2 h and steadily increased thereafter until 24 h subsequent to the 12°C treatment. The induction levels in shoots were higher than those in roots. It is interesting that the level of OsMEK1 mRNA was not induced in shoots and roots of 7-d-old seedlings that

Mitogen-Activated Protein Kinase for Chilling Signal
Figure 1. Comparison of the deduced amino acid sequences of OsMEK1 and closely related plant MEKs. A, Alignment of amino acid sequence in the catalytic domain of OsMEK1 (accession no. AF216314) with that of other MEK homologs from plants: maize (Zea mays) Zm-MEK1 (Hardin and Wolniak, 1998); Arabidopsis AtMAP2K2 (Jouannic et al., 1996), AtMKK2 (Ichimura et al., 1998b), AtMEK1 (Morris et al., 1997), AtMKK3 (Ichimura et al., 1998b), AtMKK4 (Ichimura et al., 1998b), and AtMKK5 (Ichimura et al., 1998a); tobacco NP2 (Shibata et al., 1995), and tomato (Lycopersicon esculentum) LeMEK1 (Hackett et al., 1998). Sequences were aligned, and gaps (dashes) have been introduced to maximize the alignment. Numbers within parentheses indicate the percentage of identity to OsMEK1. Roman numerals in italics under the sequences indicate the 11 major conserved subdomains found in Ser/Thr protein kinases. In the consensus sequence, dots indicate conservative substitution of amino acid residues, and asterisks indicate the invariant residues in all MEKs sequences. The Ser and/or Thr residues in the conserved consensus motif S/TXXXXXS/T between subdomains VII and VIII of MEKs are indicated with gray background. B, A phylogenetic tree of plant MEKs was created with Clustal X and TreeView programs with 1,000 times boot strapping (Page, 1996; Thompson et al., 1997). The distance scale represents evolutionary distance expressed as the number of substitutions per amino acid.
were subjected to a lower temperature (4°C; Fig. 2C). Instead, the levels of OsMEK1 mRNA decreased in roots during a 24-h period at 4°C. To clarify whether there was a rapid response to 4°C, OsMEK1 mRNA levels were analyzed within a short time course study (5, 10, 20, 40, and 60 min). Results indicated that OsMEK1 did not respond to 4°C treatment in a period of 1 h (data not shown). Thus, it could be concluded that OsMEK1 is induced by 12°C stress but not by 4°C stress. The data contrast previously identified cold-induced genes of rice, which have been shown to be responsive to 4°C to 6°C temperature treatments (Aguan et al., 1991; Binh and Oono, 1992; Saijo et al., 2000).

Expression of *lip19* Is Responsive to 4°C Treatment But Not to 12°C Treatment in Rice Seedlings

The rice *lip19* gene encoding a bZIP-type DNA-binding protein is inducible by low temperatures (5°C; Aguan et al., 1993). Thus, the Lip19 protein was suggested to be a transcription factor involved in a low-temperature signal transduction pathway. In this study, we compared the expression of *lip19* at 12°C and 4°C. Northern blots showed that the accumulation of the *lip19* transcript in roots and shoots of 7-d-old rice seedlings was substantially induced by 4°C treatment during a 24-h period (Fig. 3). However, the *lip19* transcript levels were only slightly induced (shoots) or decreased (roots) in the 12°C-treated seedlings during the same time course (Fig. 3). These data suggest that the expression of *lip19* is regulated by a signal transduction pathway that is activated within the 4°C temperature range. The results of the differential expression of OsMEK1 and *lip19* in response to different ranges of low-temperature treatments implied that there are distinct signaling systems that perceive and transduce different temperature signals in rice.

OsMAPI Isolation and Expression in Response to Low-Temperature Treatment

After cloning and characterizing the OsMEK1, we hypothesized that there might be an MAPK that functions in the same moderate temperature signal transduction pathway. Therefore, we attempted to isolate the MAPK gene by using expressed sequence tag (EST) sequences. Two cDNA fragments of 446 bp (M446) and 406 bp (M406) were amplified by PCR...
using two primer sets designed from rice EST clones (accession nos. C22363 and AU033195, respectively). Subcloned fragments were used as probes to screen a rice cDNA library. Three clones representing three different MAPKs were isolated. One of the clones screened with the probe M446, designated OsMAP1, was found to be induced by 12°C treatment. The other two clones (OsMAP2 and OsMAP3) screened with the probe M406 were not responsive to low temperatures (data not shown). The open reading frame of OsMAP1 encodes a putative protein (OsMAP1) that has 369 amino acid residues with an estimated molecular mass of 43.0 kD and a pI of 5.41 (Fig. 4A). OsMAP1 has the MAPK signature phosphorylation motif, TGY, between subdomains VII and VIII and thus belongs to the first subfamily of MAPKs (Seger and Krebs, 1995). OsMAP1 shares 91% identity with two other MAPK homologs, Aspk9 from oat (Avena sativa; Huttly and Phillips, 1995) and WCK-1 from wheat (Takezawa, 1999) at the amino acid sequence levels (Fig. 4A). A phylogenetic tree revealed that these monocot MAPKs constitute a novel subgroup of a plant MAPK superfamily (Fig. 4B). OsMAP1 also shows more than 70% identity to other stress-related plant MAPKs that belong to the PERK1 and PERK2 subgroups (Ligterink, 2000; Fig. 4B).

Expression of OsMAP1 Is Responsive to 12°C Treatment But Not to 4°C Treatment

Change in the levels of OsMAP1 mRNA was analyzed by northern-blot analysis. In anther tissue at the booting stage, a 12°C treatment for 48 h increased the OsMAP1 mRNA. However, OsMAP1 induction was less than that of OsMEK1 in response to 12°C (Fig. 5A). Seven-day-old seedlings were used to determine accumulation patterns of OsMAP1 in response to low temperatures (Fig. 5B). The data showed that the OsMAP1 mRNA rapidly increased in 2 h in root tissue, whereas a steady decrease in the transcript level was observed thereafter during a 24-h time period. A higher level of induction was observed in 12°C-treated shoots (6 h), although the induction was transient (Fig. 5B). In contrast, the OsMAP1 mRNA levels did not fluctuate in 4°C-treated roots and shoots during the same 24-h time period (Fig. 5B). The expression pattern of OsMAP1 contrasts those of cold-inducible MAPKs in PERK2 subgroup such as AtMPK3 (Mizoguchi et al., 1996) and MMK4 (Jonak et al., 1996), which are responsive to 4°C treatments. The observation that expression of OsMAP1 is induced by 12°C treatment and not by 4°C treatment is in good accordance with the OsMEK1 expression. These data suggest a possible involvement of OsMEK1 and OsMAP1 in moderately low-temperature signaling.

Effects of Abscisic Acid (ABA), NaCl, and Drought Stresses on the Expression of OsMEK1 and OsMAP1

It has been widely reported that cold-inducible genes also respond to water deficit (Jonak et al., 1996; Shinozaki and Yamaguchi-Shinozaki, 1996). Evidence has also shown that an MAPK cascade is involved in several signal transduction pathways in plants (Hirt, 1997; Mizoguchi et al., 1997; Ligterink, 2000). Thus, we examined the effects of ABA, NaCl, and water deficit on the expression of OsMEK1 and OsMAP1. Figure 6A shows that the accumulation of OsMEK1 mRNA was observed in 7-d-old seedlings that are drought stressed. In roots, drought-responsive induction of OsMEK1 was detected within 1 h of treatment and reached a peak at 2 h of treatment; thereafter, the levels of the transcript gradually declined (Fig. 6A). However, the response of OsMEK1 was found to be much slower in shoots (the induction peak appeared at 10 h of drought stress; Fig. 6A). The differential response is probably because roots desiccated prior to shoots in our experimental condition. OsMEK1 responded to exogenous ABA in a manner similar to drought stress in roots, whereas no clear induction was observed in ABA-treated shoots. OsMEK1 did not show clear responsiveness to the 0.2 m NaCl treatment during a period of 24 h (Fig. 6A). Accumulation of OsMAP1 mRNA was examined under the same conditions. The patterns of OsMAP1 induction were very similar to those of OsMEK1, except for the response of shoots to ABA. These data support the supposition that both genes are controlled by a similar regulatory mechanism.

OsMEK1 Interacts with OsMAP1 But Not with OsMAP2 and OsMAP3 in Yeast Cells

Similar responsiveness of OsMEK1 and OsMAP1 to environmental stimuli may suggest that the two proteins interact in vivo. To test this supposition, a yeast two-hybrid assay was used. Results in Figure 7 showed that OsMEK1 fused to the LexA DNA-binding domain interacted with OsMAP1 that was fused to the B42 activation domain. The interaction of OsMEK1 and OsMAP1 resulted in the expression of HIS3, which enabled the yeast cells to grow on the selective medium lacking Trp, Leu, and His. The yeast cells cotransformed with the LexA-fused OsMEK1 and the B42-fused OsMAP2 or OsMAP3 constructs did not grow on the selective medium, suggesting that there was no interaction among these proteins. A filter assay of β-galactosidase activity also confirmed the OsMAP1-specific interaction with OsMEK1 (data not shown). These results strongly suggest that OsMEK1 is a partner of OsMAP1 in rice.
Figure 4. Structural comparison of the deduced amino acid sequences of eight stress-responsive plant MAPKs and OsMAP1. A, Alignment of the deduced amino acid sequence of OsMAP1 (accession no. AF216315) with that of other MAPK homologs from plants: Aspk9 from oat (Huttly and Phillips, 1995), WCK-1 from wheat (Takezawa, 1999), PsMAPK from pea (Pisum sativum; Stafrastrom et al., 1993), SIPK (Zhang and Klessig, 1997) and WIPK (Seo et al., 1995) from tobacco, ZmMPK from maize (Berberich et al., 1999), AtMPK3 from Arabidopsis (Mizoguchi et al., 1993), and MMK4 from alfalfa (Jonak et al., 1996). Sequences are aligned, and gaps (dashes) have been introduced to maximize the alignment. Numbers within parentheses indicate the percentage of identity to OsMAP1. Roman numerals in italics under the sequences indicate the 11 major conserved subdomains found in Ser/Thr protein kinases. In the consensus sequence, dots indicate conservative substitution of amino acid residues, and asterisks indicate the invariant residues in all nine MAPKs. The conserved TEY phosphorylation motif is underlined. B, A phylogenetic tree of representative plant MAPKs. The tree was drawn with Clustal X (Page, 1996) and TreeView (Thompson et al., 1997) programs with 1,000 times bootstrapping. The distance scale represents evolutionary distance expressed in the number of substitutions per amino acid.
12°C Treatment Activates an Approximately 43-kD MAPK-Like Kinase in Rice Seedlings

An in-gel kinase activity assay was used to search for the kinase(s) involved in low temperature stress. Two artificial kinase substrates, MBP and casein, were independently embedded in the separating gel. Results showed that the 12°C treatment of rice seedlings activated an approximately 43-kD protein kinase that used MBP as a substrate. The kinase activity steadily increased during the 24 h of the cold stress. In contrast, the approximately 43-kD protein kinase activity steadily decreased in 4°C-treated seedlings during the same time period (Fig. 8A). These data support the idea that 4°C and 12°C treatment are perceived by different signaling pathways in rice. The 43-kD kinase activity was not detected when casein was used as a substrate, indicating that the 43-kD kinase prefers MBP as a substrate (Fig. 8B). It is to be noted that although further analysis is needed, molecular mass and substrate preference of the 43-kD kinase are in good accordance with those of OsMAP1. The temperature-dependent patterns of the approximately 43-kD MBP kinase activation and OsMAP1 expression imply OsMAP1 is a possible candidate for the approximately 43-kD MBP kinase.

DISCUSSION

By subtractive cDNA screening, we have cloned a cDNA, OsMEK1, encoding a putative MEK that interacts in vivo in yeast with an MAPK from rice. The putative OsMEK1 protein shares high homology (92% identity) with the maize ZmMEK1 and shows extensive homology with other MEK homologs identified in plants (Fig. 1). The deduced OsMAP1 protein shows 91% amino acid identity to Aspk9 (Huttley and Phillips, 1995) and WCK-1 (Takezawa, 1999), and more than 70% amino acid identity to other plant stress-responsive MAPK homologs (Fig. 5). OsMEK1 and OsMAP1 contain the 11 catalytic subdomains of Ser/Thr protein kinases. OsMEK1 also contains the conserved plant MEK-specific consensus motif (S/TXXXXXS/T; Fig. 1). Northern-blot analysis showed that OsMEK1 is ubiquitously expressed; however, the levels of mRNA accumulation were increased in anthers and seedlings during moderately low temperature (12°C) exposure (Fig. 2). The patterns of OsMEK1 and OsMAP1 expression in response to environmental stresses, including 12°C, 4°C, drought stress, salt stress, and ABA, were found to be similar,
suggesting both genes are possibly operating in the same pathway under similar regulation (Figs. 2, 5, and 6).

Similar to MAPK cascade pathways in animals and yeast, plant MAPK cascades appear to play important roles in regulating cell division and coordinating responses to environmental stresses (Hirt, 1997; Asai et al., 2002). Studies on the kinase activity and transcript levels of components of MAPK pathways led to the connection between the involvement of plant MAPK cascades and the auxin-induced cell cycle reentry (Mizoguchi et al., 1994), leaf wounding (Stratmann and Ryan, 1997), pollen development (Wilson et al., 1997), and innate immunity (Asai et al., 2002). Evidence has shown that MAPK pathways are likely involved in signal transduction under drought and low temperature stresses (Jonak et al., 1996). Arabidopsis AtMPK3 expression is strongly induced by cold stress (Mizoguchi et al., 1996). Because the sequence of OsMAP1 is most similar to the subgroup 2 MAPKs of dicots, including MMK4 and ATMPK3, OsMAP1 may have a similar function. In some MAPKs in this group, environmental stimuli can activate MAPK at transcriptional and posttranslational levels (Seo et al., 1995; Jonak et al., 1996; Bögre et al., 1997). Coordinate induction of OsMEK1 and OsMAP1 by 12°C treatment suggests that OsMEK1 and OsMAP1 proteins may be involved in a moderate temperature-specific MAPK signaling pathway.

Stress-induced transcription factors have been studied extensively due to their possible involvement in stress signaling (Shinozaki and Yamaguchi-Shinozaki, 1996; Eckardt, 2001). Kusano and colleagues (Aguan et al., 1993) have isolated a cold-inducible gene (lip19) encoding a homolog of bZIP transcription factor from rice. Although direct evidence has not been shown, Lip19 is considered to be involved in the regulation of cold-induced gene expression because a maize ortholog (mLip15) was found to bind to the promoter region of a cold-inducible gene of maize (Kusano et al., 1995). Northern-blot analysis showed that lip19 expression is induced by 4°C but not by 12°C treatment (Fig. 3). These data suggest that the Lip19 protein is involved in a specific signal transduction pathway induced within the 4°C temperature range.

Molecular responses to low temperatures have been extensively studied in a variety of plants, and many cold-regulated genes have been identified (Hughes and Dunn, 1996; Thomashow et al., 1997). The general strategy for isolating cold-regulated genes has used a low temperature range from 2°C to 6°C. A number of cold-regulated genes have been isolated and found to be inducible within this range. The same temperature range has been used to screen cold-induced genes of rice (Aguan et al., 1991; Binh and Oono, 1992). As a result, it has been confirmed that rice has a signal transduction pathway for this low temperature range. On the other hand, male sterility and its related physiological and morphological changes occur at 12°C or even higher. Therefore, it is possible that rice contains an additional signaling pathway to perceive this moderate temperature range as well. A previous report suggested there are distinctive pathways for the two temperature ranges. An 18-kD polypeptide has been shown to accumulate when rice seedlings were treated at 5°C, whereas the protein was not induced at 15°C (Koga et al., 1991). In this study, we have shown that the transcripts of OsMEK1 and OsMAP1 significantly accumulate under 12°C treatment, but not under 4°C treatment, in roots and shoots of rice seedlings (Figs. 2C and 5B). In a converse manner, the expression of lip19 was strongly induced by 4°C but not by 12°C treatment (Fig. 4). Our expression analysis with OsMEK1, OsMAP1, and lip19 clearly demonstrated there is discrimination in signal transduction between the 12°C and 4°C temperature ranges in terms of gene expression. Furthermore, the activation of a approximately 43-kD protein kinase that preferentially uses MBP as a substrate was observed in 12°C-treated shoots but not in 4°C-treated shoots (Fig. 8). Although it needs to be determined if the approximately 43-kD protein
kinase is identical to OsMAP1, it should be noted that discrimination of the two low temperature ranges can be observed at the transcriptional and posttranscriptional levels. It has been recently reported that a 56-kD calcium-dependent protein kinase (CDPK) is activated by the treatment of rice at 12°C (Martin and Busconi, 2001). Because activation of the 56-kD CDPK was observed after a longer (12 h) chilling period than that of the approximately 43-kD protein kinase, it is unlikely that the CDPK is an upstream component of the approximately 43-kD protein kinase. However, it is possible that several signaling pathways are involved in the signal transduction within the 12°C temperature range. It is worth noting that the activation of the approximately 43-kD protein kinase was not rapid and transient, but gradual during the treatment of 24 h, showing striking contrasts to the SIPK activation by salicylic acid (Zhang and Klessig, 1997) and WIPK by wounding in tobacco (Seo et al., 1995). SIPK and WIPK were rapidly and transiently activated within 5 min, and the activation could not be detected after 1 h of treatment, whereas the activation of the approximately 43-kD protein kinase lasted for 24 h.

It will be of great interest to elucidate the sensing mechanism for discriminating the two low temperature ranges. Reports show that a number of cold-inducible genes are also responsive to drought stress (Shinozaki and Yamaguchi-Shinozaki, 1996). Because OsMEK1 and OsMAP1 are induced by drought stress (Fig. 6), differences in the levels of dehydration may account for the differential expression of the genes by 12°C and 4°C treatments. However, our initial characterization suggested that 4°C-treated seedlings have slightly lower relative water contents than 12°C-treated seedlings within a 24-h time period, although both treatments reduce relative water contents (J.Q. Wen and R. Imai, unpublished data). ABA accumulation could also explain the differential expression because OsMEK1 and OsMAP1 were responsive to exogenous ABA application (Fig. 6). It was reported that ABA accumulated in rice seedlings under cold stress. The levels of ABA accumulation at 5°C were higher than that at 10°C (Lee et al., 1993). It is less feasible that higher levels of ABA accumulation occur at 12°C than at 4°C. Therefore, it is possible that the difference in the expression of OsMEK1 and OsMAP1 in response to 12°C and 4°C treatments is not due to different status of dehydration or ABA accumulation, but is due directly to the difference in the temperature. Thus, it is logical to consider that the rice plant has a mechanism to distinguish the two different ranges of low temperature, 12°C and 4°C, to elicit distinctive signals and thereafter activate specific responses.

Moderate temperatures at 12°C or higher induce male sterility at the booting stage of rice. Exposure to 12°C for 4 d at the tetrad stage of anther development resulted in male sterility in 80% of spikelets (Satake and Hayase, 1970; Nishiyama, 1984). Physiological and morphological changes associated with the 12°C chilling treatment have been described (Nishiyama, 1976, 1984). The identification of two MAPK signaling components and their involvement in a moderate temperature signaling pathway will provide some new insights at the molecular level of male sterility in rice, although a profound study is needed to clarify the functions of OsMEK1 and OsMAP1.

Figure 8. 12°C treatment of rice seedlings activates an approximately 43-kD protein kinase that preferentially uses MBP as a substrate. Seven-day-old rice seedlings were treated at 12°C or 4°C for the indicated times (hours). Untreated (25°C) seedlings were used as a control. Proteins extracted from treated or untreated shoots were separated by SDS-PAGE embedded with MBP (A) or casein (B) as a substrate. The protein kinase that is activated by 12°C treatment is indicated by an arrow in A. The size of molecular markers are shown in kilodaltons.
MATERIALS AND METHODS

Plant Materials, Growth Conditions, and Stress Treatment

Seeds of japonica rice (Oryza sativa cv. Yukihikari) were surface-sterilized in 70% (v/v) ethanol for 5 min, followed by further sterilization in 1.5% (v/v) sodium hypochlorite for 25 min, and were finally washed in distilled water. The sterilized seeds were soaked in distilled water for 12 h for imbibition. Fully imbibed seeds were germinated for 1 d at 25°C in the dark. Germinated seeds were evenly placed onto a plastic mesh grid supported by a plastic container filled with water just to the base of the mesh grid. The container was kept in a growth chamber at 25°C under continuous illumination (256 μmol m⁻² s⁻¹). After growing for 7 d, rice seedlings were subject to environmental stress treatments described below.

Low-temperature treatment was conducted by transferring the mesh grid with 7-d-old seedlings onto a plastic container filled with water prequillibrated at 4°C or 12°C in a growth chamber for 24 h prior to the treatment. The seedlings were treated at 4°C or 12°C for 1, 2, 6, 10, and 24 h under continuous illumination.

In a similar manner, ABA or NaCl treatments were performed by transferring the mesh grid with seedlings onto the container filled with 50 mM ABA solution or 0.2 M NaCl solution. Drought treatment was performed by transferring the mesh grid with seedlings (seedling roots were blotted with paper towel to remove the water prior to transferring) onto the container just to the base of the mesh grid. The seedlings were treated at 4°C or 12°C for 24 h in the dark.

Northern-Blot Analysis

Twenty micrograms of total RNA that was isolated from stressed or control samples using Trizol reagent (Invitrogen) was separated on a 1.0% (v/v) formaldehyde denaturing agarose gels and then transferred onto Hybond-N⁺ membranes (Amersham Pharmacia Biotech) according to standard methods (Sambrook et al., 1989). RNA blots were hybridized with 32P-labeled OsMEK1 or OsMAP1 full-length cDNA at 65°C for 16 h and were washed once with 2× SSC and 0.1% (w/v) SDS for 15 min, and twice with 0.1× SSC and 0.1% (w/v) SDS for 20 min at 65°C. After washing, blots were exposed to MR x-ray film (BioMax; Kodak, New Haven, CT) with an intensifying screen at −80°C.

DNA Sequencing and Analysis

The cloned DNA insert was sequenced by the dyeideox method using a Thermo Sequenase version 2.0 kit (Amersham Pharmacia Biotech) with a DNA sequencer (model 373A; Applied Biosystems, San Jose, CA). A homology search in the DNA/protein databases was carried out using the BLAST program. Analyses of the DNA sequences were performed using DNAnase software (Hitachi Software Engineering, Yokohama, Japan) or GENETYX-MAC software (Software Development, Tokyo).

In-Gel Kinase Activity Assay

Crude protein extracts were prepared from control (0 h) and low-temperature-treated (12°C or 4°C) rice shoots. Approximately 0.5 g of plant samples was ground with 1 mL of extraction buffer (50 mM HEPES, pH 7.5, 5 mM EDTA, 5 mM EGTA, 10 mM dithiothreitol [DTT], 10 mM Na3VO4, 10 mM NaF, 50 mM β-glycerophosphate, 1 mM phenylmethylsulfonyl fluoride, and one complete protease inhibitor mixture tablet [Amersham Pharmacia Biochemicals, Piscataway, NJ]). The protein extracts of each sample were separated by 10% polyacrylamide gel electrophoresis (SDS-PAGE), transferred to a nitrocellulose membrane (Amersham Biosciences, Piscataway, NJ), and blocked with 5% (w/v) nonfat dry milk in Tris-buffered saline (TBS) containing 0.1% (v/v) Tween 20 for 1 h at room temperature. The membrane was incubated with the antibody against phosphotyrosine (ATTO Life Science, Tokyo) at room temperature for 1 h. After washing, the membrane was incubated with the secondary antibody, followed by visualization of protein phosphorylation with the enhanced chemiluminescence (ECL) blotting system (Amersham Pharmacia Biotech). The results were analyzed using the ImageJ software (National Institutes of Health, Bethesda, MD).
Na$_3$VO$_4$) at room temperature for 20 min. After changing to the fresh supernatants were quickly frozen in liquid nitrogen and were stored at −80°C. The in-gel kinase assay was performed according to the procedures described previously (Zhang and Klessig, 1997) with slight modification. Ten micrograms of protein extracts was electrophoretically separated by 12% (w/v) SDS-polyacrylamide gels embedded with 0.5 mg mL$^{-1}$ bovine serum albumin, and 0.1% (v/v) Triton X-100 three times, each for 30 min at room temperature. The gel was renatured in the same buffer without bovine serum albumin and Triton X-100 at 4°C overnight with three changes of buffer. The gel was then equilibrated with the reaction buffer (25 mM Tris-HCl, pH 7.5, 2 mM EGTA, 10 mM MgCl$_2$, 1 mM DTT, and 0.3 mM Na$_3$VO$_4$) at room temperature for 20 min. After changing to the fresh reaction buffer, the reaction was initiated by adding 200 nM ATP and 50 μCi [$\gamma$-32P]ATP (3,000 Ci mmol$^{-1}$). The gel was incubated for 60 min at room temperature with shaking, and the reaction was terminated by transferring the gel into 5% (w/v) trichloroacetic acid and 1% (w/v) sodium pyrophosphate. The unincorporated [$\gamma$-32P]ATP was removed by washing with the same solution for 5 h with four changes. The gel was then dried and exposed to MR film (BioMax; Kodak).

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LITERATURE CITED


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Mitogen-Activated Protein Kinase for Chilling Signal

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