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## Sequence analysis of the *Hsp70* family in moss and evaluation of their functions in abiotic stress responses

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The 70-kD heat shock proteins (Hsp70s) are highly conserved molecular chaperones that play essential roles in cellular processes including abiotic stress responses. *Physcomitrella patens* serves as a representative of the first terrestrial plants and can recover from serious dehydration. To assess the possible relationship between *P. patens* Hsp70s and dehydration tolerance, we analyzed the *P. patens* genome and found at least 21 genes encoding Hsp70s. Gene structure and motif composition were relatively conserved in each subfamily. The intron-exon structure of *PpcpHsp70-2* was different from that of other *PpcpHsp70s*; this gene exhibits several forms of intron retention, indicating that introns may play important roles in regulating gene expression. We observed expansion of *Hsp70s* in *P. patens*, which may reflect adaptations related to development and dehydration tolerance, and results mainly from tandem and segmental duplications. Expression profiles of rice, *Arabidopsis* and *P. patens* Hsp70 genes revealed that more than half of the Hsp70 genes were responsive to ABA, salt and drought. The presence of overrepresented *cis*-elements (DOFCOREZM and GCCCORE) among stress-responsive Hsp70s suggests that they share a common regulatory pathway. Moss plants overexpressing *PpcpHsp70-2* showed salt and dehydration tolerance, further supporting a role in adaptation to land. This work highlights directions for future functional analyses of Hsp70s.

Plants cannot move to avoid harm, and have evolved a wide array of mechanisms to adapt to stressful environments. Heat shock proteins (HSPs) are stress proteins that were initially identified as responsive to heat stress<sup>1</sup>. HSPs serve as pivotal molecular chaperones by preventing aggregation of denatured proteins and promoting opportune protein folding under heat stress<sup>2–4</sup>. According to their approximate molecular weight, HSPs have been classified into five families: Hsp100, Hsp90, Hsp70, Hsp60 and small (s)Hsp<sup>5</sup>. Among them, Hsp70 (also known as DnaK-like) superfamily members together with their co-chaperone GrpE and Hsp40 (DnaJ-like) proteins, form a system for protein folding, degradation, and transport processes throughout the cell<sup>6</sup>. They also play essential roles in photosynthesis, signal transduction, transcriptional activation, and abiotic stress responses<sup>7,8</sup>. Structurally, Hsp70s are characterized by three distinct domains: an N-terminal adenosine triphosphatase (ATPase) domain, a substrate-binding domain, and a highly variable C-terminal domain.

Photosynthetic eukaryotes possess at least four types of Hsp70s, each of which localizes to a different cellular compartment: cytoplasm, mitochondrion (MT), chloroplast (CP) and endoplasmic reticulum (ER)<sup>9</sup>. The Hsp70s targeted to a given subcellular compartment share a similar evolutionary history. The ER and cytoplasmic Hsp70s evolved by gene duplication and subsequent divergence, whereas the MT and CP Hsp70s evolved by gene transfer from the endosymbiont to the nucleus<sup>10</sup>. In *Arabidopsis*, at least 18 Hsp70 superfamily members have been identified, and the genes show distinct expression profiles during different developmental stages and under thermal stress<sup>11</sup>. Moreover, the Hsp70s in peanut (*Arachis hypogaea* L.) have been confirmed play an important role in conferring drought tolerance<sup>12</sup>. Stromal Hsp70 chaperones also play a key role in chloroplast protein import<sup>13,14</sup>.

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Organism	Cytoplasm	ER	Mitochondrion	Chloroplast	Truncated	Hsp110/SSE	Number of Genes
<i>E. coli</i>	0	0	1	0	2	0	3
<i>S. cerevisiae</i>	4	1	3	0	1	3	12
<i>C. reinhardtii</i>	1	2	1	1	1	0	6
<i>P. patens</i>	10	2	4	5	0	0	21
<i>S. moellendorffii</i>	4	2	1	2	1	2	12
<i>O. sativa</i>	11	6	3	2	0	0	24
<i>A. thaliana</i>	5	3	2	2	1	4	18
<i>P. trichocarpa</i>	10	4	2	2	2	0	20

**Table 1.** *Hsp70* gene numbers in various species.

The model plant *P. patens* is dehydration tolerant and is able to recover upon rehydration, even after dehydration leading to 92% loss of fresh weight<sup>15</sup>. This ability of *P. patens* to tolerate severe dehydration makes it an ideal candidate for elucidating the molecular mechanisms by which plants respond to dehydration stress. *P. patens* is also an excellent model plant for studying plant physiology and development due to its amenability to gene knockout and allele replacement by homologous recombination<sup>16</sup>. Additionally, *P. patens* occupies a key position evolutionarily, serving as a link between green algae and seed plants<sup>17</sup>. *P. patens* can thus be used as a bryophyte representative of the first terrestrial plants<sup>18</sup>. As protective proteins, Hsp70s in *P. patens* have attracted attention for their potential roles in the process of adaptation to land, which would necessitate mechanisms for protection against stresses related to changes in temperature, light, and water availability<sup>19</sup>.

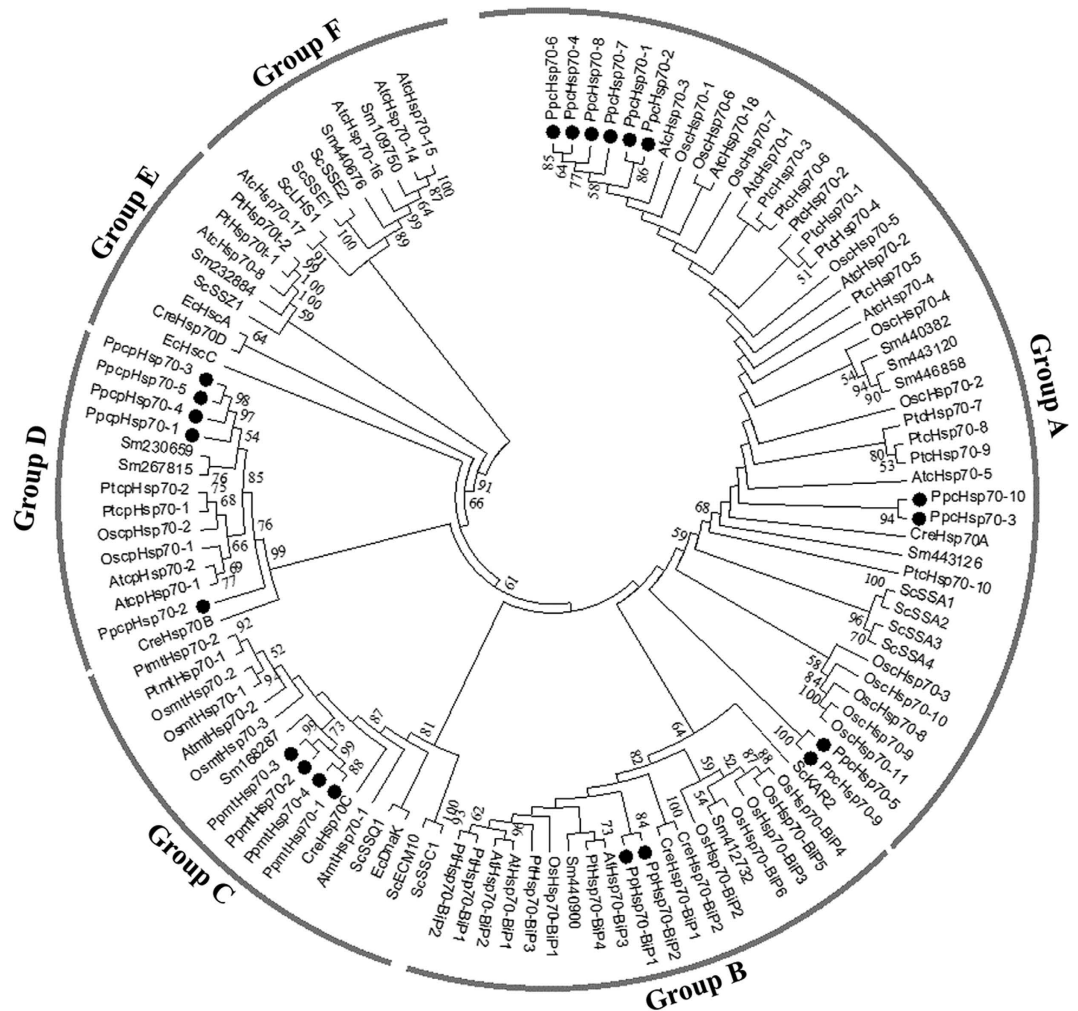
In this study, we identified *Hsp70* homologs in *P. patens*, analyzed the trends of *Hsp70* evolution among species, and examined the expression patterns of *Hsp70* genes during different developmental stages and during abiotic stress treatment. Analysis of overrepresented *cis*-elements among clusters was performed to identify conserved motifs potentially responsible for specific regulatory pathways. Furthermore, we prepared moss *cpHsp70-2* overexpression lines and found that they showed salt and dehydration tolerance. Our results lay the foundation for functional analysis of the roles of Hsp70s in stress tolerance of *P. patens*.

## Results

**Phylogenetic Analyses of the Hsp70 Superfamily.** To identify putative *P. patens* *Hsp70* genes, we first searched Phytozome databases using a published *Arabidopsis* *Hsp70* protein with conserved domain sequences as query; 29 genes were obtained using a maximum E-value of 1e-5 (Supplementary Table S1). Domain searches in SMART (<http://smart.embl-heidelberg.de/smart>) identified the *Hsp70* domain in 21 of the corresponding predicted protein sequences. It was previously reported that 24, 18 and 20 *Hsp70* genes are present in rice, *Arabidopsis* and poplar, respectively. *Escherichia coli* has three *Hsp70* genes: *DnaK*, *HscA* and *HscC*, whereas *Saccharomyces cerevisiae* contains 12 family members. In contrast to algal genomes, which have only a single cytosolic *Hsp70*, *P. patens* and other land plants have apparently required the expansion of protective proteins over the course of evolution<sup>20</sup>. The *Hsp70* genes identified in *P. patens* encode proteins ranging from 509 to 714 amino acids (aa) in length. Detailed information on the *Hsp70* genes in *P. patens*, including their gene IDs and the characteristics of their encoded proteins are listed in Supplementary Table S2.

To investigate the evolutionary relationships among *Hsp70*s from different species including both eukaryotes and prokaryotes, we identified *Hsp70* genes from *E. coli*, *S. cerevisiae*, *C. reinhardtii*, *S. moellendorffii*, *O. sativa*, *Arabidopsis*, and *P. trichocarpa* (Table 1). A Neighbour-joining (NJ) phylogenetic tree was generated by aligning the full-length *Hsp70* protein sequences from these species. The *Hsp70*s were classified into six major groups (from group A to F), each appearing to correspond to a particular predicted subcellular localization, except groups E and F (Fig. 1). Group A was the largest subfamily, with 45 members including ten members with moss paralogs. This group comprised members localized in the cytoplasm, distributed from *E. coli* to *P. trichocarpa*. Group B had 20 members, which were predicted to be localized in the ER lumen based on the *Arabidopsis* and rice orthologs. Two moss *Hsp70*s belonged to the same group as BiP.KAR2 in the yeast *S. cerevisiae*. Group C had 17 members, consisting of proteins likely found in the mitochondrion matrix, with four moss proteins forming a divergent group. Group D consisted of 14 members with five moss paralogs in the plastid stroma, and *C. reinhardtii* *Hsp70B* was the basal member of this group. Group E comprised five members that perhaps represented truncated genes, based on *P. trichocarpa* paralogs<sup>21</sup>. Group F formed an Hsp110/SSE subfamily, members of which are similar to *Hsp70* in structure and belong to the *Hsp70* superfamily. No moss proteins were included in Groups E and F.

The Predotar and LocTree3 tools predicted that moss PpcHsp70-1 to PpcHsp70-10 localize to the cytoplasm. PpHsp70-BiP1 and PpHsp70-BiP2 were predicted binding proteins (BiPs) localizing in the ER. Integration analysis of the phylogenetic tree and subcellular localization predictions indicates that the moss *Hsp70* proteins also function in different compartments like other land plants. Specifically, Group A members are likely to function preferentially in the cytoplasm, Group B in the ER, Group C in the mitochondrion matrix, and Group D in plastid stroma. In *P. patens*, the *Hsp70* superfamily genes encode 10 cytosolic *Hsp70*s, 2 BiPs, 5 plastid *Hsp70*s (*cpHsp70*s), 4 mitochondrial *Hsp70*s (*mtHsp70*s). In general, the relationships displayed in the phylogenetic tree were consistent with the traditional taxonomic classification, while the number of chloroplast *Hsp70*s varied a lot.



**Figure 1. Phylogenetic tree of Hsp70 superfamily in eight species.** The tree was constructed using the Neighbor-Joining (NJ) method based on the amino acid sequences of Hsp70 members from *Escherichia coli* (Ec), *Saccharomyces cerevisiae* (Sc), *Chlamydomonas reinhardtii* (Cr), *Physcomitrella patens* (Pp), *Selaginella moellendorffii* (Sm), *Oryza sativa* (Os), *Arabidopsis thaliana* (At), and *Populus trichocarpa* (Pt). The Hsp70s were classified into six groups, Group A localized in the cytoplasm, Group B localized in the ER (endoplasmic reticulum), Group C localized in the mitochondrion, Group D localized in the chloroplast according to the phylogenetic analyses, Group E comprised truncated genes, and Group F was a Hsp110/SSE subfamily. The 21 Hsp70 proteins of the *P. patens* were marked with black dots, and were classified into 4 groups. Numbers at each branch indicate the percentage support for the node among 1,000 bootstrap replicates.

### Multiple Sequence Alignment, Domain, and Gene Structure Analysis of Hsp70 Family Members in *P. patens*.

Multiple sequence alignment showed that Hsp70s in moss were similar to Hsp70s of other species, and included three distinct domains (Fig. 2a). The highly conserved N-terminal adenosine triphosphatase (ATPase) domain (approximately 400 amino acids) contained three Hsp70 signature sequences in groups A, B, C and D. The substrate-binding domain (approximately 200 amino acids) was extremely well conserved, but the C-terminal domain was highly variable (Fig. 2b). Most of the moss predicted Hsp70 proteins contained these domains. However, cHsp70-1 lacked part of the N terminal-ATPase domain and the substrate-binding domain. In addition, cHsp70-5 and cHsp70-9 did not include the C-terminal domain. We next used the Hsp70 proteins from *P. patens* to construct a phylogenetic tree by Mega 6.06 (Fig. 3a, left). In the cytoplasmic group, a conserved retention signal EEVD was found at the C terminus, except in cHsp70-5 and cHsp70-9. The mitochondrial Hsp70 homologs possessed the conserved signature sequences GDAWV and YSPSQI. Interestingly, whereas Hsp70-Bip1 and Hsp70-Bip2 were homologous to ER proteins, they had HED/EL sequences at the C terminus, in contrast to the HDEL ER retention signal of Hsp70 in other land plants. The motif for five chloroplast Hsp70s was conserved (DVIDADFTDSK), while the plastid signal of cpHsp70-2 was slightly different from that of other four cpHsp70s.

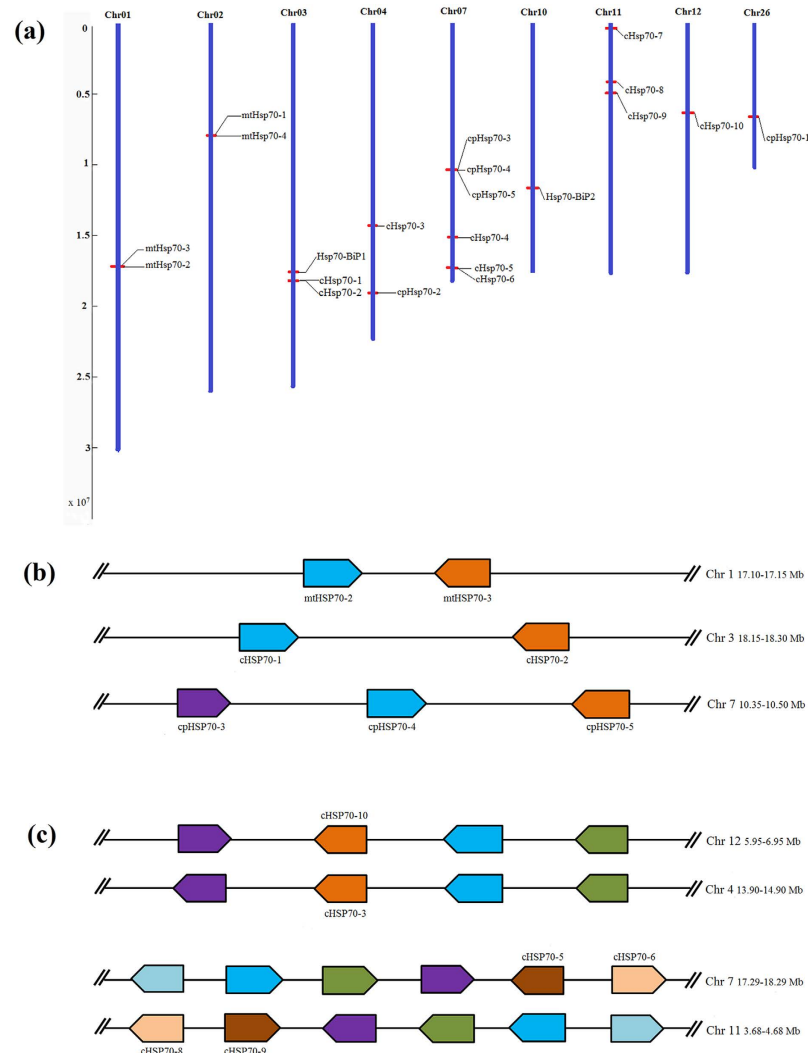
Using MEME, 20 consensus motifs were detected in moss Hsp70 proteins, with lengths ranging from 15–50 aa (Fig. 3b, and Supplementary Table S3). Most Hsp70s contained motifs 1, 2, 4, 5, 7, 10, 11, and 12, which corresponded to the conserved ATPase domain. Motifs 3, 8, 15 and 16 were included in the substrate peptide domain. Motif 20 was uniquely found in the chloroplast group, whereas motif 14 was absent from those same proteins. The











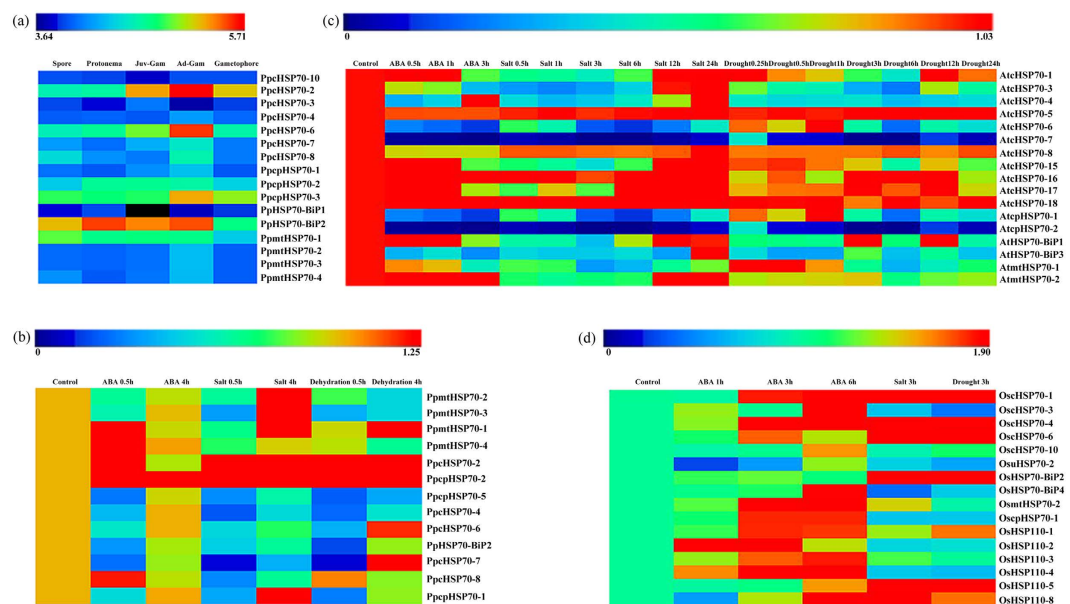
**Figure 4. Chromosomal locations and gene duplications of *P. patens* Hsp70s.** (a) The 21 Hsp70 genes were mapped to 9 chromosomes. Schematic diagram of *P. patens* Hsp70s based on the sequence map was provided by the Phytozome website. Gene names are listed to the left of the chromosomes, and map markers are listed to the right. (b) Evidence for tandem duplication of *P. patens* Hsp70s. Diagram shows chromosomal locations of Hsp70 genes and linked homologous genes in *P. patens* identified in PTGBase (<http://ocri-genomics.org/PTGBase/>). Pentagons point in the 5'→3' direction. (c) Evidence for segmental duplication of *P. patens* Hsp70s. Paralogous gene pairs generated by gene duplication within the Hsp70 family of *P. patens* were analyzed using the Plant Genome Duplication Database (<http://chibba.agtec.uga.edu/duplication/>). The black line represents syntenic blocks in *P. patens* chromosomes, and the different colors of pentagons represent different genes. The Hsp70 gene names are marked above or below the pentagons. Synonymous (Ks) and nonsynonymous substitution (Ka) rates are presented for each pair. Gene pairs were generated by tandem duplication (T) and whole-genome duplication (W).

identified large blocks of synteny between Chr7 and 11 (including *cHsp70-5/cHsp70-9*, *cHsp70-6/cHsp70-8* and six other paired genes) by investigating the flanking regions within 500 kb in either direction of Hsp70 genes. The synonymous substitution rate (Ks) values of three paired genes (*cHsp70-3/cHsp70-10*, *cHsp70-5/cHsp70-9*, *cHsp70-6/cHsp70-8*) ranged from 0.7 to 1.4, and the ratios of the nonsynonymous substitution rate (Ka) to the synonymous substitution rate (Ks) were 0.21, 0.01 and 0.05, respectively (Table 2).

**Hsp70 Genes in Land Plants are Responsive to ABA, Salt or Drought.** We obtained publicly available microarray data to explore the expression profiles of Hsp70 genes at different stages of development and under abiotic stress treatments in moss, rice and *Arabidopsis*. As Fig. 5a and Supplementary Table S4 show, the expression of two cytoplasm-group genes (*cHsp70-2*, *cHsp70-6*), and two chloroplast-group genes (*cpHsp70-2* and *cpHsp70-3*) in *P. patens* increased gradually with developmental stage from spore to protonema through adult gametophore, suggesting that these genes involved in the development of moss. Other genes maintained a steady expression level throughout multiple stages of development. For example, a gene encoding a homolog of the binding proteins in the ER (*Hsp70-BiP1*) showed high expression in both protonema and the adult gametophore.

No.	Gene 1	Gene 2	Ka	Ks	Ka/Ks	Duplication
1	<i>PpcHsp70-5</i>	<i>PpcHsp70-9</i>	0.15	0.71	0.21	W
2	<i>PpcHsp70-6</i>	<i>PpcHsp70-8</i>	0.01	1.4	0.01	W
3	<i>PpcHsp70-3</i>	<i>PpcHsp70-10</i>	0.04	0.84	0.05	W
4	<i>PpcHsp70-1</i>	<i>PpcHsp70-2</i>	0.0008	0.0030	0.2774	T
5	<i>PpmtHsp70-2</i>	<i>PpmtHsp70-3</i>	1.94	4.43	0.44	T
6	<i>PpcpHsp70-3</i>	<i>PpcHsp70-4</i>	NA	NA	NA	T
7	<i>PpcpHsp70-4</i>	<i>PpcHsp70-5</i>	NA	NA	NA	T

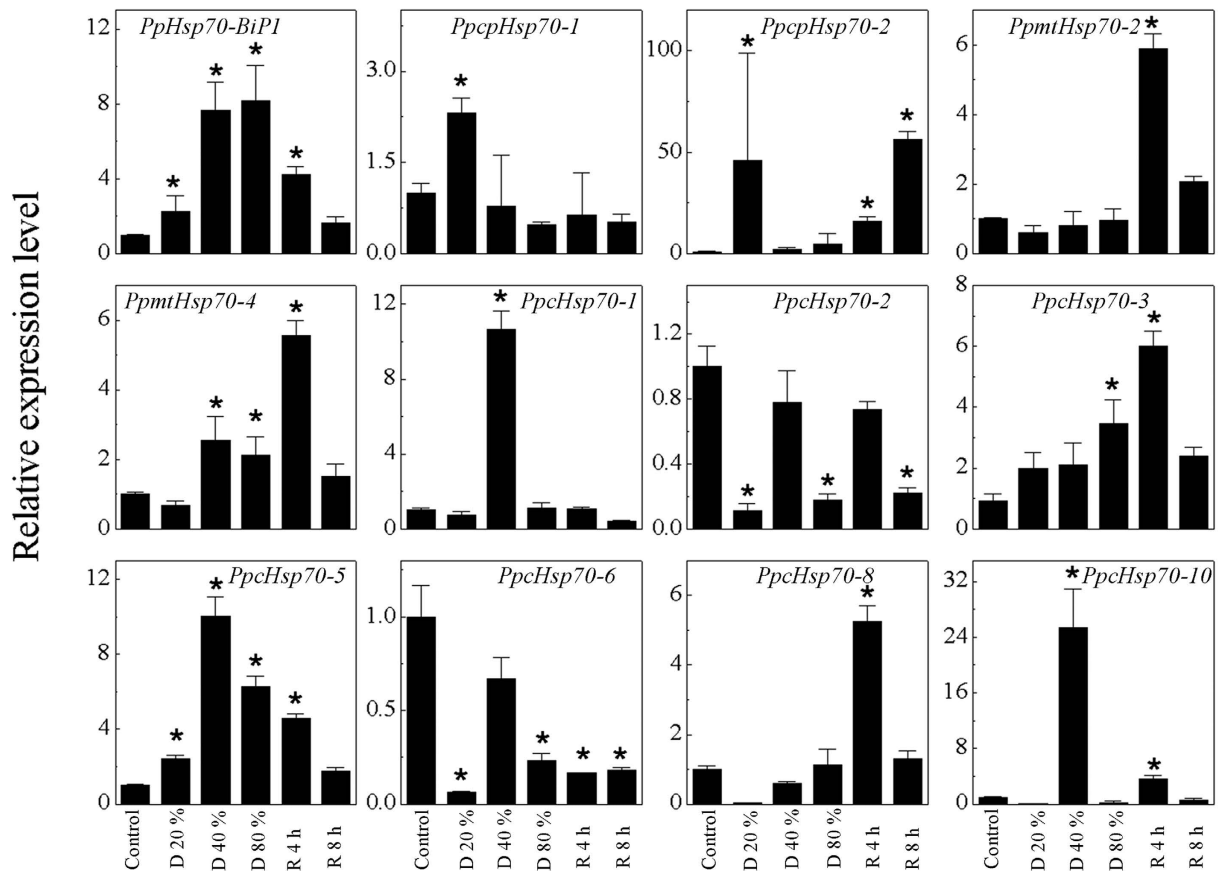
**Table 2.** Divergence between paralogous *Hsp70* gene pairs in *P. patens*. Synonymous (Ks) and nonsynonymous substitution (Ka) rates were presented for each pair. Gene pairs were generated by tandem duplication (T) and whole-genome duplication or other large-scale segmental duplication (W).



**Figure 5.** *Hsp70* expression profiles for *P. patens*, *O. sativa*, and *Arabidopsis* are shown. The *Arabidopsis* microarray gene expression data were obtained from AtGenExpress. The public expression data in rice were obtained from the Michigan State University (MSU) Rice Genome Annotation (<http://rice.plantbiology.msu.edu>) databases. The *P. patens* transcriptome data were obtained from Phytozome 10.3 (<http://phytozome.jgi.doe.gov/pz/portal.html>). (a) The heat map shows expression of *Hsp70* genes in different developmental stages (spore, protonema, juvenile stage, adult stage and gametophore) according to available microarray-based data. The expression profile was generated with log-transformed average values (b) *P. patens* *Hsp70* superfamily genes expression under ABA (0.5 h and 4 h), salt (0.5 h and 4 h) and dehydration treatment (0.5 h and 4 h). (c) *Arabidopsis* *Hsp70* superfamily genes expression under ABA (0.5 h, 1 h and 3 h), salt (0.5 h, 1 h, 3 h, 6 h, 12 h and 24 h), drought treatment (0.25 h, 0.5 h, 1 h, 3 h, 6 h, 12 h and 24 h). (d) Rice *Hsp70* superfamily genes expression under ABA (1 h, 3 h and 6 h), salt (3 h), and drought (3 h) treatment. The expression profile of (b–d) was generated with the fold changes using the average values for each treatment divided by the values of the control.

In *P. patens*, *cHsp70-2* and *cpHsp70-2* were highly induced by ABA, salt and dehydration treatment (4–11 fold increase) and maintained high expression as the time of treatments continued. The expression of other *Hsp70* genes in *P. patens* decreased significantly except for *mtHsp70-1*, *mtHsp70-4* and *cpHsp70-8*, which was initially induced dramatically by salt and then dropped rapidly. In rice, more than half of the *Hsp70* genes were highly induced by ABA, salt and dehydration treatments, whereas *OscpHSP70-1* expression was only slightly induced by ABA treatment. By contrast, most *Arabidopsis* *Hsp70* genes, such as chloroplastic *AtcpHsp1* and *AtcpHsp2*, exhibited a pattern of a decreased expression, with slight quantitative differences. Among all chloroplast *Hsp70* genes, only moss *cpHsp70* was up-regulated highly and steadily under ABA, salt and dehydration treatment (none were up-regulated in rice or *Arabidopsis*), suggesting that moss *cpHsp70s* might have been critical for the adaptation to land.

To further explore the *P. patens* *Hsp70* response to dehydration stress and rehydration, we used qRT-PCR to determine relative normalized expression (Fig. 6). At the beginning of dehydration treatment, decreased expression was observed for most of the *P. patens* *Hsp70* genes, e.g., *mtHsp70-2*, *mtHsp70-4*, *cHsp70-2*, *cHsp70-6*, *cHsp70-8*, and *cHsp70-10*. By contrast, at the beginning of rehydration most *Hsp70* gene expression increased, as for *cpHsp70-2*, *mtHsp70-2*, *mtHsp70-4*, *cHsp70-3*, *cHsp70-5*, *cHsp70-8*, and *cHsp70-10*. However, *cHsp70-1*



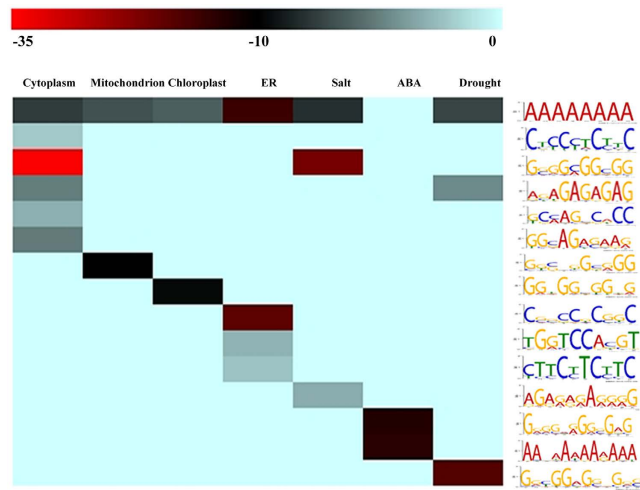
**Figure 6. Relative normalized expression of *P. patens* Hsp70 superfamily genes during treatment with dehydration stress and rehydration.** The line-chart shows relative expression of Hsp70 genes at different points during treatment with dehydration stress and rehydration, as monitored by RT-qPCR (with *Actin* as control). Control, *P. patens* gametophores with no treatment; D 20%, *P. patens* gametophores air-dried to 20% water loss; D 40%, *P. patens* gametophores air-dried to 40% water loss; D 80%, *P. patens* gametophores air-dried to 80% water loss; R 4 h, D 80% *P. patens* gametophores re-watered for 4 h; R 8 h, D 80% *P. patens* gametophores re-watered for 8 h. There were five replicates for each treatment, and the experiment repeated at least three times. Values are mean  $\pm$  S.D,  $n = 5$ . An asterisk indicates that the value of treatment is different from control ( $p < 0.05$ ).

transcripts accumulation increased 10-fold after dehydration treatment leading to 40% water loss, and those of *cpHsp70-2* increased 46-fold after dehydration to 20% water loss. Thus, the Hsp70 expression patterns during dehydration and rehydration reveal these genes to be quite sensitive to such stress in *P. patens*. Overall, these results indicate the likely function of moss Hsp70 superfamily genes, especially chloroplastic *cpHsp70-2*, in abiotic stress defense.

#### **Cis-element Analysis of Hsp70 Promoter Sequences Points to Conserved Regulatory Pathways.**

To explore the evolution of the regulation of Hsp70 genes in land plants, we performed a comprehensive *cis*-element analysis for seven clusters of Hsp70 genes: cytoplasm localized, mitochondrion localized, chloroplast localized, ER localized, salt induced, ABA induced, drought or dehydration induced (for details of clusters see Supplementary Tables S5 and S6). Certain *cis*-elements were selectively enriched in various clusters (Fig. 7 and Supplemental Table S6), although there was an obvious difference in the range of *cis*-elements distributed among the different clusters. Seven clusters were enriched for the MARTBOX, which is the most common element in flowering plants and is suggested to play role in transcriptional regulation<sup>26</sup>. The SORLIP2AT element, which is over-represented in light-induced promoters of phytochrome genes (*phyA*) in *Arabidopsis*<sup>27</sup>, was significantly enriched in cluster 3. Another element, DOFCOREZM, associated with plant metabolism and drought responses<sup>28,29</sup>, was overrepresented in cluster 6. The GCCCORE was enriched in cluster 5 and is reported to be present in promoters of many pathogenesis-related genes with a role in JA signaling pathways or plant defense signal perception<sup>30,31</sup>. A novel element (GGCGGAGGGGG) was prominently enriched in cluster 7, with E-value 7.6E-19. These results suggest that clusters of Hsp70 genes share common regulatory factors and indicate conservation of elements in the evolution of stress regulatory networks in land plants.





**Figure 7.** *Cis*-element analysis of promoter sequences of genes for *Hsp70*s localized to different cellular locations and induced under different abiotic stress treatments. Over-representation of known *cis*-elements in promoters of *Hsp70* superfamily genes was extracted according to the E-value. Logo representations of known *cis*-elements are on the vertical axis, and the different cellular locations and treatments are on the horizontal axis. Colored boxes represent log 10-transformed average E-value of *cis*-element and cellular locations and treatment with a significant statistical link.

**Moss Plants Overexpressing *PpcpHsp70-2* Show Salt and Dehydration Tolerance.** To address the question of whether *PpcpHsp70-2* plays important roles in abiotic stress responses *in vivo*, transgenic moss overexpressing *PpcpHsp70-2* under the control of the CaMV35S promoter was generated and tested for salt and dehydration responses. These plants exhibited clearly increased tolerance of salt and dehydration, relative to WT plants (Fig. 8). Chlorophyll fluorescence of two overexpression lines and WT grew weaker during the salt and dehydration treatment, but WT lost photosynthetic activity faster than did the transgenic lines (Fig. 8b,c). These data support the conclusion that *PpcpHsp70-2* exerts a function not only in protein import but also in abiotic stress defense.

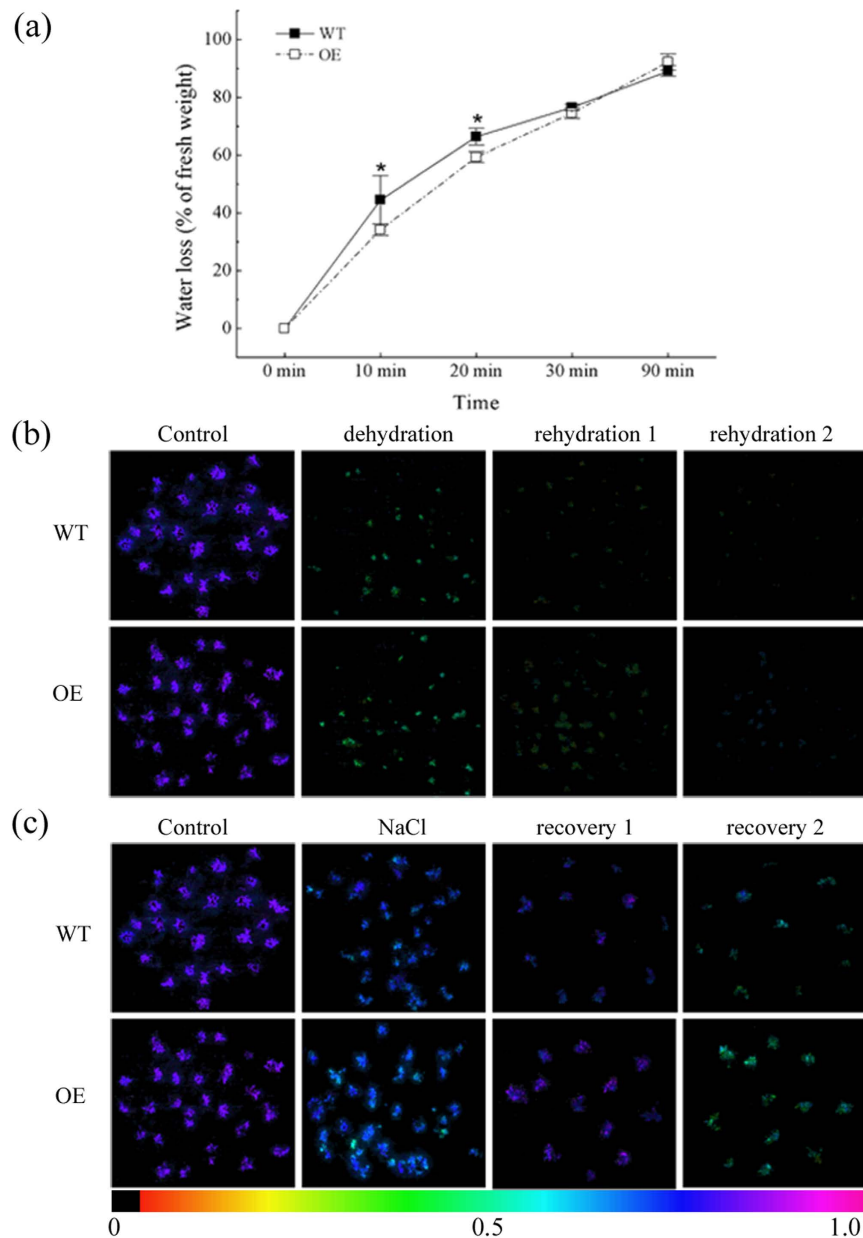
## Discussion

**The *Hsp70* Superfamily in *P. patens*.** *Hsp70* proteins exist widely and play significant roles in organisms ranging from prokaryotes to the land plants. In this work, we aimed to characterize *Hsp70* genes in *P. patens* because *Hsp70* proteins occupy a central position in the cellular chaperone network, interacting with chaperones of other families. To elucidate the evolutionary relationships between *Hsp70* proteins in moss and other organisms, a combined phylogenetic tree was produced. Our phylogenetic analysis revealed that the *Hsp70* family includes many paralogous genes with different functions, according to the six major clades displayed in the tree. Group E and F were divided earliest and the genes of these two groups, which were distributed broadly in many species, might be non-functional. Subsequently, Group D diverged and a large number of chloroplast *Hsp70* proteins of different green plants were clustered in the same large clade, which suggests a common ancestry of plastid *Hsp70* in diverse land plants. In particular, *PpcpHsp70-2* exhibited a distance from other *PpcpHsp70*s and was placed close to *CreHsp70-2*, which suggests this moss chloroplast *Hsp70* might have evolved from that in green algae. In general, the fact that *Hsp70* genes from various species were fell into the same large groups according to their predicted cellular locations, indicative of evolutionary conservation among organisms.

We identified 21 genes in the moss genome encoding the domains characteristic of *Hsp70* proteins. For example, PpmtHsp70-1 contained an N-terminal ATPase domain, a substrate-binding domain, and a C-terminal domain and shared three typical signature motifs (Fig. 2), which coincide with the structural characteristics of the *Hsp70* superfamily<sup>9</sup>. Though there have been studies on the cytosolic and chloroplast *Hsp70* families of moss<sup>5,14</sup>, this work represents the first comprehensive study of the entire moss *Hsp70* superfamily.

We found four mtHsp70 proteins in moss, one more than in rice<sup>32</sup>. PpmtHsp70s possessed the conserved signature sequences, suggesting that they are true mitochondrial *Hsp70* homologs<sup>33</sup>. The mRNA level of a mitochondrial *Hsp70* gene from the Antarctic moss *Pohlia nutans* was previously reported to increase after water deprivation and continually increase after re-watering<sup>34</sup>. Interestingly, we found a similar expression pattern for *mtHsp70-2* and *Hsp70-BiP2* in *P. patens* during dehydration and rehydration. In addition, there are two *Hsp70*-BiPs in both moss and *S. moellendorffii*, fewer than in rice and *Arabidopsis*. As demonstrated in tobacco, constitutive overexpression of *Hsp70*-BiPs is enough to confer tolerance to water stress<sup>35</sup>. The evolutionary similarity of the moss mtHsp70 and *Hsp70*-BiPs to those of the flowering plants suggests that the moss *Hsp70* proteins might also share the common localization and function.

We identified 10 cytosolic *Hsp70* genes in moss, one more than previously reported<sup>19</sup>. Among these were genes for seven canonical proteins (including the EEVD at C terminus) and three nonclassical cytosolic *Hsp70* proteins (cHsp70-1, cHsp70-5 and cHsp70-9). It has been reported that EEVD sequences are involved in binding



**Figure 8. Overexpression *PpcpHsp70-2* plants showed salt and dehydration tolerance.** (a) Time courses of water loss from gametophores of wild-type (WT) and over-expression *PpcpHsp70-2* (OE) plants. Water loss was calculated as the percentage of initial fresh weight. (b) Chlorophyll fluorescence of wild-type and overexpression plants during the course of dehydration and rehydration. *P. patens* gametophores air-dried to 80% water loss (dehydration) and then re-watered for 1 d (rehydration 1) and 2 d (rehydration 2) at room temperature. (c) Chlorophyll fluorescence of wild-type and overexpression plants after NaCl treatment and recovery at normal growth conditions. *P. patens* gametophores were treated on plates with 500 mM NaCl for 3 d and then transferred to normal conditions for recovery periods of 1 d (recovery 1) and 2 d (recovery 2). There were five replicates for each treatment, and the experiment repeated at least three times. Values are mean  $\pm$  S.D,  $n = 5$ . An asterisk indicates that the value of treatment is different from control ( $p < 0.05$ ).

proteins such as Hop (Hsp70 Hsp90 organizing protein) through tetratricopeptide motifs<sup>36</sup>. The seven canonical cytosolic Hsp70 proteins might play similar important roles in moss as in other land plants. By contrast, we did not find evidence for expression of the nonclassical *Hsp70* genes in the profiling data reported by Hiss<sup>37</sup>, which provides evidence that *cHsp70-1*, *cHsp70-5* and *cHsp70-9* genes probably are pseudogenes (Fig. 4). The function and impact of these pseudogenes in moss remains to explore in the future.

Shi *et al.*<sup>14</sup> previously described three cpHsp70 proteins, and we found genes corresponding to five cpHsp70 proteins in our study, thanks to improved genome sequencing information. Although cpHsp70-3, cpHsp70-4 and cpHsp70-5 had the same predicted length, pI and molecular weight, their corresponding genomic positions were different. Compared with other plant species (Fig. 1), moss had more cpHsp70 proteins, suggesting that they

might have been important in adaptation to the land environment. PpcpHsp70-1, PpcpHsp70-3, PpcpHsp70-4 and PpcpHsp70-5 were clustered into a separate clade and formed a sister group with two predicted proteins of *S. moellendorffii*, whereas PpcpHsp70-2 was placed in a sister group with Hsp70B of *C. reinhardtii*. Knockout of *PpcpHsp70-2* is lethal<sup>14</sup>, and considering the difference in plastid motif between cpHsp70-2 and other cpHsp70s, cpHsp70-2 might play vital and unique role in the response of moss to land environment. The chloroplast-localized Hsp70 proteins from *P. patens*, *Arabidopsis* and rice have been reported to be essential for protein import into chloroplasts and for chloroplast differentiation under high temperatures<sup>38</sup>. Recently, Liu *et al.*<sup>13</sup> demonstrated that a stromal Hsp70 in *P. patens* serves as a motor protein via ATP hydrolysis for the import of proteins into chloroplasts. In addition, stromal Hsp70s in *Arabidopsis* are important for thermotolerance of germinating seeds<sup>39</sup>, indicating that plastid physiology is important for seeds to endure heat stress. In rice, OsHsp70CP1 is essential for chloroplast development under heat-stress conditions<sup>38</sup>. Thus, land plants might share a general mechanism by which the stromal Hsp70s play roles in stress tolerance, possibly related to maintenance of chloroplast photosystem activity.

**Duplications Played Major Roles in the Diversification of Hsp70 Gene Families.** The *P. patens* genome is approximately 480 Mb organized as 27 chromosomes. Rensing *et al.*<sup>40</sup> reported that *P. patens* genome duplication might have occurred between 30 and 60 million years ago, based on the construction of linearized phylogenetic trees. It was also predicted that tandem and segmental duplications contributed to expand the number and roles of gene families<sup>41</sup>.

In moss, *mtHsp70-2* and *mtHsp70-3*, *cHsp70-1* and *cHsp70-2*, *cpHsp70-3* and *cpHsp70-4*, *cpHsp70-4* and *cpHsp70-5* are all pairs of tandemly arrayed genes (Fig. 4b) that are closely related in the NJ tree (Fig. 3a, left), suggesting that they are the result of tandem duplication. Conversely, other pairs of Hsp70 genes (*cHsp70-3/cHsp70-10*, *cHsp70-5/cHsp70-9* and *cHsp70-6/cHsp70-8*) are located at collinear positions on different chromosomes, and thus appear to have been copied during whole-genome duplication or other large-scale segmental duplication events. Their low Ka/Ks ratios indicate that these three gene pairs might have evolved under the influence of purifying selection, a phenomenon that has also been observed for Hsp70 genes in *P. trichocarpa*<sup>21</sup>. Gene duplication often leads to expansion and functional diversity of this gene family<sup>42</sup>. Accordingly, our data support a model for the evolution of the moss Hsp70 family involving a whole-genome duplication accompanied by multiple segmental and tandem duplications, suggesting that the moss Hsp70 gene family might serve diverse functions in resistance to land-related stresses.

**Hsp70 Genes could be Vital in Responses to Abiotic Stress.** The Hsp70 ATPase is thought to be one of the most ancient proteins according to molecular clock analysis<sup>43</sup>. Hsp70 functions have been widely reported in various species, but mainly in heat shock responses and protein import, whereas research in drought response-related functions of Hsp70 is limited. The ER Hsp70, i.e., Bip of tobacco and soybean positively regulate drought resistance<sup>44</sup>. In addition, ER-resident Hsp70-5 of *Citrus* has a key function in seed desiccation tolerance<sup>44</sup>. Here, we found evidence that *P. patens* Hsp70 genes are expressed constitutively during development and differentially during stress treatment (dehydration and rehydration), suggesting that Hsp70 genes have played critical roles in growth and in stress responses from the origin of land plants. Most Hsp70 genes showed high expression in the gametophore stage, indicating their possible roles in the growth of *P. patens* (Fig. 5). The finding that Hsp70 genes showed different expression during dehydration and rehydration stress demonstrates their sensitivity to stress and indicates their possible role in *P. patens* stress tolerance (Fig. 6). In *Chaetomorpha valida*, a bloom-forming green alga, *CvHsp70* most probably acts as stress-responsive gene that participates in protecting *C. valida* from environmental stresses<sup>8</sup>, suggesting that cytosolic Hsp70 might have evolved protective functions to help maintain rapid growth and allow successful colonization. In *Symbiodinium*, the cytosolic Hsp70 has been suggested as a potential stress biomarker<sup>45</sup>. These findings, together with our result that expression of *cpHsp70-2* was highest in *P. patens* during dehydration (R20%), and that *cpHsp70-2* was the most highly expressed after 8-h rehydration, illustrate that chloroplastic Hsp70 likely plays a prominent role in both growth processes and responses to drought stress. Furthermore, mRNA levels of *cpHsp70* continually increased after dehydration in *P. patens*, suggesting that the chloroplast might also be involved in preventing cellular dehydration and improving stress tolerance. It has been reported that *cis*-acting elements regulate the molecular processes of developmental and diverse stress responses<sup>46–48</sup>. Several elements including SORLIP2AT, DOFCOREZM, GCCCORE, and a novel one (GGCGGAGGGGGG) were overrepresented in the promoter regions of groups of Hsp70 genes responsive to salt, ABA or drought (Supplementary Tables S5 and S6), which implies that Hsp70s are involved in responses to stress through shared evolutionarily conserved pathways.

From the data above, we hypothesized that moss *cpHsp70* played a critical role not only in protein import but also in adaptation to dehydration stress. Considering its unique intron-exon structure, strongly active intron retention alternative splicing events, copy number, and known function under abiotic stresses, as shown in Additional Data 2<sup>24</sup>, we chose *PpcpHsp70-2* for further analysis. *PpcpHsp70-2* was previously found to be essential in moss, as the knockout was lethal<sup>14</sup>. Here, we found that moss plants overexpressing *PpcpHsp70-2* exhibited clear salt and dehydration tolerance (Fig. 8), which provides clear evidence for a role of *cpHsp70* in dehydration stress tolerance.

## Conclusion

In this study, we have identified 21 Hsp70 genes from the genome sequence of *P. patens*. A comprehensive analysis of these genes, including of gene structure, phylogeny, gene duplication, expression profile, enriched *cis*-elements and dehydration tolerance, was performed. Our phylogenetic and evolutionary analysis based on Hsp70 sequences points to a number of gene duplication events having taken place in this gene superfamily. Further, overexpression analysis showed that *PpcpHsp70-2* is involved in salt and dehydration tolerance. The information



presented in this study provides detailed characterization of the *P. patens* Hsp70 protein superfamily and lays a foundation for further functional studies of these genes in *P. patens* development and dehydration stress.

## Materials and Methods

**Identification of Putative Hsp70 Proteins in *P. patens*.** For Hsp70 retrieval in *P. patens* genome database v3.1 ([http://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org\\_Ppatens\\_er](http://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Ppatens_er)), *Arabidopsis* Hsp70 proteins containing conserved domain sequences were used as query to identify potential moss Hsp70 proteins, with a maximum E-value of  $1e-5$  (Supplementary Tables S1 and S2). Functional domains of PpHsp70 sequences were analyzed using SMART (<http://smart.embl-heidelberg.de/>) and PROSITE (<http://prosite.expasy.org/>). Predotar v.1.03 (<https://urgi.versailles.inra.fr/predotar/predotar.html>) and LocTree3 (<https://roslab.org/services/loc-tree3/>) were used to predict the protein subcellular localizations<sup>49</sup>.

**Multiple Sequence Alignment and Domain Analysis.** Multiple sequence alignment of all Hsp70 proteins was performed using MegAlign (v.7 Lasergene). To identify signature domains of Hsp70 proteins in *P. patens*, InterProScan 5 (<http://www.ebi.ac.uk/Tools/pfa/iprscan5/>) and SMART (<http://smart.embl-heidelberg.de/>) web programs were used<sup>50</sup>. ClustalX2.1 software and the ESPript tool were used to analyze the PpHsp70 sequences and structures<sup>51</sup>.

**Motif and Gene Structure Prediction.** Conserved motifs were identified using MEME (<http://meme.nbcrc.net/meme/tools/meme>), with parameters set as follows: numbers of repetitions = any, minimum motif width = 6, maximum motif width = 50, and maximum number of motifs to identify was 20; default values were used for other parameters<sup>52</sup>. Information on intron-exon structure was illustrated using Gene Structure Display Server (<http://gsds.cbi.pku.edu.cn/>). To identify the various *cis*-elements in the promoter of each cluster, 2 kb upstream sequences were extracted. Upstream sequences were downloaded from the Rice Annotation Project Database (<http://rapdb.dna.affrc.go.jp/>). The *Arabidopsis* Information Resource (<http://www.arabidopsis.org/>) and Joint Genome Institute Launches Phytozome v10.3 (<http://phytozome.jgi.doe.gov/pz/portal.html#>), respectively. *Cis*-element analysis was performed using MEME (<http://meme.nbcrc.net/meme/tools/meme>), with parameters set as follows: numbers of repetitions = any, minimum motif width = 6, maximum motif width = 12, and maximum number of motifs to identify was 50; default values were used for other parameters<sup>52</sup>. The elements were annotated with PLACE (Supplementary Tables S3, S5 and S6, <https://sogo.dna.affrc.go.jp/cgi-bin/sogo.cgi?lang=en&pj=640&action=page&page=newplace>).

**Phylogenetic Analyses.** The amino acid sequences encoded by the complete *Hsp70* gene families from other species, including *Escherichia coli*, *Saccharomyces cerevisiae*, *Chlamydomonas reinhardtii*, *Selaginella moellendorffii*, *Oryza sativa*, *Arabidopsis*, and *Populus trichocarpa*, were retrieved from Phytozome v10.3 (<http://phytozome.jgi.doe.gov/pz/portal.html#>) or NCBI (<http://www.ncbi.nlm.nih.gov/>) using BLAST searches. A phylogenetic tree was constructed in MEGA 6.06 (<http://www.megasoftware.net/history.php>) using the Neighbor-Joining (NJ) method. The bootstrap values reported for each branch reflect the percentage of 1,000 replicate trees containing that branch.

**Chromosomal Location and Gene Duplication Analysis.** Chromosomal analysis was performed using Matlab programming language. The chromosomal positions of the *Hsp70* genes and the lengths of the chromosomes were obtained from Phytozome (<http://phytozome.jgi.doe.gov/pz/portal.html#>). Tandem and segmental duplications of *Hsp70* superfamily genes in *P. patens* were identified in PTG Base (<http://ocri-genomics.org/PTGBase/>) and Plant Genome Duplication Database (PGDD; <http://chibba.agtec.uga.edu/duplication/>), respectively.

**Analysis of Publicly Available Microarray Data.** Microarray data (bulk accession numbers E-MTAB-914, E-MTAB-916, E-MTAB-917) from the public repository ARRAYEXPRESS (Hiss *et al.*<sup>37</sup>) (<http://www.ebi.ac.uk/arrayexpress/>) were used to analyze the expression profiles of *P. patens* *Hsp70* genes at different developmental stages (spore, protonema, juvenile, adult stage and gametophore) and under different treatments (dehydration, ABA and salt). The *P. patens* transcriptome data were obtained from Phytozome 10.3 (<http://phytozome.jgi.doe.gov/pz/portal.html>). In addition, the samples of rice and *Arabidopsis* used in the microarray data analysis included three abiotic stress conditions, i.e., salt, ABA and drought. The *Arabidopsis* microarray gene expression data were obtained from AtGenExpress. The public expression data in rice was obtained from the Michigan State University (MSU) Rice Genome Annotation (<http://rice.plantbiology.msu.edu>) databases (Supplementary Table S4).

**Plant Material, Stress Treatment and Chlorophyll Fluorescence Analysis.** *Physcomitrella patens* (Gransden) wild type was maintained on BCD medium supplemented with 5 mM ammonium tartrate and 1 mM CaCl<sub>2</sub> overlaid with cellophane, at 23 °C under continuous light (60 to 80 μmol photons m<sup>-2</sup> s<sup>-1</sup>) for 2 weeks then transferred on the growth matrix block for another two weeks to get gametophytes. To examine the response to dehydration and rehydration stress in Fig. 6, we treated *P. patens* samples as follows. *P. patens* gametophytes were treated with air drying and water recovery, with 6 samples collected: dehydration samples (D), with relative water-content loss to 20%, 40%, 80%, and rehydration samples (R), with water recovery time to the 80% water-loss samples (4 h and 8 h).

The *cpHsp70-2* overexpression plants were a gift from Dr. Steven Theg in UC. Davis. In these plants, a *cpHsp70-2* knockout cassette (cloned into pCR4 TOPO vector) and rescue plasmid (*cpHsp70-2* cDNA cloned into pART7 vector) with 35S promoter and the OCS terminator were co-transformed moss protoplasts to generate rescued transgenic plants<sup>14</sup>. We refer to these rescued transgenic plants as *cpHsp70-2* overexpression transgenic plants because the mRNA and protein expression levels of these transgenic plants was much higher than those

of wild-type moss<sup>13,14</sup>. The *cpHsp70-2* overexpression transformants and wild-type (WT) plants were grown for 4 weeks to obtain gametophytes. Then, 500 mM NaCl was used for salt treatment for 3 d, followed by recovery. For water loss measurement, leafy gametophores were weighed and placed on the laboratory bench (the relative humidity was between 30 and 40%) at 22 °C. Weight loss of the leafy gametophores was monitored for 1.5 h at the indicated time intervals. Water loss was expressed as the percentage of initial fresh weight. The leafy gametophores were then transferred to water for rehydration. Chlorophyll fluorescence of leaf gametophores was monitored using an IMAGING-PAM chlorophyll fluorometer and Imaging Win software (Walz, Effeltrich, Germany), as described previously, was measured under salt, dehydration and rehydration treatments. A dark-light induction curve was applied to assess dark- and light-adapted parameters. Plants were given a saturating pulse (>1,800 μmol photons·m<sup>-2</sup>·s<sup>-1</sup>) and the levels of  $F_v/F_m$  were determined after 20 min of dark adaptation.  $F_v/F_m$  was calculated as  $(F_m - F_0)/F_m$ . False-colour images of the  $F_v/F_m$  parameter are presented through the Imaging Win software<sup>53</sup>.

**Quantitative Expression Analysis by Real-time PCR.** Total RNA was isolated from dehydrated/rehydrated samples using TRIzol following the supplier's instructions (Invitrogen, Argentina). RNA concentration was measured using a Nanodrop-2000 spectrophotometer (Thermo scientific). For each sample, 1 μg RNA was treated with DNaseI and reverse-transcribed using the PrimeScript™ RT reagent Kit with gDNA Eraser (Takara, Japan). Reverse transcription quantitative real-time PCR (RT-qPCR) was carried out in a 25-μl reaction mix containing: 1 μl each primer (10 μM concentration), 1 μl cDNA sample and SYBP Premix Ex Taq II (Tli RNaseH Plus). RT-qPCR was performed using 96-well plates (Bio-Rad CFX96), with the program: 95 °C for 30 s, 39 cycles of 95 °C for 5 s and 60 °C for 30 s, followed by melting curve analysis (60 to 95 °C). The RT-qPCR assays were carried out with three biological replicates for each condition. The relative normalized expression was calculated using Bio-Rad CFX96 software with *Actin* expression (F: 5'CAGGGTGCAGTGCATTG3', R: 5'TCGGCAACGGAGACATAAGAGTA3') for normalization.

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## Author Contributions

Conceived and designed the experiments: L.L. Performed the experiments: T.T. and P.L. Analyzed the data: A.Y., G.L., H.Y. and T.T. Wrote the paper: L.L., A.Y. and T.T.

## Additional Information

**Supplementary information** accompanies this paper at <http://www.nature.com/srep>

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