REFERENCES

Abe, H., Uraoa, T., Ito, K., Sekic, M., Shinozaki, K., and Yamakushi-Shinozaki, K. (2003). Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) function as transcriptional activators in abscisic acid signaling. *The Plant Cell* **15**, 63-78.

Agrawal, G. K., Rakwal, R., Tamogami, S., Yonekura, M., Kubo, A., and Saji, H. (2002). Chitosan activates defense/stress response(s) in the leaves of *Oryza sativa* seedlings. *Plant Physiology and Biochemistry* **40**, 1061-1069.

Ali, G. M., and Komatsu, S. (2006). Proteomic analysis of rice leaf sheath during drought stress. *Journal of Proteome Research* **5**, 396–403.

Amborabe, B. E., Bonmort, J., Fleurat-Lessard, P., and Roblin, G. (2008). Early events induced by chitosan on plant cells. *Journal of Experimental Botany* **59**, 2317-2324.

Anjum, A. S., Xie, X. Y., Wang, L. C., Saleem, M. F., Man, C., and Wang, L. (2011). Morphological, physiological and biochemical responses of plants to drought stress. *African Journal of Agricultural Research* **6**, 2026-2032.

Ashraf, M. (2010). Inducing drought tolerance in plants: recent advances. *Biotechnology Advances* **28**, 169-183.

Ashraf, M., Akram, N. A., Al-Qurainy, F., and Foolad, M. R. (2011). Drought tolerance: roles of organic osmolytes, growth regulators, and mineral nutrients. Vol. 111, pp. 249-296.

Bittelli, M., Flury, M., Campbell, G., and Nichils, E. J. (2001). Reduction of transpiration through foliar application of chitosan. *Agricultural and Forest Meteorology* **107**, 167-175.

Boonlertnirun, S., Boonruang, C., and Suvanasara, R. (2008). Application of chitosan in rice production. *Journal of the Minerals Metals and Materials Society* **8**, 47-52.

Boonlertnirun, S., Sarabol, E., Meechoui, S., and Sooksatan, I. (2007). Drought recovery and grain yield potential of rice after chitosan application. *Kasetsart Journal (Natural Science)* **41**, 1-6.

Centre-for-Agricultural-Information (2013). "Thailand foreign agricultural trade statistics 2012." Office of Agricultural Economics.

Chamnanmanoontham, N. (2009). Early expression of the novel salt-responsive gene in rice *Oryza sativa* L. after salt and various abiotic stresses, Chulalongkorn University.

Chandra Babu, R., Zhang, J., Blum, A., David Ho, T. H., Wu, R., and Nguyen, H. T. (2004). *HVA1*, a LEA gene from barley confers dehydration tolerance in transgenic rice (*Oryza sotiva* L.) via cell membrane protection. *Plant Science* **166**, 855-862.

Chantarachot, T. (2012). Relationship between *OsCam1-1* and *OsNUC* gene expression in salt stress response in rice *Oryza sativa* L., Chulalongkorn University.

Chaves, M. M., Maroco, J. P., and Pereira, J. S. (2003). Understanding plant responses to drought : from genes to the whole plant. *Functional Plant Biology* **30**, 239-264.

Chen, J. Q., NMeng, X. P., Zhang, Y., Xia, M., and Wang, W. P. (2008). Over-expression of *OsDREB* genes lead to enhanced drought tolerance in rice. *Biotechnology Letters* **30**, 2191-2198.

Choudhary, N., Sairam, R., and Tyagi, A. (2005). Expression of Δ^1-pyrroline-5-carboxylate synthetase gene during drought in rice (*Oryza sativa* L.). *Indian Journal of Biochemistry and Biophysics* **42**, 366-370.

Cramer, G. R., Van Sluyter, S. C., Hopper, D. W., Pascovici, D., Keighley, T., and Haynes, P. A. (2013). Proteomic analysis indicates massive changes in metabolism prior to the inhibition of growth and photosynthesis of grapevine (*Vitis vinifera* L.) in response to water deficit. *BMC Plant Biology* **13**, 49.

Dardick, C., Chen, J., Richter, T., Ouyang, S., and Ronald, P. (2007). The rice kinase database. A phylogenomic database for the rice kinome. *Plant Physiology* **143**, 579-586.

Duan, J., and Cai, W. (2012). *OsLEA3-2*, an abiotic stress induced gene of rice plays a key role in salt and drought tolerance. *PLoS One* **7**, e45117.

Dubouzet , J. G., Sakuma, Y., Ito, Y., Kasuga, M., Dubouzet, G. E., Miura, S., Seki, M., Shinozaki , K., and Yamaguchi-Shinozaki, T. (2003). *OsDREB* genes in rice, *Oryza sativa* L., encode transcription activators that function in drought-, high-salt- and cold-responsive gene expression. *The Plant Journal* **33**, 751-763.

Dzung, N. A., Khanh, V. T. P., and Dzung, T. T. (2011). Research on impact of chitosan oligomers on biophysical characteristics, growth, development and drought resistance of coffee. *Carbohydrate Polymers* **84**, 751-755.

Farouk, S., and Abdul Qados, A. M. S. (2013). Osmotic adjustment and yield of cowpea in response to drought stress and chitosan. *Indian Journal of Applied Research* **3**, 1-6.

Ferri, M., Tassoni, A., Franceschetti, M., Righetti, L., Naldrett, M. J., and Bagni, N. (2009). Chitosan treatment induces changes of protein expression profile and stilbene distribution in *Vitis vinifera* cell suspensions. *Proteomics* **9**, 610-624.

Fukayama, H., Ueguchi, C., Nishikawa, K., Katoh, N., Ishikawa, C., Masumoto, C., Hatanaka, T., and Misoo, S. (2012). Overexpression of Rubisco activase decreases the photosynthetic CO_2 assimilation rate by reducing Rubisco content in rice leaves. *Plant and Cell Physiology* **53**, 976-986.

Gao, C., and Han, B. (2009). Evolutionary and expression study of the aldehyde dehydrogenase (ALDH) gene superfamily in rice (*Oryza sativa*). *Gene* **431**, 86-94.

Garg, A. K., Kim, J. K., Owens, T. G., Ranwala, A. P., Choi, Y. D., Kochian, L. V., and Wu, R. J. (2002). Trehalose accumulation in rice plants confers high tolerance levels to different abiotic stresses. *Proceedings of the National Academy of Sciences of the United States of America* **99**, 15898-15903.

Ghanbari, A. A., Shakiba, M. R., Toorchi, M., and Choukan, R. (2013). Morpho-physiological responses of common bean leaf to water deficit stress. *European Journal of Experimental Biology* **3**, 487-492.

Goff, S. A., Ricke, D., Lan, T. H., Presting, G., Wang, R., and Dunn , M. (2002). A draft sequence of the rice genome (*Oryza sativa* L. spp. japonica). *Science* **296**, 92–100.

Gutha, L. R., and Reddy, A. R. (2008). Rice *DREB1B* promoter shows distinct stress-specific responses, and the overexpression of cDNA in tobacco confers improved abiotic and biotic stress tolerance. *Plant Molecular Biology* **68**, 533-555.

Hadiarto, T., and Tran, L.-S. P. (2011). Progress studies of drought-responsive genes in rice. *Plant Cell Reports* **30**, 297-310.

Harish Prashanth, K. V., and Tharanathan, R. N. (2007). Chitin/chitosan: modifications and their unlimited application potential—an overview. *Trends in Food Science and Technology* **18**, 117-131.

Henkes, S., Sonnewald, U., Badur, R., Flachmann, R., and Stitt, M. (2001). A small decrease of plastid transketolase activity in antisense tobacco transformants has dramatic effects on photosynthesis and phenylpropanoid metabolism. *The Plant Cell* **13**, 535-551.

Hien, D. T., Jacobs, M., Angenon, G., Hermans, C., Thu, T. T., Son, L. V., and Roosens, N. H. (2003). Proline accumulation and Δ^1-pyrroline-5-carboxylate synthetase gene properties in three rice cultivars differing in salinity and drought tolerance. *Plant Science* **165**, 1059-1068.

Ho, C. L., Wu, Y., Shen, H. B., Provart, N. J., and Geisler, M. (2012). A predicted protein interactome for rice. *Rice* **5**, 1-14.

Huang, J., Sun, S. J., Xu, D. Q., Yang, X., Bao, Y. M., Wang, Z. F., Tang, H. J., and Zhang, H. (2009). Increased tolerance of rice to cold, drought and oxidative stresses mediated by the overexpression of a gene that encodes the zinc finger protein ZFP245. *Biochemical and Biophysical Research Communications* **389**, 556-561.

Huh, S. M., Noh, E. K., Kim, H. G., Jeon, B. W., Bae, K., Hu, H. C., Kwak, J. M., and Park, O. K. (2010). Arabidopsis annexins AnnAt1 and AnnAt4 interact with each other and regulate drought and salt stress responses. *Plant and Cell Physiology* **51**, 1499-1514.

Hur, J., Jung, K.-H., Lee, C.-H., and An, G. (2004). Stress-inducible *OsP5CS2* gene is essential for salt and cold tolerance in rice. *Plant Science* **167**, 417-426.

Igarashi, Y., Yoshiba, Y., Sanada, Y., Yamaguchi-Shinozaki, K., Wada, K., and Shinozaki, K. (1997). Characterization of the gene for Δ^1-pyrroline-5-carboxylate synthetase and correlation between the expression of the gene and salt tolerance in *Oryza sativa* L. *Plant Molecular Biology* **33**, 857-865.

Iordachescu, M., and Imai, R. (2008). Trehalose biosynthesis in response to abiotic stresses. *Journal of Integrative Plant Biology* **50**, 1223-1229.

Iriti, M., Picchi, V., Rossoni, M., Gomarasca, S., Ludwig, N., Gargano, M., and Faoro, F. (2009). Chitosan antitranspirant activity is due to abscisic acid-dependent stomatal closure. *Environmental and Experimental Botany* **66**, 493-500.

Ito, Y., Katsura, K., Maruyama, K., Taji, T., Kobayashi, M., Seki, M., Shinozaki, K., and Yamaguchi-Shinozaki, K. (2006). Functional analysis of rice DREB1/CBF-type transcription factors involved in cold-responsive gene expression in transgenic rice. *Plant and Cell Physiology* **47**, 141-153.

Jaleel, C. A., Manivannan, P., Wahid, A., Farooq, M., Al-Juburi, H. J., Somasundaram, R., and Panneerselvam, R. (2009). Drought stress in plants: a review on morphological characteristics and pigments composition. *International Journal of Agriculture and Biology* **11**, 100-105.

Jami, S. K., Clark, G. B., Ayele, B. T., Roux, S. J., and Kirti, P. B. (2012). Identification and characterization of annexin gene family in rice. *Plant Cell Reports* **31**, 813-825.

Jaresitthikunchai, J., Phaonakrop, N., Kittisenachai, S., and Roytrakul, S. (2009). Rapid in-gel digestion protocol for protein identification by peptide mass fingerprint.

In "The 2nd Biochemistry and Molecular Biology Conference: Biochemistry and Molecular Biology for Regional Sustainable Development", Khon Kaen, Thailand.

Ji, K., Wang, Y., Sun, W., Lou, Q., Mei, H., Shen, S., and Chen, H. (2012). Drought-responsive mechanisms in rice genotypes with contrasting drought tolerance during reproductive stage. *Journal of Plant Physiology* **169**, 336-344.

Jia, H., Oguchi, R., Hope, A. B., Barber, J., and Chow, W. S. (2008). Differential effects of severe water stress on linear and cyclic electron fluxes through Photosystem I in spinach leaf discs in CO_2-enriched air. *Planta* **228**, 803–812.

Jiao, Z., Li, Y., Li, J., Xu, X., Li, H., Lu, D., and Wang, J. (2012). Effects of exogenous chitosan on physiological characteristics of potato seedlings under drought stress and rehydration. *Potato Research* **55**, 293-301.

Johansson, C., Samskog, J., Sundstrom, L., Wadensten, H., Bjorkesten, L., and Flensburg, J. (2006). Differential expression analysis of *Escherichia coli* proteins using a novel software for relative quantitation of LC-MS/MS data. *Proteomics* **6**, 4475-4485.

Johnson, M. P., and Ruban, A. V. (2010). Arabidopsis plants lacking PsbS protein possess photoprotective energy dissipation. *The Plant Journal* **61**, 283-289.

Jung, K.-H., Dardick, C., Bartley, L. E., Cao, P., Phetsom, J., Canlas, P., Seo, Y.-S., Shultz, M., Ouyang, S., and Yuan, Q. (2008). Refinement of light-responsive transcript lists using rice oligonucleotide arrays: evaluation of gene-redundancy. *PLoS One* 3, e3337.

Kananont, N., Pichayangkura, R., Chanprame, S., Chadchawan , S., and Limpanavech, P. (2010). Chitosan specificity for the *in vitro* seed germination of two *Dendrobium* orchids (Asparagales: Orchidaceae). *Scientia Horticulturae* **124**, 239-247.

Kasajima, I., Ebana, K., Yamamoto, T., Takahara, K., Yano, M., Kawai-Yamada, M., and Uchimiya, H. (2011). Molecular distinction in genetic regulation of nonphotochemical quenching in rice. *Proceedings of the National Academy of Sciences of the United States of America* **108**, 13835-13840.

Ke, Y., Han, G., He, H., and Li, J. (2009). Differential regulation of proteins and phosphoproteins in rice under drought stress. *Biochemical and Biophysical Research Communications* **379**, 133-138.

Khan, W., Prithiviraj, B., and Smith, D. L. (2003). Chitosan and chitin oligomers increase phenylalanine ammonia-lyase and tyrosine ammonia-lyase activities in soybean leaves. *Journal of Plant Physiology* **160**, 859-863.

Khan, W. M., Prithiviraj, B., and Smith, D. L. (2002). Effect of foliar applicaton of chitin and chitosan oligosaccharides on photosynthesis of maize and soybean. *Photosynthetica* **40**, 621-624.

Klomsakul, P. (2004). Effects of exogenous abscisic acid on growth, proline accumulation and Δ^1–pyroline-5-carboxylate synthetase gene expression during drought-and salt-stress conditions in rice (*Oryza sativa* L), Chulalongkorn University.

Koo, H. Y., Zulfugarov, I. S., Oh, M. H., Moon, Y. H., Jansson, S., An, G., and Lee, C. H. (2005). The function of the PsbS protein in relation to non-photochemical energy dependent quenching in rice plants. *In* "Photosynthesis: Fundamental Aspects to Global Perspectives".

Laemmli, U. K. (1970). Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature* **227**, 680-685.

Lee, S. L., Choi, H., Doo, I., Oh, K., Choi, E. J., Schroeder-Taylor, A. T., Low, P. S., and Lee, Y. (1999). Oligogalaturonic acid and chitosan reduce stomatal aperture by inducing the evolution of reactive oxygen species from guard cells of tomato and Commelina communis. *Plant Physiology and Biochemistry* **121**, 147–152.

Li, H.-W., Zang, B.-S., Deng, X.-W., and Wang, X.-P. (2011). Overexpression of the trehalose-6-phosphate synthase gene *OsTPS1* enhances abiotic stress tolerance in rice. *Planta* **234**, 1007-1018.

Limpanavech, P., Chaiyasuta, S., Vongpromek, R., Pichyangkura, R., Khunwasi, C., Chadchawan , S., Lotrakul, P., Bunjongrat, R., Chaidee, A., and Bangyeekhun, T. (2008). Chitosan effects on floral production, gene expression, and anatomical changes in the Dendrobium orchid *Scientia Horticulturae* **116**, 65-72.

Lin, W., Hu, X., Zhang, W., John Rogers, W., and Cai, W. (2005). Hydrogen peroxide mediates defence responses induced by chitosans of different molecular weights in rice. *Journal of Plant Physiology* **162**, 937-944.

Lizama-Uc, G., Estrada-Mota, I. A., Caamal-Chan, G. M., Souza-Perera, R. A., Oropeza, C., Islas-Flores, I., and Zuniga-Aguilar, J. J. (2007). Chitosan activates a MAP-kinase pathway and modifies abundance of defense-related transcripts in calli of *Cocos nucifera* L. *Physiological and Molecular Plant Pathology* 70, 130-141.

Lowry, O. H., Rosebrough, N. J., Fair, A. L., and Randall, R. J. (1951). Protein measurement with the Folin phenol reagent. *The Journal of Biological Chemistry* **193**, 265–275.

Maksup, S., Roytrakul, S., and Supaibulwatana, K. (2012). Physiological and comparative proteomic analyses of Thai jasmine rice and two check cultivars in response to drought stress. *Journal of Plant Interactions* 1-13.

Maneeprasopsuk, P. (2004). Comparison of gene expression between the original rice *Oryza sativa* L. cv. Leung Pratew123 and the salt-tolerant lines in salt-stressed condition, Chulalongkorn University.

Matsukura, S., Mizoi, J., Yoshida, T., Todaka, D., Ito, Y., Maruyama, K., Shinozaki, K., and Yamaguchi-Shinozaki, K. (2010). Comprehensive analysis of rice DREB2-type genes that encode transcription factors involved in the expression of abiotic stress-responsive genes. *Molecular Genetics and Genomics.* **283**, 185-196.

Mazzucotelli, E., Mastrangelo, A. M., Crosatti, C., Guerra, D., Stanca, A. M., and Cattivelli, L. (2008). Abiotic stress response in plants: when post-transcriptional and post-translational regulations control transcription. *Plant Science* **174**, 420-431.

Miller, G., Suzuki, N., Yilmaz, S. C., and Mitter, R. (2010). Reactive oxygen species homeostasis and signalling during drought and salinity stresses. *Plant, Cell and Environment* **33**, 453-467.

Montesinos-Pereira, D., Barrameda-Medina, Y., Romero, L., Ruiz, J. M., and Sanchez-Rodriguez, E. (2014). Genotype differences in the metabolism of proline and polyamines under moderate drought in tomato plants. *Plant Biology*, doi: 10.1111/plb.12178.

Mosher, S., and Kemmerling, B. (2013). *PSKR1* and *PSY1R*-mediated regulation of plant defense responses. *Plant Signaling and Behavior* **8**, e24119.

Nijhawan, A., Jain, M., Tyagi, A. K., and Khurana, J. P. (2008). Genomic survey and gene expression analysis of the basic leucine zipper transcription factor family in rice. *Plant Physiology* **146**, 333-350.

Nuruzzaman, M., Manimekalai, R., Sharoni, A. M., Satoh, K., Kondoh, H., Ooka, H., and Kikuchi, S. (2010). Genome-wide analysis of NAC transcription factor family in rice. *Gene* **465**, 30-44.

Ouyang, S., Zhu, W., Hamilton, J., Lin, H., Campbell, M., Childs, K., Thibaud-Nissen, F., Malek, R. L., Lee, Y., Zheng, L., Orvis, J., Haas, B., Wortman, J., and Buell, C. R. (2007). The TIGR Rice Genome Annotation Resource: improvements and new features. *Nucleic Acids Research* **35**, D883-D887.

Perkins, D. N., Pappin, D. J. C., Creasy, D. M., and Cottrell, J. S. (1999). Probability-based protein identification by searching sequence databases using mass spectrometry data. *Electrophoresis* **20**, 3551-3567.

Peterson, G. L. (1983). Determination of total protein. *Methods in Enzymology* **91**, 95-121.

Pfaffl, M. W. (2001). A new mathematical model for relative quantification in real-time RT-PCR. *Nucleic Acids Research* **29**, 2002-2007.

Photchanacha, S., Singkaew, J., and Thamthong, J. (2006). Effects of chitosan seed treatment on *colletotrichum* sp and seedling growth of chili cv. Jinda. *Acta Horticulturae* **712**, 585-588.

Pongprayoon, W., Roytrakul, S., Pichayangkura, R., and Chadchawan , S. (2012). The effect of chitosan on rice *(Oryza sativa* L.) growth under drought stress. *In* "Proceedings: 1^{st} ASEAN Plus Three Graduate Research Congress", pp. ST-282-ST288.

Pongprayoon, W., Roytrakul, S., Pichayangkura, T., and Chadchawan , S. (2013). The role of hydrogen peroxide in chitosan-induced resistance to osmotic stress in rice (*Oryza sativa* L.). *Plant Growth Regulation* **70**, 159-173.

Povero, G., Loreti, E., Pucciariello, C., Santaniello, A., Di Tommaso, D., Di Tommaso, G., Kapetis, D., Zolezzi, F., Piaggesi, A., and Perata, P. (2011). Transcript profiling of chitosan-treated Arabidopsis seedlings. *Journal of Plant Research* **124**, 619-629.

Priya, P., and Jain, M. (2013). RiceSRTFDB: a database of rice transcription factors containing comprehensive expression, cis-regulatory element and mutant information to facilitate gene function analysis. *Database*, bat027.

Rabbani, M. A., Maruyama, K., Abe, H., Khan, M. A., Katsura, K., Ito, Y., and Yoshiwara, K. (2003). Monitoring expression profiles of rice genes under cold, drought, and high-salinity stresses and abscisic acid application using cDNA microarray and RNA gel-blot analyses. *Plant Physiology* **133**, 1755-1767.

Reddy, A. R., Chitanya, K. V., and Vivekanandan, M. (2004). Drought-induced responses of photosynthesis and antioxidant metabolism in higher plants. *Journal of Plant Physiology* **161**, 1189-1202.

Rohila, J. S., and Yang, Y. (2007). Rice mitogen-activated protein kinase gene family and its role in biotic and abiotic stress response. *Journal of Integrative Plant Biology* **49**, 751-759.

Ross, C. A., Liu, Y., and Shen, Q. J. (2007). The WRKY gene family in rice (*Oryza sativa*). *Journal of Integrative Plant Biology* **49**, 827-842.

Rumeau, D., Bécuwe-Linka, N., Beyly, A., Louwagie, M., Garin, J., and Peltier, G. (2005). New subunits NDH-M,-N, and-O, encoded by nuclear genes, are essential for plastid Ndh complex functioning in higher plants. *The Plant Cell* **17**, 219-232.

Sa-nguanmoo, N. (2013). Comparative proteomics of rice *Oryza sativa* L. root proteins under drought stress condition, Chulalongkorn University.

Saeed, A. I., Sharov, V., White, J., Li, J., Liang, W., Bhagabati, N., Braisted, J., Klapa, M., Currier T, Thiagarajan, M., Sturn, A., Snuffin, M., Rezantsev, A., Popov, D., Ryltsov, A., Kostukovich, E., Borisovsky , I., Liu, Z., Vinsavich, A., Trush, V., and Quackenbush, J. (2003). TM4: a free, open-source system for microarray data management and analysis *Biotechniques* **34**, 374-378.

Saeng-ngam, S., Takpirom, W., Buaboocha, T., and Chadchawan , S. (2012). The role of *OsCam1-1* salt stress sensor in ABA accumulation and salt tolerance in rice. *Journal of Plant biology* **55**, 198-208.

Salam, M. A., Jammes, F., Hossain, M. A., YE, W., Nakamura, Y., Mori, I. C., Kwak, J. M., and Murata, Y. (2012). MAP Kinase, MPK9 and MPK12 regulate chitosan-induced stomatal closure. *Bioscience Biotechnology and Biochemistry* **76**, 1785-1787.

Salekdeh, G. H., Siopongco, J., Wade, L. J., Ghareyazie, B., and Bennett, J. (2002). Proteomic analysis of rice leaves during drought stress and recovery. *Proteomics* **2**, 1131-1145.

Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989). "Molecular Cloning: A Laboratory Manual," Cold Spring Harbor Laboratory Press., Cold Spring Harbor, USA

Saneoka, H., Moghaieb, R. E., Premachandra, G. S., and Fujita, K. (2004). Nitrogen nutrition and water stress effects on cell membrane stability and leaf water relations in *Agrostis palustris* Huds. *Environmental and Experimental Botany* **52**, 131-138.

Song, C. P., Agarwal, M., Ohtaa, M., Guoa, Y., Halfte, r. U., Wang, P., and Zhu, J. K. (2005). Role of an Arabidopsis AP2/EREBP-type transcriptional repressor in abscisic acid and drought stress responses. *The Plant Cell* **17**, 2384-2396.

Sripinyowanich, S. (2010). Characterization of the novel salt stress responsive gene in rice *Oryza sativa* L., Chulalongkorn University, Faculty of Science.

Sripinyowanich, S., Klomsakul, P., Boonburapong, B., Bangyeekhun, T., Asami, T., Gu, H., Buaboocha, T., and Chadchawan , S. (2013). Exogenous ABA induces salt tolerance in indica rice (*Oryza sativa* L.) : The role of *OsP5CS1* and *OsP5CR* gene expression during salt stress. *Environmental and Experimental Botany* **86**, 94-105.

Srivastava, N., Gonugunta, V. K., Puli, M. R., and Raghavendra, A. S. (2009). Nitric oxide production occurs downstream of reactive oxygen species in guard cells during stomatal closure induced by chitosan in abaxial epidermis of *Pisum sativum*. *Planta* **229**, 757-765.

Suvanasara, R., and Boonlertnirun, S. (2013). Studies on appropriate chitosan type and optimum concentration on rice seed storability. *ARPN Journal of Agricultural and Biological Science* **8**, 196-200.

Takáč, T., Pechan, T., Šamajová, O., Ovečka, M., Richter, H., Eck, C., Niehaus, K., and Šamaj, J. (2012). Wortmannin treatment induces changes in Arabidopsis root proteome and post-Golgi compartments. *Journal of Proteome Research* **11**, 3127-3142.

Thikart, P., Kowanij, D., Selanan, T., Vajrabhaya, M., Bangyeekhun, T., and Chadchawan, S. (2005). Genetic variation and stress tolerance of somaclonal variegated rice and its original cultivar. *Journal of Scientific Research Chulalongkorn University* **30**, 63-75.

Thorsell, A., Portelius, E., Blennow, K., and Westman, B. A. (2007). Evaluation of sample fractionation using microscale liquid-phase isoelectric focusing on mass spectrometric identification and quantitation of proteins in a SILAC experiment. *Rapid Communications in Mass Spectrometry* **21**, 771-778.

Tian, L., DellaPenna, D., and Dixon, R. A. (2007). The pds2 mutation is a lesion in the Arabidopsis homogentisate solanesyltransferase gene involved in plastoquinone biosynthesis. *Planta* **226**, 1067-1073.

Tian, X. H., Li, X. P., Zhou, H. L., Zhang, J. S., Gong, Z. Z., and Chen, S. Y. (2005). *OsDREB4* genes in rice encode AP2-containing proteins that bind specifically to the dehydration-responsive element. *Journal of Integrative Plant Biology* **47**, 467-476.

Twyman, R. M. (2004). "Principles of proteomics," Garland Science/BIOS Scientific, Abingdon, UK

Udomchalotorn, T., Maneeprasobsuk, S., Bangyeekhun, E., Boon-long, P., and Chadchawan , S. (2009). The role of the bifunctional enzyme, fructose-6-phosphate-2-kinase/fructose-2,6-biphosphatase, in carbon partitioning during salt stress and salt tolerance in rice (*Oryza sativa* L.). *Plant Science* **176**, 334-341.

Vajrabhaya, M., and Vajrabhaya, T. (1991). Somaclonal variation of salt tolerance in rice. *In* "Biotechnology in Agriculture and Forestry" (Y. P. S. Bajaj, ed.), pp. 368-382. Berlin Heidelberg : Springer-Verlag.

Wang, H., Siopongco, J., Wade, L. J., and Yamauchi, A. (2009). Fractal analysis on root systems of rice plants in response to drought stress. *Environmental and Experimental Botany* **65**, 338-344.

Wang, Q., Guan, Y., Wu, Y., Chen, H., Chen, F., and Chu, C. (2008). Over-expression of a rice *OsDREB1F* gene increases salt, drought, and low temperature tolerance in both Arabidopsis and rice. *Plant Molecular Biology* **67**, 589-602.

Wang, X.-S., Zhu, H.-B., Jin, G.-L., Liu, H.-L., Wu, W.-R., and Zhu, J. (2007). Genome-scale identification and analysis of *LEA* genes in rice (*Oryza sativa* L.). *Plant Science* **172**, 414-420.

Xiang, Y., Huang, Y., and Xiong, L. (2007). Characterization of stress-reponsive CIPK genes in rice for stress tolerance improvement. *Plant Physiology* **144**, 1416-1428.

Xu, C., and Huang, B. (2010). Differential proteomic responses to water stress induced by PEG in two creeping bentgrass cultivars differing in stress tolerance. *Journal of Plant Physiology* **167**, 1477-1485.

Xu, D. Q., Huang, J., Guo, S. Q., Yang, X., Bao, Y. M., Tang, H. J., and Zhang, H. S. (2008). Overexpression of a TFIIIA-type zinc finger protein gene *ZFP252* enhances drought and salt tolerance in rice (*Oryza sativa* L.). *FEBS Letters* **582**, 1037-1043.

Yamaguchi-Shinozaki, K., and Shinozaki, K. (2006). Transcriptional regulatory networks in cellular responses and tolerance to dehydration and cold stresses. *Annual Review of Plant Biology* **57**.

Yang, A., Dia, X., and Zhang, W. H. (2012a). A R2R3-type MYB gene, *OsMYB2*, is involved in salt, cold, and dehydration tolerance in rice. *Journal of Experimental Botany* **63**, 2541-2556.

Yang, F., Hu, J., Li, J., Wu, X., and Qian, Y. (2009). Chitosan enhances leaf membrane stability and antioxidant enzyme activities in apple seedlings under drought stress. *Plant Growth Regulation* **58**, 131-136.

Yang, H. L., Liu, Y. J., Wang, C. L., and Zeng, Q. Y. (2012b). Molecular evolution of trehalose-6-phosphate synthase (TPS) gene family in Populus, Arabidopsis and rice. *PLoS One* **7**, e42438.

Yang, S., Vanderbeld, B., Wan, J., and Huang, Y. (2010). Narrowing down the targets: towards successful genetic engineering of drought-tolerant crops. *Molecular Plant* **3**, 469-490.

Yanhui, C., Xiaoyuan, Y., Kun, H., Meihua, L., Jigang, L., Zhaofeng, G., Zhiqiang, L., Yunfei, Z., Xiaoxiao, W., Xiaoming, Q., Yunping, S., Li, Z., Xiaohui, D., Jingchu, L., Xing-Wang, D., Zhangliang, C., Hongya, G., and Li-Jia, Q. (2006). The MYB transcription factor superfamily of Arabidopsis: expression analysis and phylogenetic comparison with the rice MYB family. *Plant Molecular Biology* **60**, 107-124.

Yin, H., Li, S., Zhao, X., Du, Y., and Ma, X. (2006). cDNA microarray analysis of gene expression in *Brassica napus* treated with oligochitosan elicitor. *Plant Physiology and Biochemistry* **44**, 910-916.

Yin, H., Zhao, X. M., and Du, Y. G. (2010). Oligochitosan: a plant diseases vaccine_a review *Carbohydrate Polymers* **82**, 1-8.

Yooyongwech, S., Cha-um, S., and Supaibulwatana, K. (2012). Proline related genes expression and physiological changes in indica rice response to water-deficit stress. *Plant OMICS: Journal of Plant Molecular Biology & Omics* **5**.

Zeng, D. (2012). Physiological effects of chitosan coating on wheat growth and activities of protective enzyme with drought tolerance. *Open Journal of Soil Science* **2**, 282-288.

Zheng, X., Chen, B., Lu, G., and Han, B. (2009). Overexpression of a NAC transcription factor enhances rice drought and salt tolerance. *Biochemical and Biophysical Research Communications* **379**, 985-989.

Zou, M., Guan, Y., Ren, H., Zhang, F., and Chen, F. (2008). A bZIP transcription factor, OsABI5, is involved in rice fertility and stress tolerance. *Plant Molecular Biology* **66**, 675-683.

Zulfugarov, I. S., Mishra, S. R., and Lee, C.-H. (2010). Quantitative analysis of cyclic electron flow in rice plants (*Oryza sativa* L.) lacking PsbS protein of photosystem II. *Proceedings of ANAS (Biological Sciences)* **65**, 90-95.

APPENDIX

APPENDIX A
CHEMICALS AND REAGENTS

1. Reagent for rice planting

1.1 modified WP nutrient solution (Vajrabhaya and Vajrabhaya, 1991)

The solution 1 liter contains:

Chemicals	Content (mg)
Macroelements:	
Potassium nitrate (KNO_3)	580
Calcium sulfate ($CaSO_4$)	500
Magnesium sulfate ($MgSO_4.7H_2O$)	450
Triple superphosphate	250
Ammonium sulfate ($(NH_4)_2SO_4$)	100
Microelements:	
Di-sodium ethylene diamine tetraacetate (Na_2EDTA)	160
Ferrous sulfate ($FeSO_4.7H_2O$)	120
Manganese sulfate ($MnSO_4.H_2O$)	15
Boric acid (H_3BO_3)	5
Zinc sulfate ($ZnSO_4.7H_2O$)	1.5
Potassium iodide (KI)	1.0
Sodium molybdate ($Na_2MoO_4.2H_2O$)	0.1
Copper sulfate ($CuSO_4.5H_2O$)	0.05
Cobalt chloride ($CoCl_2.6H_2O$)	0.05

2. Reagents for identification of chitosan responsive proteins in LPT123 and LPT123-TC171 rice during drought stress

Chemicals	Content	
1. protein concentration measurement (Lowry's method)		
- reagent A (alkaline copper reagent)	CTC	5 ml
	(0.2% $CuSO_4.7H_2O$ + 0.4% Tartaric acid)	
	20% Na_2CO_3	5 ml
	0.8 N NaOH	10 ml
	5% SDS	20 ml
- reagent B (diluted Folin-Ciocalteu's phenol reagent)	Folin-Ciocalteu phenol	1 ml
	distilled water	5 ml
2. protein separation (SDS-PAGE)		
2.1 SDS-polyacrylamide gel preparation		
- separating gel (12.5 %)[a]	distilled water	4,200 µl
	40% acrylamide	3,125 µl
	1.5 M Tris. HCl pH 8.8	2,500 µl
	10% SDS	125 µl
	10% APS	50 µl
	TEMED[b]	6 µl
- stacking gel (4%)[a]	distilled water	1,900 µl
	40% acrylamide	300 µl
	0.5 M Tris. HCl pH 6.8	742 µl
	10% SDS	30 µl
	10% APS	23 µl
	TEMED[b]	3.5 µl

[a] The components were mixed in the order shown.

[b] Polymerize will begin as soon as TEMED has been added.

2. Reagents for identification of chitosan responsive proteins in LPT123 and LPT123-TC171 rice during drought stress *(cont.)*

Chemicals	Content	
2. protein separation (SDS-PAGE)		
2.2 SDS-PAGE running		
- protein loading dye	50 mM Tris.HCl pH 6.8	
	10% glycerol	
	2% SDS	
	1% β-mercaptoethanol	
	0.02% bromophenol blue	
	adjust volume with distilled water	
- Tris-glycine electrophoresis buffer	25 mM Tris pH 8.3	
	250 mM glycine	
	0.1% SDS	
	adjust volume to 1 L with distilled water	
2.3 gel staining (Coomassie Brilliant Blue)		
- staining solution	Coomassie Brilliant Blue R250	5 g
	acetic acid	100 ml
	methanol	500 ml
	distilled water	400 ml
- destaining solution	acetic acid	100 ml
	methanol	200 ml
	distilled water	700 ml

3. **Reagents for expression analysis of a chitosan-responsive gene during drought stress, *transcriptional repressor***

Chemicals	Content	
1. total RNA extraction		
- RNA extraction buffer	100 mM Tris pH 9.0	
	100 mM NaCl	
	20 mM EDTA pH 8.0	
	1% (w/v) Lauryl sarcosinate[a]	
	0.1% (v/v) diethylpyrocarbonate (DEPC)	
	0.1% (v/v) β-mercaptoethanol[b]	
- DEPC treated TE buffer	10 mM Tris (pH 8.0)	
	1 mM EDTA (pH 8.0)	
	0.1% (v/v) diethylpyrocarbonate (DEPC)	
2. agarose gel electrophoresis		
- 6x RNA loading dye	30% (v/v) glycerol in water	
	0.25% (w/v) bromophenol blue	
	0.25% (w/v) xylene cyanol FF	
- 5x TBE buffer	Tris base	54 g
	Boric acid	27.5 g
	0.5 M EDTA pH 8.0	20 ml
	adjust volume to 1,000 ml with distilled water	
3. DNA-free RNA preparation		
- DEPC treated water	distilled water	1,000 ml
	diethylpyrocarbonate (DEPC)	1 ml

[a] add after autoclave

[b] add before use

APPENDIX B
PROTOCOLS

1. Identification of chitosan-responsive proteins in LPT123 and LPT123-TC171 rice during drought stress

1.1 Protein separation (SDS-PAGE)

1.1.1 Gel staining with Coomassie Brilliant Blue

Separated protein was detected with Coomassie Brilliant Blue staining. The gel was immersed in staining solution and shaken gently at room temperature until the protein bands appeared. The solution was taken away before the gel was soaked in destaining solution and agitated slowly for an hour. During this period, the destaining solution was changed 3-4 times. After that the gel was destained overnight or until the background was clear.

2. Expression analysis of a chitosan-responsive gene during drought stress, *transcriptional repressor*

2.1 Agarose gel electrophoresis

In order to check RNA quality, the RNA sample was run on 0.8% agarose gel electrophoresis. Agarose solution was prepared by melting agarose powder in 0.5x TBE buffer. 1 µl of RNA sample was mixed with 1 µl of 6x RNA loading dye and 4 µl of DEPC-treated water and then loaded into a well. The electrophoresis was carried out at 100 Volt. The RNA was stained with 0.5 µg/ml of ethidium bromide for 15 minutes and visualized under UV light by using gel documentation system (Gel DOC^{TM}2000, Bio-Rad, USA).

APPENDIX C
STANDARD CURVES AND PROTEIN LADDER

1. Identification of chitosan-responsive proteins in LPT123 and LPT123-TC171 rice during drought stress

1.1 Protein concentration measurement

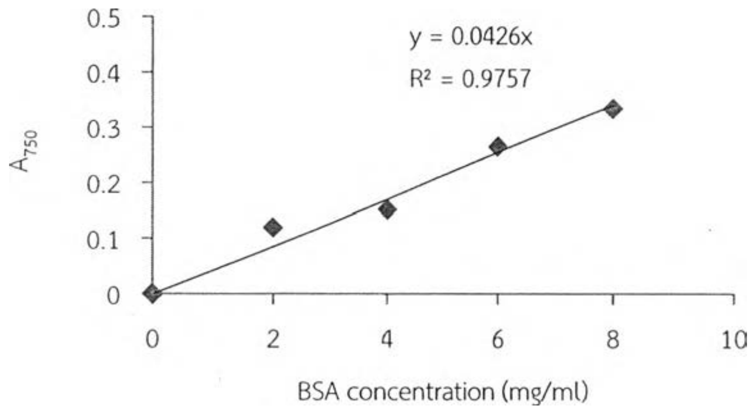

Figure C.1 Standard curve of standard protein (BSA)

1.2 Protein separation (SDS-polyacrylamide gel electrophoresis)

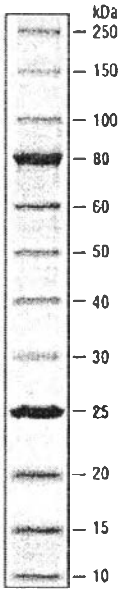

Figure C.2 Protein ladder 10-250 kDa (New England Biolabs, USA)

2. Expression analysis of a chitosan-responsive gene during drought stress, *transcriptional repressor*

2.1 Quantitative reverse transcription polymerase chain reaction (qRT-PCR)

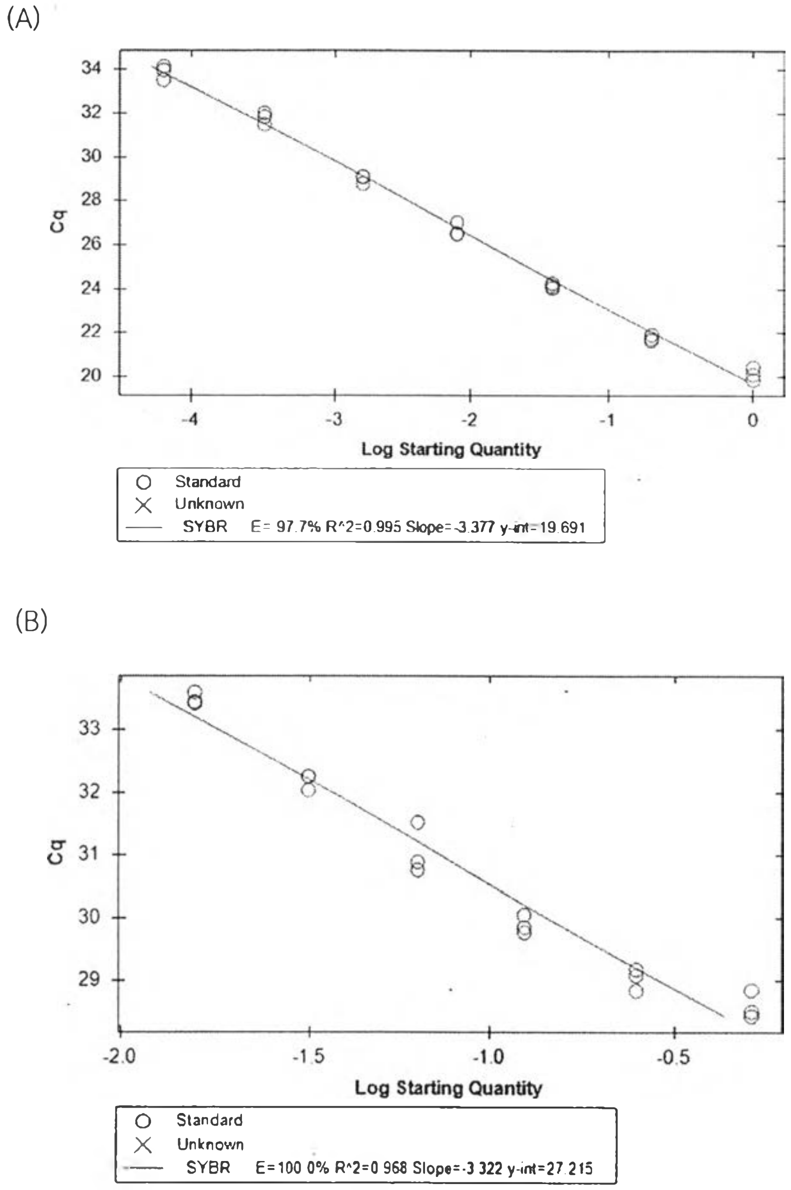

Figure C.3 Standard curve of (A) *EF-1α*, a reference gene and (B) *transcriptional repressor*

APPENDIX D
CHITOSAN RESPONSIVE PROTEINS DURING DROUGHT STRESS IN LEAF AND ROOT TISSUES OF LPT123 AND LPT123-TC171 RICE

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Up-regulated proteins							
Cellular homeostasis							
LOC_Os03g21000	Thioredoxin	membrane, plastid	gi|222624850	1093.73	MNLAFAKATK	4.3e-109	C
Growth and development							
LOC_Os04g52340	expressed protein		gi|38568023	1281.89	CYLRLSDNSR	9.9e-181	F
Nucleic acid metabolic process							
LOC_Os01g36460	MYB family transcription factor		gi|297720083	753.17	AAAVPAVR	6.0e-08	C
LOC_Os01g49150	anti-silencing protein, ASF1-like domain containing protein	cytoplasm, nucleus	gi|125571604	1183.31	NILADKPSVTK	6.5e-161	C
LOC_Os04g39160	RNA-dependent RNA polymerase	nucleolus	gi|75327281	831.43	KGFSIGPK	0	C
LOC_Os05g48990	homeobox domain containing protein	cytoplasm, nucleus	gi|50511480	1005.29	QRGGSGSSGGR	9.8e-271	C
LOC_Os07g12320	WD domain, G-beta repeat domain containing protein	nucleolus	gi|22296462	1158.91	VVRYPVAGGDK	5.5e-283	N
LOC_Os03g27310	histone H3		gi|38569184	992.45	RCSSTDLR	2.6e-34	C
Other metabolic process							
LOC_Os03g45250	2-aminoethanethiol dioxygenase		gi|29244630	961.46	TPEPAPLLK	3.3e-166	C
LOC_Os03g55230	cytochrome P450		gi|115455481	899.89	DRTTDHR	7.8e-181	C
LOC_Os04g33370	cytochrome P450	membrane	gi|116309420	994.40	AMERFVAR	5.6e-281	C
LOC_Os05g48640	ATROPGEF7/ROPGEF7		gi|115465411	704.23	SSGSRGR	5.9e-302	F
LOC_Os06g41390	N-terminal asparagine amidohydrolase		gi|218198552	2141.70	FLQGSGGRELVAALMGNPGLR	4.9e-192	C
LOC_Os11g10480	Dehydrogenase	cytosol, plasma membrane	gi|296248168	773.38	ATAGKVXK	2.1e-155	C
LOC_Os01g33300	Polygalacturonase		gi|115437052	1033.63	AVTMDNVIR	5.5e-219	C

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os03g47010	glycosyl hydrolase family 10 protein		gi|115454551	671.48	VLAVSGK	0	C
LOC_Os04g24140	ribose-5-phosphate isomerase A	cytosol	gi|115457638	707.73	RVAAHR	1.2e-143	C
LOC_Os06g19550	oxidoreductase, short chain dehydrogenase/reductase family	ER	gi|125555016	524.46	FSGSE	4.8e-129	C
LOC_Os07g09190	Transketolase	plastid	gi|115470975	916.17	SRMHTIR	0	C
LOC_Os07g38850	Prenyltransferase	plastid	gi|34393498	2182.10	FLRPHTIRGTALGSMSLVAR	2.0e-173	C
LOC_Os10g42720	acyltransferase	plastid	gi|115483650	849.84	LCCSRR	1.7e-233	C
LOC_Os03g49180	alkaline phytoceramidase	ER, membrane	gi|115454765	551.09	DMAAK	2.0e-143	C
LOC_Os02g30620	dnaJ domain containing protein		gi|115446299	576.17	SAVSGR	0	C
LOC_Os07g34850	aspartic proteinase nepenthesin		gi|115472515	1658.11	DSHRIAFLSDATAAGK	1.3e-235	C
LOC_Os07g34920	aspartic proteinase nepenthesin precursor		gi|50725948	1123.14	ESSCSRMPR	5.4e-10	C
LOC_Os10g33774	leucoanthocyanidin reductase		gi|110289263	970.60	DLQSLGPLK	1.2e-173	C
LOC_Os11g32580	chalcone synthase	membrane, nucleus, vacuole	gi|115485725	544.82	AGIER	3.8e-220	C
Protein modification							
LOC_Os01g48020	S-locus-like receptor protein kinase	plasma membrane	gi|125571523	765.07	EATGNFK	0	C
LOC_Os04g55760	OsWAK55 - OsWAK receptor-like protein kinase	plasma membrane	gi|297603478	766.11	SFGTEAR	0	C
LOC_Os07g31190	OsWAK71 - OsWAK receptor-like cytoplasmic kinase OsWAK-RLCK	plasma membrane	gi|115472179	869.73	ELDGIPAR	0	C
LOC_Os09g29520	OsWAK81 - OsWAK receptor-like cytoplasmic kinase OsWAK-RLCK	plasma membrane	gi|297609620	1783.16	RCLEMCGENRPSMK	5.3e-182	N

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Signal transduction							
LOC_Os03g58870	expressed protein		gi|158937154	971.339	AYSSSSTLR	1.1e-05	C
LOC_Os06g35814	ras-related protein	endosome, Golgi apparatus, plasma membrane	gi|115468476	942.82	AITSAYYR	2.2e-112	C
LOC_Os08g40990	receptor-like protein kinase 1		gi|115477354	1264.62	SIDPQMFEGNK	0	C
LOC_Os12g37550	PPR repeat domain containing protein	plastid	gi|115489080	1049.58	AIIDAFGKSK	1.5e-161	C
Stress response/defense							
LOC_Os02g18140	NBS type disease resistance protein		gi|115445571	884.65	AEWTIHK	0	C
LOC_Os03g13160	non-symbiotic hemoglobin 2	cell wall, cytosol, plasma membrane	gi|115451755	1048.58	AFASASNGAVR	3.3e-86	C
LOC_Os04g14220	disease resistance protein RPM1	plasma membrane	gi|21616908	661.43	MQHCA	8.8e-157	C
LOC_Os05g16660	WD domain, G-beta repeat domain containing protein	cytosol	gi|218200913	708.09	MSATRK	4.6e-41	C
LOC_Os06g17920	NBS-LRR disease resistance protein	plasma membrane	gi|55296580	470.42	AGVLI	0.0013	N
LOC_Os07g18050	RNA-binding motif protein	nucleus	gi|115471551	850.36	GAECPYR	2.1e-274	C
LOC_Os08g37210	patatin	cytoplasm	gi|125561902	642.49	LVEVGK	1.8e-220	C
LOC_Os09g20330	annexin		gi|222641446	594.75	TTFAR	2.4e-138	N
LOC_Os11g29990	NBS-LRR type disease resistance protein		gi|77550937	1046.78	LSSLMVPER	0	C
Transport							
LOC_Os01g57370	cyclic nucleotide-gated ion channel 2	membrane	gi|297720463	565.24	KPPPK	0	C
LOC_Os03g13380	transmembrane 9 superfamily member	Golgi apparatus, membrane	gi|115451783	616.38	VEKGGK	0	C

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transport *(cont.)*							
LOC_Os04g41320	nucleotide-sugar transporter family protein	Golgi apparatus, membrane	gi|38345234	678.45	KPLLPI	3.1e-209	C
LOC_Os09g26820	exo70 exocyst complex subunit	cytosol	gi|115479365	882.65	SFLGRFR	0	C
Transposon/retrotransposon							
LOC_Os02g26630	transposon protein, putative, unclassified, expressed		gi|218190703	987.13	CQEGLPKR	0	C
LOC_Os02g39220	transposon protein, putative, unclassified, expressed		gi|47497275	415.47	IVAGG	0	C
LOC_Os03g43490	retrotransposon protein, putative, unclassified, expressed		gi|108709984	881.64	VSAGHSTPK	9.0e-100	C
LOC_Os04g24165	retrotransposon protein, putative, unclassified, expressed		gi|21328112	830.35	GSAAGGAGQR	1.8e-08	C
LOC_Os05g26600	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|34394299	488.62	GKGGNG	1.5e-67	C
LOC_Os07g25160	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|50582701	887.02	MDPAVEAR	1.0e-06	N
LOC_Os09g01020	retrotransposon protein, putative, unclassified, expressed		gi|52077437	880.45	TSGSGGGGSSK	4.9e-266	C
LOC_Os10g15180	retrotransposon protein, putative, unclassified, expressed		gi|21672048	533.09	GTAER	9.3e-233	C
LOC_Os10g24510	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|18652533	1933.97	SFGLTNAPAFFMNLMNK	0	C
LOC_Os10g34120	retrotransposon protein, putative, Ty1-copia subclass, expressed		gi|110289286	1149.33	MNMAIISKAR	0	C

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os11g28800	retrotransposon protein, putative, Ty3-gypsy subclass		gi|77550812	1034.16	EISRLVYR	7.5e-96	N
LOC_Os12g43480	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|77557127	717.19	GMSAHAK	0	C
Unknown							
LOC_Os01g35810	expressed protein		gi|22138476	1228.51	RRPAHWHGGR	2.5e-88	C
LOC_Os01g36940	OsFBX13 - F-box domain containing protein		gi|125526369	687.34	AVGGEQK	4.7e-126	C
LOC_Os01g40220	DEFL7 - Defensin and Defensin-like DEFL family	endosome	gi|125531815	1893.51	MATTNTAPFPHTGGDGMR	0.12	F
LOC_Os01g43060	expressed protein		gi|115438610	1121.19	KAGPPTDPLPK	1.4e-94	C
LOC_Os01g56530	DUF260 domain containing protein		gi|56785215	1027.67	GAAEFAAVHR	6.5e-129	C
LOC_Os02g03950	zinc finger, C3HC4 type family protein		gi|218189993	712.00	RSTPPR	9.5e-144	C
LOC_Os02g34830	tetratricopeptide repeat domain containing protein		gi|222623045	935.48	CKEDEEK	8.8e-189	C
LOC_Os02g43770	DUF630/DUF632 domains containing protein		gi|125583115	654.07	DGTHVQ	4.6e-185	C
LOC_Os02g45030	latency associated nuclear antigen		gi|218188721	689.56	SGGGVSAR	6.1e-09	C
LOC_Os02g52960	PHD-finger domain containing protein		gi|125583819	2266.62	ARAEGLPEGAAPGVGVDLYAQAR	0	C
LOC_Os03g15300	hypothetical protein		gi|108707269	856.49	WKNGSHK	1.8e-85	N
LOC_Os03g32790	expressed protein		gi|115453727	812.48	MSRYLK	1.0e-100	C
LOC_Os03g38130	conserved hypothetical protein	mitochondrion	gi|50399983	762.85	HVRPKK	1.5e-99	C
LOC_Os03g38740	Dicer		gi|41469333	753.21	DLIAGHK	0	C

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os03g48280	expressed protein		gi|50838970	1869.78	AIGALSSYDAGATGEEAMR	5.5e-90	C
LOC_Os03g55430	expressed protein		gi|149390995	527.98	SSTFS	1.9e-65	C
LOC_Os03g56510	OsFBX112 - F-box domain containing protein		gi|24899441	1065.28	CAATCKSLR	9.0e-203	C
LOC_Os04g15680	expressed protein		gi|115457368	812.67	LGGISPDR	1.5e-12	C
LOC_Os04g33020	expressed protein		gi|218190840	921.36	QRVHEVR	8.6e-24	C
LOC_Os05g16315	translation initiation factor IF-2		gi|49389059	1529.29	GRAATAAAMWAAPLR	3.7e-23	C
LOC_Os05g23530	expressed protein		gi|115463067	1204.68	LRSCILSETK	0	C
LOC_Os06g05200	zinc finger, C3HC4 type domain containing protein		gi|55296364	557.74	TPVSR	2.3e-06	C
LOC_Os06g09620	expressed protein		gi|218194252	736.56	KLALHR	0.00047	C
LOC_Os06g15560	expressed protein		gi|215740613	683.28	WTQH	3.0e-101	C
LOC_Os06g30400	expressed protein	plastid	gi|52076486	781.09	SPLPVSGK	7.9e-69	C
LOC_Os06g42810	UBA and UBX domain-containing protein		gi|115469078	777.586	MAAGDAAR	1.3e-242	C
LOC_Os06g43770	expressed protein		gi|115469186	1098.65	VGAVQAAATRR	2.0e-127	C
LOC_Os06g44870	expressed protein		gi|218198686	946.46	EAAPLPPPR	2.3e-55	C
LOC_Os07g43480	expressed protein		gi|218200071	875.68	TTLRATGR	3.3e-156	C
LOC_Os08g13740	expressed protein		gi|125540467	737.32	TDMIDK	2.7e-146	C
LOC_Os08g16860	OsFBX282 - F-box domain containing protein		gi|37805887	678.48	GAKNYK	7.6e-206	C
LOC_Os08g20090	expressed protein		gi|115445961	522.12	RGGMS	3.7e-16	C

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os08g23360	signal recognition particle 68 kDa protein		gi|218200939	595.91	GKYTK	4.5e-222	C
LOC_Os10g05030	expressed protein		gi|51091822	463.43	GGGGGC	6.0e-11	C
LOC_Os10g05510	expressed protein		gi|18642674	804.50	DSGGSVKR	4.2e-63	C
LOC_Os10g17940	OsFBX382 - F-box domain containing protein		gi|297727435	1091.64	KVAAPPGHCR	1.9e-264	C
LOC_Os11g02340	expressed protein		gi|77548414	884.23	RPTGVAQR	3.8e-124	C
LOC_Os11g04510	expressed protein		gi|297727959	682.34	FCDNK	2.4e-163	N
LOC_Os11g05790	expressed protein		gi|115487566	1038.97	LLLLVAAATR	1.4e-08	C
LOC_Os11g06050	expressed protein		gi|77548777	714.42	ADEKHD	1.8e-135	C
LOC_Os11g11400	expressed protein		gi|77549306	876.02	AALMQPSC	5.9e-64	C
LOC_Os11g14820	expressed protein		gi|125597205	955.64	GPGCRRPR	1.2e-65	C
LOC_Os11g31790	hypothetical protein		gi|115485671	1446.01	MACTEMMKSAVR	1.2e-214	C
LOC_Os11g39050	expressed protein		gi|125557110	775.87	RESDDR	3.0e-21	C
LOC_Os12g07200	expressed protein	nucleus	gi|77553134	800.51	IKPEASR	2.2e-73	C
LOC_Os12g38800	RNA recognition motif containing protein		gi|297729321	526.41	SGSLY	5.2e-223	C
Down-regulated proteins							
Cellular component organization							
LOC_Os01g13270	AGC_PVPK_like_kin82y.4 - ACG kinases include homologs to PKA, PKG and PKC		gi|115435510	910.90	EKPAAAPTK	1.7e-288	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Cellular process							
LOC_Os09g20684	SMP-30/Gluconolaconase/LRE-like region containing protein	cell wall, ER, plasma membrane	gi|115478873	1924.84	GADNDDVAPTVAVRVTAAGK	3.4e-196	A
Growth and development							
LOC_Os01g68598	expressed protein		gi|115441801	746.32	LPKYAR	1.0e-68	A
LOC_Os04g38470	expressed protein		gi|125548557	843.44	SMMFSAR	9.2e-59	A
LOC_Os05g43960	no apical meristem protein	plastid	gi|222632226	463.15	ASTGK	8.6e-285	A
LOC_Os06g44860	OsSPL10 - SBP-box gene family member	nucleus	gi|115469324	1471.02	TYFSPGDMLAVDR	1.4e-236	A
LOC_Os10g02980	formin	cytoskeleton, cytoplasm	gi|110288553	1700.23	LLAEEMQAINKGLEK	3.3e-198	A
LOC_Os09g12500	EMB1381		gi|218201867	1007.33	FASDVREGK	6.6e-271	A
Nucleic acid metabolic process							
LOC_Os01g01960	transcriptional repressor	nucleus	gi|52076211	1852.62	FELDMLLESVNAATKR	0	A
LOC_Os01g56780	plus-3 domain containing protein	nucleus	gi|297597703	584.60	ARLVK	0	A
LOC_Os01g67970	ZOS1-20 - C2H2 zinc finger protein	nucleus	gi|115441715	756.65	KTGHSVK	0	D
LOC_Os02g39140	helix-loop-helix DNA-binding domain containing protein	cytosol	gi|222623194	1517.83	MASTSALEMAGMDR	1.2e-51	A
LOC_Os02g42040	MIF4G domain containing protein		gi|49389189	924.64	SSVEHVLR	0	A
LOC_Os02g44360	scarecrow transcription factor family protein	plastid	gi|4056615	946.39	APPLPAILR	5.8e-137	A
LOC_Os02g49270	NOL1/NOP2/sun family protein	nucleolus	gi|45735882	1057.31	ADPSSDDPQK	0	D
LOC_Os03g22800	OsFBT5 - F-box and tubby domain containing protein		gi|122236825	951.18	SHRGGGGAPR	1.1e-218	A
LOC_Os03g42420	B3 DNA binding domain containing protein	vacuole	gi|115454161	1982.44	EVVMERGGGGGGGDQWHVR	2.2e-215	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Nucleic acid metabolic process *(cont.)*							
LOC_Os04g48370	RNA polymerase IV subunit	nucleus	gi|115460018	881.51	FFVESVR	6.2e-243	A
LOC_Os06g43220	AP2 domain containing protein	nucleus	gi|125556211	789.28	NMLLMR	5.9e-112	A
LOC_Os06g51450	PHD-finger domain containing protein	nucleus	gi|297606567	643.54	LLASLK	6.5e-36	A
LOC_Os07g36250	peptide chain release factor protein	plastid	gi|115472651	713.53	LLNDLK	1.2e-239	L
LOC_Os08g03390	pre-mRNA-splicing factor SLU7		gi|115474617	1015.81	ELLLGQSEK	1.8e-298	A
LOC_Os09g24800	MYB family transcription factor		gi|19072764	456.25	AAAPK	4.1e-111	A
LOC_Os12g31430	helix-loop-helix DNA-binding domain containing protein	nucleus	gi|14626293	629.12	ATIPAR	3.6e-13	A
LOC_Os12g33100	guanylate kinase		gi|115488800	946.10	GTVVVAWSK	6.4e-202	A
LOC_Os12g41700	LSD1 zinc finger domain containing protein		gi|115489526	886.94	NILLYPR	4.8e-94	A
LOC_Os04g18090	histone H1	intracellular, nucleus	gi|215707123	848.28	AKPAAPAPK	1.7e-96	A
LOC_Os02g01230	ribosomal protein	Golgi apparatus, ribosome	gi|41052902	731.56	LKDATGK	8.7e-269	D
LOC_Os08g39500	60S ribosomal protein L31	cell wall, cytosal, ribosome	gi|115477176	475.14	GLGTK	6.8e-31	A
Other metabolic process							
LOC_Os01g22520	dihydrolipoyl dehydrogenase 1, mitochondrial precursor	membrane, mitochondrion	gi|115436320	743.49	AAEALLR	1.7e-263	A
LOC_Os01g24030	AMP-binding enzyme	peroxisome	gi|115436398	1219.96	VTAAAIFDSVAR	0	A
LOC_Os01g66000	NADH dehydrogenase I subunit N	intracellular, membrane, thylakoid	gi|56784479	1141.69	LPAAPGEDGCR	2.7e-116	A
LOC_Os02g22680	integral membrane protein DUF6 containing protein	plasma membrane, vacuole	gi|218190638	585.34	YGMAK	3.1e-145	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os04g01590	arginase	plastid	gi|115456826	842.93	LKAELLR	3.9e-179	A
LOC_Os04g20260	UDP-glucoronosyl and UDP-glucosyl transferase		gi|297722919	1030.01	DGAMSHQLR	1.7e-281	A
LOC_Os04g23720	lectin protein kinase family protein	plasma membrane	gi|297722977	815.20	IILDITK	0	A
LOC_Os04g32330	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor	cytosol, ribosome, mitochondrion	gi|115458104	851.58	GLVVPVIR	2.8e-231	A
LOC_Os04g39140	acetyltransferase, GNAT family	plastid	gi|115458850	820.39	DELAAFR	1.3e-169	A
LOC_Os04g44950	short-chain dehydrogenase/reductase	cell wall	gi|115459602	622.76	EASFLG	1.7e-160	A
LOC_Os05g29050	phospholipase D p1		gi|218196631	768.24	FRYER	0	L
LOC_Os05g42150	OsGH3.4 - Probable indole-3-acetic acid-amido synthetase	cytoplasm, plastid	gi|115464735	1122.46	NAAPMFAFVR	0	A
LOC_Os05g47640	threonine synthase, chloroplast precursor	cytosol, plastid	gi|115465273	1180.06	ADFGAVMDVLK	2.8e-286	A
LOC_Os06g13460	SAM dependent carboxyl methyltransferase family protein		gi|297724651	834.06	AIIEVYK	2.2e-89	D
LOC_Os06g17090	UDP-glycosyltransferase		gi|125554921	536.73	AGAYR	2.4e-193	A
LOC_Os06g19960	aconitate hydratase protein	cell wall, cytosol, mitochondrion, plastid	gi|297605667	644.89	GFAVPR	0	A
LOC_Os07g25540	flavin monooxygenase		gi|218199513	921.88	DSVHVLPR	3.6e-215	A
LOC_Os09g04730	dehydrogenase/reductase SDR family member 2	peroxisome	gi|115478070	1662.12	VNCIAPGFVPTNFAR	6.7e-127	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os10g04860	aldehyde oxidase		gi|125531085	1432.02	SSDGIEIGAAVSISK	0	A
LOC_Os10g18510	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein		gi|218184318	683.01	MPSPPR	3.6e-215	A
LOC_Os10g35840	shikimate/quinate 5-dehydrogenase	plastid	gi|10140790	844.21	IGEDALTK	8.8e-276	A
LOC_Os10g41170	dehydrogenase	cytosol	gi|222613266	2190.66	APKMATMAAGVALHLHLQGMK	7.4e-174	A
LOC_Os11g47970	AAA-type ATPase family protein	cell wall, membrane, extracellular region, nucleus, thylakoid, plastid	gi|62733297	1867.63	IVDSFPGQSIDFFGALR	1.9e-255	L
LOC_Os12g15400	CXE carboxylesterase		gi|115488038	705.17	GHELSY	5.3e-237	A
LOC_Os12g33958	NADH-ubiquinone oxidoreductase 49 kDa subunit	mitochondrion, membrane	gi|89280745	1032.75	GPGVCWDSR	3.3e-212	A
LOC_Os12g37660	pectinesterase	cytoplasm, cell wall	gi|125588509	720.84	MWDDR	2.9e-126	A
LOC_Os01g19220	beta-D-xylosidase	cell wall, extracellular region	gi|14164501	540.79	VGLPR	0	A
LOC_Os02g54420	hypro1	membrane	gi|218188373	641.67	AAPDIR	1.7e-167	L
LOC_Os04g33740	glycosyl hydrolases	cell wall	gi|293651274	1216.82	GARLGLAXLYR	2.3e-181	A
LOC_Os04g46560	lactate/malate dehydrogenase	plasma membrane, cytosol	gi|115459790	941.08	EFAPAIPAK	2.1e-187	D
LOC_Os07g09670	galactosyltransferase family protein	Plastid	gi|34393273	888.15	KSTNIVAR	0	A
LOC_Os08g25410	conserved hypothetical protein		gi|38423992	1332.60	AAEGLGAAYTRVR	2.0e-136	A
LOC_Os01g61200	GDSL-like lipase/acylhydrolase		gi|15624048	1101.75	NIVGEEEASR	2.1e-187	A
LOC_Os01g37825	M16 domain containing zinc peptidase	mitochondrion, plastid	gi|57899335	603.42	AEVGTK	0	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os04g40750	expressed protein		gi|38345334	1264.93	VLADGEAAAHRR	6.9e-118	A
LOC_Os05g35400	DnaK family protein	plasma membrane, nucleolus, cell wall, vacuole, nucleus	gi|115464027	701.73	TMVPVR	0	A
LOC_Os08g41550	ubiquitin carboxyl-terminal hydrolase		gi|222640904	1455.80	SLGPLKVSGHVSFK	1.6e-292	A
LOC_Os09g10270	SKP1-like protein 1B	intracellular, cytoplasm, nucleolus, nucleus	gi|49387822	1422.59	MAASAAAADGAADGEK	1.6e-86	A
LOC_Os11g12520	serpin domain containing protein		gi|125576685	1325.14	DELAGLVGRLAGR	6.5e-216	A
LOC_Os11g36050	prefoldin subunit	cytosol	gi|115485941	856.82	MHEALEK	1.1e-73	A
LOC_Os12g31840	ZOS12-05 - C2H2 zinc finger protein	intracellular	gi|115488688	1020.59	LMEEDNKK	0	A
LOC_Os08g14570	NADPH reductase	ER, plastid	gi|222640169	499.84	TPAGR	0	A
LOC_Os11g42290	transferase family protein	cytosol	gi|297728623	615.35	ARVGGR	2.0e-237	A
Protein modification process							
LOC_Os01g60440	HEAT repeat family protein		gi|115440729	598.57	TSSTGM	0	A
LOC_Os02g28980	peptidyl-prolyl isomerase	cytosol, nucleus, membrane	gi|115446187	601.60	DGGILK	0	A
LOC_Os02g40664	zinc finger family protein	plasma membrane	gi|115447343	823.79	MEGMWR	0	A
LOC_Os03g55880	expressed protein		gi|222630337	573.78	GGRASK	7.4e-18	A
LOC_Os05g06120	ubiquitin conjugating enzyme protein	cytosol	gi|52353591	601.08	VSAAVR	0	A
LOC_Os05g38830	HECT-domain domain containing protein	intracellular	gi|53749320	928.65	DNILVSAAK	2.1e-283	A
LOC_Os10g10870	protein kinase family protein		gi|297610190	1922.81	VSRLIDLVDPALQDVNR	1.4e-156	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Signal transduction							
LOC_Os01g57510	receptor protein kinase	plasma membrane, vacuole	gi|125572261	909.14	MAAVSSSSR	0	A
LOC_Os03g57780	protein kinase		gi|108711496	686.70	SEGGPGGK	0	A
LOC_Os04g15630	xa21	plasma membrane	gi|38346890	934.41	SLVMSLNR	0	A
LOC_Os04g15660	receptor kinase		gi|38346024	706.77	NMGTLR	0	A
LOC_Os04g45170	leucine-rich repeat family protein	plasma membrane	gi|115459628	1721.72	MFACVDDDLLANVPK	2.9e-94	A
LOC_Os04g54070	receptor-like kinase	plasma membrane, vacuole	gi|115460788	733.88	GMLGDNK	0	A
LOC_Os04g57640	RCD1	nucleus, cytoplasm	gi|115461248	534.01	MPSGK	0	L
LOC_Os07g17160	expressed protein		gi|125557936	704.95	KSVMTK	3.1e-248	A
LOC_Os11g47140	OsWAK123 - OsWAK receptor-like protein kinase	plasma membrane, cell wall, vacuole	gi|62734468	917.79	ITNNKSNK	0	A
Stress response/defense							
LOC_Os01g57310	rp1		gi|297720459	1886.22	EDIIKVWLCCHEER	0	A
LOC_Os01g57720	expressed protein		gi|297597754	1097.04	NSDGSSPCMK	0	A
LOC_Os03g51140	HEAT repeat family protein	membrane, nucleus, cytosol	gi|115455003	1845.84	EVVVPITGPLIRILGDR	0	A
LOC_Os04g08370	Leucine Rich Repeat family protein		gi|297722797	768.10	DDSSFAK	0	A
LOC_Os05g34230	disease resistance protein RGA3		gi|115463901	961.21	VTGSVLTER	0	A
LOC_Os06g49390	NBS-LRR disease resistance protein		gi|115480968	1473.08	LLQELSKFQVNR	1.4e-195	A
LOC_Os07g33730	NB-ARC domain containing protein		gi|28564734	1622.74	VHGSPLAAKFIGASLR	0	A
LOC_Os08g09430	disease resistance protein RPM1	plasma membrane	gi|156600226	810.63	DLGKLHK	8.0e-59	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Stress response/defense *(cont.)*							
LOC_Os09g39380	monodehydroascorbate reductase	plastid, peroxisome, plasma membrane, extracellular region	gi|115480733	1584.02	EVDDADKLVAAIQAK	2.6e-228	A
LOC_Os10g10360	NBS-LRR disease resistance protein		gi|115481324	936.76	SWELFQK	0	A
LOC_Os11g02080	expressed protein		gi|3282394	985.76	MMTITMIN	8.2e-19	A
LOC_Os11g11550	NBS-LRR disease resistance protein	plasma membrane	gi|115484771	582.40	CCSGV	0	A
LOC_Os11g47447	stripe rust resistance protein Yr10	plasma membrane	gi|108864692	943.42	LRQFLLR	5.5e-212	A
Transport							
LOC_Os01g07870	ABC transporter family protein	vacuole, membrane, extracellular region	gi|27368883	852.67	AMSEMLR	0	L
LOC_Os01g40380	amino acid/ transporter II	vacuole, membrane	gi|53791740	535.10	FGVGR	5.4e-31	A
LOC_Os01g41720	expressed protein	membrane	gi|53793543	1939.20	EEIIFELLKYLGGSTTK	0	A
LOC_Os01g64890	CorA-like magnesium transporter protein	plasma membrane	gi|115441289	556.43	ADSHK	2.3e-220	A
LOC_Os01g66560	signal recognition particle 72 kDa protein		gi|115441529	660.58	SDAIEK	0	A
LOC_Os02g02170	transporter, major facilitator family	membrane	gi|115443757	815.67	DNLNLTK	5.5e-290	A
LOC_Os02g44570	mitochondrial carrier protein	mitochondrion, membrane	gi|115447769	787.12	CGAPKVR	0	A
LOC_Os03g18550	mitochondrial carrier protein	mitochondrion, membrane	gi|108707653	1804.03	LQLTSSPYTGVSHCVR	1.5e-147	A
LOC_Os03g21490	ABC transporter, ATP-binding protein	plastid	gi|115452835	1543.13	EGEIHALMGQNGSGK	8.6e-159	A
LOC_Os03g37984	amino acid permease family protein		gi|38093761	1144.40	TGAGAGPVFDPR	1.0e-27	A
LOC_Os03g46740	ABC transporter, ATP-binding protein	plastid	gi|125547633	1856.45	MGGLLAIPMAVARVSSLR	5.6e-22	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transport *(cont.)*							
LOC_Os03g48180	peptide transporter PTR2	plasma membrane	gi|50872461	402.02	GAAAN	0	A
LOC_Os03g50300	CASP	Golgi apparatus, membrane	gi|62733538	974.58	DKITLSSGR	0	D
LOC_Os04g38010	transporter family protein	membrane	gi|297723201	939.41	HQGVTMPR	0	A
LOC_Os05g01750	TruB family pseudouridylate synthase	plastid	gi|297603679	936.66	KVEDFFR	4.4e-249	L
LOC_Os05g30640	leucine zipper protein-like	cytoplasm	gi|125562609	580.79	CSSDL	1.1e-268	A
LOC_Os06g36090	ABC-2 type transporter	plasma membrane	gi|115468502	575.30	AFIPK	0	A
LOC_Os08g31140	heavy metal-associated domain containing protein		gi|115476332	1128.85	GVQSVEINRK	6.9e-128	A
LOC_Os09g32200	mitochondrial carrier protein	mitochondrion, membrane	gi|115479927	954.60	LPDVEGAVR	0	A
LOC_Os10g21266	ATP synthase subunit beta	cell wall, membrane, mitochondrion, plastid, thylakoid	gi|19920171	1327.38	AHGGVSVFGGVGER	8.7e-79	D
LOC_Os11g08980	preprotein translocase secA family protein	plastid	gi|108864090	728.70	TSSMMR	8.0e-211	A
LOC_Os11g31470	expressed protein	nuclear envelope	gi|125534514	1660.32	WPHNGPITFSPPRR	3.7e-261	A
LOC_Os11g43049	exo70 exocyst complex subunit	cytoplasm	gi|297728641	748.83	LDAMAGR	1.5e-60	A
Transposon/retrotransposon							
LOC_Os01g27280	retrotransposon protein, putative, unclassified, expressed		gi|54290434	834.80	AAVFWNK	2.2e-208	A
LOC_Os01g47200	retrotransposon protein, putative, unclassified, expressed		gi|115438995	831.26	ESALTIAK	9.7e-222	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os01g54119	retrotransposon protein, putative, unclassified, expressed		gi|115439891	1788.56	LDSGSVKDQDQLEEAR	0	A
LOC_Os01g66870	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|222619663	995.86	GGYEKGAEGK	1.5e-273	A
LOC_Os02g20030	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|57900438	694.33	KGTMSR	6.8e-09	A
LOC_Os02g27890	retrotransposon, putative, centromere-specific, expressed		gi|51090669	867.58	RAAAHGER	7.5e-25	A
LOC_Os02g46020	transposon protein, putative, unclassified, expressed		gi|34015189	874.70	GGGGGKGETR	2.8e-57	A
LOC_Os03g02630	retrotransposon protein, putative, unclassified		gi|108705868	742.97	DPLNKR	3.7e-126	A
LOC_Os03g15400	retrotransposon protein, putative, unclassified, expressed		gi|108707280	1049.55	ATSWRSSTR	3.4e-148	A
LOC_Os03g32119	retrotransposon protein, putative, unclassified, expressed		gi|108709008	1268.54	KVLEMFNMDK	0	A
LOC_Os03g32650	transposon protein, putative, unclassified, expressed		gi|19697447	932.59	QKIIEMR	0	A
LOC_Os03g33380	retrotransposon, putative, centromere-specific, expressed		gi|29126391	900.32	QEEPSIAK	1.2e-159	A
LOC_Os03g38570	retrotransposon protein, putative, unclassified, expressed		gi|41469319	1014.75	GYLHFEPR	0	A
LOC_Os04g17010	retrotransposon protein, putative, unclassified, expressed		gi|38345214	925.79	ADMYDAIK	0	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os04g26290	retrotransposon protein, putative, unclassified, expressed		gi|116309492	663.60	GRFASK	0	D
LOC_Os04g52540	retrotransposon protein, putative, unclassified, expressed		gi|54291680	787.46	ALGFPER	0	A
LOC_Os05g01850	transposon protein, putative, unclassified, expressed		gi|52353574	659.02	ESLIAK	1.2e-07	A
LOC_Os05g08030	retrotransposon protein, putative, unclassified, expressed		gi|54291442	711.34	NKQNPN	0	A
LOC_Os05g15320	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|53981178	951.77	ADDLEMDK	5.9e-25	A
LOC_Os05g15490	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|222631468	823.75	DAPISPQP	0.019	A
LOC_Os05g17840	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|50878385	603.45	GYIPR	0	A
LOC_Os05g19460	retrotransposon protein, putative, unclassified, expressed		gi|125561428	970.70	IVSHEMQE	1.7e-73	D
LOC_Os05g46670	transposon protein, putative, unclassified, expressed		gi|258644667	1698.09	APIVSGGGHRHGGAAAER	7.5e-57	A
LOC_Os06g14270	retrotransposon protein, putative, unclassified		gi|222635331	1045.45	IVMAMAARGK	3.1e-35	A
LOC_Os06g17800	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|23237845	1548.02	KLTDLMQAVEEQK	0	A
LOC_Os06g22160	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|50725094	2029.60	MLGMNGNTFIALHDLLVR	1.8e-129	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os06g32580	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|297724919	1475.64	LQRLYINPEMAK	2.6e-237	A
LOC_Os07g13070	transposon protein, putative, CACTA, En/Spm sub-class		gi|33147057	594.86	HGPAGR	5.8e-22	A
LOC_Os07g19120	retrotransposon protein, putative, unclassified		gi|27817962	1084.22	GMNKVDLHR	1.3e-52	A
LOC_Os07g36770	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|125600667	645.01	MAPPSK	5.1e-287	A
LOC_Os07g42234	retrotransposon protein, putative, unclassified, expressed		gi|115473321	1551.68	EDGSWVESEEEKK	0	A
LOC_Os08g01570	retrotransposon protein, putative, unclassified, expressed		gi|115474393	1831.23	APTTIDLDAETSSASKPK	0	A
LOC_Os08g29440	retrotransposon, putative, centromere-specific, expressed		gi|22138455	1019.78	ATASTELTAR	1.6e-24	A
LOC_Os08g38690	retrotransposon protein, putative, SINE subclass, expressed		gi|297608786	1063.24	SYATEKTHK	2.4e-125	A
LOC_Os09g02250	transposon protein, putative, unclassified, expressed		gi|115477948	1154.76	AVLADGAVLAVR	0	A
LOC_Os09g21420	transposon protein, putative, unclassified, expressed		gi|218202079	692.67	STNGSTE	6.0e-103	A
LOC_Os09g32930	retrotransposon protein, putative, SINE subclass, expressed		gi|37999050	552.02	SSACK	0	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os10g03130	retrotransposon protein, putative, unclassified, expressed		gi|18997217	999.71	EIKADNAIK	2.0e-262	A
LOC_Os10g13530	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|19225021	2224.02	MSFVISLTLLTIIKELCSR	0	A
LOC_Os10g16470	retrotransposon protein, putative, unclassified, expressed		gi|13992678	939.43	DHAEGVRR	0	A
LOC_Os10g24160	retrotransposon protein, putative, Ty3-gypsy subclass		gi|78708451	514.37	GSKPK	1.8e-259	A
LOC_Os10g24650	retrotransposon, putative, centromere-specific, expressed		gi|13129454	630.42	GSILIK	5.4e-70	A
LOC_Os10g38570	retrotransposon protein, putative, unclassified		gi|18071399	872.45	MPDGGELR	4.1e-33	D
LOC_Os10g42650	retrotransposon protein, putative, unclassified, expressed		gi|125575799	964.29	DVVHIARR	5.0e-99	A
LOC_Os11g07300	retrotransposon protein, putative, LINE subclass, expressed		gi|222615603	1865.30	MMAEDGVPLAESEWLR	1.3e-93	A
LOC_Os11g09395	retrotransposon protein, putative, unclassified, expressed		gi|77549155	1775.68	LLPAEVEVGMGRPXRR	3.0e-172	A
LOC_Os11g12090	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|108864166	727.04	KLPGSVK	0	A
LOC_Os11g20780	retrotransposon protein, putative, unclassified, expressed		gi|62734014	808.08	RPGAGLNK	5.9e-302	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os11g33420	transposon protein, putative, CACTA, En/Spm sub-class		gi|77551334	672.27	LLVSIK	3.4e-116	A
LOC_Os12g03660	transposon protein, putative, unclassified		gi|218184837	1340.92	TIYIDQDSAMGK	6.7e-197	A
LOC_Os12g36580	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|218199408	1019.87	MPTPPPLPR	3.8e-238	A
LOC_Os12g42640	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|77557110	849.01	NECALNK	0	A
Unknown							
LOC_Os01g05530	expressed protein		gi|115434524	756.59	ENPLKR	0	A
LOC_Os01g11500	zinc finger, C3HC4 type domain containing protein		gi|50508512	570.28	AAPADK	1.4e-46	D
LOC_Os01g20110	expressed protein	membrane, thylakoid, plastid	gi|115436176	646.61	SLAKTK	1.7e-242	A
LOC_Os01g24840	conserved hypothetical protein		gi|53792293	758.81	DVPSGER	6.2e-117	D
LOC_Os01g26070	expressed protein		gi|125558331	1056.34	EQEGHSNEK	0.0085	A
LOC_Os01g31560	expressed protein		gi|218188280	603.21	GGGDAGGGG	1.8e-46	A
LOC_Os01g35320	expressed protein		gi|56784757	894.25	GGGHRPWK	2.9e-05	A
LOC_Os01g37790	expressed protein		gi|115437600	616.45	SATSPR	0	A
LOC_Os01g38490	expressed protein		gi|218188485	654.65	GPAASPR	1.5e-44	A
LOC_Os01g38710	nucleic acid binding protein		gi|125570867	619.78	TAADDK	1.5e-154	A
LOC_Os01g41370	FBD domain containing protein		gi|115438184	456.05	GAPGR	5.1e-287	A
LOC_Os01g50630	hypothetical protein		gi|51091353	768.23	GFISAFK	0.0015	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os01g51730	expressed protein		gi|50725769	922.17	MASSAGATGR	1.1e-07	A
LOC_Os01g54770	expressed protein		gi|15623852	498.09	TPGPK	1.7e-247	D
LOC_Os01g58754	expressed protein		gi|242117506	1936.59	MPTFHTIGDGHRHTTTL	0.9995	A
LOC_Os01g62680	hypothetical protein		gi|56784693	1357.61	SAVMPVPLLIMR	4.0e-97	A
LOC_Os01g68130	expressed protein		gi|297598157	934.16	DPMSRSAR	1.2e-205	A
LOC_Os02g01740	U5 small nuclear ribonucleoprotein		gi|222622018	1177.58	TWAAAPEAHAR	0	A
LOC_Os02g03920	200 kDa helicase		gi|125537961	1037.87	SGATGSPCMR	2.5e-56	A
LOC_Os02g07654	expressed protein		gi|49387592	1506.85	MVVAEWAAGTWLR	0.27	A
LOC_Os02g16740	expressed protein		gi|125581590	554.07	RLGLP	3.0e-37	A
LOC_Os02g30974	expressed protein		gi|125539634	758.12	EQPGGGGR	4.1e-132	A
LOC_Os02g45160	aluminum-activated malate transporter		gi|115447863	836.76	KGQTEMK	4.2e-260	A
LOC_Os02g46540	expressed protein		gi|41053262	1538.16	VGDGAATATRHDAAAR	4.5e-18	A
LOC_Os02g47230	Disease resistance/zinc finger/chromosome condensation-like region protein		gi|222629483	1821.97	GLVLAVVGSSYSKMIGLK	5.8e-105	A
LOC_Os02g49670	zinc knuckle family protein, expressed		gi|115448451	692.02	ANSCSR	2.1e-265	A
LOC_Os02g50370	helicase domain-containing protein		gi|115448551	1060.20	AFPGPSKDDK	0	L
LOC_Os03g02020	stress responsive A/B Barrel domain containing protein		gi|108705799	937.63	RVVFCTR	2.4e-154	A
LOC_Os03g04830	expressed protein		gi|115450653	495.78	GPPVK	4.6e-247	A
LOC_Os03g04990	expressed protein		gi|115450679	864.74	KEYADLK	0	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os03g05650	expressed protein		gi|108706214	763.55	YPNGSAR	2.2e-98	A
LOC_Os03g11890	potyvirus VPg interacting protein		gi|108706872	1362.48	RSDLNSEMLQR	0	A
LOC_Os03g21140	RNA-binding zinc finger protein		gi|205688046	773.70	IPYQQK	0	A
LOC_Os03g37170	expressed protein		gi|53749421	610.44	FILAF	7.7e-09	A
LOC_Os03g42440	expressed protein		gi|115454165	801.01	ALRGAASR	1.6e-40	A
LOC_Os03g43060	OsFBX96 - F-box domain containing protein		gi|46805647	1765.34	DGGSAQPAQAAAGLGLRAR	7.1e-10	A
LOC_Os03g45440	expressed protein		gi|31415963	767.08	ETEGMGK	5.7e-82	A
LOC_Os03g57020	expressed protein		gi|54291435	491.86	ESGEA	0.064	A
LOC_Os04g01610	expressed protein		gi|116310893	906.05	SSSPPPPSR	4.0e-303	A
LOC_Os04g04040	expressed protein		gi|32482893	983.66	MWYEVGGK	1.2e-88	A
LOC_Os04g10150	expressed protein		gi|78708625	1240.51	GRGGGGLGSGDGLGK	3.0e-05	A
LOC_Os04g26440	hypothetical protein		gi|32490342	549.14	GMWAS	1.1e-32	A
LOC_Os04g28234	Rf1, mitochondrial precursor	mitochondrion	gi|32489924	658.37	DMLHK	0	A
LOC_Os04g32600	expressed protein		gi|297602641	887.13	GKEPSSER	3.2e-65	L
LOC_Os04g38290	expressed protein		gi|297723203	1808.34	NMASGSGVEGEGLGIPYR	1.7e-265	A
LOC_Os04g45080	expressed protein		gi|32489831	783.03	AAMHPTR	4.5e-98	A
LOC_Os04g46430	expressed protein		gi|297727743	799.53	VLEVGER	0.0018	A
LOC_Os04g47010	expressed protein	plastid	gi|115459856	872.38	DAALEILK	1.2e-120	A
LOC_Os04g53770	SDA1		gi|115460742	958.77	TGGLSNRQK	0	A
LOC_Os04g57700	expressed protein		gi|115461260	688.85	MVRGDP	1.2e-104	A
LOC_Os05g02780	glycine-rich protein A3		gi|115461767	707.89	MGGGKDK	1.5e-122	A
LOC_Os05g10830	proteophosphoglycan ppg4		gi|297725787	872.94	HPPQAAPR	0.00011	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os05g11310	expressed protein		gi|48475255	1125.78	EVVPKLSLIK	3.2e-223	A
LOC_Os05g15110	expressed protein		gi|47848112	723.51	GGDALHR	7.2e-06	A
LOC_Os05g15230	plant protein of unknown function domain containing protein	mitochondrion	gi|115462809	843.98	TITRTPR	2.1e-242	A
LOC_Os05g33930	expressed protein		gi|222631577	932.73	LITAMKLK	4.5e-50	A
LOC_Os05g41130	OsFBX168 - F-box domain containing protein		gi|50080303	1064.50	TQVPACNMK	2.7e-187	A
LOC_Os05g45490	hydrolase, acting on carbon-nitrogen		gi|115465069	878.90	NATFAISR	0	A
LOC_Os05g48070	expressed protein		gi|115465341	733.92	SGANEEK	5.6e-194	A
LOC_Os05g50370	dnaJ domain containing protein		gi|222632684	1457.01	LWEVNDGRDAGVK	0	A
LOC_Os06g02830	expressed protein		gi|115466064	1640.53	ADAIINNINSKNNNK	0	A
LOC_Os06g04980	OsFBX185 - F-box domain containing protein		gi|115466332	849.45	GMLNLMR	3.6e-279	A
LOC_Os06g05390	expressed protein	plastid	gi|222634949	1226.82	ASADFVNSGGMR	1.7e-178	A
LOC_Os06g05980	transporter family protein	membrane	gi|297605201	724.35	AEPPRR	1.5e-147	A
LOC_Os06g07300	jacalin-like lectin domain containing protein		gi|297724515	822.24	MSTKLVK	5.2e-72	A
LOC_Os06g23590	expressed protein		gi|125555227	1118.75	AGAMASPTAGIR	1.2e-72	A
LOC_Os06g27800	tm-1GCR237 protein,		gi|115468048	810.51	TKSVLHK	0	A
LOC_Os07g02110	expressed protein		gi|54290268	1131.22	AATAAAGGLLCR	4.3e-05	A
LOC_Os07g13570	expressed protein		gi|125560407	784.38	GEHDGGGR	4.4e-05	A
LOC_Os07g14910	expressed protein		gi|53792422	601.28	VAAGER	0.056	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os07g18610	OsFBLD7 - F-box, LRR and FBD domain containing protein		gi|34393661	1189.80	SGTLDGLEELR	9.2e-265	L
LOC_Os07g33090	expressed protein		gi|23616995	900.90	ANSEALLAL	1.5e-81	A
LOC_Os07g42040	DC1 domain-containing protein		gi|24059842	2127.76	MAPCTSSRHQLASFGGHLR	2.9e-16	A
LOC_Os07g46590	SNF2 family N-terminal domain containing protein		gi|21820011	701.18	LKVGGTK	0	A
LOC_Os07g48360	helicase conserved C-terminal domain containing protein		gi|222612908	698.70	YEFSR	2.5e-40	A
LOC_Os08g06810	expressed protein		gi|42409011	1093.98	RLPSNPTPGR	4.0e-11	A
LOC_Os08g07090	expressed protein		gi|37806094	710.87	LTPGAPR	1.0e-50	L
LOC_Os08g08910	hypothetical protein		gi|53791742	1009.63	RQPIPTAVK	3.1e-09	A
LOC_Os08g14600	expressed protein		gi|40253497	976.76	TSAAAVAACR	1.4e-103	A
LOC_Os08g25340	hypothetical protein		gi|42408175	804.90	SASNSGQR	0.0019	A
LOC_Os08g31890	expressed protein		gi|125561556	941.70	HTDKITTK	1.5e-209	A
LOC_Os08g33960	expressed protein		gi|50252931	703.89	AETASAR	0.00071	A
LOC_Os08g35080	hypothetical protein		gi|42407650	808.12	MSGSTSPK	1.1e-35	A
LOC_Os09g03800	expressed protein		gi|47497793	995.14	NYASTIISK	2.2e-25	A
LOC_Os09g13650	microtubule-associated protein		gi|115478462	986.77	KNESQILR	7.9e-85	A
LOC_Os09g19880	expressed protein		gi|48716729	1881.34	FHDTQKAKPDFTVGYK	0	A
LOC_Os09g21670	expressed protein		gi|125563572	744.54	VNTIGNK	7.7e-229	A
LOC_Os09g21689	expressed protein		gi|115478951	910.86	SKPSGLPAR	3.2e-65	A
LOC_Os09g25000	spotted leaf 11	plastid	gi|115479177	1617.83	MVARCAHADVGGGFR	4.6e-254	L
LOC_Os09g26110	expressed protein		gi|222641623	431.38	GSRGG	8.2e-83	A

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os09g28470	leucine-rich repeat family protein		gi|115479563	881.43	APGPLSWR	1.3e-279	A
LOC_Os09g29030	expressed protein		gi|46806314	1007.99	MNLTSGSHM	2.8e-96	A
LOC_Os09g29790	PPR repeat domain containing protein	mitochondrion	gi|125606055	980.69	WMTSLATR	0	A
LOC_Os09g30070	expressed protein		gi|218202329	711.76	NAVSHGK	0	A
LOC_Os09g37870	expressed protein		gi|218202588	720.44	MDAAADK	1.4e-46	A
LOC_Os10g05730	armadillo/beta-catenin repeat family protein	plasma membrane	gi|115481140	1161.25	QAHMIQDMR	0	A
LOC_Os10g08530	expressed protein		gi|78707884	603.43	DIEAR	1.4e-167	A
LOC_Os10g18490	cytokinin-O-glucosyltransferase 2		gi|222612625	2138.60	MGPLIRLVAVPDGMGPDDDR	1.6e-61	A
LOC_Os10g24004	expressed protein		gi|222612738	993.81	EGSMLMGGGR	4.3e-45	A
LOC_Os11g04267	expressed protein		gi|125576149	873.01	APSRVQSK	2.5e-197	A
LOC_Os11g04630	expressed protein		gi|77548646	477.04	QGGMA	6.4e-35	A
LOC_Os11g08050	expressed protein		gi|62732911	764.60	EDTWSK	0	A
LOC_Os11g08750	pectinesterase		gi|115484549	742.88	KTVVVAK	3.8e-211	A
LOC_Os11g11650	expressed protein		gi|218185406	764.72	CTNDQK	7.9e-69	A
LOC_Os11g12680	expressed protein		gi|62734553	873.13	GMAAASLPR	3.0e-76	A
LOC_Os11g13560	serpin domain containing protein	cytosol	gi|62701807	542.19	AVEPK	3.7e-94	A
LOC_Os11g17350	expressed protein		gi|46063441	1102.92	NSFKGLITPK	0.86	A
LOC_Os11g22800	expressed protein		gi|62733897	920.02	GESVSGDGGR	7.1e-84	A
LOC_Os11g33110	Cupin domain containing protein	extracellular region	gi|51535348	1604.43	MKDLLACQLPLMR	0.49	A
LOC_Os11g34100	expressed protein		gi|54291526	1229.70	TTAAAEVGEAGVR	0.00087	A
LOC_Os11g37010	expressed protein		gi|125534864	671.96	SNDLPK	2.4e-147	A
LOC_Os11g45120	conserved hypothetical protein		gi|50509844	688.57	ELTGLR	3.4e-13	L

Table D.1 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os12g04110	pentatricopeptide		gi|108862162	535.36	GDMGR	0	A
LOC_Os12g05340	expressed protein		gi|77553006	932.55	KGALFGADR	9.0e-61	A
LOC_Os12g07310	citrate-binding protein precursor		gi|125535927	715.71	SKTKPR	1.5e-99	A
LOC_Os12g10320	plant-specific domain TIGR01627 family protein		gi|115487782	948.58	AIHFVSMK	1.6e-157	A
LOC_Os12g32580	expressed protein		gi|108862733	1764.62	TSSNQGEPVLKWQMGS	1.1e-37	A
LOC_Os12g38540	expressed protein		gi|297613404	543.64	AVSIR	2.4e-153	A
LOC_Os12g41430	expressed protein		gi|218187216	1134.30	MEGAEVEGEGK	2.2e-80	A

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Up-regulated proteins							
Nucleic acid metabolic process							
LOC_Os02g27790	splicing factor 3B subunit 1	plastid	gi|297721205	838.28	LSPEEHK	0	N
LOC_Os03g09820	transcription initiation factor IIB	cytoplasm, nucleus	gi|24414276	1718.20	HLGEEAGTAMEMGVVR	1.0e-162	C
Other metabolic process							
LOC_Os02g13965	lectin protein kinase family protein	plasma membrane	gi|50251219	2306.47	RFNITDAIVQPNMNISSDGAK	0	C
LOC_Os02g52730	ferredoxin--nitrite reductase	plastid, membrane mitochondrion, extracellular region	gi|218191633	1055.98	AVLLDTGRGR	0	F
LOC_Os11g42480	transferase family domain containing protein	plastid	gi|77552250	627.12	VPEER	1.8e-236	C
LOC_Os01g43160	polygalacturonase		gi|125526876	1207.11	IAGDVGGHPDDR	1.1e-243	C
LOC_Os09g25890	trehalose-6-phosphate synthase		gi|125605767	824.15	LRAAAAPR	0	C
LOC_Os05g16980	terpene synthase 8		gi|50300552	1792.09	DVRILFGTCNDILEK	1.3e-59	C
LOC_Os07g29620	OsSCP39 - Putative Serine Carboxypeptidase homologue	cytosol, vacuole	gi|115472071	561.21	MGPTR	1.2e-289	C
Protein modification process							
LOC_Os01g45380	protein kinase domain containing protein		gi|115438805	1281.40	CCPSSLANVMK	2.2e-215	C
LOC_Os02g08190	CYPRO4		gi|115444595	890.24	DGADINMR	0	C
LOC_Os03g30890	S-locus-like receptor protein kinase	plasma membrane	gi|57164475	759.46	MLENVR	0	C
LOC_Os05g50970	protein phosphatase 2C		gi|222637237	806.81	SMKQPSN	0.0083	C
LOC_Os12g10740	leucine-rich repeat family protein	plasma membrane, vacuole	gi|115487826	759.12	LLGEDGR	0	C

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Signal transduction							
LOC_Os06g47890	OsFBO9 - F-box and other domain containing protein	cytosol, nucleus, intracellular	gi|115469678	1637.85	RHPLVDAMVVSEIR	0	C
LOC_Os12g41140	expressed protein		gi|108862930	945.75	EHDMWTK	1.1e-252	C
Stress response/defense							
LOC_Os01g33684	disease resistance RPP13-like protein 1		gi|115437084	650.23	GNWMK	0	C
LOC_Os11g11790	NBS-LRR type disease resistance protein	plasma membrane	gi|222615745	673.54	TVRATK	0	C
Transport							
LOC_Os02g46850	oligopeptide transporter	membrane	gi|297721523	636.44	LVGHGR	0.37	C
LOC_Os06g20354	PPR repeat domain containing protein		gi|115467750	1082.37	GIMNMLFDK	1.3e-180	C
Transposon/retrotransposon							
LOC_Os03g33060	retrotransposon protein, putative, unclassified, expressed		gi|49388922	842.79	EPADVWK	0.076	C
LOC_Os03g47310	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|108710375	728.94	EGVPSNK	0	C
LOC_Os04g45390	retrotransposon protein, putative, unclassified, expressed		gi|21740446	578.15	SSGDGR	1.6e-292	C
LOC_Os05g40110	retrotransposon protein, putative, unclassified, expressed		gi|222640687	635.03	LAEMR	1.5e-198	N
LOC_Os07g45630	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|34394325	1124.63	TPPADAPISQK	0	C
LOC_Os12g08420	retrotransposon protein, putative, unclassified, expressed		gi|77553191	736.82	SSLITMA	1.2e-65	C
LOC_Os12g26660	retrotransposon protein, putative, LINE subclass, expressed		gi|19386855	704.97	FKVLAK	2.1e-52	C

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown							
LOC_Os01g06310	glycine-rich cell wall structural protein precursor		gi|115434618	724.71	GGMFGGGK	4.4e-75	C
LOC_Os01g40070	expressed protein		gi|21902022	855.59	LATGEPLR	6.1e-300	C
LOC_Os01g71180	pentatricopeptide repeat protein PPR1106-17		gi|20160775	600.69	GRSIIG	0	C
LOC_Os03g05890	expressed protein		gi|108706243	638.83	AAGLGPR	8.3e-74	C
LOC_Os03g32636	hypothetical protein		gi|108709059	954.93	SGSIPLRVK	1.7e-36	N
LOC_Os03g47584	expressed protein		gi|50881422	2136.12	DMAASNSTTCPRLIPMSIR	6.0e-135	C
LOC_Os03g55950	H-BTB1 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with H family conserved sequence		gi|115455589	628.12	MSVHR	1.9e-282	N
LOC_Os05g31180	hypothetical protein		gi|51038079	704.55	VDSAASR	6.8e-17	C
LOC_Os05g50690	pentatricopeptide		gi|297724361	808.66	LLDMMR	2.6e-253	C
LOC_Os06g24130	expressed protein		gi|54291307	902.16	ENWENGR	3.3e-34	C
LOC_Os06g30960	expressed protein		gi|52075895	709.42	APGRGPR	1.3e-125	C
LOC_Os07g02360	expressed protein		gi|115470309	886.44	DMNMSFK	5.6e-100	C
LOC_Os08g05810	DEAD-box ATP-dependent RNA helicase		gi|143456125	724.19	TGHAGRK	0	C
LOC_Os11g07760	hypothetical protein		gi|108864062	1653.24	AGEGAIGEGGNIIVEIR	2.2e-32	C
LOC_Os11g26560	expressed protein		gi|62733138	647.90	ATSAGSR	1.5e-97	N
LOC_Os11g44630	calmodulin binding protein		gi|125535215	626.83	GTPILK	3.2e-111	C
Down-regulated proteins							
Cellular component organization							
LOC_Os02g40770	SET domain containing protein	nucleolus	gi|218191189	1457.51	EKTGDMGLSMAPPK	0	A

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Cellular process							
LOC_Os03g64290	myosin	cytoskeleton	gi|31193918	774.99	LMINNR	0	A
Growth and development							
LOC_Os03g47820	PINHEAD	cytosol ,nucleus	gi|251764800	1659.52	VCNPSVGQWNMINK	0	A
Nucleic acid metabolic process							
LOC_Os02g09100	isoleucyl-tRNA synthetase, cytoplasmic	cytosol	gi|218190198	529.62	GVVTR	0	A
LOC_Os02g27060	high mobility group		gi|115446099	745.61	RDMPPN	3.9e-250	A
LOC_Os02g33770	homeodomain		gi|115446577	743.57	KHAMLK	4.3e-228	A
LOC_Os03g15420	dynamin family protein		gi|115452033	734.10	DLVGDSK	0	A
LOC_Os05g49460	CTP synthase		gi|115465531	520.51	GGTMR	6.7e-272	A
LOC_Os05g51040	tesmin/TSO1-like CXC domain containing protein		gi|222632736	904.60	GIYTLILL	6.1e-110	L
LOC_Os11g47630	ZOS11-10 - C2H2 zinc finger protein		gi|50252254	904.02	NIMEGGRK	0.0013	A
LOC_Os12g31880	translation initiation factor	plasma membrane	gi|218186906	1255.28	VGSGPSRVTLER	7.6e-270	A
Other metabolic process							
LOC_Os02g47470	cytochrome P450		gi|297721537	781.93	GGGDALHR	2.0e-253	A
LOC_Os04g36620	hydrolase, alpha/beta fold family domain containing protein	vacuole	gi|115458578	1921.50	ALTIGQMQGKFQMVVVR	3.2e-184	A
LOC_Os08g19420	O-methyltransferase	cytosol	gi|115475736	711.80	AFPHIK	1.9e-202	A
LOC_Os08g30240	1-aminocyclopropane-1-carboxylate oxidase homolog 1		gi|222640493	693.90	AAAGHLR	4.1e-120	A
LOC_Os08g32870	aldehyde dehydrogenase	cytosol, cell wall, plastid	gi|224709986	1050.47	IMASAAPMVK	4.0e-32	A

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os09g26360	Pectinesterase	cell wall	gi|115479305	463.83	GGGFK	0	A
LOC_Os12g07150	amidase family protein	plasma membrane, vacuole, ER	gi|77553129	1677.79	HYKKPEVFYDLLK	0	A
LOC_Os12g17070	radical SAM enzyme	cytoplasm, plastid	gi|115488116	1821.86	SFYAFGLGSASYINGIR	7.1e-258	A
LOC_Os11g24374	OsSCP55 - Putative Serine Carboxypeptidase homologue		gi|218185657	1087.14	ISEDIEAGVR	4.0e-209	A
Protein modification process							
LOC_Os02g41500	OsWAK13 - OsWAK receptor-like protein kinase	plasma membrane	gi|125582933	885.55	DNGAVVAIK	5.4e-260	A
LOC_Os05g25540	STRUBBELIG-RECEPTOR FAMILY 6 precursor		gi|115463171	721.75	DTMDPK	1.1e-252	A
LOC_Os09g17910	expressed protein		gi|50252384	1051.58	GCSLPIIHR	0	A
LOC_Os10g41390	protein kinase domain containing protein		gi|78709014	1758.17	GYLIDFNLANDLHQK	0	A
Stress response/defense							
LOC_Os02g14460	peroxidase precursor	cytosol, cell wall, extracellular region	gi|115445245	864.13	AAASSTTTR	5.7e-178	A
LOC_Os02g18080	NB-ARC domain containing protein		gi|125538990	1049.44	ESGQCWKR	0	A
LOC_Os03g17240	ankyrin repeat-containing protein	plasma membrane	gi|24796795	472.98	AGAVR	7.7e-144	A
LOC_Os04g41370	Leucine Rich Repeat family protein		gi|32483316	651.47	RIVHK	0	L
Transport							
LOC_Os05g02140	clathrin assembly protein	plasma membrane, cytosol, nucleus	gi|22535662	1255.30	RLLVMGAVEPR	4.5e-08	A
LOC_Os09g29239	purine permease	membrane	gi|115479663	808.65	MDVEATK	6.0e-190	A

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transport *(cont.)*							
LOC_Os10g11354	MATE efflux family protein	membrane, vacuole	gi|110288754	819.51	DVLGFLR	2.5e-255	A
Transposon/retrotransposon							
LOC_Os01g09490	transposon protein, putative, unclassified, expressed		gi|115435016	1319.27	DISADITAVQMR	0	A
LOC_Os01g63960	retrotransposon protein, putative, Ty1-copia subclass, expressed		gi|52353388	1485.80	GGGGGQQRGGNTGNGGR	0	A
LOC_Os03g36200	retrotransposon protein, putative, unclassified		gi|108709305	878.75	DVYDLQK	1.1e-128	A
LOC_Os03g44070	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|22074751	921.49	AHPEASIAK	4.1e-230	A
LOC_Os03g60670	retrotransposon protein, putative, unclassified, expressed		gi|222626062	733.17	TISTVGR	9.4e-09	L
LOC_Os04g05180	retrotransposon protein, putative, unclassified		gi|38347261	820.02	MGHFADK	8.0e-282	A
LOC_Os04g50830	retrotransposon protein, putative, LINE subclass, expresse		gi|58532025	874.52	GKNMAAAGR	0	A
LOC_Os06g10740	transposon protein, putative, unclassified, expressed		gi|115467022	1039.71	LMIFFLQK	0	A
LOC_Os06g39890	retrotransposon protein, putative, unclassified, expressed		gi|77548345	829.58	RASGIGDR	4.6e-10	A
LOC_Os07g41270	retrotransposon protein, putative, unclassified, expressed		gi|40253429	670.55	GPAGGRR	6.5e-19	A
LOC_Os10g17140	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|19881559	848.07	IRTMPSK	1.8e-174	A

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os10g25080	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|78708515	603.63	FAPDR	0	A
LOC_Os11g29530	retrotransposon protein, putative, unclassified, expressed		gi|77550985	1404.32	IVPDIASLHDVVK	0	A
LOC_Os12g24220	retrotransposon protein, putative, unclassified, expressed		gi|77554862	961.52	CLDPSTNR	0	A
LOC_Os12g27710	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|77555338	1039.96	QSGPNWKPK	0	A
Unknown							
LOC_Os01g13730	WD domain, G-beta repeat domain containing protein	plasma membrane, intracellular	gi|222618072	852.34	STDEFTR	2.1e-249	A
LOC_Os01g52780	HVA22		gi|222619195	778.17	DMAVNSK	0	A
LOC_Os02g02360	expressed protein		gi|125580555	857.35	RAGVGGEGR	9.7e-293	A
LOC_Os02g31090	collagen-binding protein		gi|51536026	777.70	SCRVEK	4.2e-102	A
LOC_Os03g06430	expressed protein		gi|125542494	991.10	GGGGMEEALR	2.0e-49	D
LOC_Os03g25760	calmodulin-binding protein		gi|31249708	1158.17	SFNGAAAPATPR	0	A
LOC_Os03g31500	expressed protein		gi|218196709	840.58	VGPGNNER	0	A
LOC_Os03g32620	pentatricopeptide		gi|115453719	627.23	EIIVR	8.9e-06	A
LOC_Os04g42560	expressed protein		gi|51090641	714.29	AGKGEVR	8.9e-06	A
LOC_Os04g55260	thiamine-repressible mitochondrial transport protein THI74		gi|115460932	586.68	VDVQK	1.8e-206	A
LOC_Os05g16315	translation initiation factor IF-2		gi|222615783	1050.63	SGDGGAGSAAMR	7.8e-07	A
LOC_Os06g11820	expressed protein		gi|51535091	632.41	GRSGTR	5.9e-167	A

Table D.2 Chitosan responsive proteins during the drought stress in root tissue of LPT123 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os06g30940	pentatricopeptide		gi|115468242	490.81	TSGVK	0	A
LOC_Os06g44820	PPR repeat domain containing protein		gi|51535142	1006.13	NRMLAVCK	0	A
LOC_Os07g27300	RNA-binding protein Luc7-like		gi|115471921	913.72	VELLNAEK	0	A
LOC_Os09g06570	expressed protein		gi|115478102	784.65	LAAVVGIGS	9.2e-59	A
LOC_Os09g16600	expressed protein		gi|41393223	1092.87	ALGPPTALPTR	9.7e-32	A
LOC_Os09g23170	expressed protein		gi|218202107	806.02	CLDLATN	3.4e-68	A
LOC_Os09g24940	expressed protein		gi|50251543	864.65	RAPATKPK	5.4e-134	A
LOC_Os09g37870	expressed protein		gi|218202588	719.18	MDAAADK	1.4e-46	L
LOC_Os11g06670	expressed protein		gi|215768810	1123.98	GLHGECLAIR	1.9e-193	L
LOC_Os11g13950	hypothetical protein		gi|62733877	848.13	DCYVHR	1.1e-44	A
LOC_Os11g14500	expressed protein		gi|77556907	829.67	ALTLWAR	0.057	A
LOC_Os12g05144	hypothetical protein		gi|108862200	1210.90	VDYSDKSTAAR	2.4e-51	A
LOC_Os12g33250	lig A		gi|77555925	1053.42	DGDGDAMTTR	4.4e-84	A
LOC_Os12g38880	tetratricopeptide-like helical		gi|222617355	470.04	AGAPR	2.6e-267	A

Table D.3 Chitosan-responsive proteins in LPT123 rice mapped in the RNA and protein synthetic processes by using MapMan software

gene ID	annotation	bin name
LOC_Os03g09820	transcription initiation factor IIB	RNA.transcription
LOC_Os03g38570	retrotransposon protein, putative, unclassified, expressed	RNA.transcription
LOC_Os04g39160	RNA-dependent RNA polymerase	RNA.transcription
LOC_Os04g48370	RNA polymerase IV subunit	RNA.transcription
LOC_Os10g13530	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	RNA.transcription
LOC_Os11g12090	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	RNA.transcription
LOC_Os10g24510	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	RNA.transcription
LOC_Os02g27790	splicing factor 3B subunit 1	RNA.processing.splicing
LOC_Os08g03390	pre-mRNA-splicing factor SLU7	RNA.processing.splicing
LOC_Os08g05810	DEAD-box ATP-dependent RNA helicase	RNA.processing.RNA helicase
LOC_Os03g38740	dicer	RNA.processing.degradation dicer
LOC_Os01g13730	WD domain, G-beta repeat domain containing protein	RNA.processing
LOC_Os07g12320	WD domain, G-beta repeat domain containing protein	RNA.processing
LOC_Os12g38880	tetratricopeptide-like helical	RNA.processing
LOC_Os01g66560	signal recognition particle 72 kDa protein	protein.targeting.secretory pathway.unspecified
LOC_Os08g23360	signal recognition particle 68 kDa protein	protein.targeting.secretory pathway.unspecified
LOC_Os11g08980	preprotein translocase secA family protein	protein.targeting.chloroplast
LOC_Os02g01230	ribosomal protein	protein.synthesis.ribosomal protein.prokaryotic. unknown organellar.30S subunit.S5
LOC_Os08g39500	60S ribosomal protein L31	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L31
LOC_Os06g20354	PPR repeat domain containing protein	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L15
LOC_Os07g36250	peptide chain release factor protein	protein.synthesis.release
LOC_Os12g31880	translation initiation factor	protein.synthesis.initiation
LOC_Os05g16660	WD domain, G-beta repeat domain containing protein	protein.synthesis.initiation
LOC_Os10g10870	protein kinase family protein	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase X
LOC_Os11g47140	OsWAK123 - OsWAK receptor-like protein kinase	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII

Table D.3 Chitosan-responsive proteins in LPT123 rice mapped in the RNA and protein synthetic processes by using MapMan software *(cont.)*

gene ID	annotation	bin name
LOC_Os02g13965	lectin protein kinase family protein	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII
LOC_Os09g29520	OsWAK81 - OsWAK receptor-like cytoplasmic kinase OsWAK-RLCK	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII
LOC_Os05g25540	STRUBBELIG-RECEPTOR FAMILY 6 precursor	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII
LOC_Os03g30890	S-locus-like receptor protein kinase	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII
LOC_Os05g50970	protein phosphatase 2C	protein.posttranslational modification
LOC_Os12g38880	tetratricopeptide-like helical	protein.posttranslational modification
LOC_Os01g45380	protein kinase domain containing protein	protein.posttranslational modification
LOC_Os10g41390	protein kinase domain containing protein	protein.posttranslational modification
LOC_Os01g71180	pentatricopeptide repeat protein PPR1106-17	protein.posttranslational modification
LOC_Os01g60440	HEAT repeat family protein	protein.posttranslational modification
LOC_Os01g13270	AGC_PVPK_like_kin82y.4 - ACG kinases include homologs to PKA, PKG and PKC	protein.posttranslational modification
LOC_Os08g41550	ubiquitin carboxyl-terminal hydrolase	protein.degradation.ubiquitin.ubiquitin protease
LOC_Os09g10270	SKP1-like protein 1B	protein.degradation.ubiquitin.E3.SCF.SKP
LOC_Os01g36940	OsFBX13 - F-box domain containing protein	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os06g47890	OsFBO9 - F-box and other domain containing protein	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os03g22800	OsFBT5 - F-box and tubby domain containing protein	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os05g41130	OsFBX168 - F-box domain containing protein	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os09g25000	spotted leaf 11	protein.degradation.ubiquitin.E3.RING
LOC_Os02g40664	zinc finger family protein	protein.degradation.ubiquitin.E3.RING
LOC_Os02g03950	zinc finger, C3HC4 type family protein	protein.degradation.ubiquitin.E3.RING
LOC_Os05g38830	HECT-domain domain containing protein	protein.degradation.ubiquitin.E3.HECT
LOC_Os05g06120	ubiquitin conjugating enzyme protein	protein.degradation.ubiquitin.E2
LOC_Os11g13560	serpin domain containing protein	protein.degradation.serine protease
LOC_Os11g24374	OsSCP55 - Putative Serine Carboxypeptidase homologue	protein.degradation.serine protease
LOC_Os11g12520	serpin domain containing protein	protein.degradation.serine protease

Table D.3 Chitosan-responsive proteins in LPT123 rice mapped in the RNA and protein synthetic processes by using MapMan software *(cont.)*

gene ID	annotation	bin name
LOC_Os07g29620	OsSCP39 - Putative Serine Carboxypeptidase homologue	protein.degradation.serine protease
LOC_Os01g37825	M16 domain containing zinc peptidase	protein.degradation.metalloprotease
LOC_Os01g57720	expressed protein	protein.degradation.autophagy
LOC_Os07g34920	aspartic proteinase nepenthesin precursor	protein.degradation.aspartate protease
LOC_Os07g34850	aspartic proteinase nepenthesin	protein.degradation.aspartate protease
LOC_Os06g42810	UBA and UBX domain-containing protein	protein.degradation
LOC_Os05g01750	TruB family pseudouridylate synthase	protein.aa activation.pseudouridylate synthase
LOC_Os02g09100	isoleucyl-tRNA synthetase, cytoplasmic	protein.aa activation.isoleucine-tRNA ligase

Table D.4 Chitosan-responsive proteins in LPT123 rice mapped in the overview of metabolic pathway by using MapMan software

gene ID	annotation	bin name
LOC_Os04g01590	arginase	amino acid metabolism.degradation.glutamate family.arginine
LOC_Os05g47640	threonine synthase, chloroplast precursor	amino acid metabolism.synthesis.aspartate family.threonine.threonine synthase
LOC_Os03g45250	2-aminoethanethiol dioxygenase	amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine
LOC_Os01g19220	beta-D-xylosidase	cell wall.degradation.cellulases and beta -1,4-glucanases
LOC_Os01g19220	beta-D-xylosidase	cell wall.degradation.mannan-xylose-arabinose-fucose
LOC_Os03g47010	glycosyl hydrolase family 10 protein	cell wall.degradation.mannan-xylose-arabinose-fucose
LOC_Os01g33300	polygalacturonase	cell wall.degradation.pectate lyases and polygalacturonases
LOC_Os01g43160	polygalacturonase	cell wall.degradation.pectate lyases and polygalacturonases
LOC_Os07g09670	galactosyltransferase family protein	cell wall.hemicellulose synthesis
LOC_Os11g08750	pectinesterase	cell wall.pectin esterases.PME
LOC_Os09g26360	pectinesterase	cell wall.pectin esterases.PME
LOC_Os12g37660	pectinesterase	cell wall.pectin esterases.PME
LOC_Os08g32870	aldehyde dehydrogenase	fermentation.aldehyde dehydrogenase
LOC_Os03g49180	alkaline phytoceramidase	lipid metabolism."exotics" (steroids, squalene etc).sphingolipids
LOC_Os01g24030	AMP-binding enzyme	lipid metabolism.FA synthesis and FA elongation. acyl coA ligase
LOC_Os05g29050	phospholipase D p1	lipid metabolism.lipid degradation. lysophospholipases.phospholipase D
LOC_Os10g42720	acyltransferase	lipid metabolism.Phospholipid synthesis
LOC_Os04g33740	glycosyl hydrolases	major CHO metabolism.degradation.sucrose. invertases.cell wall
LOC_Os09g25890	trehalose-6-phosphate synthase	minor CHO metabolism.trehalose.potential TPS/TPP
LOC_Os09g25890	trehalose-6-phosphate synthase	minor CHO metabolism.trehalose.TPS
LOC_Os10g21266	ATP synthase subunit beta	mitochondrial electron transport / ATP synthesis. F1-ATPase
LOC_Os12g33958	NADH-ubiquinone oxidoreductase 49 kDa subunit	mitochondrial electron transport / ATP synthesis. NADH-DH.localisation not clear
LOC_Os04g46560	lactate/malate dehydrogenase	TCA / org. transformation.other organic acid transformaitons.cyt MDH
LOC_Os04g32330	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor	TCA / org. transformation.TCA.2-oxoglutarate dehydrogenase

Table D.4 Chitosan-responsive proteins in LPT123 rice mapped in the overview of metabolic pathway by using MapMan software *(cont.)*

gene ID	annotation	bin name
LOC_Os06g19960	aconitate hydratase protein	TCA / org. transformation.TCA.aconitase
LOC_Os01g22520	dihydrolipoyl dehydrogenase 1, mitochondrial precursor	TCA / org. transformation.TCA.pyruvate DH.E3
LOC_Os02g52730	ferredoxin-nitrite reductase	N-metabolism.nitrate metabolism.nitrite reductase
LOC_Os05g01750	TruB family pseudouridylate synthase	nucleotide metabolism.deoxynucleotide metabolism.pseudouridine synthase
LOC_Os12g33100	guanylate kinase	nucleotide metabolism.phosphotransfer and pyrophosphatases.guanylate kinase
LOC_Os05g49460	CTP synthase	nucleotide metabolism.synthesis.pyrimidine.CTP synthetase
LOC_Os04g24140	ribose-5-phosphate isomerase A	OPP.non-reductive PP.ribose 5-phosphate isomerase
LOC_Os11g47970	AAA-type ATPase family protein	PS.calvin cycle.rubisco interacting
LOC_Os01g20110	expressed protein	PS.lightreaction.NADH DH
LOC_Os01g66000	NADH dehydrogenase I subunit N	PS.lightreaction.NADH DH
LOC_Os08g30240	1-aminocyclopropane-1-carboxylate oxidase homolog 1	redox.ascorbate and glutathione
LOC_Os09g39380	monodehydroascorbate reductase	redox.ascorbate and glutathione.ascorbate
LOC_Os11g32580	chalcone synthase	secondary metabolism.flavonoids.chalcones
LOC_Os10g33774	leucoanthocyanidin reductase	secondary metabolism.flavonoids.dihydroflavonols
LOC_Os07g09190	transketolase	secondary metabolism.isoprenoids.non-mevalonate pathway.DXS
LOC_Os05g16980	terpene synthase 8	secondary metabolism.isoprenoids.terpenoids
LOC_Os07g38850	Prenyltransferase	secondary metabolism.isoprenoids.tocopherol biosynthesis
LOC_Os09g20684	SMP-30/Gluconolaconase/LRE-like region containing protein	secondary metabolism.N misc.alkaloid-like
LOC_Os08g14570	NADPH reductase	secondary metabolism.phenylpropanoids
LOC_Os11g42480	transferase family domain containing protein	secondary metabolism.phenylpropanoids
LOC_Os12g17070	radical SAM enzyme	tetrapyrrole synthesis.coproporphyrinogen III oxidase
LOC_Os10g35840	shikimate/quinate 5-dehydrogenase	tetrapyrrole synthesis.glu-tRNA reductase

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Up-regulated proteins							
Cellular component organization							
LOC_Os02g51430	SEC6	plasma membrane, cytosol	gi|46390198	838.99	EHINVTK	0	G
LOC_Os08g29730	intracellular protein transport protein USO1-related	Golgi apparatus	gi|115476230	845.20	LENDNSR	6e-183	G
Growth and development							
LOC_Os04g52340	expressed protein		gi|38568023	1281.89	CYLRLSDNSR	9.9e-181	F
LOC_Os03g55680	expressed protein	plastid	gi|31415945	602.94	MADHD	1.4e-101	G
Nucleic acid metabolic process							
LOC_Os01g08990	expressed protein		gi|9558424	864.77	QVAHGLGGK	4.0e-145	G
LOC_Os01g17990	expressed protein		gi|56785021	876.52	DILINYK	1.2e-209	G
LOC_Os01g40430	WRKY27		gi|14588696	821.23	DGCQWR	6.4e-170	G
LOC_Os01g67970	ZOS1-20 - C2H2 zinc finger protein	nucleus	gi|115441715	756.65	KTGHSVK	0	D
LOC_Os02g49270	NOL1/NOP2/sun family protein	nucleolus	gi|45735882	1057.31	ADPSSDDPQK	0	D
LOC_Os04g28090	MYB family transcription factor	plastid	gi|38346500	881.69	AAVMKYGK	0	G
LOC_Os09g30466	nuclear ribonuclease Z	plastid	gi|297727071	962.34	VVALTEGFK	8.3e-193	G
LOC_Os12g40570	WRKY94	nucleus	gi|222617410	848.86	EALAPPPR	1.1e-197	G
LOC_Os02g01230	ribosomal protein	Golgi apparatus, ribosome	gi|41052902	731.56	LKDATGK	8.7e-269	D
LOC_Os05g32670	pentatricopeptide repeat-containing protein		gi|54287525	987.85	AVLLFRNR	1.5e-129	G
Other metabolic process							
LOC_Os01g34700	dienelactone hydrolase family protein	plastid, cytosol	gi|115437234	571.36	ANGSPK	5.9e-151	G

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os01g70570	acyltransferase		gi|297598246	985.48	VVGAQIRSR	6.9e-276	G
LOC_Os03g37010	glycosyltransferase		gi|115453815	722.13	GAYSLGR	0	G
LOC_Os05g48640	ATROPGEF7/ROPGEF7		gi|115465411	704.23	SSGSRGR	5.9e-302	F
LOC_Os06g13460	SAM dependent carboxyl methyltransferase family protein		gi|297724651	834.06	AIIEVYK	2.2e-89	D
LOC_Os06g18010	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein	cytosol	gi|86361432	1744.49	AVAGGGSSHRCLAEFAR	4.1e-246	G
LOC_Os06g43384	cytochrome P450		gi|115469134	970.69	HGPVMMLR	37e-158	G
LOC_Os09g25640	5-nucleotidase domain-containing protein	mitochondrion	gi|115479249	835.09	SFLQITK	4.1e-294	G
LOC_Os11g07090	pectinesterase	cell wall , membrane	gi|125533563	533.62	DGVSR	7.9e-275	G
LOC_Os12g17600	ribulose bisphosphate carboxylase small chain, chloroplast precursor	cytosol, ribosome, thylakoid, plastid, extracellular region, membrane	gi|115488144	937.42	AYPDAFVR	1.4e-94	G
LOC_Os03g19330	glycosyltransferase		gi|108707732	955.15	HGGKVTSDR	3.4e-251	G
LOC_Os04g46560	lactate/malate dehydrogenase	plasma membrane, cytosol	gi|115459790	941.08	EFAPAIPAK	2.1e-187	D
LOC_Os03g26030	expressed protein	mitochondrion, membrane	gi|218192930	1796.32	EDMFDLAKPGVGMEDK	0	G
LOC_Os09g23070	malonyl-CoA decarboxylase, mitochondrial precursor	peroxisome	gi|115478995	1106.02	SLAADYDVPR	1.5e-273	G
LOC_Os12g01930	lipase-related		gi|108862093	1076.78	KLMEILVSK	5.8e-192	G
LOC_Os05g03630	dnaJ domain containing protein		gi|46391158	847.38	GEGMPITK	5.1e-113	G

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os12g26470	aspartic proteinase nepenthesin-1 precursor		gi|77555282	574.86	AAVASR	5.1e-113	G
LOC_Os01g27340	glutathione S-transferase	cytoplasm	gi|218188239	1861.98	NPFGQDASFPGRGSASLR	1.1e-25	G
LOC_Os07g44930	dirigent		gi|23495731	936.09	ALPPPSSLR	1.0e-107	G
Protein modification process							
LOC_Os01g36550	protein kinase family protein		gi|125526343	1210.52	GIEYIHDHTK	3.1e-289	G
LOC_Os03g28130	OsFBX94 - F-box domain containing protein		gi|115453413	832.28	TFAELPR	3.7e-222	G
LOC_Os03g59390	CAMK_CAMK_like.24 - CAMK includes calcium/calmodulin dependent protein kinases	plasma membrane	gi|115456103	750.96	HGVMHR	6.0e-293	G
LOC_Os12g25180	expressed protein	plasma membrane	gi|115488408	744.24	MRLIGR	1.2e-24	G
Signal transduction							
LOC_Os02g05930	phytosulfokine receptor precursor		gi|51873286	1019.10	SEQAASIST	5.4e-276	G
LOC_Os04g51110	WD repeat-containing protein	intracellular, plasma membrane	gi|115460308	840.43	TQWLHR	0	G
Stress response/defense							
LOC_Os10g36703	CPuORF40 - conserved peptide uORF-containing transcript		gi|15144310	1226.09	GAIAIPCRVDR	1.6e-56	G
LOC_Os01g57270	disease resistance RPP13-like protein 1		gi|125527941	757.22	SMKLHK	1.8e-254	G
LOC_Os09g14010	disease resistance protein RPS2	plasma membrane	gi|51091428	664.59	LTKFR	0	G
LOC_Os10g25487	NBS-LRR disease resistance protein		gi|115481862	755.28	LPSSIIK	0	G
LOC_Os11g29920	NB-ARC domain containing protein		gi|77550930	1857.60	MQGIKPSASKNIISAWK	0	G

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transport							
LOC_Os03g50300	CASP	Golgi apparatus, membrane	gi|62733538	974.58	DKITLSSGR	0	D
LOC_Os06g29900	integral membrane protein	vacuole, membrane	gi|52077393	776.36	EASGQMR	3.8e-53	G
LOC_Os10g21266	ATP synthase subunit beta	cell wall, membrane, mitochondrion, thylakoid, plastid	gi|19920171	1327.38	AHGGVSVFGGVGER	3.7e-261	D
LOC_Os11g34130	expressed protein		gi|108864467	446.64	AGGDK	2.6e-251	G
Transposon/retrotransposon							
LOC_Os01g39520	retrotransposon, putative, centromere-specific, expressed		gi|51090446	578.78	NSSSGK	2.9e-24	G
LOC_Os01g74560	transposon protein, putative, Pong sub-class, expressed		gi|28564717	540.26	DAIHS	1.3e-130	G
LOC_Os03g40070	transposon protein, putative, unclassified, expressed		gi|218196275	945.49	IVSGAMTLR	2.7e-59	G
LOC_Os03g52190	retrotransposon protein, putative, unclassified, expressed		gi|38345754	902.68	AQRNLMR	0	G
LOC_Os04g26290	retrotransposon protein, putative, unclassified, expressed		gi|116309492	663.60	GRFASK	0	D
LOC_Os05g19460	retrotransposon protein, putative, unclassified, expressed		gi|125561428	970.70	IVSHEMQE	1.7e-73	D
LOC_Os08g05240	retrotransposon protein, putative, unclassified, expressed		gi|51091853	952.80	LNEGGITPR	1.0e-38	G
LOC_Os08g23240	retrotransposon protein, putative, unclassified, expressed		gi|222612643	568.40	THVGR	1.3e-45	G

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os10g11870	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|115451351	675.70	IGALMR	0.17	G
LOC_Os10g13590	retrotransposon protein, putative, Ty1-copia subclass		gi|50300531	562.95	GALMGD	2.4e-19	G
LOC_Os10g20960	retrotransposon protein, putative, unclassified, expressed		gi|78708310	552.89	IGIPR	0	G
LOC_Os10g38570	retrotransposon protein, putative, unclassified		gi|18071399	872.45	MPDGGELR	4.1e-33	D
LOC_Os11g40640	transposon protein, putative, unclassified, expressed		gi|218186130	895.64	VALHQGDR	0	G
Unknown							
LOC_Os01g01930	expressed protein		gi|52076208	821.22	CCARVR	3.6e-121	G
LOC_Os01g11500	zinc finger, C3HC4 type domain containing protein		gi|50508512	570.28	AAPADK	1.4e-46	D
LOC_Os01g12690	plant-specific domain TIGR01568 family protein	plasma membrane	gi|125524987	848.09	FSVDASPK	5.7e-201	G
LOC_Os01g24840	conserved hypothetical protein		gi|53792293	758.81	DVPSGER	6.2e-117	D
LOC_Os01g40220	DEFL7 - Defensin and Defensin-like DEFL family		gi|125531815	1893.51	MATTNTAPFPHTGGDGMR	0.12	F
LOC_Os01g44090	X8 domain containing protein		gi|125524660	752.38	RGVGLPR	0.00064	G
LOC_Os01g54530	hydrolase, acting on carbon-nitrogen		gi|14209549	659.33	PSSTIR	1.8e-254	G
LOC_Os01g54770	expressed protein		gi|15623852	498.09	TPGPK	1.7e-247	D
LOC_Os02g03700	expressed protein		gi|115443997	781.22	SMVSGEAT	1.3e-50	G
LOC_Os02g20560	fasciclin domain containing protein	plasma membrane	gi|297721111	2189.05	HACDAGDAHIVNLHWVFAR	0.13	G

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os02g37520	RNA-binding protein FUS		gi|125582681	2159.86	AMVAAPAAVAEAQPAAAAAATAIR	5.3e-40	G
LOC_Os02g48620	tetratricopeptide repeat	plasma membrane, plastid, cytosol	gi|218191467	651.55	RLHVK	0	G
LOC_Os03g17060	RNA recognition motif containing protein		gi|115452257	1495.50	MALSSSLLHRLLR	7.4e-89	G
LOC_Os03g25720	GA20734-PA		gi|115453221	1117.26	DQGSQANGTGGK	1.9e-145	G
LOC_Os03g27900	ZIM motif family protein		gi|297722193	1948.01	SADGVVVSPAPAPAAAQERR	2.8e-105	G
LOC_Os03g42820	LIM domain-containing protein	plasma membrane	gi|57164484	886.75	KTLDHMK	5.1e-287	G
LOC_Os04g11200	expressed protein		gi|218184627	973.11	LGGRGCLDK	0.0016	G
LOC_Os04g44880	expressed protein		gi|125549125	835.02	HALVAPTK	9.7e-48	G
LOC_Os05g06960	hypothetical protein		gi|297723733	835.08	VARTTCK	1.2e-33	G
LOC_Os05g14390	expressed protein		gi|50300527	728.40	EPLKNK	1.2e-120	G
LOC_Os05g30490	harpin-induced protein 1 domain containing protein	plasma membrane	gi|115463481	806.56	FVSGPFR	2.7e-139	G
LOC_Os06g05580	OsFBDUF30 - F-box and DUF domain containing protein		gi|125554088	2230.99	TLSFVVYEADLSNGSRMWR	8.4e-81	G
LOC_Os07g03140	ternary complex factor MIP1		gi|218199018	969.05	EQRVTLPK	1.3e-288	G
LOC_Os07g06750	VQ domain containing protein	plastid	gi|125557320	1504.68	MSSTSSSPPPPSKAK	1.5e-90	G
LOC_Os07g18860	expressed protein		gi|33147052	1589.13	IRGQAGVEGESATSTK	9.4e-66	G
LOC_Os07g36450	PPR repeat domain containing protein		gi|115472667	840.19	DLIVALAK	4.7e-142	G
LOC_Os08g15230	heat shock protein-related		gi|125560774	674.70	KIIFR	4.7e-87	G
LOC_Os08g29615	expressed protein		gi|297726377	698.41	AAIALLK	1.0e-52	G

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os08g42890	pectinesterase inhibitor domain containing protein		gi|125562389	970.42	VSPVADIDR	5.6e-91	G
LOC_Os10g25660	OsFBX385 - F-box domain containing protein	nucleus	gi|115481874	859.33	MEPGAALR	2.9e-238	G
LOC_Os10g26560	expressed protein		gi|15217315	692.02	GIFLSR	3.2e-104	G
LOC_Os11g09030	expressed protein		gi|115484565	537.48	SCADS	9.8e-55	G
LOC_Os11g12290	proteophosphoglycan		gi|47497220	944.77	SVTQVREK	5.0e-05	G
LOC_Os11g19130	expressed protein		gi|77549991	714.14	ANHSASK	6.5e-296	G
LOC_Os11g26840	expressed protein		gi|77550702	857.97	QDGGGGGRR	1.5e-33	G
LOC_Os11g32910	expressed protein		gi|77550702	857.97	QDGGGGGRR	1.5e-33	G
LOC_Os11g32910	expressed protein		gi|115485755	1028.89	LPEGMELPK	4.4e-91	G
LOC_Os11g36400	expressed protein	plasma membrane, cytosol, nucleus, extracellular region	gi|115485961	2056.32	TLSGMMRGILHDLESLIR	3.7e-229	G
LOC_Os11g39850	expressed protein		gi|77552006	939.26	SPLRLQAR	0	G
LOC_Os12g28370	expressed protein		gi|77555631	948.27	EGTAASADAR	2.9e-87	G
LOC_Os12g36180	auxilin	cytosol	gi|222617242	729.40	HSSMPGV	5.9e-52	G
Down-regulated proteins							
Cellular component organization							
LOC_Os08g03560	chloroplast unusual positioning protein	membrane, plastid	gi|115474639	695.44	HSLGGPK	0	O
LOC_Os11g18830	survival motor neuron containing protein		gi|115485137	808.66	NMDAVSR	1.1e-197	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Cellular process							
LOC_Os05g02670	kinesin motor domain containing protein	plasma membrane	gi|218201602	1127.61	KPLPLMEDGK	5.0e-245	O
LOC_Os10g34710	myosin-2 heavy chain, non-muscle	plasma membrane, cytoskeleton, ER, cytoplasm, endosome	gi|78708833	561.02	AFAVR	0	O
Growth and development							
LOC_Os02g05440	expressed protein	nucleus, intracellular	gi|115444213	757.81	STIVPSR	7.5e-183	O
LOC_Os02g15250	late embryogenesis abundant domain-containing protein		gi|115445331	832.19	NRAAESGK	6.0e-245	O
LOC_Os02g47880	tetratricopeptide repeat domain containing protein	plasma membrane	gi|115448207	416.83	GTVAA	0	O
LOC_Os03g37320	expressed protein		gi|37700342	689.93	SKVSAAK	3.1e-115	O
LOC_Os03g47820	PINHEAD	nucleus, cytosol	gi|31712081	549.17	GGMIR	0	O
LOC_Os05g43920	auxin response factor 14	nucleus	gi|51451357	896.25	RFSADMR	0	O
Nucleic acid metabolic process							
LOC_Os01g13100	KH domain containing protein	mitochondrion	gi|115435482	635.71	GGTMQK	2.1e-258	O
LOC_Os01g59350	transcription factor	nucleus, cytoplasm	gi|17025924	645.73	ADTSPR	2.7e-171	O
LOC_Os01g66030	OsMADS2 - MADS-box family gene with MIKC type-box	cytoplasm, nucleus	gi|115441465	894.57	MLEDENK	9.0e-110	O
LOC_Os03g48490	centromere protein	mitochondrion	gi|297601509	828.42	LDVAGLIK	0	O
LOC_Os03g60130	transcription elongation factor protein	nucleus	gi|37718881	428.72	GGAPK	2.2e-169	O
LOC_Os05g48240	dynamin family protein	vacuole, thylakoid, cytoplasm, membrane, cytoskeleton	gi|222619050	512.47	ATGHK	6.2e-289	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Nucleic acid metabolic process *(cont.)*							
LOC_Os06g48290	homeobox associated leucine zipper	nucleus	gi|75112038	1848.93	VTVMGGGGGETGKSSSSYSS	1.2e-136	O
LOC_Os07g12320	WD domain, G-beta repeat domain containing protein	nucleolus	gi|22296462	1158.91	VVRYPVAGGDK	5.5e-283	N
LOC_Os07g36250	peptide chain release factor protein	plastid	gi|115472651	713.53	LLNDLK	1.2e-239	L
LOC_Os07g48900	expressed protein	plastid, nucleus	gi|24059889	966.51	LDPAASPAAR	3.6e-89	O
LOC_Os09g31438	OsSPL17 - SBP-box gene family member	nucleus	gi|297727091	1771.89	MATGGSGGGGGGGGGGDDVHGR	1.2e-177	O
LOC_Os11g05130	PHD-finger family protein		gi|62701668	1002.12	ADLISPPYK	0	O
LOC_Os12g09250	bZIP transcription factor domain containing protein		gi|194396129	725.14	DAVPGLR	2.4e-106	O
LOC_Os12g13170	transcription factor	nucleus	gi|77554088	505.90	SSEGK	8.8e-173	O
LOC_Os01g61920	Core histone H2A/H2B/H3/H4 domain containing protein	cytosol, plastid, plasma membrane, vacuole	gi|15226944	1003.10	IFLENVIR	5.0e-51	O
LOC_Os08g35300	expressed protein		gi|125561762	697.58	NNIIPE	9.5e-105	O
LOC_Os08g36330	POLE2B - Putative DNA polymerase epsilon complex subunit	nucleus	gi|42409427	773.06	ATPSAATR	2.4e-87	O
LOC_Os03g58204	ribosomal protein L4	plastid, membrane, plasma membrane, nucleolus, cytosol, cell wall, vacuole, ribosome	gi|297722605	1281.93	NLPGVDVANVER	6.7e-214	O
LOC_Os08g42560	tRNA synthetase class II core domain containing protein	mitochondrion, cytosol	gi|115477547	628.95	AAGAAAAK	0	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process							
LOC_Os01g09260	cytokinin dehydrogenase precursor		gi|296439589	498.57	GVAPR	1.2e-285	O
LOC_Os01g11300	cytochrome P450		gi|115435230	583.49	AEPIR	2.1e-274	O
LOC_Os01g51410	glycine dehydrogenase	plastid, cytoplasm, mitochondrion	gi|115439533	2051.12	SFIGMGYYNTHVPAVILR	0	O
LOC_Os03g57220	hydroxyacid oxidase 1	ribosome, cytosol, peroxisome, plastid	gi|115455773	1189.78	FVLPPYLTLK	2.0e-191	O
LOC_Os04g02050	bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase	plastid, cytosol	gi|222628257	1372.94	RAMVEIYPHNK	5.1e-161	O
LOC_Os04g53330	RNA recognition motif containing protein	cytosol	gi|115460668	1319.97	KNMPEKPEMGK	3.4e-196	O
LOC_Os05g29050	phospholipase D p1		gi|218196631	768.24	FRYER	0	L
LOC_Os05g38150	amino acid kinase	plastid, cytoplasm, membrane	gi|115464247	756.00	LTIKPGK	0	O
LOC_Os06g04270	transketolase, chloroplast	plastid	gi|28190676	1084.79	AVTDKPTLIK	0	O
LOC_Os07g14630	glucosyltransferase-11		gi|297725509	1342.70	VDGLPELMEGLR	5.3e-143	O
LOC_Os09g17890	expressed protein		gi|50252380	1156.75	VESRQFTYK	1.5e-175	O
LOC_Os09g22000	hydrolase, HAD superfamily, Cof family		gi|115478973	471.65	GNGVK	1.9e-200	O
LOC_Os09g27820	1-aminocyclopropane-1-carboxylate oxidase protein		gi|115479473	900.49	YKSVIHR	1.2e-173	O
LOC_Os10g05020	cytochrome P450	ER	gi|115481092	1344.18	MGSRLEVIVADR	4.3e-283	O
LOC_Os11g13990	AAA-type ATPase family protein	plasma membrane	gi|62733734	562.84	AHIPK	0	O
LOC_Os11g15570	Ser/Thr protein phosphatase family protein		gi|115485009	659.82	KQGAEK	1.4e-227	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os11g18570	cytochrome P450		gi|115485127	836.69	TAHKLIR	2.3e-268	O
LOC_Os11g47970	AAA-type ATPase family protein	cell wall, nucleus, plastid, thylakoid, membrane, extracellular region	gi|62733297	1867.63	IVDSFPGQSIDFFGALR	1.9e-255	L
LOC_Os12g04100	cytochrome P450		gi|115487218	880.89	KPTTHGLK	1.1e-284	O
LOC_Os12g19304	Fe-S metabolism associated domain containing protein	plastid	gi|108862504	489.87	GEPTS	5.5e-203	O
LOC_Os02g54420	hypro1	membrane	gi|218188373	641.67	AAPDIR	1.7e-167	L
LOC_Os04g39864	Os4bglu11 - beta-glucosidase homologue, similar to Os4Bglu12 exoglucanase/beta-glucosidase		gi|297723235	500.47	ILPSA	3.0e-60	O
LOC_Os04g44840	glycosyl hydrolase family 3 protein	vacuole, membrane	gi|115459584	549.14	GYPGR	0	O
LOC_Os08g14330	aldose 1-epimerase	cytosol	gi|40253263	707.03	TFVLTK	3.5e-185	O
LOC_Os12g20150	phosphoglucan, water dikinase, chloroplast precursor	plastid	gi|115488252	715.88	RAILSR	0	O
LOC_Os01g12381	GDSL-like lipase/acylhydrolase	vacuole	gi|56783999	1522.87	AGPADYDARTGCLR	1.5e-153	O
LOC_Os05g06140	lipase		gi|297603863	991.82	SMIAMIDGR	1.5e-282	O
LOC_Os06g34120	GDSL-like lipase/acylhydrolase		gi|125555604	633.39	MAPGSR	1.3e-208	O
LOC_Os08g33200	1-phosphatidylinositol-4-phosphate 5-kinase/ zinc ion binding protein		gi|115476510	832.10	QGMVSGKK	0	O
LOC_Os01g16200	serpin domain containing protein	extracellular region	gi|222618162	629.05	AGGPTAR	2.4e-211	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123-TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Other metabolic process *(cont.)*							
LOC_Os01g49430	DnaK family protein	membrane, plastid, nucleolus, nucleus, ribosome, cell wall, cytoplasm, vacuole	gi|222619078	1101.34	EYMAADEEK	1.5e-273	O
LOC_Os03g43390	F-box/LRR domain containing protein	plastid, nucleus, intracellular	gi|297601356	576.14	DCAGR	0	O
LOC_Os03g52070	OsSCP20 - Putative Serine Carboxypeptidase homologue		gi|115455123	1445.20	LQGYIVGNPITGSK	2.5e-207	O
LOC_Os04g30230	F-box/LRR-repeat protein 14		gi|38605924	1152.94	HQYECEKC	8.4e-168	O
LOC_Os04g53780	leucoanthocyanidin reductase		gi|115460744	582.73	ANAGPR	3.8e-172	O
Protein modification process							
LOC_Os01g12420	receptor-like protein kinase		gi|115435380	855.82	VGQVSLVR	0	O
LOC_Os03g15770	tyrosine protein kinase domain containing protein		gi|297600699	478.50	VAGTM	1.1e-39	O
LOC_Os04g59320	protein kinase domain containing protein	plasma membrane	gi|125592152	628.13	KGAPAGK	0	O
LOC_Os06g37750	S-locus-like receptor protein kinase		gi|115468660	1275.11	YVKYCTTVDK	0	O
LOC_Os06g45460	OsFBX202 - F-box domain containing protein		gi|52076509	912.51	LSVPRSVR	8.7e-221	O
LOC_Os09g29520	OsWAK81 - OsWAK receptor-like cytoplasmic kinase OsWAK-RLCK	plasma membrane	gi|297609620	1783.16	RCLEMCGENRPSMK	5.3e-182	N
LOC_Os10g03440	avr9/Cf-9 rapidly elicited protein 74		gi|125573869	1134.26	CPISLELMR	3.2e-230	O
Signal transduction							
LOC_Os01g72700	expressed protein		gi|115442331	941.45	NLTVLDLR	0	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Signal transduction *(cont.)*							
LOC_Os04g48760	leucine-rich repeat family protein	plasma membrane	gi|38345533	699.25	HGLVFK	0	O
LOC_Os04g57640	RCD1	nucleus, cytoplasm	gi|115461248	534.01	MPSGK	0	L
LOC_Os06g35910	FYVE zinc finger domain containing protein		gi|115468484	1028.68	FHPIICSR	0	O
Stress response/defense							
LOC_Os01g64960	chlorophyll A-B binding protein	plastid, membrane, thylakoid	gi|115441299	484.75	AAPAR	2.5e-136	O
LOC_Os04g41759	expressed protein	cell wall	gi|116310366	626.18	VPQGAR	3.3e-198	O
LOC_Os02g18510	stripe rust resistance protein Yr10	plasma membrane, cytoplasm	gi|297599021	834.10	AGGVYKLK	0	O
LOC_Os03g50210	DUF292 domain containing protein		gi|115454891	743.19	SVPVSVR	1.7e-183	O
LOC_Os05g25850	superoxide dismutase, mitochondrial precursor	mitochondrion	gi|115463191	2863.92	GVTTVALPDLPYDYGALEPAIS GEIMR	3.0e-124	O
LOC_Os06g17920	NBS-LRR disease resistance protein	plasma membrane	gi|55296580	470.42	AGVLI	0.0013	N
LOC_Os06g40740	expressed protein	plastid	gi|218198530	999.88	AAAAGGSGGLLR	0	O
LOC_Os06g41660	CC-NBS-LRR protein		gi|125556102	1457.59	NKDEAIDAQLVNK	0	O
LOC_Os08g44770	copper/zinc superoxide dismutase	plastid	gi|115477837	1099.13	LACGVVGLTPL	1.3e-109	O
LOC_Os09g20330	annexin		gi|222641446	594.75	TTFAR	2.4e-138	N
LOC_Os10g33440	NB-ARC domain containing protein		gi|16905161	636.56	AGSKMK	0	O
LOC_Os11g29110	Leucine Rich Repeat family protein		gi|218185734	519.88	TGGSAK	0	O
LOC_Os11g45980	NBS-LRR type disease resistance protein	plasma membrane, cytoplasm	gi|115486673	916.03	LKNLMPGK	0	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transport							
LOC_Os01g07870	ABC transporter family protein	extracellular region, membrane, vacuole	gi|27368883	852.67	AMSEMLR	0	L
LOC_Os03g15690	phosphate carrier protein, mitochondrial precursor	mitochondrion, cell wall, vacuole, plastid, membrane	gi|29893603	957.24	AAGVGLEEGR	9.5e-192	O
LOC_Os03g51430	SEC14 cytosolic factor family protein		gi|115455039	1113.54	AALGPLSSSGKK	3.1e-161	O
LOC_Os05g01750	TruB family pseudouridylate synthase	plastid	gi|297603679	936.66	KVEDFFR	1.1e-268	L
LOC_Os08g06230	nucleolar GTP-binding protein 1	membrane	gi|115474885	811.88	EISVPLR	1.3e-251	O
LOC_Os11g23890	peptide transporter PTR2	membrane	gi|62734474	632.07	ACILR	0	O
LOC_Os12g29220	nodulin MtN3 family protein	plasma membrane, membrane	gi|297613157	634.21	SMSSKP	2.2e-50	O
Transposon/retrotransposon							
LOC_Os01g23330	retrotransposon, putative, centromere-specific, expressed		gi|55296789	1332.99	RGPPVSGSGGAVHR	9.5e-19	O
LOC_Os01g32700	transposon protein, putative, unclassified, expressed		gi|56201732	755.41	EPLIKR	1.3e-20	O
LOC_Os02g24270	retrotransposon protein, putative, unclassified, expressed		gi|115445925	723.34	ESSGSEK	0	O
LOC_Os03g17110	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|108707497	1061.57	DINCDIANK	3.3e-173	O
LOC_Os03g24010	retrotransposon protein, putative, unclassified, expressed		gi|108708221	810.22	TMLEMR	4.8e-300	O
LOC_Os03g35430	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|31126663	1043.47	VNVVADALSR	0	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os03g35940	retrotransposon protein, putative, Ty1-copia subclass		gi|14018100	995.39	FNMQDSKK	0	O
LOC_Os03g59090	retrotransposon protein, putative, unclassified, expressed		gi|48717051	952.70	TPSAAASPPR	1.2e-05	O
LOC_Os04g15510	retrotransposon protein, putative, unclassified, expressed		gi|38346882	1821.12	TPTIPTCSKMEAAEGGR	6.7e-230	O
LOC_Os04g17190	transposon protein, putative, Mutator sub-class, expressed		gi|38346848	1140.25	IYICLDGCK	0	O
LOC_Os04g19760	retrotransposon protein, putative, unclassified, expressed		gi|38344604	641.52	SHKSGK	0	O
LOC_Os04g22990	retrotransposon protein, putative, unclassified, expressed		gi|38343986	1383.85	SAARIYMPAMFK	0	O
LOC_Os05g22560	retrotransposon protein, putative, unclassified, expressed		gi|34394824	1081.38	IPRVAGAAGGGR	1.7e-16	O
LOC_Os05g34330	retrotransposon protein, putative, unclassified, expressed		gi|50511456	603.16	FGPAGR	1.5e-239	O
LOC_Os05g38910	retrotransposon protein, putative, unclassified, expressed		gi|38637205	533.05	VAGMR	1.9e-10	O
LOC_Os06g03590	retrotransposon protein, putative, unclassified, expressed		gi|218184355	1086.90	GRGGVGCGVGGR	4.7e-16	O
LOC_Os07g24930	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|56784802	1058.64	LTVAGDGNRR	2.5e-17	O
LOC_Os07g25160	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|50582701	887.02	MDPAVEAR	1.0e-06	N

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os07g26020	retrotransposon protein, putative, unclassified, expressed		gi|34394102	1068.87	KVCVRPLAK	2.3e-277	O
LOC_Os07g40130	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|222628946	1530.20	MAPTARPSPRPPPR	7.1e-10	O
LOC_Os08g17450	retrotransposon protein, putative, unclassified, expressed		gi|57899524	1304.58	RGSFDLAGILEK	0.045	O
LOC_Os08g26160	retrotransposon, putative, centromere-specific, expressed		gi|49387892	494.54	HPSGV	0.0042	O
LOC_Os08g26960	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|50509439	719.07	TGEGLKD	0.00019	O
LOC_Os10g32030	retrotransposon protein, putative, unclassified, expressed		gi|14140296	752.06	DHIQLK	0	O
LOC_Os11g17700	retrotransposon protein, putative, unclassified, expressed		gi|62733179	755.96	DPGPSER	0	O
LOC_Os11g18070	retrotransposon protein, putative, unclassified, expressed		gi|49387656	774.36	DIIIFR	4.0e-20	O
LOC_Os11g18700	retrotransposon protein, putative, unclassified, expressed		gi|62701895	1361.80	LKDFHSSLIMR	0	O
LOC_Os11g20010	retrotransposon protein, putative, unclassified, expressed		gi|77550216	2294.80	VGQVMISAPATASDVPVPLWEK	2.6e-180	O
LOC_Os11g22160	retrotransposon protein, putative, unclassified, expressed		gi|62733358	728.02	VAGVGNGR	0	O
LOC_Os11g28800	retrotransposon protein, putative, Ty3-gypsy subclass		gi|77550812	1034.16	EISRLVYR	7.5e-96	N

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os11g36880	retrotransposon protein, putative, unclassified, expressed		gi|222616196	722.28	AEMLDK	0	○
LOC_Os12g04250	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|56202277	831.82	LDDGGVEK	0.00068	○
LOC_Os12g23030	retrotransposon protein, putative, unclassified, expressed		gi|77554811	1293.87	VIVFGGDFRQR	0	○
LOC_Os12g35410	retrotransposon protein, putative, unclassified, expressed		gi|77556548	841.84	IGSLLPSR	0	○
Unknown							
LOC_Os01g01500	expressed protein		gi|52075670	826.85	VHAGSNSR	1.3e50	○
LOC_Os01g14280	expressed protein		gi|56784570	1531.83	KGQLMLGGAEGGSGVR	1.2e-06	○
LOC_Os01g27030	hypothetical protein		gi|14091822	524.97	VAAHK	1.8e-69	○
LOC_Os01g27370	expressed protein		gi|48716554	1854.47	TGARAVVHCIYYETSK	6.2e-14	○
LOC_Os01g33869	expressed protein		gi|56201970	735.62	RGGSFGR	0	○
LOC_Os01g43500	expressed protein		gi|222617756	914.22	RHVAASMK	0.0041	○
LOC_Os01g49400	expressed protein		gi|18844896	1154.32	CMHADAGAAPR	1.7e-82	○
LOC_Os01g52830	DUF1264 domain containing protein		gi|115439703	567.59	HAPFP	4.1e-136	○
LOC_Os01g60960	DUF260 domain containing protein	nucleus	gi|222619472	1209.35	DLQAQVPAGRR	8.6e-56	○
LOC_Os01g63890	G10 protein	cytosol, nucleus	gi|115441153	566.33	GCASGD	5.7e-82	○
LOC_Os01g68610	pentatricopeptide repeat protein PPR1106-17		gi|115441803	1026.25	KLMSAEGMK	0	○
LOC_Os02g03840	expressed protein	plastid, plasma membrane	gi|115444017	1754.58	KESMISNNEVSNFEK	2.8e-256	○
LOC_Os02g15670	expressed protein		gi|50251672	616.01	AGGQQR	5.8e-50	○

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os02g21030	expressed protein		gi|46391043	834.84	GGGNDIMR	1.9e-99	O
LOC_Os02g30070	expressed protein		gi|48716176	631.27	DLLGTL	3.7e-48	O
LOC_Os02g49750	expressed protein		gi|58737179	660.44	ASDGRR	2.4e-05	O
LOC_Os02g50370	helicase domain-containing protein		gi|115448551	1060.20	AFPGPSKDDK	0	L
LOC_Os02g57600	expressed protein		gi|115449795	583.01	GYDTK	2.9e-158	O
LOC_Os03g05220	expressed protein		gi|46806233	1042.22	VLVGEARSGR	0.28	O
LOC_Os03g08940	expressed protein		gi|125544919	832.62	AILSAGMR	1.7e-34	O
LOC_Os03g11250	expressed protein	plastid	gi|108706801	1714.03	GPGTDERGATAGGGGVVTR	1.6e-63	O
LOC_Os03g12560	expressed protein	plastid, cell wall	gi|115451681	1919.20	RAGPVAAVPDGVAVADVVEK	1.7e-137	O
LOC_Os03g15300	hypothetical protein		gi|108707269	856.49	WKNGSHK	1.8e-85	N
LOC_Os03g21020	RNA recognition motif containing protein		gi|222624851	707.31	LFTSLK	3.2e-207	O
LOC_Os03g22350	Brix domain containing protein		gi|115452957	745.82	MPASVAR	5.6e-194	O
LOC_Os03g22880	nucleolar protein 5A	nucleolus, cell wall	gi|218200199	1641.91	TLLIMSHDQLKCQG	4.1e-197	O
LOC_Os03g25190	OsFBX87 - F-box domain containing protein	plastid	gi|125544015	674.22	TMGLPR	1.0e-163	O
LOC_Os03g32980	expressed protein		gi|48716919	516.21	AVLSE	7.7e-39	O
LOC_Os03g38350	expressed protein		gi|108709496	685.25	QPDGLR	3.5e-82	O
LOC_Os03g42480	expressed protein		gi|115454171	1023.72	LTGHPSASVR	5.3e-40	O
LOC_Os03g48626	expressed protein	vacuole	gi|125587550	725.53	GAPGVAVR	1.2e-26	O
LOC_Os03g51230	SNF2 family N-terminal domain containing protein		gi|116235007	663.82	KFMPK	0	O
LOC_Os03g59560	hypothetical protein		gi|23616972	1460.40	GESPRPHGLVQQR	5.3e-08	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os04g04070	expressed protein		gi|32482895	559.08	VAAGSR	1.3e-98	O
LOC_Os04g09800	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A		gi|58531994	682.49	TAAPPVK	0	O
LOC_Os04g22220	SCP-like extracellular protein		gi|125547615	472.51	GSGPR	1.1e-89	O
LOC_Os04g32600	expressed protein		gi|297602641	887.13	GKEPSSER	3.2e-65	L
LOC_Os04g41930	expressed protein		gi|116310693	649.06	DSTDGR	6.9e-70	O
LOC_Os04g46100	expressed protein		gi|222629303	840.54	MVMSQSK	1.5e-223	O
LOC_Os04g48484	expressed protein		gi|297720487	721.32	AAYIRK	0.068	O
LOC_Os04g57739	expressed protein		gi|115461266	460.43	GRDGG	1.3e-45	O
LOC_Os05g06540	expressed protein		gi|115462215	897.57	EKIDPAAR	2.2e-247	O
LOC_Os05g26860	expressed protein		gi|222625353	832.48	MNNDDPK	3.1e-07	O
LOC_Os05g33010	heat shock protein DnaJ		gi|46981328	691.51	AAFRAR	1.9e-74	O
LOC_Os05g37810	expressed protein		gi|53749260	1131.86	SSLSPLLLFR	8.6e-127	O
LOC_Os05g38300	expressed protein		gi|34395201	1096.04	HAVAEGAPSTR	0.00013	O
LOC_Os06g07100	RING-H2 finger protein		gi|115466640	417.01	SPGAS	6.3e-195	O
LOC_Os06g07150	expressed protein		gi|55296049	720.72	SYLIGGL	4.7e-55	O
LOC_Os06g12430	expressed protein		gi|53792740	1616.11	LGHLLFAITEPMMK	6.8e-24	O
LOC_Os06g12510	Pentatricopeptide		gi|51535410	740.06	KPAGLSAP	7.8e-284	O
LOC_Os06g20270	hypothetical protein		gi|125555061	737.81	TFVENK	1.6e-84	O
LOC_Os06g31190	intracellular protein transport protein USO1-related	plasma membrane, plastid	gi|125597372	1091.68	GGEEGEEEEK	0	O
LOC_Os06g36370	expressed protein		gi|297725799	928.20	DPAAEAEAR	0.00027	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os07g02640	expressed protein		gi|222636344	963.27	DACMVTLR	4.9e-179	O
LOC_Os07g09530	ankyrin repeat family protein		gi|11862971	783.22	PNLPSEK	0.020	O
LOC_Os07g10550	cyclin-related protein		gi|115471103	1116.29	GGVNLTVEEAK	0	O
LOC_Os07g18610	OsFBLD7 - F-box, LRR and FBD domain containing protein		gi|34393661	1189.80	SGTLDGLEELR	9.2e-265	L
LOC_Os07g28180	expressed protein		gi|222631387	761.03	EDPGGMR	0.0015	O
LOC_Os07g46180	PWWP domain containing protein		gi|115473797	579.09	FAADR	0	O
LOC_Os07g47030	expressed protein		gi|115473937	1652.69	IMPFVSIEVHLPKK	0	O
LOC_Os08g04140	X8 domain containing protein		gi|34394886	1860.09	SHANRSLVAAAAPGSLPSR	0.28	O
LOC_Os08g05550	expressed protein		gi|115474807	799.19	AAGGLVRR	3.3e-134	O
LOC_Os08g06659	expressed protein		gi|18565420	567.66	PPNLK	0.0091	O
LOC_Os08g07090	expressed protein		gi|37806094	710.87	LTPGAPR	1.0e-50	L
LOC_Os08g10110	hypothetical protein		gi|47848098	969.52	SVHLVQMR	7.2e-20	O
LOC_Os08g11520	expressed protein		gi|45736225	565.35	ATATTT	2.4e-83	O
LOC_Os08g28200	expressed protein		gi|218201062	819.38	ELIECR	2.7e-45	O
LOC_Os08g30590	C1-like domain containing protein		gi|297726401	1414.54	QEEEGPDHCCR	0	O
LOC_Os09g10204	expressed protein		gi|115478300	777.97	DPPAQPR	9.4e-66	O
LOC_Os09g20960	expressed protein		gi|50251558	514.10	GPADR	0.0019	O
LOC_Os09g25000	spotted leaf 11	plastid	gi|115479177	1617.83	MVARCAHADVGGGFR	4.6e-254	L
LOC_Os09g27120	expressed protein		gi|51536007	597.81	FFGAR	8.9e-77	O
LOC_Os10g05530	OsFBX372 - F-box domain containing protein		gi|218184137	889.74	EVADDGASK	1.5e-108	O

Table D.5 Chitosan responsive proteins during the drought stress in leaf tissue of LPT123-TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os10g19200	vegetative cell wall protein gp1 precursor		gi|297728977	1177.42	SSPPSQTSMTR	0.0026	O
LOC_Os11g03260	lig A		gi|50511390	803.72	CQEAAAR	3.7e-05	O
LOC_Os11g04510	expressed protein		gi|297727959	682.34	FCDNK	2.4e-163	N
LOC_Os11g18470	expressed protein		gi|56382051	580.75	IKALH	2.5e-127	O
LOC_Os11g18890	expressed protein		gi|62734042	635.79	ASGCSR	6.1e-78	O
LOC_Os11g32360	expressed protein		gi|297728407	786.07	RAPSNDK	1.4e-220	O
LOC_Os11g37810	expressed protein		gi|13873037	817.39	QESGDAGR	0.059	O
LOC_Os11g45120	conserved hypothetical protein		gi|50509844	688.57	ELTGLR	3.4e-13	L
LOC_Os12g15520	expressed protein		gi|115488050	922.76	RLIAAHSR	4.0e-168	O
LOC_Os12g19660	expressed protein		gi|40737001	750.59	ADGGGYGR	7.0e-06	O
LOC_Os12g32190	expressed protein		gi|115488702	831.94	DVSVTKGK	1.8e-245	O

Table D.6 Chitosan responsive proteins during the drought stress in root tissue of LPT123–TC171 rice

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Up-regulated proteins							
Cellular component organization							
LOC_Os04g39670	expressed protein		gi|297602896	773.92	CQNILK	5.6e-187	G
Metabolic process							
LOC_Os02g52730	ferredoxin--nitrite reductase	mitochondrion, extracellular region, plastid, membrane	gi|218191633	1055.98	AVLLDTGRGR	0	F
LOC_Os06g21760	jasmonate O-methyltransferase		gi|297724791	950.12	LFVRMER	9.9e-126	G
LOC_Os07g47590	expressed protein	nucleus	gi|115474015	848.16	RIQMER	1.9e-177	G
Signal transduction							
LOC_Os05g24010	receptor protein kinase-like		gi|218196519	1043.47	DVMDPVLQK	0	G
LOC_Os07g39530	BTBN16 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hypocotyl 3 NPH3 domain	plastid	gi|218199914	1384.41	IQALEQEILSLK	0	G
Stress response/defense							
LOC_Os05g40150	RGH2B		gi|115464497	1077.78	YPSVSTIRR	0	G
LOC_Os11g27430	NB-ARC domain containing protein	cytoplasm, plasma membrane	gi|77550667	1006.20	LATMAVRTK	0	G
Transposon/retrotransposon							
LOC_Os03g47410	retrotransposon protein, putative, unclassified, expressed		gi|29150404	1183.82	ADALTKGLPAAR	0	G
LOC_Os11g28770	retrotransposon protein, putative, unclassified, expressed		gi|108864375	930.06	KERPASDK	0	G

Table D.6 Chitosan responsive proteins during the drought stress in root tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os11g42720	retrotransposon protein, putative, unclassified, expressed		gi|77552314	470.88	GAAPR	0	G
LOC_Os12g03760	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|77553605	751.33	HDEPVR	0	G
Unknown							
LOC_Os01g43330	extra-large G-protein-related		gi|222618874	623.35	GCGSSR	0	G
LOC_Os02g31090	collagen-binding protein		gi|51536026	777.70	SCRVEK	4.2e-102	G
LOC_Os03g06430	expressed protein		gi|125542494	991.10	GGGGMEEALR	2.0e-49	D
LOC_Os07g23494	expressed protein		gi|22324439	771.84	ANSLGRR	3.4e-109	G
LOC_Os07g26760	expressed protein		gi|222632653	994.42	GGEWGMGER	5.5e-13	G
LOC_Os07g30450	expressed protein		gi|34394108	2277.79	AHGYDNGSVEVSGGTAEAENGTR	3.4e-13	G
LOC_Os08g03620	tetratricopeptide repeat domain containing protein		gi|222639859	665.60	SSGGTTR	0	G
LOC_Os10g25570	expressed protein		gi|408100	774.10	XRAPDR	0.00017	G
LOC_Os10g41850	expressed protein		gi|78709030	934.88	AVFLGLCR	7.2e-178	G
LOC_Os12g19860	expressed protein		gi|77554991	730.35	SLVAEGR	1.9e-74	G
LOC_Os12g33590	hypothetical protein		gi|77555959	679.90	SMGDQK	4.6e-112	G
Down-regulated proteins							
Nucleic acid metabolic process							
LOC_Os01g64000	bZIP transcription factor	nucleus	gi|20161640	500.64	AGVVR	6.4e-209	O
LOC_Os02g27790	splicing factor 3B subunit 1	plastid	gi|297721205	838.28	LSPEEHK	0	N
LOC_Os05g51040	tesmin/TSO1-like CXC domain containing protein		gi|222632736	904.60	GIYTLILL	6.1e-110	L

Table D.6 Chitosan responsive proteins during the drought stress in root tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Nucleic acid metabolic process *(cont.)*							
LOC_Os07g32040	eukaryotic translation initiation factor 3 subunit E	plasma membrane, cytosol, nucleus	gi|115472263	651.22	STMEPA	4.7e-238	○
LOC_Os10g10170	PPR repeat domain containing protein	plastid	gi|222612526	522.02	FGGSR	0	○
LOC_Os11g20689	exosome complex exonuclease	cytosol	gi|62734004	1017.86	NLEDILMR	2.2e-64	○
LOC_Os11g45250	ribonucleases P/MRP protein subunit POP1 containing protein		gi|77552547	513.50	TPGLK	0	○
Other metabolic process							
LOC_Os03g42130	gibberellin 20 oxidase 2		gi|125560614	784.31	VVVNVEK	7.5e-160	○
LOC_Os04g32010	thiamine pyrophosphate enzyme, C-terminal TPP binding domain containing protein	plastid	gi|115458074	1463.16	ARAGPDAGAHGAAEGR	2.1e-18	○
LOC_Os07g37990	glycosyltransferase sugar-binding region containing DXD motif	mitochondrion, Golgi apparatus	gi|27817893	849.23	QGMGVTEK	0	○
LOC_Os10g21100	glycosyl hydrolase family 10 protein		gi|115481642	706.21	AAMDKR	0	○
LOC_Os08g39840	lipoxygenase, chloroplast precursor	cytoplasm, thylakoid, plastid, membrane	gi|115477206	701.26	EKATVR	0	○
LOC_Os11g37330	pentatricopeptide repeat domain containing protein	mitochondrion	gi|77551591	750.11	CRCAGK	0	○
LOC_Os02g21520	chalcone isomerase 3	plastid	gi|115445809	1860.49	VGIETFDASSVFDSIFK	1.2e-143	○
LOC_Os06g08640	transferase family protein	cytosol	gi|115466808	769.76	QQVGALR	1.7e-233	○
Protein modification process							
LOC_Os10g06030	OsWAK103 - OsWAK receptor-like protein kinase	plasma membrane	gi|125564281	1816.85	SNNLASCFQSCMAKGK	2.7e-68	○

Table D.6 Chitosan responsive proteins during the drought stress in root tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Protein modification process *(cont.)*							
LOC_Os10g12620	protein kinase domain containing protein		gi|110288802	999.56	FIHSVRNK	0	O
Stress response/defense							
LOC_Os01g18890	peroxidase precursor	cell wall, vacuole, membrane	gi|222618253	879.73	MGGAFRAR	2.5e-65	O
LOC_Os04g41370	Leucine Rich Repeat family protein		gi|32483316	651.47	RIVHK	0	L
LOC_Os04g59190	peroxidase precursor	cell wall, vacuole, membrane	gi|115461478	822.01	VPRPGGNK	4.6e-176	O
LOC_Os11g45060	NB-ARC domain containing protein		gi|125601283	1042.23	LKDAMAHEK	2.1e-43	O
Transport							
LOC_Os01g59870	LTPL65 - Protease inhibitor/seed storage/LTP family protein precursor	membrane	gi|297720515	1642.58	GGGDGDGGGADVAGGGAGAGGR	3.5e-11	O
Transposon/retrotransposon							
LOC_Os01g19420	transposon protein, putative, unclassified, expressed		gi|115466696	589.42	AANSAR	0.00060	O
LOC_Os02g06670	retrotransposon protein, putative, unclassified, expressed		gi|297720403	835.33	MSRSSIR	3.6e-05	O
LOC_Os02g18020	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|47848560	711.41	RPSTPR	9.8e-158	O
LOC_Os03g60670	retrotransposon protein, putative, unclassified, expressed		gi|222626062	733.17	TISTVGR	9.4e-09	L
LOC_Os04g06020	transposon protein, putative, CACTA, En/Spm sub-class		gi|38346252	560.03	IADLE	5.5e-132	O

Table D.6 Chitosan responsive proteins during the drought stress in root tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Transposon/retrotransposon *(cont.)*							
LOC_Os04g14770	retrotransposon protein, putative, unclassified, expressed		gi|38344129	637.60	ATPPPR	0	O
LOC_Os05g40110	retrotransposon protein, putative, unclassified, expressed		gi|222640687	635.03	LAEMR	1.5e-198	N
LOC_Os06g37140	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|297721175	653.41	YCANK	1.9e-12	O
LOC_Os09g06730	retrotransposon protein, putative, unclassified, expressed		gi|218201716	1210.90	SAMTSFGVLGVK	7.3e-103	O
LOC_Os09g17930	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|222641403	739.50	APQSPIK	8.8e-292	O
LOC_Os10g15079	retrotransposon protein, putative, unclassified, expressed		gi|110288842	879.49	FFATPLGK	0	O
LOC_Os10g20480	transposon protein, putative, CACTA, En/Spm sub-class, expressed		gi|110288928	1396.91	FQDNAGHGFHAAK	0	O
LOC_Os11g28230	retrotransposon protein, putative, unclassified, expressed		gi|52353550	676.21	EGGLFR	1.0e-297	O
LOC_Os11g31310	retrotransposon protein, putative, Ty3-gypsy subclass, expressed		gi|108864420	618.52	TIDAAK	1.9e-280	O
LOC_Os12g14530	retrotransposon protein, putative, unclassified		gi|28269481	1120.46	EGAPDDASMGR	1.6e-15	O
LOC_Os12g27096	retrotransposon protein, putative, Ty1-copia subclass, expressed		gi|108862649	818.19	GDVKICK	0	O
Unknown							
LOC_Os01g06380	expressed protein		gi|15528633	667.17	SAMMGR	1.3e-208	O

Table D.6 Chitosan responsive proteins during the drought stress in root tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os01g49154	expressed protein		gi|115439233	655.91	VDALLQ	1.0e-75	O
LOC_Os02g22160	DNA binding protein		gi|115445863	508.92	VMGFG	7.1e-242	O
LOC_Os02g27290	expressed protein		gi|47497543	633.62	GGTEDR	2.1e-84	O
LOC_Os02g44260	zinc-binding protein		gi|49388501	786.79	MQSPAVR	3.3e-125	O
LOC_Os02g44710	expressed protein		gi|115447799	1028.33	EDVGGAVRVK	3.2e-72	O
LOC_Os03g32636	hypothetical protein		gi|108709059	954.93	SGSIPLRVK	1.7e-36	N
LOC_Os03g55950	H-BTB1 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with H family conserved sequence		gi|115455589	628.12	MSVHR	1.9e-282	N
LOC_Os04g32470	expressed protein		gi|28411941	881.21	GMLAVTGCG	0.00031	O
LOC_Os04g46110	fibroin heavy chain precursor		gi|297723339	761.38	GDSSGAIR	4.8e-149	O
LOC_Os04g47010	expressed protein	plastid	gi|115459856	962.97	LMDEPTSR	1.2e-120	O
LOC_Os05g40000	expressed protein		gi|46576002	854.36	AAAAQGLPR	3.5e-137	O
LOC_Os06g14180	expressed protein		gi|52076977	879.97	HNAAAAAKK	5.3e-143	O
LOC_Os07g28010	AGAP001055-PA		gi|218192651	627.96	APAGEQG	3.7e-07	O
LOC_Os07g39890	expressed protein		gi|222637367	713.55	IQPVEK	5.1e-97	O
LOC_Os08g28300	expressed protein		gi|47497553	917.49	AAAATAASVGK	6.4e-12	O
LOC_Os09g13920	expressed protein		gi|55771373	1011.96	GMSGLMTGDK	1.7e-11	O
LOC_Os09g37870	expressed protein		gi|218202588	719.18	MDAAADK	1.4e-46	L
LOC_Os10g03780	OsFBX351 - F-box domain containing protein		gi|20042917	606.10	CIADK	0	O
LOC_Os10g34440	expressed protein		gi|18087883	1289.19	VVMEGLLDRGGK	4.6e-176	O
LOC_Os11g03850	PPR repeat domain containing protein		gi|125576095	699.13	APGTPTR	1.1e-140	O

Table D.6 Chitosan responsive proteins during the drought stress in root tissue of LPT123–TC171 rice *(cont.)*

gene ID	protein identification	cellular compartment	Acc. no. NCBInr	mass (Da)	peptide sequence	E-value	Venn diagram
Unknown *(cont.)*							
LOC_Os11g06670	expressed protein		gi|215768810	1123.98	GLHGECLAIR	1.9e-193	L
LOC_Os11g10180	OsFBX412 - F-box domain containing protein		gi|115484649	705.34	MASGADR	1.6e-237	O
LOC_Os11g11650	expressed protein		gi|62733749	830.14	QLKELVT	0	O
LOC_Os11g26560	expressed protein		gi|62733138	647.90	ATSAGSR	1.5e-97	N
LOC_Os11g34950	expressed protein		gi|115485867	678.65	LMLFR	1.4e-199	O
LOC_Os12g23550	expressed protein		gi|77555124	721.44	HPLAER	2.2e-238	O

Table D.7 Chitosan-responsive proteins in LPT123-TC171 rice mapped in the RNA and protein synthetic processes by using MapMan software

gene ID	annotation	bin name
LOC_Os03g52190	retrotransposon protein, putative, unclassified, expressed	RNA.transcription
LOC_Os03g35430	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	RNA.transcription
LOC_Os10g20960	retrotransposon protein, putative, unclassified, expressed	RNA.transcription
LOC_Os05g22560	retrotransposon protein, putative, unclassified, expressed	RNA.transcription
LOC_Os01g23330	retrotransposon, putative, centromere-specific, expressed	RNA.transcription
LOC_Os11g28770	retrotransposon protein, putative, unclassified, expressed	RNA.transcription
LOC_Os02g27790	splicing factor 3B subunit 1	RNA.processing.splicing
LOC_Os09g30466	nuclear ribonuclease Z	RNA.processing.ribonucleases
LOC_Os11g20689	exosome complex exonuclease	RNA.processing.ribonucleases
LOC_Os07g12320	WD domain, G-beta repeat domain containing protein	RNA.processing
LOC_Os01g68610	pentatricopeptide repeat protein PPR1106-17	RNA.processing
LOC_Os11g03850	PPR repeat domain containing protein	RNA.processing
LOC_Os01g74560	transposon protein, putative, Pong sub-class, expressed	protein.synthesis.ribosomal protein.unknown.unknown
LOC_Os02g01230	ribosomal protein	protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S5
LOC_Os03g58204	ribosomal protein L4	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L4/L1
LOC_Os05g32670	pentatricopeptide repeat-containing protein	protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L34
LOC_Os07g36250	peptide chain release factor protein	protein.synthesis.release
LOC_Os03g22350	Brix domain containing protein	protein.synthesis.misc ribosomal protein.BRIX
LOC_Os07g32040	eukaryotic translation initiation factor 3 subunit E	protein.synthesis.initiation
LOC_Os03g60130	transcription elongation factor protein	protein.synthesis.elongation
LOC_Os01g12420	receptor-like protein kinase	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII
LOC_Os09g29520	OsWAK81 - OsWAK receptor-like cytoplasmic kinase OsWAK-RLCK	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII
LOC_Os03g15770	tyrosine protein kinase domain	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII

Table D.7 Chitosan-responsive proteins in LPT123-TC171 rice mapped in the RNA and protein synthetic processes by using MapMan software *(cont.)*

gene ID	annotation	bin name
LOC_Os01g36550	protein kinase family protein	protein.posttranslational modification.kinase. receptor like cytoplasmatic kinase VII
LOC_Os06g12510	Pentatricopeptide	protein.posttranslational modification
LOC_Os10g12620	protein kinase domain containing protein	protein.posttranslational modification
LOC_Os03g59390	CAMK_CAMK_like.24 - CAMK includes calcium/calmodulin dependent protein kinases	protein.posttranslational modification
LOC_Os03g43390	F-box/LRR domain containing protein	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os04g30230	F-box/LRR-repeat protein 14	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os03g28130	OsFBX94 - F-box domain containing protein	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os10g03780	OsFBX351 - F-box domain containing protein	protein.degradation.ubiquitin.E3.SCF.FBOX
LOC_Os06g07100	RING-H2 finger protein	protein.degradation.ubiquitin.E3.RING
LOC_Os09g25000	spotted leaf 11	protein.degradation.ubiquitin.E3.RING
LOC_Os07g47590	expressed protein	protein.degradation.ubiquitin.E3.RING
LOC_Os03g52070	OsSCP20 - Putative Serine Carboxypeptidase homologue	protein.degradation.serine protease
LOC_Os01g16200	serpin domain containing protein	protein.degradation.serine protease
LOC_Os12g26470	aspartic proteinase nepenthesin-1 precursor	protein.degradation.aspartate protease
LOC_Os05g01750	TruB family pseudouridylate synthase	protein.aa activation.pseudouridylate synthase
LOC_Os08g42560	tRNA synthetase class II core domain containing protein	protein.aa activation.glycine-tRNA ligase

Table D.8 Chitosan-responsive proteins in LPT123-TC171 rice mapped in the overview of metabolic pathway by using MapMan software

gene ID	annotation	bin name
LOC_Os03g40070	transposon protein, putative, unclassified, expressed	amino acid metabolism.degradation.aspartate family.asparagine.L-asparaginase
LOC_Os01g51410	glycine dehydrogenase	amino acid metabolism.degradation.serine-glycine-cysteine group.glycine
LOC_Os04g32010	thiamine pyrophosphate enzyme, C-terminal TPP binding domain containing protein	amino acid metabolism.synthesis.branched chain group.common
LOC_Os05g38150	amino acid kinase	amino acid metabolism.synthesis.glutamate family.proline
LOC_Os02g20560	fasciclin domain containing protein	cell wall.cell wall proteins.AGPs.AGP
LOC_Os04g44840	glycosyl hydrolase family 3 protein	cell wall.degradation.mannan-xylose-arabinose-fucose
LOC_Os10g21100	glycosyl hydrolase family 10 protein	cell wall.degradation.mannan-xylose-arabinose-fucose
LOC_Os11g07090	Pectinesterase	cell wall.pectin esterases.PME
LOC_Os10g11870	transposon protein, putative, CACTA, En/Spm sub-class, expressed	glycolysis.cytosolic branch.fructose-2,6-bisphosphatase (Fru2,6BisPase)
LOC_Os09g23070	malonyl-CoA decarboxylase, mitochondrial precursor	lipid metabolism.FA synthesis and FA elongation.MCD
LOC_Os12g01930	lipase-related	lipid metabolism.lipid degradation.lipases
LOC_Os05g06140	Lipase	lipid metabolism.lipid degradation.lipases. triacylglycerol lipase
LOC_Os05g29050	phospholipase D p1	lipid metabolism.lipid degradation. lysophospholipases.phospholipase D
LOC_Os01g70570	Acyltransferase	lipid metabolism.phospholipid synthesis
LOC_Os12g20150	phosphoglucan, water dikinase, chloroplast precursor	major CHO metabolism.degradation.starch.glucan water dikinase
LOC_Os08g14330	aldose 1-epimerase	minor CHO metabolism.others
LOC_Os10g21266	ATP synthase subunit beta	mitochondrial electron transport / ATP synthesis.F1-ATPase
LOC_Os04g46560	lactate/malate dehydrogenase	TCA / org. transformation.other organic acid transformaitons.cyt MDH
LOC_Os02g52730	ferredoxin-nitrite reductase	N-metabolism.nitrate metabolism.nitrite reductase
LOC_Os04g02050	bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase	S-assimilation.ATPS
LOC_Os05g01750	TruB family pseudouridylate synthase	nucleotide metabolism.deoxynucleotide metabolism.pseudouridine synthase
LOC_Os11g47970	AAA-type ATPase family protein	PS.calvin cycle.rubisco interacting
LOC_Os12g17600	ribulose bisphosphate carboxylase small chain, chloroplast precursor	PS.calvin cycle.rubisco small subunit
LOC_Os06g04270	transketolase, chloroplast	PS.calvin cycle.transketolase

Table D.8 Chitosan-responsive proteins in LPT123-TC171 rice mapped in the overview of metabolic pathway by using MapMan software *(cont.)*

gene ID	annotation	bin name
LOC_Os01g64960	chlorophyll A-B binding protein	PS.light reaction.photosystem II.PSII polypeptide subunits
LOC_Os03g57220	hydroxyacid oxidase 1	PS.photorespiration.glycolate oxydase
LOC_Os02g21520	chalcone isomerase 3	secondary metabolism.flavonoids.chalcones
LOC_Os04g53780	leucoanthocyanidin reductase	secondary metabolism.flavonoids.dihydroflavonols
LOC_Os06g08640	transferase family protein	secondary metabolism.phenylpropanoids

APPENDIX E

BIOINFORMATIC ANALYSES OF A *TRANSCRIPTIONAL REPRESSOR*

1. Predicted co-expression network of transcriptional repressor analyzed with rice interactions viewer in the Bio-Analytic Resource for Plant Biology (http://bar.utoronto.ca)

Table E.1 Predicted partner of transcriptional repressor

gene ID	annotation	subcellular localization	interolog confidence value	interolog confidence	Pearson correlation coefficient
LOC_Os01g01960	transcriptional repressor	nucleus	1	low	1
LOC_Os01g08560	DnaK family protein	nucleus, mitochondria, Golgi apparatus, ER	1	low	0.241
LOC_Os01g15310	LSM domain containing protein	nucleus	2	medium	0.583
LOC_Os01g16540	NEDD8-activating enzyme E1 catalytic subunit	nucleus	1	low	0.738
LOC_Os01g23630	transcription initiation factor IID, 18kD subunit family protein	ER, cytoplasm	1	low	0.411
LOC_Os01g33080	fimbrin-like protein 2	cytoplasm	1	low	0.125
LOC_Os01g36930	ubiquitin carboxyl-terminal hydrolase 6	nucleus	1	low	0.736
LOC_Os01g38970	carbamoyl-phosphate synthase large chain	cytoplasm	1	low	0.739
LOC_Os01g43030	tetratricopeptide repeat domain containing protein	vacuole	2	medium	N/A
LOC_Os01g46932	vacuolar protein-sorting-associated protein 25	nucleus	1	low	N/A
LOC_Os01g47600	HMG1/2	chloroplast	18	high	0.64
LOC_Os01g62620	DHHC zinc finger domain containing protein	cytoplasm	1	low	0.655
LOC_Os01g65580	mitotic checkpoint family protein	cell membrane	1	low	0.697
LOC_Os01g72790	cyclin-dependent kinase	chloroplast	1	low	0.792
LOC_Os01g73310	actin	cytoplasm	1	low	0.127
LOC_Os02g02860	glutamyl-tRNA synthetase	mitochondria, cytoplasm, chloroplast	1	low	0.677
LOC_Os02g04660	arginine N-methyltransferase 5	nucleus	1	low	0.319
LOC_Os02g14000	actin-related protein 2/3 complex subunit 3	nucleus	1	low	0.85
LOC_Os02g15220	bromodomain containing protein	vacuole	1	low	0.84
LOC_Os02g22780	T-complex protein	cytoplasm	1	low	0.381
LOC_Os02g32490	AMP-binding enzyme	nucleus, peroxisome	1	low	0.547
LOC_Os02g33450	Peroxiredoxin	cytoplasm, chloroplast	1	low	0.443

Table E.1 Predicted partner of transcriptional repressor *(cont.)*

gene ID	annotation	subcellular localization	interolog confidence value	Interolog confidence	Pearson correlation coefficient
LOC_Os02g34750	leucine-rich repeat receptor-like protein kinase 1	nucleus	1	low	0.522
LOC_Os02g38300	SNF7 domain containing protein	chloroplast	1	low	0.583
LOC_Os02g39800	SET domain containing protein	nucleus	1	low	N/A
LOC_Os02g45180	ORM1	nucleus	1	low	0.733
LOC_Os02g45820	mitochondrial import inner membrane translocase subunit Tim	mitochondria	4	medium	0.249
LOC_Os02g51780	ribonuclease protein	chloroplast	4	medium	0.432
LOC_Os02g55300	CAF1 family ribonuclease containing protein	nucleus	1	low	0.57
LOC_Os02g57150	tubulin-specific chaperone A	nucleus	1	low	0.252
LOC_Os02g58640	tumor susceptibility gene 101	vacuole	1	low	0.646
LOC_Os03g04980	PHD-finger domain containing protein	mitochondria	1	low	0.639
LOC_Os03g07080	endonuclease/exonuclease/phosphatase family domain containing protein	mitochondria	1	low	0.687
LOC_Os03g07850	tRNA methyltransferase	chloroplast	1	low	0.607
LOC_Os03g10990	retinoblastoma-binding protein-like	nucleus	1	low	0.679
LOC_Os03g13850	cell cycle checkpoint protein RAD17	nucleus	1	low	0.355
LOC_Os03g13970	26S proteasome non-ATPase regulatory subunit 4	nucleus	4	medium	N/A
LOC_Os03g17700	N/A	nucleus	1	low	0.393
LOC_Os03g29470	transcription initiation factor IID	nucleus	4	medium	0.727
LOC_Os03g46390	ras-related protein	cell membrane	1	low	0.53
LOC_Os03g51140	HEAT repeat family protein	peroxisome, chloroplast, cell wall	1	low	0.613
LOC_Os03g51550	WD repeat-containing protein 5	nucleus	4	medium	0.272
LOC_Os03g53190	Core histone H2A/H2B/H3/H4 domain containing protein	nucleus, mitochondria	1	low	0.694

Table E.1 Predicted partner of transcriptional repressor *(cont.)*

gene ID	annotation	subcellular localization	interolog confidence value	interolog confidence	Pearson correlation coefficient
LOC_Os03g53960	transcriptional adaptor	nucleus	2	medium	0.834
LOC_Os03g57760	N/A	ER	1	low	0.769
LOC_Os03g57790	ubiquitin-conjugating enzyme	nucleus, cytoplasm	2	medium	N/A
LOC_Os04g01130	chromatin modification-related protein EAF3	nucleus, cytoplasm	42	high	N/A
LOC_Os04g02820	elongation factor	cytoplasm	1	low	0.754
LOC_Os04g35060	nicotinate phosphoribosyltransferase family domain containing protein	nucleus	1	low	0.773
LOC_Os04g36700	proteasome subunit	nucleus	1	low	0.631
LOC_Os04g38870	14-3-3 protein	nucleus	1	low	0.599
LOC_Os04g39040	UBA and UBX domain-containing protein	peroxisome, chloroplast mitochondria,	1	low	0.776
LOC_Os04g40840	elongator complex protein 3	nucleus, cytoplasm	4	medium	0.478
LOC_Os04g46450	zinc finger, C3HC4 type domain containing protein	nucleus	6	medium	0.855
LOC_Os04g54330	acetyltransferase, GNAT family	nucleus	1	low	0.598
LOC_Os04g54340	double-strand break repair protein MRE11	nucleus	1	low	0.725
LOC_Os04g55050	amidase	nucleus	1	low	N/A
LOC_Os05g01020	N/A	chloroplast	32	high	0.892
LOC_Os05g05860	retrotransposon protein, putative, unclassified, expressed	nucleus	1	low	0.599
LOC_Os05g06350	importin subunit alpha	nucleus, cytoplasm	8	medium	0.527
LOC_Os05g29010	POLA4 - Putative DNA polymerase alpha complex subunit	chloroplast	1	low	0.146
LOC_Os05g38710	lipin, N-terminal conserved region family protein	nucleus	1	low	0.589
LOC_Os05g42300	NAF1 domain containing protein	cell membrane	1	low	0.56
LOC_Os05g46330	MYB family transcription factor	mitochondria	2	medium	0.754
LOC_Os05g48030	anti-silencing protein, ASF1-like domain containing protein	nucleus	1	low	0.67

Table E.1 Predicted partner of transcriptional repressor *(cont.)*

gene ID	annotation	subcellular localization	interolog confidence value	interolog confidence	Pearson correlation coefficient
LOC_Os05g51490	SIT4 phosphatase-associated protein domain containing protein	nucleus	1	low	0.8
LOC_Os06g04580	transcription factor TFIIF	cytoplasm	8	medium	0.742
LOC_Os06g06460	histone H3	nucleus	1	low	0.287
LOC_Os06g06510	histone H3	nucleus	4	medium	0.321
LOC_Os06g07878	peptidase, T1 family	nucleus	1	low	0.653
LOC_Os06g15360	RAD23 DNA repair protein	mitochondria, nucleus	1	low	0.782
LOC_Os06g21340	rho GDP-dissociation inhibitor 1	cytoplasm	1	low	0.243
LOC_Os06g38470	histone deacetylase 19	nucleus, cytoplasm	372	high	0.718
LOC_Os06g48800	OsHKT2,4 - Na+ transporter	cell membrane	3	medium	0.417
LOC_Os06g48810	OsHKT2,1 - Na+ transporter	cell membrane	1	low	-0.009
LOC_Os06g50910	Phosphatidylinositol kinase and FAT containing domain protein	nucleus	1	low	0.157
LOC_Os07g02350	casein kinase II subunit alpha-2	nucleus	10	medium	0.848
LOC_Os07g03160	WD domain, G-beta repeat domain containing protein	cytoplasm	1	low	0.228
LOC_Os07g06980	histone deacetylase	cell membrane	6	medium	0.67
LOC_Os07g13280	RNA recognition motif containing protein	nucleus	1	low	N/A
LOC_Os07g22220	F-box-like/WD repeat-containing protein TBL1XR1-A	mitochondria	1	low	0.802
LOC_Os07g31370	ras-related protein	nucleus, Golgi apparatus	1	low	0.52
LOC_Os07g32480	mitotic checkpoint serine/threonine-protein kinase BUB1	nucleus	1	low	0.235
LOC_Os07g36140	core histone H2A/H2B/H3/H4	nucleus	10	medium	N/A
LOC_Os07g37640	IKI3 family protein	chloroplast	4	medium	0.584
LOC_Os07g43360	MYST-like histone acetyltransferase 1	nucleus	1	low	0.784
LOC_Os08g08040	LSM domain containing protein	cell membrane	1	low	0.578

Table E.1 Predicted partner of transcriptional repressor *(cont.)*

gene ID	annotation	subcellular localization	interolog confidence value	interolog confidence	Pearson correlation coefficient
LOC_Os08g09320	YL1 nuclear protein C-terminal domain containing protein	cytoplasm	6	medium	0.663
LOC_Os08g38570	WD domain, G-beta repeat domain containing protein	cell membrane	4	medium	0.668
LOC_Os08g39140	heat shock protein	cytoplasm	1	low	0.279
LOC_Os08g44770	copper/zinc superoxide dismutase	chloroplast	1	low	0.386
LOC_Os09g01640	CAX-interacting protein 4	nucleus	2	medium	0.828
LOC_Os09g02284	DNA-directed RNA polymerase subunit	nucleus	1	low	0.701
LOC_Os09g19750	expressed protein	mitochondria	1	low	0.584
LOC_Os09g21770	ES43 protein	nucleus	4	medium	0.647
LOC_Os09g38020	Core histone H2A/H2B/H3/H4 domain containing protein	nucleus	4	medium	N/A
LOC_Os10g02630	transposon protein, putative, CACTA, En/Spm sub-class, expressed	cell membrane	2	medium	N/A
LOC_Os10g10990	transcription initiation factor IIF, alpha subunit domain containing protein	mitochondria	1	low	N/A
LOC_Os10g28040	histone acetyltransferase GCN5	nucleus	6	medium	0.675
LOC_Os10g33060	hcr2-5D	chloroplast	1	low	0.059
LOC_Os10g33770	importin-beta N-terminal domain containing protein	nucleus, cytoplasm, cell membrane	8	medium	0.301
LOC_Os10g34750	LIG1 - Putative DNA ligase I	nucleus	1	low	0.601
LOC_Os10g35580	protein ATEB1A-like microtubule associated protein	cell membrane	6	medium	0.176
LOC_Os10g41450	mediator of RNA polymerase II transcription subunit 31	nucleus	1	low	0.607
LOC_Os10g41520	casein kinase II subunit beta-4	nucleus, chloroplast	18	high	0.849
LOC_Os11g03430	CDC45B - Putative DNA replication initiation protein	nucleus	8	medium	0.176
LOC_Os11g34840	MMP37-like protein, mitochondrial precursor	nucleus	1	low	N/A
LOC_Os11g43640	retrotransposon protein, putative, unclassified	nucleus	4	medium	N/A

Table E.1 Predicted partner of transcriptional repressor *(cont.)*

gene ID	annotation	subcellular localization	interolog confidence value	interolog confidence	Pearson correlation coefficient
LOC_Os12g35030	plus-3 domain containing protein	chloroplast	1	Low	0.762
LOC_Os12g38970	VIP4	cytoplasm	1	Low	0.741

2. *In silico* characterization of stress-responsive *cis*-elements in promoter of *transcriptional repressor* from Rice Stress-Responsive Transcription Factor Database (http://www.nipgr.res.in/RiceSRTFDB.html)

Table E.2 *In silico* characterization of stress-responsive *cis*-elements in 2 kb upstream region of *transcriptional repressor*

location	strand	site name	signal sequence	stress response
35	(-)	GT1GMSCAM4	GAAAAA	Pathogen-induced stress | salinity stress
78	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
78	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
151	(-)	WBOXATNPR1	TTGAC	Pathogen-induced stress response
227	(-)	MYB1AT	WAACCA	stress responsive
351	(+)	GT1GMSCAM4	GAAAAA	Pathogen-induced stress | salinity stress
427	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
427	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
446	(+)	WBOXATNPR1	TTGAC	Pathogen-induced stress response
447	(+)	ASF1MOTIFCAMV	TGACG	Abiotic and biotic stress | xenobiotic stress
479	(-)	MYB2AT	TAACTG	drought stress
479	(-)	MYB2CONSENSUSAT	YAACKG	stress responsive
479	(+)	MYBCORE	CNGTTR	drought stress
486	(-)	MYBCORE	CNGTTR	drought stress
489	(-)	MYB2AT	TAACTG	drought stress
489	(-)	MYB2CONSENSUSAT	YAACKG	stress responsive
489	(+)	MYBCORE	CNGTTR	drought stress

'Location' refers to the position upstream to the translation start codon (ATG).
R=A/G, Y=C/T, K=G/T, S=C/G, W=A/T, B=C/G/T, H=A/C/T, V=A/C/G, N=A/C/G/T

Table E.2 *In silico* characterization of stress-responsive *cis*-elements in 2 kb upstream region of *transcriptional repressor (cont.)*

location	strand	site name	signal sequence	stress response
529	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
529	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
582	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
582	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
590	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
590	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
627	(-)	ACGTATERD1	ACGT	drought stress
627	(+)	ACGTATERD1	ACGT	drought stress
673	(+)	DRE2COREZMRAB17	ACCGAC	drought stress | salinity stress | cold stress
673	(+)	DRECRTCOREAT	RCCGAC	drought stress | salinity stress | cold stress | heat stress
733	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
733	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
870	(+)	MYB1AT	WAACCA	stress responsive
904	(-)	ACGTATERD1	ACGT	drought stress
904	(+)	ACGTATERD1	ACGT	drought stress
909	(-)	ABRELATERD1	ACGTG	drought stress
909	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
909	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
910	(+)	ABRELATERD1	ACGTG	drought stress
910	(+)	ACGTABREMOTIFA2OSEM	ACGTGKC	drought stress | salinity stress
910	(-)	ACGTATERD1	ACGT	drought stress

'Location' refers to the position upstream to the translation start codon (ATG).

R=A/G, Y=C/T, K=G/T, S=C/G, W=A/T, B=C/G/T, H=A/C/T, V=A/C/G, N=A/C/G/T

Table E.2 *In silico* characterization of stress-responsive *cis*-elements in 2 kb upstream region of *transcriptional repressor (cont.)*

location	strand	site name	signal sequence	stress response
910	(+)	ACGTATERD1	ACGT	drought stress
1132	(+)	AGCBOXNPGLB	AGCCGCC	salinity stress
1240	(-)	ACGTATERD1	ACGT	drought stress
1240	(+)	ACGTATERD1	ACGT	drought stress
1317	(-)	MYB1AT	WAACCA	stress responsive
1429	(+)	ACGTATERD1	ACGT	drought stress
1429	(-)	ACGTATERD1	ACGT	drought stress
1431	(-)	DRE2COREZMRAB17	ACCGAC	drought stress | salinity stress | cold stress
1431	(-)	DRECRTCOREAT	RCCGAC	drought stress | salinity stress | cold stress | heat stress
1543	(-)	GT1GMSCAM4	GAAAAA	Pathogen-induced stress | salinity stress
1628	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
1628	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
1677	(-)	ASF1MOTIFCAMV	TGACG	Abiotic and biotic stress | xenobiotic stress
1678	(-)	WBOXATNPR1	TTGAC	Pathogen-induced stress response
1708	(+)	ACGTATERD1	ACGT	drought stress
1708	(-)	ACGTATERD1	ACGT	drought stress
1766	(+)	MYB2AT	TAACTG	drought stress
1766	(+)	MYB2CONSENSUSAT	YAACKG	stress responsive
1766	(-)	MYBCORE	CNGTTR	drought stress

'Location' refers to the position upstream to the translation start codon (ATG).
R=A/G, Y=C/T, K=G/T, S=C/G, W=A/T, B=C/G/T, H=A/C/T, V=A/C/G, N=A/C/G/T

Table E.2 *In silico* characterization of stress-responsive *cis*-elements in 2 kb upstream region of *transcriptional repressor (cont.)*

location	strand	site name	signal sequence	stress response
1812	(-)	MYCATERD1	CATGTG	drought stress
1812	(+)	MYCATRD22	CACATG	drought stress
1812	(-)	MYCCONSENSUSAT	CANNTG	abiotic stress
1812	(+)	MYCCONSENSUSAT	CANNTG	abiotic stress
1879	(+)	AGCBOXNPGLB	AGCCGCC	salinity stress
1897	(+)	MYB2CONSENSUSAT	YAACKG	stress responsive
1897	(-)	MYBCORE	CNGTTR	drought stress
1949	(-)	ASF1MOTIFCAMV	TGACG	Abiotic and biotic stress | xenobiotic stress
1950	(-)	WBOXATNPR1	TTGAC	Pathogen-induced stress response

'Location' refers to the position upstream to the translation start codon (ATG).

R=A/G, Y=C/T, K=G/T, S=C/G, W=A/T, B=C/G/T, H=A/C/T, V=A/C/G, N=A/C/G/T

3. *In silico* gene expression analysis of *transcriptional repressor* from Rice Oligonucleotide Array Database (http://www.ricearray.org)

Experiment ID : GSE6901

Experiment title : Expression data for stress treatment in rice seedlings

Overall design : Seven-day-old light-grown rice seedlings grown under controlled conditions and those subjected to various abiotic stress conditions were used for RNA extraction and hybridization on Affymetrix microarrays. Three biological replicates of each sample were used for microarray analysis. For salt treatment (SS), the rice seedlings were transferred to a beaker containing 200 mM NaCl solution for 3 h. For desiccation (DS), rice seedlings were dried for 3 h between folds of tissue paper at 28 °C, in a culture room. For cold treatment (CS), the seedlings were kept at 4 °C for 3 h. The seedlings kept in water for 3 h, at 28 °C, served as control (seedling).

Table E.3 Average expression level of *transcriptional repressor* in GSE6901

probe ID	average expression level			
	seedling_7d	drought	Salt	Cold
Os.6597.1.S1_at	10.8192	12.0525	11.4856	10.9699
Os.6597.2.S1_x_at	6.8677	8.2761	7.9137	7.4722

Experiment ID : GSE24048

Experiment title : Expression data from field droughted rice plants

Overall design : Two rice cultivars, Bala and Azucena, were grown in 1.2 m^2 plots under flooded conditions in Wuhan, China being sown on 2nd June 2007. Starting at 59 days after sowing, drought was imposed by withholding water, while a set of control plots had continued flooding conditions. At 2 pm on the 83^{rd} day after sowing (after 24 days of drought) the second youngest fully expanded leaf was taken off three plants in two plots per block, the leaves had the top and bottom 4 cm removed and the central portion of the leaf was placed in a bag and then into liquid N_2. For the controls there was only one plot of the genotypes per block. There was one bag for each block and three replicate blocks. A total of 6 droughted leaf samples (3 Bala and 3 Azucena) and six control leaf samples (3 Bala and 3 Azucena) were collected for RNA extraction and hybridization on Affymetrix microarrays.

Table E.4 Average expression level of *transcriptional repressor* in GSE24048

probe ID	average expression level			
	Control Azucena	control Bala	droughted Azucena	droughted Bala
Os.6597.1.S1_at	10.0808	10.5762	10.6141	10.8179
Os.6597.2.S1_x_at	4.9859	5.9418	5.6612	6.5479

Experiment ID : E-MEXP-2401

Experiment title : Transcription profiling of *Oryza sativa* subtypes Cultivar Nagina-22 (N22) and IR64 subtypes under normal and drought conditions

Overall design : Comparative analysis of Drought responsive transcriptome between Indica rice genotypes with contrasting drought tolerance. High quality RNA was extracted from the whole seedlings (Combined root and leaf samples) using TRI Reagent (Ambion, Inc. USA) and pooled from 12 independent stressed and non-stressed plant samples separately, and treated with DNase-I (QIAGEN GmbH, Germany). Subsequently, RNA cleanup was carried out using RNeasy Plant Mini Kit (QIAGEN GmbH, Germany) and 5 ug of total RNA from each sample in triplicates were reverse-transcribed to double stranded cDNA using the GeneChip One-Cycle cDNA Synthesis Kit. The biotin-labelled cRNA was made using the GeneChip IVT Labelling Kit (Affymetrix, CA, USA). Twenty microgram of cRNA samples was fragmented and out of which which 7.5 ug cRNA were hybridized for 16 hours at 45 °C to the Affymetrix GeneChip Rice Genome Array (Santa Clara, CA, USA). After washing and staining with R-phycoerythrin streptavidin in a Fluidics Station, using the Genechip Fluidics Station 450, the arrays were scanned by the Genechip 3000 Scanner. The chip images were scanned and extracted using default settings and the CEL files were produced with the Affymetrix GeneChip Operating Software (GCOS 1.2). The resulting .CEL files were imported into the GeneSpring GX 10 (Agilent Technologies Inc, Santa Clara CA) and normalized with the PLIER16 algorithm. The resulting expression values were log2-transformed. Average log signal intensity values of three technical replicates for each sample were used for advance analysis.

Table E.5 Average expression level of *transcriptional repressor* in E-MEXP-2401

probe ID	average expression			
	IR64_control	IR64_drought	N22_control	N22_drought
Os.6597.1.S1_at	11.5700	11.7144	11.701	12.0297
Os.6597.2.S1_x_at	8.0244	8.2276	8.2685	8.1317

Experiment ID : GSE26280

Experiment title : Genome-wide temporal-spatial gene expression profiling of drought responsiveness in rice

Overall design : The gene expression patterns across six tissues including leaves and roots at tillering stage and panicle elongation stage, leaves and young panicle at booting stage (TL: leaves at tillering stage; TR: roots at tillering stage; PL: leaves at panicle elongation stage; PR: roots at panicle elongation stage; BP: young panicle at booting stage; BL: leaves at booting stage) were characterized by using the Affymetrix rice microarray platform based on a drought tolerant rice line derived from IR64.

Table E.6 Average expression level of *transcriptional repressor* in GSE26280*

probe ID	normal leaves tillering	drought leaves tillering	normal leaves panicle elongation	drought leaves panicle elongation
Os.6597.1.s1_at	10.5673	11.4656	10.6073	12.1902
Os.6597.2.s1_x_at	6.2366	5.4836	6.6876	8.0533

* Only the expression level of *transcriptional repressor* in leaves at tillering and panicle elongation stages under normal and drought stress condition are shown.

4. Comparison of protein sequences of *transcriptional repressor* in rice and *sin3-like* in Arabidopsis

```
AT3G01320.1           MKRIRDDVYASGSQFRRPLGSSRGQLCGQSPVHGSGD-TEEEEGGSRRVSQKLTTNDAL
AT5G15020.1           MKRIRDDIYATGSQFKRPLGSSRGESYEQSPITGGGS-IGE-----GGINTQKLTTDDAL
AT1G10450.1           MKRAREDVHTDTQKRKPEV-------------SSRGETNKLPR------------TIDAL
AT1G59890.2           MKRVREEVYVEPQMRGPTV-------------SSRGETNGRPSTISGGGTTGGLTTVDAL
AT1G24190.1           --------------------------------------------MVGGGSAQKLTTNDAL
AT1G70060.1           --------------------------------------------MVGGSSAQKLTTNDAL
LOC_Os01g01960.1      ------------------------------------------------------------
LOC_Os05g01020.2      MKAAPT---ASQHLKRPNLARSD-----PSPMPAPAPAPAPSQQGQGPSQNQKLTTNDAL

AT3G01320.1           SYLREVKEMFQDQREKYDRFLEVMKDFKAQRTDTGGVIARVKELFKGHNNLIYGFNTFLP
AT5G15020.1           TYLKEVKEMFQDQRDKYDMFLEVMKDFKAQKTDTSGVISRVKELFKGHNNLIFGFNTFLP
AT1G10450.1           TYLKAVKDIFHDNKEKYESFLELMKEFKAQTIDTNGVIERIKVLFKGYRDLLLGFNTFLP
AT1G59890.2           TYLKAVKDMFQDNKEKYETFLGVMKDFKAQRVDTNGVIARVKDLFKGYDDLLLGFNTFLP
AT1G24190.1           AYLKAVKDKFQDQRGKYDEFLEVMKNFKSQRVDTAGVITRVKELFKGHQELILGFNTFLP
AT1G70060.1           AYLKAVKDKFQDKRDKYDEFLEVMKDFKAQRVDTTGVILRVKELFKGNRELILGFNTFLP
LOC_Os01g01960.1      -----------------------MRDFKSERIDTNGVIIRVKTLFNGYPELILGFNTFLP
LOC_Os05g01020.2      LYLKAVKDKFQDKRDKYDEFLEVMRDFKSGRIDTAGVIIRVKTLFNGHHELILGFNAFLP
                                             *::**:   ** *** *:* **:*  :*: ***:***

AT3G01320.1           KGYEITLIEEDDAL--PKKTVEFEQAINFVNKIKMRFKHDEHVYKSFLEILNMYRKENKE
AT5G15020.1           KGFEITLDD-VEAP--SKKTVEFEEAISFVNKIKTRFQHNELVYKSFLEILNMYRKDNKD
AT1G10450.1           KGYKITLLPEEEKP---KIRVDFKDAIGFVTKIKTRFGDDEHAYKRFLDILNLYRKEKKS
AT1G59890.2           KGYKITLQPEDEKP---KKPVDFQVAIEFVNRIKARFGGDDRAYKKFLDILNMYRKETKS
AT1G24190.1           KGFEITLQPEDGQPPL-KKRVEFEEAISFVNKIKTRFQGDDRVYKSFLDILNMYRRDSKS
AT1G70060.1           KGFEITLRPEDDQPAAPKKPVEFEEAISFVNKIKTRFQGDDRVYKSFLDILNMYRKENKS
LOC_Os01g01960.1      KGYAIKLQE-------EKKPVDFVEAINFVNKIKNRFQHDEHVYKAFLDILNMYRKDNKS
LOC_Os05g01020.2      KGFAIKLQD------LEKKPVDFMEAINFVNKIKARFQQEDHVYKSFLGILNMYRLHNKS
                      **: *.*          *  *:*  ** **.:** **  :: .** ** ***:** ..*.

AT3G01320.1           IKEVYNEVSILFQGHLDLLEQFTRFLPASLPSHSAAQHSRSQAQQYSDRG-SDPPLLHQM
AT5G15020.1           ITEVYNEVSTLFEDHSDLLEEFTRFLPDSLAPHTEAQLLRSQAQRYDDRG-SGPPLVRRM
AT1G10450.1           ISEVYEEVTMLFKGHEDLLMEFVNFLPNCPESAPS-----TKNAVPRHKG-TATTAMHSD
AT1G59890.2           INEVYQEVTLLFQDHEDLLGEFVHFLPDFRGSVSVNDPLFQRNTIPRDRN-STFPGMHPK
AT1G24190.1           ITEVYQEVAILFRDHSDLLVEFTHFLPDTSATASIP-S---VKTSVRERGVS--------
AT1G70060.1           ITEVYHEVAILFRDHHDLLGEFTHFLPDTSATASTNDS---VKVPVRDRGIKSLPTMRQI
LOC_Os01g01960.1      IQDVYHEVAVLFADHKDLLEEFQHFLPDTSVPPQAVAPSRP-GIRRDDRT-SLVPPASRN
LOC_Os05g01020.2      IQDVYGEVAALFRDYPDLLEEFKHFLPDTSTAPEPVTVPRGVSSRHDDRG-PLMPSARNA
                      * :** **: **  : *** :* .***                    .:

AT3G01320.1           QVEKERRRERAVALRGD--YSVERYDLNDDKTMVKIQREQRKRLDKENRARRGRDLDDRE
AT5G15020.1           FMEKDRRRERTVASRGDRDHSVDRSDLNDDKSMVKMHRDQRKRVDKDNRERRSRDLEDGE
AT1G10450.1           K-----K-------------------------------------------RKQRCKLE--
AT1G59890.2           H---FEK-------------------------------------------KIKRSRHD--
AT1G24190.1           L---ADKKDRIITPHPDHDYGTEHIDQDRERPIKKENKEHMRGTNKENEHR------DAR
AT1G70060.1           D---LDKKDRIITSHPNRALKTENMDVDHERSLLKDSKEEVRRIDKKNDFMDDRDRKDYR
LOC_Os01g01960.1      E-----KRDKAHPHA--DRESVDRPDLD--------HVIQR---------RRPKDRHDYD
LOC_Os05g01020.2      Q---IIKRERAYPSTVDRDFSIDRPDPE--------DDPHRRRVDKGRDGKVDRSRKDYE
                            :                                                  :

AT3G01320.1           -------AGQDNLHHFPEKRKSSRRAEALEA--------------YSGSAS-HSEKDNLK
AT5G15020.1           -------AEQDNLQHFSEKRKSSRRMEGFEA--------------YSGPAS-HSEKNNLK
AT1G10450.1           ---------------------------DYSGHSDQREDGDENLVTCSADSP-VG-EGQ--
AT1G59890.2           ---------------------------EYTELSDQREDGDENLVAYSAGNS-LG-KSLAN
AT1G24190.1           D----FEPHSKKEQFLNKKQKLHIRGDDPAEISNQ-----SKLSGAVPSSSTYDEKGAMK
AT1G70060.1           G----LDHDSHKEHFFNSKKKLIRKDDDSAEMSDQ-AREGDKFSGAIPSSSTYDEKGH--
LOC_Os01g01960.1      RGDKDGELDSKDLDIGLKRKPFPRKMEDPTSADAHHGGPLENHGILGASASLYDNKDALK
LOC_Os05g01020.2      TDVKDVEYDSKDLDGGQRKRKLARKMDGALADT--------QQGGVSTSTSPYDDKDALK
                                                                           :
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AT3G01320.1                SMYKQAFVFCEKVKDRLCSQDDYQTFLKCLNIFSNGIIQRKDLQNLVSDLLGKFPDLMDE
AT5G15020.1                SMYNQAFLFCEKVKERLCSQDDYQAFLKCLNMFSNGIIQRKDLQNLVSDVLGKFPDLMDE
AT1G10450.1                --------------------------------------------------PGYFRDYEN-
AT1G59890.2                --------------------------------------------------QGQWPGYPK-
AT1G24190.1                -SYSQDLAIVDRVKEKLN-ASEYQEFLRCLNLFSKEIISRPELQSLVGNLIGVYPDLMDS
AT1G70060.1                ---SQELAFVDRVKAKLD-TADNQEFLRCLNLYSKEIISQPELQSLVSDLIGVYPDLMDA
LOC_Os01g01960.1           SVYTQEFHFCEKVKEKLE-HDAYQEFLKCLHIYSQEIITRSELKNLVNDILQQHPDLMDG
LOC_Os05g01020.2           SAYTKEFRFCEKVKEKLE-PEAYQEFLKCLHIYSQEIITRSELKNLVNDILQHYPDLMNG
                                                                                     .

AT3G01320.1                FNQFFERCESITDGFQRLAGVMSKKLF----SSEEQLSRPMKVEEKES--EHKPE--LE-
AT5G15020.1                FNQFFERCESI-DGFQHLAGVMSKKSL----GSEENLSRSVKGEEKDR--EHKRD--VE-
AT1G10450.1                -------REDT-ETD------------TADRTEK--SA---------AS----GS-----
AT1G59890.2                -------VEDT-EGI------------QIYES-N--GG---------HE----RD-----
AT1G24190.1                FIEFLVQCEKN-EGL--LSGILTKSKSTYLLQGEGKYPQP--SLDNDRDQEHKRD---DG
AT1G70060.1                FKVFLAQCDKN-DGL--LSGIVSKKS----LWSEGKCPQPTKSLDKDTDREREKI---ER
LOC_Os01g01960.1           FNEFLEHCENI-DGF--LAGVFSKRQTGRIVKTEERKEG-----GKGTEKEPDRIEKVPA
LOC_Os05g01020.2           FNDFLEQCENI-DAF--LEGVFSKRKTSQIVKIVEKGSA-----LNSKE-----------
                                   :.  :

AT3G01320.1                ---AVKE----TEQCKKEYMGKSIQELDLSDCECCTPSYRLLPADYPIPIASQRSELGAE
AT5G15020.1                ---AAKE----KERSKDKYMGKSIQELDLSDCERCTPSYRLLPPDYPIPSVRHRQKSGAA
AT1G10450.1                -QDIGNH----K--STTKYVGTPINELDLSECTQCTPSYRLLPKDYAVEIPSYRNTLGKK
AT1G59890.2                -PDIGSQ----KNLLSTNHMAKAINELDLTDCAQCTPSYRRLPDDYPIQIPSYRNSLGEK
AT1G24190.1                LRDRDHEKERLEKAAANLKWAKPISELDLSNCEQCTPSYRLLPKNYPISIASQKTEIGKL
AT1G70060.1                YRERDREKERLEKVAASQKWAKPISELDLSNCEQCTPSYRRLPKNYPIPIASQKMEIGSQ
LOC_Os01g01960.1           YKEAPSQKPV-FSSKEKY-IYKPVSELDLSNCQRCTPSYRLLPKHYPMPPAGNKTELGAS
LOC_Os05g01020.2           --GATHKATT-FSSKDKYNLCKPISELDLSNCQRCTPSYRLLPKNYPMPPASCRTDLGAS
                                 .              . :.****::*  ****** ** .* :     :   *

AT3G01320.1                VLNDHWVSVTSGSEDYSFKHMRRNQYEESLFRCEDDRFELDMLLESVSSAARSAESLLNI
AT5G15020.1                VLNDHWVSVTSGSEDYSFKHMRRNQYEESLFRCEDDRFELDMLLESVGSAAKSAEELLNI
AT1G10450.1                TLNDHLVSVTSGSEDYSFSHMRKNQYEESLFRCEDDRYEMDMLLGSVSSAIKQVEILLEK
AT1G59890.2                VLNDHWVSVTSGSEDYSFKHMRKNQYEESLFRCEDDRFELDMLLESVSAAIKRVESLLEK
AT1G24190.1                VLNDHWVSVTSGSEDYSFSHMRKNQYEESLFKCEDDRFELDMLLESVNSTTKHVEELLTK
AT1G70060.1                VLNDHWVSVTSGSEDYSFKHMRKNQYEESLFKCEDDRFELDMLLESVISATNRVEELLAK
LOC_Os01g01960.1           VLNDHWVSVTSGSEDYSFKHMRKNQYEESLFRCEDDRFELDMLLESVNAATKRVEELIEK
LOC_Os05g01020.2           VLNDLWVSVTSGSEDYSFKHMRKNQYEESLFRCEDDRFELDMLLESVIVAIKRVEELIEK
                           .***  ************.***:********:*****:*:**** **  : . .* *:

AT3G01320.1                ITEKKISFSGSFRIEDHFTALNLRCIERLYGDHGLDVIDILNKNPATALPVILTRLKQKQ
AT5G15020.1                IIDKKISFEGSFRIEDHFTALNLRCIERLYGDHGLDVTDLIRKNPAAALPVILTRLKQKQ
AT1G10450.1                MNNNTISVDSTICIEKHLSAMNLRCIERLYGDNGLDVMDLLKKNMHSALPVILTRLKQKQ
AT1G59890.2                INNNTISIETPICIREHLSELNLRCIERLYGDYGLDVMDFLKKNSHIALPVILTRLKQKQ
AT1G24190.1                INSNELKTNSPIRVEDHLTALNLRCIERLYGDHGLDVMDVLKKNVSLALPVILTRLKQKQ
AT1G70060.1                INSNELKTDTPICIEDHLTALNLRCIERLYSDHGLDVLDLLKKNAYLALPVILTRLKQKQ
LOC_Os01g01960.1           MQDNSLKPDSPIRIDEHLTPLNLRCIERLYGDHGLDVMDVLRKNASVALPVILTRLKQKQ
LOC_Os05g01020.2           MQDNSIKPDSPIRIDEHLTPLNLRCIERLYGDHGLDVMDVLRKNASVALPVILTRLKQKQ
                           : .: :. .  : : .*:: :*********.* **** *::.**   *************

AT3G01320.1                GEWKKCRDDFDKVWANVYAKNHYKSLDHRSFYFKQQDSKNLSAKSLLAEIKELKEKSQND
AT5G15020.1                DEWTKCREGFNVVWADVYAKNHYKSLDHRSFYFKQQDSKNLSAKALVSEVKDLKEKSQKE
AT1G10450.1                EEWARCHSDFQKVWAEVYAKNHHKSLDHRSFYFKQQDSKNLSTKCLVAEVKDISEKKHQ-
AT1G59890.2                EEWARCRADFRKVWAEVYAKNHHKSLDHRSFYFKQQDSKNLSTKGLVAEIKDISERKHK-
AT1G24190.1                EEWARCRSDFDKVWAEIYAKNYYKSLDHRSFYFKQQDSKKLSMKALLAEIKEITEKKR-E
AT1G70060.1                EEWARCRTEFNKVWADIYTKNYHRSLDHRSFYFKQQDSKNLSTKALLAEIKEISEKKRGE
LOC_Os01g01960.1           EEWSRCRSDFNKVWAEIYAKNYHKSLDHRSFYFKQQDTKNLSTKSLLTEIKEINEKKRKE
LOC_Os05g01020.2           EEWSRCRSDFNKVWAEIYAKNYHKSLDHRSFYFKQQDTKNLSTKALLAAIKEVNEKKRKE
                            ** :*:  *  ***::*:**:::*************:*:** * *:: :*::.*:.:

AT3G01320.1                DDVLLSISAGYRQPINPNLEYEYLNRAIHEDMFKVVQFSCEELCSTKEQLSKVLRLWENF
AT5G15020.1                DDVVLSISAGYRQPIIPHLEYDYLDRAIHEDLFKLVQFSCEEICSTKEQTGKVLKLWANF
AT1G10450.1                EDLLQAIAVRVMPLFTPDLEFNYCDTQIHEDLYLLIKYYCEEICAT-EQSDKVMKLWITF
AT1G59890.2                EDLLRAIAVGTKPSFTPDVEFIYTDTKVHTDLYKLIKYYCEEICAT-EQSDKVMKLWVTF
AT1G24190.1                DDSLLAFAAGNRLSISPDLEFDYPDHDLHEDLYQLIKYSCAEMCST-EQLDKVMKIWTTF
AT1G70060.1                DDALLALAAGNRRTISSNMSFDYPDPDLHEDLYQLIKYSCGEMCST-EQLDKVMKVWTEF
LOC_Os01g01960.1           DDVLLAIAAGNRRPIVPNMSFDYVDSNIHEDMYKIIKYSCGEVCSSSDQLDKVVRIWTTF
LOC_Os05g01020.2           DDMLLTIASGNRRPIVPNMSFEYVDPEIHEDLYQIIKYSCGEVCSSSDQVDKVMKIWATF
                           :* : :::      :  .:.: * :  :* *:: :::: * *:*:: :*  **:::*  *
```

```
AT3G01320.1           LEAVLGVPPRAKGTDLVEDVVINPKTLDVNHSTSPNGEAAVSSGGDTARLASRKLK----
AT5G15020.1           LELMLDVAPRAKGSDSVEDVVETQHQRAFT-----SGE--ANESSDAISLVSRQLK----
AT1G10450.1           LEPIFGILSRSQDNLALEDVSKLKNNRELQDA-CLAVKETASGSN---RK---HPISP-K
AT1G59890.2           LEPMFGVPSRSETIETMKDVAKIEDNQEHHDA-SEAVKENTCDGSMASNL---KPLTPPK
AT1G24190.1           VEQIFGVPSRPQGAEDQEDVVKSMNQNVKSGS-SSAGESEGSPHNYASVADSRRSK-SSR
AT1G70060.1           LEPIFGVPSRPQGAEDREDAVKSTNHDREDQ------EDAVSPQNGASIANSMRSN-GPR
LOC_Os01g01960.1      LEPILGVQPRTHGAEDADAVKP-KSRTTKSGL-ATVGEINTTAAGA--VAKHGHDENIPQ
LOC_Os05g01020.2      LEPILGVHPRGHGVEDEKH----NSRSTKAGP-ANVEINNASTNGTVTVKHAHSDEIVPK
                      :* :: :  * .     .

AT3G01320.1           -SAANGDENSSSGTFKHG-IGLLNKDSTGKENLEDVEIANRDGVACSAVKPQKEQETGN-
AT5G15020.1           -FATNGDVHASSGVSKHGETGLLNRDSSGKENLKDGDLANKDVATCA-EKPQKDQEIGN-
AT1G10450.1           RLSKDN-----------------------------------------------TKM----
AT1G59890.2           MPNKEN-----------------------------------------------PMI----
AT1G24190.1           KANEHSQLGQTSNSERDGAAGRT----------------SDA--LCETAQHEK-ML----
AT1G70060.1           KVNESNQVRQASELDKDVTSSKT----------------SDALLSCDNTQNDK-MP----
LOC_Os01g01960.1      EQTPSSLARMVNGVATDTQNGFH----------------DVDRTARRAEEPSNTAVNGRV
LOC_Os05g01020.2      EQASCSRAILVGGVAADAQNSLQ----------------DAERTVCRDEERPKTMLDRRL


AT3G01320.1           --------EAEKRFGKPIPMDISERAAISSISIPSGAENNHCVVGKEVLPGAHEIQAKPS
AT5G15020.1           --------GAAKRSG-----DVDERVATSSSSFPSGVENNNGKVGSRDSSGSRGILSKPS
AT1G10450.1           QGSSSR---------EDVSAN--IKVKTAQ---PDKLQD---------DAAMTNEV----
AT1G59890.2           QGSSFA---------QDLPVN--TG-ESIQ---QDKLHD---------VAAITNED----
AT1G24190.1           KNV-VTSDE-KPESKQAVSIE--RAHDSTALAVDGLLDQSNGGSSIVHMTGHCNNN----
AT1G70060.1           KNL-TTPDE-RAETKQAVSIE--RAHNSNALPLDGLLPQRNGKISSLSVAGLSNSN----
LOC_Os01g01960.1      QGASPGTNEIPAVSTQNMPTE--RSAENIPVARTE--QHGNAKANLEPTSGVNASRSSHA
LOC_Os05g01020.2      QNTTPAVDVVPAVYAQNISTE--RSVESSHLSRPE--QN-HSRANMEVKPGINACSATPA
                                          :                 .           .

AT3G01320.1           DTLTDIHHDVDSIETVHSTQG--------------GDVGNSIVLANGLRSDSSKGTRNSD
AT5G15020.1           EAI-------DKVDSIQHTQG--------------VDIGRIIVLGNGLQSDTSKANSNYD
AT1G10450.1           ------------------------IQSSK----FVSP-KNDQIMEDEGN----HMV-NA
AT1G59890.2           ------------------------SQPSK----LVST-RNDLIMEGVEN----RSRVSD
AT1G24190.1           --------------LKPVTCGTELELKMNDGNGPKLEVGNKKLLTNGIAV----EITSDQ
AT1G70060.1           --------------PKPALTSGTEELKPNYVNGPRVEIGDNPVIPNGTVA----E-----
LOC_Os01g01960.1      GNDTA-AEARAGNETLPSVEGGETGRSGSTLNGGGASEGNKGRL-----------FNEAS
LOC_Os05g01020.2      GGEVV-SEAKGGNEAIMG-------SGEIRIPGSFNSKDNKHCP-----------INEYC
                                                          .                  .

AT3G01320.1           DPEGPSRNEKEEGELSPNGDFE-DNFGVYKDHGVKSTSKPENSA----------------
AT5G15020.1           ESGGPSKIEKEEGELSPVGDSE-DNFVVYEDRELKATAKTEHSV----------------
AT1G10450.1           A--SVEKHELEEGELSPTASREQSNFEVNGQNAFKPLQKVTDNVRSNKDKQS-------C
AT1G59890.2           VSMGGHKVEREEGELSPTESCEQENFEVYKENGLEPVQKLPDNEISNTDREP---KEGAC
AT1G24190.1           EMAGTSKVEREEGELSPNGDFEEDNFAVYAKTDFETFSKANDSTGNNISGDRSREGEPSC
AT1G70060.1           WFAGEAKVEREEGELSPTGDFEEDNYAVHGENDMEALSKSKENDA---------------
LOC_Os01g01960.1      ASHNTPKVEREEGELSPNGDFEEDNFAPFEDGAVDGVSKAKEGSTSRPFQGRSGEAQPSC
LOC_Os05g01020.2      GSHNHSKVEREEGELSPNGDVG-ENFGPFDGVSVDGVSKAKEDSTRRLLQGRPMDA----
                            : * *******  .   .*:       ..   *  .

AT3G01320.1           --EAEVEADAEVENED--------DADDVDSENASEASGTESGGDV-CSQD-EDREEENG
AT5G15020.1           --EAEGENDEDADDED----------GDDASEAGEDASGTESIGDE-CSQD-DNGVEEEG
AT1G10450.1           DKKGA-KNKTRAEDDKQENCHKLSENNKTASEM--LVSGTKVSCHEENNRV---------
AT1G59890.2           GTEAVTRSNALPEDDDNKITQKLSEGDENASKF--IVSASKFGGQVSSDEE---------
AT1G24190.1           L-ETRAENDAE----GDENAARSSEDSRNEYENG-DVSGTESGGGEDPE--DDLDN----
AT1G70060.1           ---------TA----DDASAPRSSDGSGNTSHNG-DVSGTDSGDGEDCYREDDIDH----
LOC_Os01g01960.1      A-EAAGENDADADDEGEESAQRSTEDSENASEGGEDASGSESGDGEECSREDHDEEEEDM
LOC_Os05g01020.2      T-EFAGENDVDADDEGEESAQM-MEDSENASEAGEDASGSESGDGEECSREDHED-EDDM
                                                     .    .*.:.

AT3G01320.1           EHDEIDGKAESEGEAEGMDPHLL---EGESELLPQSERVLLSVRPLSKHVAA-VLCDE--
AT5G15020.1           EHDEIDGKAESEGEAEGMESHLI---ED-KGLFPSSERVLLSVKPLSKHIAAAALVDE--
AT1G10450.1           ------MNCNGRGSVAGEMANGNQ--GEDGS-FAFSERFLQTVKPVAKHLSWPLQASE--
AT1G59890.2           ------HKGAESENEAGGMVNSNE--GEDGSFFTFSERYLQPVKPLAKHVPGTLQASE--
AT1G24190.1           -----NNKGESEGEA-ECMADAHDA-EENGSALPVSARFLLHVKPLVKYVPSAIALHDKD
AT1G70060.1           -----N-KVESEGEAEEGMSDGHDDTEGDMPVLSISVKNLLHVKPLAKYVPPALYDKD-N
LOC_Os01g01960.1      DHDDQDAKAESEGEAEGT-TETHD--VEGGISLPLSERFLHSVKPLAKHVPTALHDRD--
LOC_Os05g01020.2      DQDDPDAKAESEGEAAEN-TEAQD--ADAGISLPFSERSHNAVKPLAKHVPRALNDHE--
                             :     .      .           :  * :    *:*: *::       :
```

```
AT3G01320.1           --RTKDLQVFYGNDDFYVLFRLHQ------------ILYERILYAKRNCSGGELKSKNLK
AT5G15020.1           --KKKDSRVFYGNDDFYVLFRLHRVSAIDSYDLLSHILYERILSAKTYCSGSEMKLRNTK
AT1G10450.1           TCSQNDSQVFYGNDSYYVLFRLHQ------------MLYERIQTAKKHS---EKKWKAAD
AT1G59890.2           CDTRNDSRVFYGNDSLYVLFRLHQ------------MLYERIQSAKIHS---ERKWKAPD
AT1G24190.1           KDSLKNSQVFYGNDSFYVLFRLHR------------ILYERILSAKVNSSSPEGKWRTSN
AT1G70060.1           DDSRKNSQVFYGNDSFYVLFRLHQ------------ILYDRILSAKINSSSPDRKWKTSN
LOC_Os01g01960.1      ---EKSSRIFYGNDSFYVLFRLHQ------------ILYERLLSAKTNSSSAEKKWRTSK
LOC_Os05g01020.2      ---EKFSCIFYGNDSFYVLFRLHQ------------ILYERILSAKTNSSSAEKKWKASK
                          :   :*****. *******:            :**:*:  **  .   : * :  .

AT3G01320.1           DTNAGDPYARFMRVLYGLLDGSAENTKFEDECRAIIGNQSYVLFTLDKLIYRLVKQLQAI
AT5G15020.1           DTCSPDPYARFMNALFSLLNGSAENSKFEDECRAIIGNQSYVLFTLEKLIYKLVKQLQAV
AT1G10450.1           NT-TPDSYPRFMDALYNLLDGSIDNTKFEDECRAIFGAQSYVLFTLDKLVQKFVKHLHSV
AT1G59890.2           ST-STDSYTRFMEALYNLLDGSSDNTKFEDECRAIIGAQSYVLFTLDKLVQKFVKHLHAV
AT1G24190.1           TKNPTDSYARFMTALYNLLDGTSDNAKFEDDCRAIIGTQSYILFTLDKLIHKFIKHLQVV
AT1G70060.1           PTNPADSYARIMDALYNLLDGTSDNSKFEDDCRAIIGTQSYVLFTLDKLIYKLIKHLQAV
LOC_Os01g01960.1      DTNPPDLYAKFISALYNLLDGSSDNTKFEDDCRSIIGTQSYVLFTLDKLIYKVVKQLQAI
LOC_Os05g01020.2      DTNLPDQYSKFMSALYNLLDGSSDNTKFEDDCRSIIGTQSYVLFTLDKLIYKVVKQLQAI
                       .   * * ::: .*: **:*: :*.****:**.*:* ***:****:**: :.:*:*:.:

AT3G01320.1           VADEMDNKLLQLYEYEKSRKPGRVIDSVYYENVRVLVHEENIYRLECS-SLPSRLSIQLM
AT5G15020.1           VADDMDNKLLQLYEYENSRRPGRVFDSVYYENARILLHEENIYRLECS-SSPSRLSIQLM
AT1G10450.1           ASDETDTKLLQLHAYENYRKPGKFFDLVYHENACALLHEANIYRIRYS-SEGTRLSIQLM
AT1G59890.2           AADETDTKLLQLYAYENYRKPGRFFDIVYHENARALLHDQNIYRIEYS-SAQTRLGIQLM
AT1G24190.1           VADEMDNKLLQLYFYEKSRRPETIFDAVYYDNTRVLLPDENIYRIECRLSTPAKLSIQLM
AT1G70060.1           AADEMDNKLQQLYAYEKSRKPEKFLDAVYYENALVLLPDEDIYRIECEQSTPSKLSIQLL
LOC_Os01g01960.1      ATDEMDNKLLQLYLYEKSRSPGRFFDLVYHENARVLLHEESIYRFECC-SNPTKLSIQLM
LOC_Os05g01020.2      ASDEMDNKLLQLYIYEKSRSPGRFFDLVYHENARVLLHDESIYRFERR-SNPTRLSIQLM
                      .:*: *.** **: **: * *  .:* **::*.  *: : .***:.   *  ::*.***:

AT3G01320.1           DNIIEKPEAYAVSMDPTFASYMQTELLSVSSGKKEEGHDIVLQRNLTGL------Y--DL
AT5G15020.1           DNIIEKPDAYAVSMEPTFTSYLQNEFLSNSSGKKE-LQDIVLQRNMRGYNGLDDLA--VA
AT1G10450.1           NSGNNQLEVMGVAMEPAFADYLQNKCLKSVND-EE-NHGLFLNRNKKKFTSL-DESR-GM
AT1G59890.2           NSWNDQPEVTAVTVEPGFANYLQNDFLSFVSD-EE-KPGLFLKRNKAKLSGPGEESL-GM
AT1G24190.1           CNGLDKPDVTSVSIDPTFAAYLHNDFLSIQPNARE-DRRIYLNRNKRKVCREDEQ-----
AT1G70060.1           DYGHDKPDVTSISMDPTFAAYLHNVFLSYQPNAKE-NPRIYLKRNKRKNGG-DDE-----
LOC_Os01g01960.1      EYGHEKPEVTAVSIDPNFSSYLFNEYLSSMSDRKL-SEGVFLERNKRKHSNNDEPS--DS
LOC_Os05g01020.2      EYGHEKPEVTAVSIDPNFSSYLYNEYLSSISNTKL-YDDIFLGRYFPDLMLESQFYFPRL
                          :: :. .::::* *: *: .  *.     .     : * *

AT3G01320.1           CKAMEGVEVVNGLECKMSCSSYKIAYVLDTEDYFHRKKKKKKTEQLW-----------Q
AT5G15020.1           CKAMEGVQVINGLECKMSCSSYKISYVLDTEDFFHRKKKQKKSNNLS----------LAK
AT1G10450.1           PVAMERLNIINEMECRMACSSSKVKYVANTSDLLYRSKQGKPN-----------SRVSEI
AT1G59890.2           SRALEGLNIINEVECKIACSSFKVKYEPHTADLLYRRKQKKATLNPTGPENVKTSDSSEL
AT1G24190.1           LYSTDEVKIKNGLECKIACGSSKVSYVLETEDLLVRVKKRRKTLC------H---NQDSW
AT1G70060.1           LCTTDEVKIINGLECKITCSSSKVSYVLDTEDVLHRAKRRKLLNQSGLPLAHDSVCSGSL
LOC_Os01g01960.1      LKAMDGVKVANGLECKISCKTSKVSYVLDTEDFLFRLRKRRRFSPVGNVPEKL---QASK
LOC_Os05g01020.2      FSLLDIISQE--------------------------------------------------
                          : :.

AT3G01320.1           RNKVRVERFHRFLSA-------
AT5G15020.1           LSQNRIARFHKFLSASR-----
AT1G10450.1           LKQRRISRFHIMLNCRLCALPL
AT1G59890.2           SRKKRISRFHMSLNRRLVALP-
AT1G24190.1           VRQMRLQYYKNNFL--------
AT1G70060.1           IRQRRTQRYQKLLTGQ------
LOC_Os01g01960.1      TYAAKVQRFHRFLSKP------
LOC_Os05g01020.2      ----------------------
```

Figure E.1 Multiple sequence alignment of protein sequences of *transcriptional repressor* in rice and *sin3-like* in Arabidopsis performed by CLUSTAL Omega program; AT3G01320.1: *sin3-like 1*; AT5G15020.1: *sin3-like 2*; AT1G10450.1: *sin3-like 6*; AT1G59890.2: *sin3-like 5*; AT1G24190.1: *sin3-like 3*; AT1G70060.1: *sin3-like 4*; LOC_Os01g01960.1: *transcriptional repressor* and LOC_Os05g01020.2: *transcriptional repressor*. The protein sequences were obtained from The Arabidopsis Information Resource (TAIR) and Rice Genome Annotation Project (RGAP).

VITA

Miss Maiporn Maipoka was born on October 8, 1987 in Surat Thani Province, Thailand. After finishing high school from Suratpittaya school in 2006, she enrolled for Bachelor's degree in Science (Biology) at the Department of Biology, Faculty of Science, Prince of Songkla University and graduated with first class honors in 2010. She continued her study in Master degree in Science (Botany) at the Department of Botany, Faculty of Science, Chulalongkorn University. Miss Maiporn Maipoka has been financially supported for study by Development and Promotion of Science and Technology Talent Project (DPST) since 2006. In 2013, she got a scholarship from DPST to do research at Plant Growth Laboratory, Department of Biology, University of Washington, Seattle, Washington, US.

Proceeding and Poster Presentation

Maipoka, M., Pongprayoon, W., Chintakovid, N., Roytrakul S., Pichayangkura, R., and Chadchawan, S. (2012). Comparison of chitosan induced protein patterns in 'Leung Pratew123' rice (Oryza sativa L. cv Leung Pratew123) and its drought resistant mutant lines, Leung Pratew123-TC171 during drought Stress. In The 13th FAOBMB International Congress of Biochemistry and Molecular Biology "Discovery of Life Processes: From Biomolecules to Systems Biology", Bangkok, Thailand.

Oral Presentations

Maipoka, M., Pongprayoon, W., Chintakovid, N., Roytrakul S., Pichayangkura, R., and Chadchawan, S. (2012). Analysis of chitosan-responsive proteins in 'Leung Pratew123' rice leaf and its drought resistant mutant line during drought stress by GeLC-MS/MS. In "The 17th Biological Sciences Graduate Congress", Bangkok, Thailand.

Maipoka, M., Pongprayoon, W., Chintakovid, N., Roytrakul S., Pichayangkura, R., and Chadchawan, S. (2013). Comparative proteomic analysis of chitosan responsive proteins in 'Leung Pratew 123' rice and its drought resistant mutant line under drought condition. In "The 8th Science and Technology Conference for Youth", Bangkok, Thailand.

Maipoka, M., Van Volkenburgh, E., and Chadchawan, S. (2014). Effect of drought stress on water relations, growth and photosynthetic activity of Kitaake rice seedlings. In "The 18th Biological Sciences Graduate Congress", Kualalumpur, Malaysia.