TROPICAL AGRICULTURAL SCIENCE

In silico Comparisons of the *Ethylene Response Factor 1* (*ERF1*) Gene Between Malaysian Wild Banana (*Musa acuminata* ssp. *malaccensis*) and Pisang Klutuk Wulung (*Musa balbisiana*)

Gede Kamalesha¹, Fenny Martha Dwivany¹,²,³*, Husna Nugrahapraja¹ and Rika Rahma Putri¹

¹School of Life Science and Technology, Institut Teknologi Bandung, Jl. Ganeca 10, Bandung, 40132, Indonesia
²Bali International Research Center for Banana, Gedung Widyasaba lt. 3 Sayap Selatan Kampus UNUD Bukit Jimbaran Kuta Selatan Badung, Bali, 80361, Indonesia
³Bioscience and Biotechnology Research Center, Institut Teknologi Bandung, Jl. Ganeca 10, Bandung, 40132, Indonesia

ABSTRACT

Musa balbisiana (B genome) has been observed to have a higher tolerance of biotic and abiotic stresses than *Musa acuminata* (A genome). *Ethylene Response Factor 1* (*ERF1*) is a gene activator for pathogenesis-related proteins (PR proteins) such as basic chitinases and beta-1,3-glucanase. There are numerous *ERF1* gene studies about *Oryza sativa*, but information about the banana *ERF1* gene, especially in the B genome (*Musa balbisiana* "Pisang Klutuk Wulung"), has still not been explored thoroughly. Using annotated genomic data in an A genome (*Musa acuminata* ssp. *malaccensis*) and genomic data in a B genome (*Musa balbisiana* "Pisang Klutuk Wulung"), research on the *ERF1* gene can be conducted at the gene sequences and amino acid sequences levels. The *Musa acuminata* (A genome) *ERF1* gene nucleotide sequence was retrieved from the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. The *Musa balbisiana* (B genome) *ERF1* gene nucleotide sequence was identified with the nucleotide Basic Local Alignment Search Tool (BLASTn) using an A genome *ERF1* gene sequence as a query. Both *ERF1* gene nucleotide sequences and amino acid sequences in the A and B genomes were annotated and compared. Seven annotated genome *ERF1* gene sequences from the A and B genomes were identified with the probability that these genes were actively transcribed in cell activity. *ERF1* gene comparisons between the A and B genomes showed that nucleotide composition, gene structure, gene position in each respective chromosome, *ERF*

clusterization, identified motif, and amino acid composition in each of the identified motifs have similar characteristics.

INTRODUCTION

Banana plants are commonly grown in tropical and subtropical countries. They can be classified into two groups based on their genomic composition: *Musa acuminata* (A genome) and *Musa balbisiana* (B genome) (Simmonds, 1959; Sumardi & Wulandari, 2010). The Cavendish banana cultivar (AAA) covers 90% of globally planted bananas and reduces diversity, especially at the plantation site (Drenth & Kema, 2021; Food and Agriculture Organization of the United Nations [FAO], 2019). Low diversity at plantation sites may cause problems in plants like susceptibility to a particular disease, such as the devastating Fusarium wilt (also known as "Panama Disease"), which attacked the cultivar Gros Michel (de Bellaire et al., 2010; Marín et al., 2003).

The ethylene hormone regulates the plant's defense response against the pathogen through signal transduction. The first contact in this signal transduction is the ethylene response (ETR) receptor. Next, the ETR receptor activates a signal transduction cascade by releasing the block exerted by the CONSTITUTIVE TRIPLE RESPONSE 1 (CTR1) on *Ethylene Insensitive 2* (*EIN2*) (Karlova et al., 2014). Finally, this release will actuate *EIN3/EIN3-like* (*EIL*) primary transcription factor genes (Tieman et al.,

2001), leading to the activation of ethylene response factors (ERF) (Adams-Phillips et al., 2004; Bapat et al., 2010).

The ERF family, part of the AP2/ERF superfamily, is the most widely studied transcription family in plants (Riechmann & Meyerowitz, 1998). The *ERF* gene family is the gene activator for many genes (Pirrello et al., 2012). In Nakano et al. (2006), *ERF* genes were divided into groups I–X based on identified motifs besides the AP2/ERF domain. Therefore, ERF groupings based on Nakano et al. (2006) can be used as a reference to identify motifs besides AP2/ERF domain and determine the function of the sequences acquired in this study. The *ERF1* gene has been thoroughly studied in the *Arabidopsis thaliana*. It acts as a gene activator for pathogenesis-related proteins (PR proteins), such as basic-chitinases and beta-1,3-glucanase. In a previous study by Lakhwani et al. (2016), a genome-wide analysis was conducted to identify members of the AP2/ERF family in *Musa acuminata* (A genome) and *Musa balbisiana* (B genome) as well as changes leading to neofunctionalization of genes. However, information about the *ERF1* gene in the *Musa balbisiana* genome remains unexplored.

The study aimed to compare the *ERF1* genes in the A (*Musa acuminata* "DH Pahang") and B genomes (*Musa balbisiana* "Pisang Klutuk Wulung"), including their gene structure (exon-intron architecture), gene position on the chromosome, and gene function (protein clustering and motifs). Therefore, the *ERF1* gene study in *Musa*

balbisiana "Pisang Klutuk Wulung" can be conducted using the annotated genomic information data of *Musa acuminata* "DH Pahang" (D'Hont et al., 2012).

MATERIALS AND METHODS

ERF1 Gene Nucleotide Sequences and Amino Acid Sequences Identification

A genome *ERF1* gene sequences were retrieved from KEGG (Kyoto Encyclopedia of Genes and Genomes) (https://www.genome.jp/dbgetbin/www_bget?K14516+K14517) (Kanehisa & Goto, 2000). BLAST (Basic Local Alignment Search Tool) on the banana genome hub site (https://banana-genome-hub.southgreen.fr/blast) was used to identify *ERF1* gene sequences from the B genome with the highest similarity approach (Eisen, 1998). Translated protein sequences from identified *ERF1* genes of both genomes were classified with the phylogenetic tree approach. Identified *ERF1* genes and 128 amino acid *Oryza sativa* sequences (Nakano et al., 2006) was used as a phylogenetic tree construction dataset. Phylogenetic tree construction was based on Nakano et al.'s (2006) study on the platform Molecular Evolutionary Genetics Analysis (MEGA-X) (version 10.1.5) (Kumar et al., 2018).

ERF1 Gene Nucleotide Comparison in *Musa acuminata* ssp. *malaccensis* and *Musa balbisiana*

Seven nucleotide sequences were retrieved and analyzed in pairs between the *MaERF1* A and B genome genes with pairwise sequence alignment and Needleman-Wunsch as the

algorithm (Needleman & Wunsch, 1970) on the European Bioinformatics Institute site (EMBL-EBI) (https://www.ebi.ac.uk/Tools/psa/emboss_needle/) (Madeira et al., 2019).

ERF1 Gene Structure Prediction and Visualization

Seven *ERF1* of B genome gene structures were predicted using the FGENESH+ program (Solovyev, 2007). Each predicted *ERF1* gene on both A and B genomes was visualized using the CLC Sequence Viewer (version 8.0). The location of the genes in chromosomes for both *Musa acuminata* ssp. *malaccensis* and *Musa balbisiana* were retrieved from the BLAST search and visualized using MS Paint (version 11.2201.22.0).

ERF1 Motif Identification and Comparison in *Musa acuminata* ssp. *malaccensis*

ERF1 amino acid sequences in both *Musa acuminata* ssp. *malaccensis* and *Musa balbisiana* motifs were identified with Multiple Expectation maximizations for Motif Elicitation (MEME) suite (Bailey & Elkan, 1994) using ERF group IX consensus motifs from Nakano et al. (2006) as motif targets. The identified motif in the *Musa acuminata* ssp. *malaccensis* and *Musa balbisiana* amino acid sequences were visualized using the Weblogo3 program with default parameters (http://weblogo.threeplusone.com/create.cgi) (Crooks et al., 2004).

RESULTS AND DISCUSSION

ERF1 Genes Identification in *Musa balbisiana* and *Musa acuminata*

Through searching and selections from BLASTn *ERF* gene results, seven *ERF1* genes in *Musa acuminata* (A genome) were retrieved from the KEGG database with the following gene IDs from NCBI (National Centre for Biotechnology Information): "103971653" (*MaERF1_1*), "103972093" (*MaERF1_2*), "103973681" (*MaERF1_3*), "103981246" (*MaERF1_4*), "103981564" (*MaERF1_5*), "103983138" (*MaERF1_6*), "103985947" (*MaERF1_7*). Seven *ERF1* genes in *Musa balbisiana* (B genome) were identified with gene identification: *MbERF1_1*, *MbERF1_2*, *MbERF1_3*, *MbERF1_4*, *MbERF1_5*, *MbERF1_6*, and *MbERF1_7*. *ERF1* genes in A and B genomes had a similarity of above 90% (Supplementary 1).

ERF1 Genes Structure and Composition in *Musa acuminata* and *Musa balbisiana*

The *ERF1* genes in *Musa acuminata* ssp. *malaccensis* and *Musa balbisiana* have no introns. The longest *ERF1* gene was *MaERF1_7* in the A genome and *MbERF1_7* in the B genome. The shortest *ERF1* gene was *MbERF1_5* in the B genome and *MaERF1_5* in the A genome (Figure 1). Like relatively short sequences, including the intron, coding sequences, and exon compared to other genes, these are the housekeeping genes' typical genomic features (Eisenberg & Levanon, 2003; Vinogradov, 2004). M. Liu et al.'s study (2019) also showed that 79.3% of *FtERF* genes had no introns. Thus, there is a probability that these *ERF1* genes are transcribed actively in cell activities. Furthermore, the nucleotide compositions of all seven *ERF1* genes in both genomes showed a similarity percentage above 95%, the data for which have been presented in Supplementary 1. These results showed that *ERF1* genes of *Musa acuminata* ssp. *malaccensis* and *Musa balbisiana* have a close evolutionary relationship because the nucleotide varieties were minimal.

ERF1 Genes Location in *Musa acuminata* and *Musa balbisiana* Chromosomes

The *ERF1* genes' positions in A and B genome chromosomes were similar: *ERF1_1* (for A and B genomes) in chromosome 2, *ERF1_2* in chromosome 11, *ERF1_4* and *ERF1_5* in chromosome 4, *ERF1_6* in chromosome 1, and *ERF1_7* in chromosome 5. *ERF1_3* gene in both genomes was not identified in the genome database and identified as uncategorized in the chromosome in the Banana Genome Hub database (Figure 2). Chromosome 4 has the most identified *ERF1* genes, with two in the A (*MaERF4* and *MaERF5*) and B genomes (*MbERF4* and *MbERF5*). Multiple *ERF1* genes in both banana genomes resulted from gene replication, also identified in Tartary buckwheat (*Fagopycum tataricum*) (M. Liu et al., 2019).
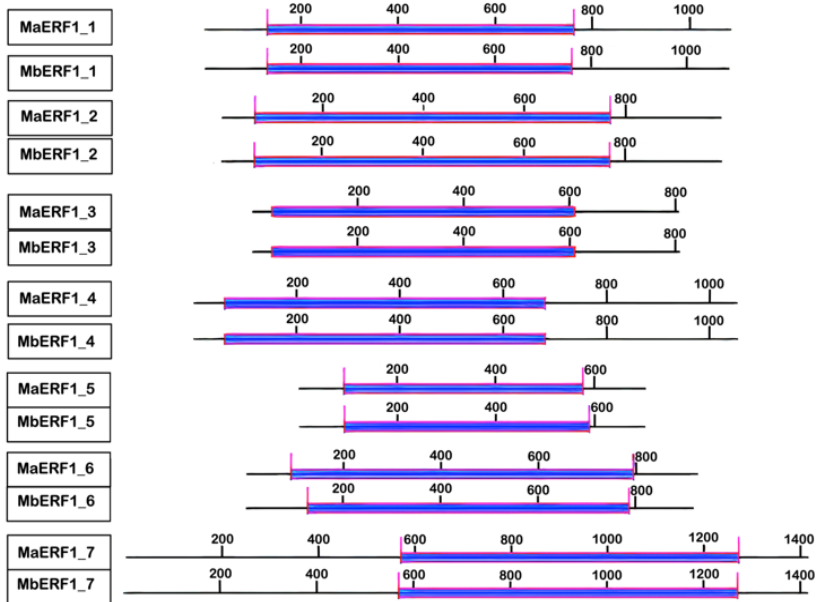
*Figure 1*. The structure of the *ERF1* gene in *Musa acuminata* (A genome) and *Musa balbisiana* (B genome). Bars are marked in the base pair (bp). The figure was visualized using the CLC Sequence Viewer (version 8.0)
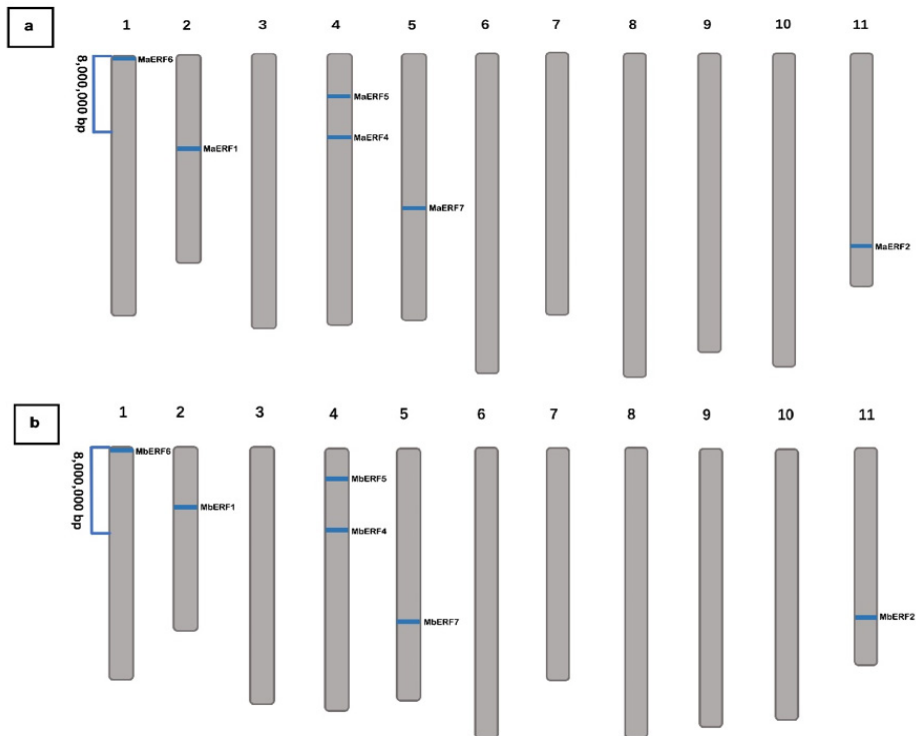

Figure 2. Position of *ERF1* genes in (a) *Musa acuminata* (A genome) and (b) *Musa balbisiana* (B genome) chromosomes. The figure was visualized using MS Paint (version 11.2201.22.0)

Phylogenetic Tree Analysis

Phylogenetic tree analysis (Figure 3) showed that MaERF1 and MbERF1 amino acid sequences (red-colored area) were in one clade with the *Oryza sativa* ERF group IX (blue-colored area). *Oryza sativa* was used as a comparison species because its *ERF* gene database was already established in a previous study by Nakano et al. (2006). *Oryza sativa* is monocotyledonous like the *Musa* species. So, based on the data, *Oryza sativa* is a widely accepted model for monocots that gives evidence of the similarities and differences between the two major groups of higher plant species and has a close lineage with *Musa* (Goff et al., 2002; Izawa & Shimamoto, 1996). The MaERF1 and MbERF1 amino acid sequences within group IX were grouped with *Oryza sativa* ERF group IXc. of the other genes, *MaERF1_1* grouped as sister taxa with *MbERF1_1*, *MaERF1_2* with *MbERF1_2*, *MaERF1_3* with *MbERF1_3*, *MaERF1_4* with *MbERF1_4*, *MaERF1_5* with *MbERF1_5*, *MaERF1_6* with *MbERF1_6*, and *MaERF1_7* with *MbERF1_7*. Phylogenetic tree analysis results showed that all *MaERF1* and *MbERF1* were ERF IXc based on ERF classification by Nakano et al. (2006), who also explained that the *ERF* gene in group IX has disease resistance roles in tomato and tobacco (Fischer & Dröge-Laser, 2004; Huang et al., 2004). *ERF1* in the A and B genomes were closely related because they are grouped as sister taxa.
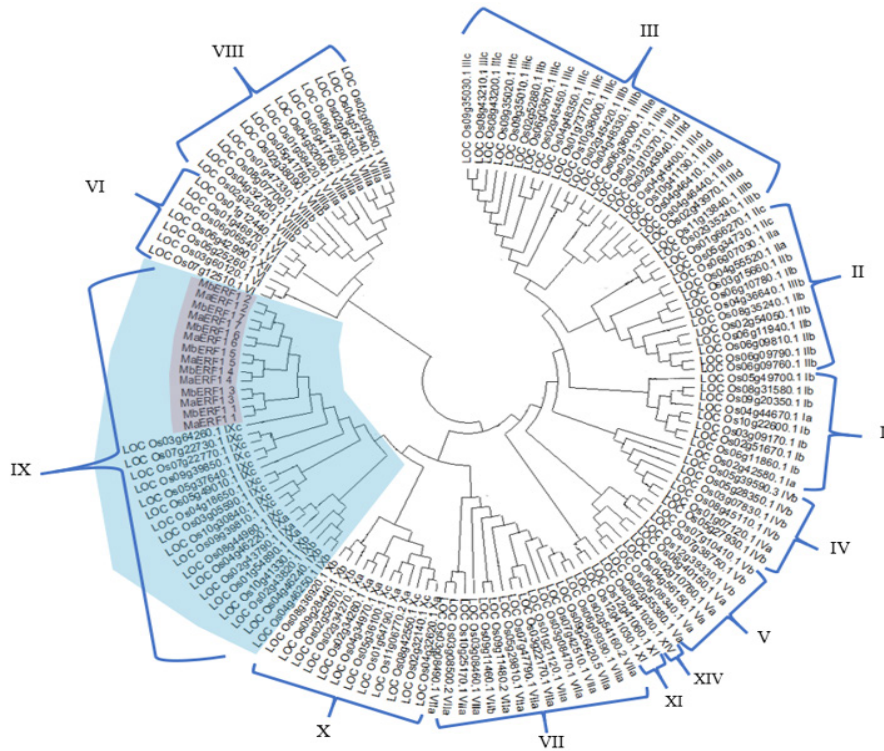
Figure 3. Phylogenetic tree of *Musa acuminata* (A genome), *Musa balbisiana* (B genome), and *Oryza sativa* *ERF* genes. The figure was constructed using MEGA-X software (version 10.1.5)

Amino Acid Motif Composition Comparison

There were four motifs in total in the MaERF1_1, MbERF1_1, MaERF1_2, MbERF1_2, MaERF1_3, MbERF1_3, MaERF1_4, MbERF1_4, MaERF1_5, MbERF1_5, MaERF1_7, and MbERF1_7 amino acid sequences (Figure 4). There was one domain AP2/ERF (red box) and three motifs which consisted of CMIX-1 (cyan box), CMIX-3 (purple box), and CMIX-4 (orange box). In addition, three motifs were detected in MaERF1_6 and MbERF1_7. AP2/ERF, CMIX-4, and CMIX-1 were detected, while in MbERF1_6, AP2/ERF, and CMIX-4 motifs were detected. On the other hand, domain AP2/ERF was detected in all MaERF1 and MbERF1 amino acid sequences, indicating that these amino acid sequences are classified as the ERF subfamily (Riechmann & Meyerowitz, 1998). Motifs besides AP2/ERF are transcription factors likely to have similar essential functions (Rashid et al., 2012; Reyes et al., 2004) that consist of transcription factors' activities, interactions between proteins, and nuclear localization (L. Liu et al., 1999).
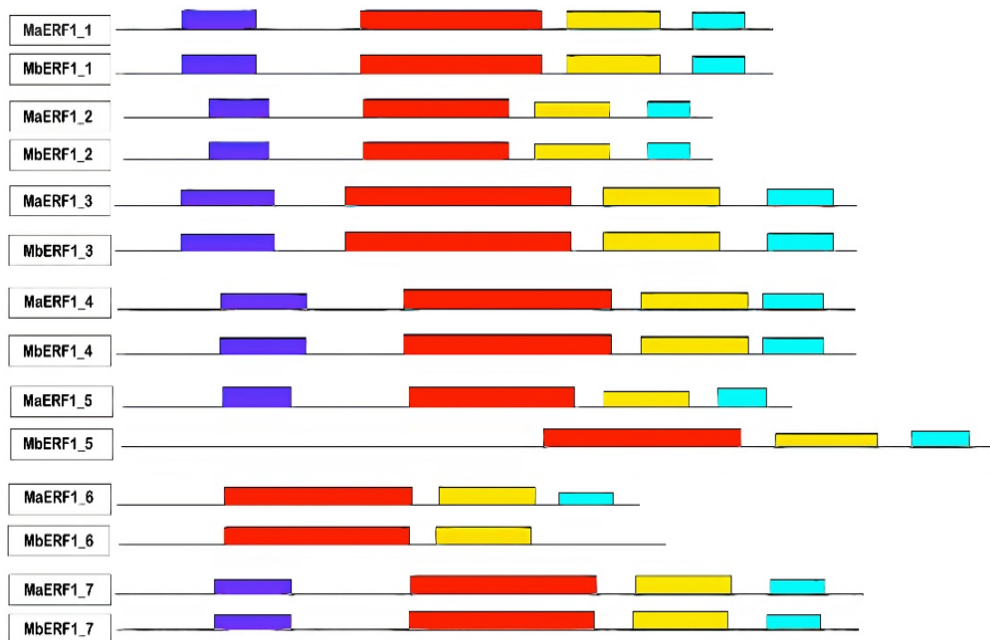
Figure 4. The amino acid motif of ERF sequences compares *Musa acuminata* (A genome) and *Musa balbisiana* (B genome) chromosomes. The box shows domain AP2/ERF (red box) and three motifs, which consist of CMIX-1 (cyan box), CMIX-3 (purple box), and CMIX-4 (orange box). The figure was visualized using the MEME suite program

Each identified amino acid motif of MaERF1 and MbERF1 was also analyzed. Overall, all the identified motifs between MaERF1 and MbERF1 have high similarities. For example, in Figure 6, both MaERF1 and MbERF1 have similar CMIX-4 motifs with slight amino acid composition differences detected at positions 4, 9, 19, and 22.
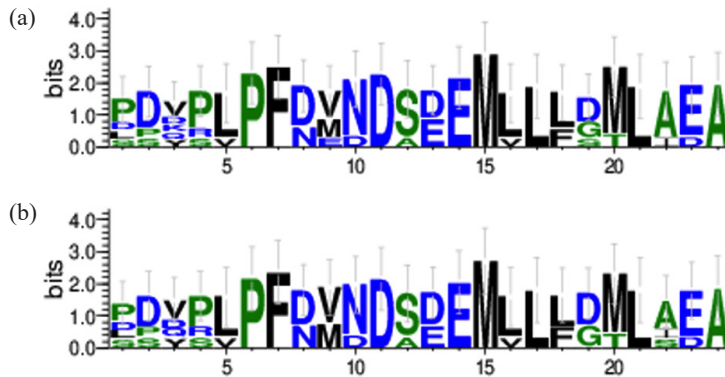
Figure 5. CMIX-3 motif sequences of (a) *Musa acuminata* (A genome) and (b) *Musa balbisiana* (B genome). The figure was visualized using the Weblogo3 program

In addition to the CMIX-4 motif, the amino acid composition of the CMIX-3 motif varied, but both generally have the same amino acid consensuses at each position (Figure 5). Based on the analysis, the CMIX-1 motif has the shortest amino acid sequence compared with other identified motifs, and variation between MaERF1 and MbERF1 in this motif was relatively low (Figure 7). On the other hand, the AP2/ERF motif was the longest in both genomes, with 58 amino acids. This result confirmed the previous study by Wessler (2005), which showed that AP2/ERF length was around 60–70 amino acids. Besides its length, domain motifs AP2/ERF in both genomes were conserved. There were two conserved amino acids in both genomes, YRG in position numbers 1–3 and RAYD in position numbers 39–42. YRG conserved motif was the rich basic hydrophilic amino acids located at N-terminus and has a function in DNA binding (Okamuro et al., 1997). On the other hand, the RAYD conserved domain has an essential function in domain structure and function. However, in both genomes, the AP2/ERF domain has L (leucine) in position number 39 rather than R (arginine) (Okamuro et al., 1997).
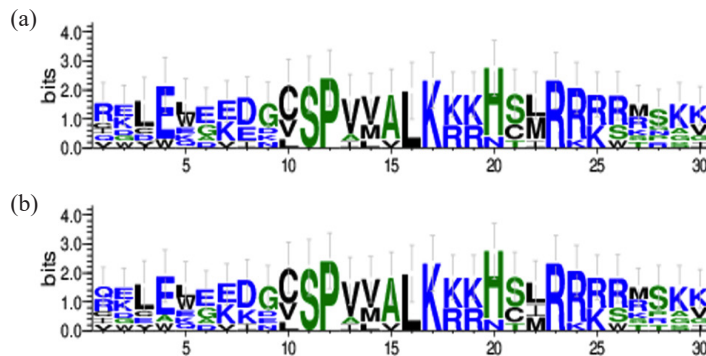
Figure 6. CMIX-4 motif sequences of (a) *Musa acuminata* (A genome) and (b) *Musa balbisiana* (B genome). The figure was visualized using the Weblogo3 program
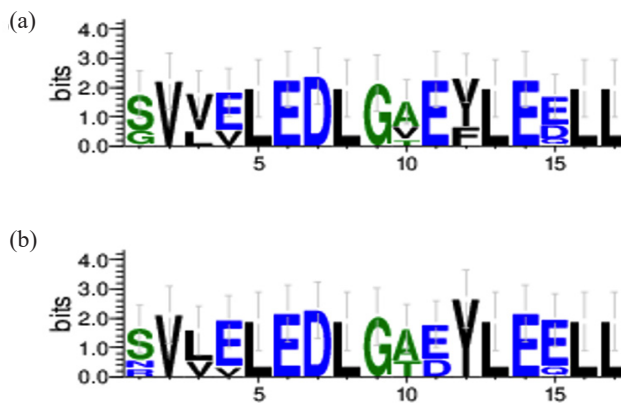

Figure 7. CMIX-1 motif sequences of (a) *Musa acuminata* (A genome) and (b) *Musa balbisiana* (B genome). The figure was visualized using the Weblogo3 program

Based on this study's comparison with Lakhwani et al. (2016), there were several differences in identified motifs outside the AP2/ERF domain. In Lakhwani et al. (2016), the identified motif in group IX of the *ERF* gene was only the LNFP motif. On the other hand, this study identified three motifs: CMIX-1, CMIX-3, and CMIIX-4. Furthermore, Lakhwani et al. (2016) showed that the identified motif outside AP2/ERF domain was named the LNFP motif, but based on Fujimoto et al. (2000), the LNFP motif is the part of the AP2/ERF domain

amino acid residues. Considering both studies used the *in silico* approach, further confirmation is needed to elucidate the differences.

CONCLUSION

Based on this study, the *ERF1* genes of *Musa acuminata* (A genome) and *Musa balbisiana* (B genome) showed high similarities in their nucleotide sequences, gene structures, and positions in the chromosome, phylogenetic clustering, and the motif predicted in the protein sequences.

Pertanika J. Trop. Agric. Sci. 45 (2): 519 - 545 (2022)

527

AUTHORS' CONTRIBUTIONS

GK, FMD, and HN designed the study. GK analyzed the data. RRP reviewed and edited the manuscript. All authors wrote, read, and approved the final version of the manuscript.

CONFLICT OF INTEREST

All authors declare no conflict of interest.

REFERENCES

Adams-Phillips, L., Barry, C., & Giovannoni, J. (2004). Signal transduction systems regulating fruit ripening. *Trends in Plant Science*, *9*(7), 331–338. https://doi.org/10.1016/j.tplants.2004.05.004

Bailey, T. L., & Elkan, C. (1994). Fitting a mixture model by expectation maximization to discover motifs in biopolymers. *Proceedings International Conference on Intelligent Systems for Molecular Biology*, *2*, 28–36.

Bapat, V. A., Trivedi, P. K., Ghosh, A., Sane, V. A., Ganapathi, T. R., & Nath, P. (2010). Ripening of fleshy fruit: Molecular insight and the role of ethylene. *Biotechnology Advances*, *28*(1), 94–107. https://doi.org/10.1016/j.biotechadv.2009.10.002

Crooks, G. E., Hon, G., Chandonia, J. M., & Brenner, S. E. (2004). WebLogo: A sequence logo generator. *Genome Research*, *14*(6), 1188–1190. https://doi.org/10.1101/gr.849004

de Bellaire, L. d. L., Foure, E., Abadie, C., & Carlier, J. (2010). Black leaf streak disease is challenging the banana Goff, S. A., Ricke, D., Lan, T. H., Presting, G., Wang, R., Dunn, M., Glazebrook, J., Sessions, A., Oeller, P., Varma, H., Hadley, D., Hutchison, D., Martin, C., Katagiri, F., Lange, B. M., Moughamer, T., Xia, Y., Budworth, P., Zhong, J., … Briggs, S. (2002). A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*). *Science*, *296*(5565), 92–100. https://doi.org/10.1126/science.1068275

Huang, Z., Zhang, Z., Zhang, X., Zhang, H., Huang, D., & Huang, R. (2004). Tomato TERF1 modulates ethylene response and enhances osmotic stress tolerance by activating expression of downstream genes. *FEBS Letters*, *573*(1–3), 110–116. https://doi.org/10.1016/j.febslet.2004.07.064

Izawa, T., & Shimamoto, K. (1996). Becoming a model plant: The importance of rice to plant science. *Trends in Plant Science*, *1*(3), 95–99. https://doi.org/10.1016/S1360-1385(96)80041-0

Kanehisa, M., & Goto, S. (2000). KEGG: Kyoto encyclopedia of genes and genomes. *Nucleic Acids Research*, *28*(1), 27–30. https://doi.org/10.1093/nar/28.1.27

Karlova, R., Chapman, N., David, K., Angenent, G. C., Seymour, G. B., & de Maagd, R. A. (2014). Transcriptional control of fleshy fruit development and ripening. *Journal of Experimental Botany*, *65*(16), 4527–4541. https://doi.org/10.1093/jxb/eru316

Kumar, S., Stecher, G., Li, M., Knyaz, C., & Tamura, K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution*, *35*(6), 1547–1549. https://doi.org/10.1093/molbev/msy096

Lakhwani, D., Pandey, A., Dhar, Y. V., Bag, S. K., Trivedi, P. K., & Asif, M. H. (2016). Genome-wide analysis of the AP2/ERF family in *Musa* species reveals divergence and neofunctionalisation during evolution. *Scientific Reports*, *6*, 18878. https://doi.org/10.1038/srep18878

Liu, L., White, M. J., & MacRae, T. H. (1999). Transcription factors and their genes in higher plants functional domains, evolution and regulation. *European Journal of Biochemistry*, *262*(2), 247–257. https://doi.org/10.1046/j.1432-1327.1999.00349.x

Liu, M., Sun, W., Ma, Z., Zheng, T., Huang, L., Wu, Q., Zhao, G., Tang, Z., Bu, T., Li, C., & Chen, H. (2019). Genome-wide investigation of the AP2/ERF gene family in tartary buckwheat (*Fagopyum tataricum*). *BMC Plant Biology*, *19*(1), 84. https://doi.org/10.1186/s12870-019-1681-6

Madeira, F., Park, Y. M., Lee, J., Buso, N., Gur, T., Madhusoodanan, N., Basutkar, P., Tivey, A., Potter, S. C., Finn, R. D., & Lopez, R. (2019). The EMBL-EBI search and sequence analysis tools APIs in 2019. *Nucleic Acids Research*, *47*(W1), W636–W641. https://doi.org/10.1093/nar/gkz268

Marín, D. H., Romero, R. A., Guzmán, M., & Sutton, T. B. (2003). Black sigatoka: An increasing threat to banana cultivation. *Plant Disease*, *87*(3), 208–222. https://doi.org/10.1094/PDIS.2003.87.3.208

Nakano, T., Suzuki, K., Fujimura, T., & Shinshi, H. (2006). Genome-wide analysis of the ERF gene family in *Arabidopsis* and rice. *Plant Physiology*, *140*(2), 411–432. https://doi.org/10.1104/pp.105.073783

Needleman, S. B., & Wunsch, C. D. (1970). A general method applicable to the search for similarities in the amino acid sequence of two proteins. *Journal of Molecular Biology*, *48*(3), 443–453. https://doi.org/10.1016/0022-2836(70)90057-4

Okamuro, J. K., Caster, B., Villarroel, R., Van Montagu, M., & Jofuku, K. D. (1997). The AP2 domain of *APETALA2* defines a large new family of DNA binding proteins in *Arabidopsis*. *Proceedings of the National Academy of Sciences of the United States of America*, *94*(13), 7076–7081. https://doi.org/10.1073/pnas.94.13.7076

Pirrello, J., Prasad, B. C., Zhang, W., Chen, K., Mila, I., Zouine, M., Latché, A., Pech, J. C., Ohme-Takagi, M., Regad, F., & Bouzayen, M. (2012). Functional analysis and binding affinity of tomato ethylene response factors provide insight on the molecular bases of plant differential responses to ethylene. *BMC Plant Biology*, *12*, 190. https://doi.org/10.1186/1471-2229-12-190

Rashid, M., Guangyuan, H., Guangxiao, Y., Hussain, J., & Xu, Y. (2012). AP2/ERF transcription factor in rice: Genome-wide canvas and syntenic relationships between monocots and eudicots. *Evolutionary Bioinformatics*, *8*, EBO-S9369. https://doi.org/10.4137/EBO.S9369

Reyes, J. C., Muro-Pastor, M. I., & Florencio, F. J. (2004). The GATA family of transcription factors in *Arabidopsis* and rice. *Plant Physiology*, *134*(4), 1718–1732. https://doi.org/10.1104/pp.103.037788

Riechmann, J. L., & Meyerowitz, E. M. (1998). The AP2/EREBP family of plant transcription factors. *Biological Chemistry*, *379*(6), 633–646. https://doi.org/10.1515/bchm.1998.379.6.633

Simmonds, N. W. (1959). *Bananas*. Longman.

Solovyev, V. (2007). Statistical approaches in eukaryotic gene prediction. In D. Balding, C. Cannings, & M. Bishop (Eds.), *Handbook of statistical genetics* (3rd ed.). Wiley-Interscience. https://doi.org/10.1002/0470022620.bbc06

Sumardi, I., & Wulandari, M. (2010). Anatomy and morphology character of five Indonesian banana cultivars (*Musa* spp.) of different ploidy level. *Biodiversitas, Journal of Biological Diversity*, *11*(4), 167–175. https://doi.org/10.13057/biodiv/d110401

Tieman, D. M., Ciardi, J. A., Taylor, M. G., & Klee, H. J. (2001). Members of the tomato *LeEIL* (*EIN3-like*) gene family are functionally redundant and regulate ethylene responses throughout plant development. *The Plant Journal*, *26*(1), 47–58. https://doi.org/10.1046/j.1365-313x.2001.01006.x

Vinogradov, A. E. (2004). Compactness of human housekeeping genes: Selection for economy or genomic design?. *Trends in Genetics*, *20*(5), 248–253. https://doi.org/10.1016/j.tig.2004.03.006

Wessler, S. R. (2005). Homing into the origin of the AP2 DNA binding domain. *Trends in Plant Science*, *10*(2), 54–56. https://doi.org/10.1016/j.tplants.2004.12.007

SUPPLEMENTARY DATA

Supplementary 1

The sequence alignment of ERF1 *genes in* Musa acuminata *ssp.* malaccensis *(A genome) and* Musa balbisiana *(B genome)*

```
#=======================================
#
# Aligned_sequences: 2
# 1: MaERF1_1
# 2: MbERF1_1
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1088
# Identity:     1071/1088 (98.4%)
# Similarity:   1071/1088 (98.4%)
# Gaps:            2/1088 ( 0.2%)
# Score: 5284.5
#
#
#=======================================

MaERF1_1        1 GGTCAGACTTGCCTCGCTCTCTTTGCCTCATCCCTTCCATGTCTCTTCGA     50
                  |||||||||||||||||||.|||||.||||||||||||||||||||||||
MbERF1_1        1 GGTCAGACTTGCCTCGCTATCTTTTCCTCATCCCTTCCATGTCTCTTCGA     50

MaERF1_1       51 CCCTCTCCGGTATATATCTTCCCCGCCCCTGCGCTTTCTCACGCTCGATA    100
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1       51 CCCTCTCCGGTATATATCTTCCCCGCCCCTGCGCTTTCTCACGCTCGATA    100

MaERF1_1      101 GCGAACCCCGCGACCCAGGCGTGCATCTCATGGATCCTTCCAATCTCCAC    150
                  |||||||.||.|||.||||||||||||||||||||||||||||||||||||
MbERF1_1      101 GCGAACACCACGAACCAGGCGTGCATCTCATGGATCCTTCCAATCTCCAC    150

MaERF1_1      151 TGTCGGAGCCACGACGAGTTCTCGTCGGAATCCTCCGGCCGGTCGCCGGA    200
                  |||||||||||||||||||||||||||||||||||.||||||||||||||
MbERF1_1      151 TGTCGGAGCCACGACGAGTTCTCGTCGGAATCCTCTGGCCGGTCGCCGGA    200

MaERF1_1      201 CTCCCTCCCCTTCAACGTCAACGACAGCGACGAGATGGTCCTGTTCGACA    250
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1      201 CTCCCTCCCCTTCAACGTCAACGACAGCGACGAGATGGTCCTGTTCGACA    250

MaERF1_1      251 TGCTGGCGGAGGCCACCGCCCCCAGGCCCGACGAGGCCAGGGACGGGGAG    300
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1      251 TGCTGGCGGAGGCCACCGCCCCCAGGCCCGACGAGGCCAGGGACGGGGAG    300

MaERF1_1      301 GCCGAGTCGAAGAGCAGGGACGAGGAAGGGCTGCTGCGGCGGCGGACGCC    350
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1      301 GCCGAGTCGAAGAGCAGGGACGAGGAAGGGCTGCTGCGGCGGCGGACGCC    350

MaERF1_1      351 GGAAGATCGGTGCTACCGCGGCGTCCGGAAGCGGCCGTGGGGCAAGTTCG    400
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1      351 GGAAGATCGGTGCTACCGCGGCGTCCGGAAGCGGCCGTGGGGCAAGTTCG    400

MaERF1_1      401 CGGCGGAGATCAGGGACTCGACCCGGAACGGGATTCGGGTGTGGTTGGGC    450
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1      401 CGGCGGAGATCAGGGACTCGACCCGGAACGGGATTCGGGTGTGGTTGGGC    450
```

```
MaERF1_1    451 ACGTTCGACACCGCGGAGGCCGCCGCGCTGGCCTACGACCAGGCGGCGCT   500
                |||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1    451 ACGTTCGACACCGCGGAGGCCGCCGCGCTGGCCTACGACCAGGCGGCGCT   500

MaERF1_1    501 GTCCATGCGGGGGCAGCTCGCGGTGCTCAATTTCCCGGTGGAGCGGGTGC   550
                |||||||||||.||.|||||||||||||||||||||||||||||||||||
MbERF1_1    501 GTCCATGCGGGGACAACTCGCGGTGCTCAATTTCCCGGTGGAGCGGGTGC   550

MaERF1_1    551 AGGCGTCGCTGCGGGAGCTGGAGTGGGGCAAGGACGACTGCTCCCCGGTG   600
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1    551 AGGCGTCGCTGCGGGAGCTGGAGTGGGGCAAGGACGACTGCTCCCCGGTG   600

MaERF1_1    601 ATGGCTCTCAAGAAGAAGCACTCCCTGAGAAGACGGCGGTCATCGAGCAT   650
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1    601 ATGGCTCTCAAGAAGAAGCACTCCCTGAGAAGACGGCGGTCATCGAGCAT   650

MaERF1_1    651 AAAGGACAAGGTGGCGCCGACCAGGATACCGAATGTTCTGGAACTGGAAG   700
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1    651 AAAGGACAAGGTGGCGCCGACCAGGATACCGAATGTTCTGGAACTGGAAG   700

MaERF1_1    701 ACCTCGGCGCAGACTACTTGGAGGAGCTCCTCAGTGTATCGGAGTCTTCA   750
                |||||.|||||||||||||||||||||||||||||||||||||||.|||||
MbERF1_1    701 ACCTTGGCGCAGACTACTTGGAGGAGCTCCTCAGTGTATCGGAGCCTTCA   750

MaERF1_1    751 AAACCATGGTAACCCTTCTCCTGCTCTCCACCGCTGCCATCTCACGCCCG   800
                |||||||||||||||||||||||||||||..||||||||||||||||||||
MbERF1_1    751 AAACCATGGTAACCCTTCTCCTGCTCTCGGCCGCTGCCATCTCACGCCCG   800

MaERF1_1    801 GAGGACCTCATCATTTCCTCCTCCATAATTGGAGAATCCAATCACCTGCT   850
                |||||||||||||||||||||||||||.||||||||||||||||||||||
MbERF1_1    801 GAGGACCTCATCATTTCCTCCTCCATGATTGGAGAATCCAATCACCTGCT   850

MaERF1_1    851 CAACCTACAGCCACACTCCATGAAACTCGGATCCAGCT--CCCCCTCACC   898
                |||||.||||||||||||||||||||||||||||||||  ||||||||||
MbERF1_1    851 CAACCCACAGCCACACTCCATGAAACTCGGATCCAGCTCCCCCCCCTCACC   900

MaERF1_1    899 ATTTTTTATTCTTCTTCCCCTCTCCCTCCCTCTCTCTCTCTCTCTCTATC   948
                |||||||||||||||||||.||||||||||||||||||||||||||||||
MbERF1_1    901 ATTTTTTATTCTTCTTCTCCTCTCCCTCCCTCTCTCTCTCTCTCTCTATC   950

MaERF1_1    949 GAAAGCCCCCATCAGATAAGCAGTGCTGCATTATTATGCGGGCCCCGAAA   998
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1    951 GAAAGCCCCCATCAGATAAGCAGTGCTGCATTATTATGCGGGCCCCGAAA   1000

MaERF1_1    999 ACGATGTAAGAAAAGATGTACATGTCTGTTTCAGATCCATTGAATCCACG   1048
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_1    1001 ACGATGTAAGAAAAGATGTACATGTCTGTTTCAGATCCATTGAATCCACG   1050

MaERF1_1    1049 GGAAAGTTGAGCACGACGCCTTTGCTCTCTTCACATCA   1086
                 ||||||||||||||||||||||||||||||||||||||
MbERF1_1    1051 GGAAAGTTGAGCACGACGCCTTTGCTCTCTTCACATCA   1088
```

```
#=======================================
#
# Aligned_sequences: 2
# 1: MaERF1_2
# 2: MbERF1_2
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 992
# Identity:     967/992 (97.5%)
# Similarity:   967/992 (97.5%)
# Gaps:           2/992 ( 0.2%)
# Score: 4732.5
#
#
#=====================================

MaERF1_2          1 GCTCGAGAAGAAGCAAGGAGGTGGGCGAAACCCTGCGCTCTGCCTCGTTC     50
                    ||||||||||||||||||||||||||.||||||.||||||||||||||||
MbERF1_2          1 GCTCGAGAAGAAGCAAGGAGGTGGGCAAACCCTACGCTCTGCCTCGTTC     50

MaERF1_2         51 CTCCCTTTCCTCCCTATGGACTACTACCTCTTCGACTCCCTGAACCACGA    100
                    |||||||.||||||||||||||||||||||||||||||||||||||||||
MbERF1_2         51 CTCCCTCTCCTCCCTATGGACTACTACCTCTTCGACTCCCTGAACCACGA    100

MaERF1_2        101 ACACTCGCCGGAATCCTCCACCGGTTCCACCGAGCCCTTTCCATGGGCCG    150
                    ||||||||||||||.||.||.||||||||.|||||||||||.||||||||
MbERF1_2        101 ACACTCGCCGGAATCGTCTACCGGTTCCCCCGAGCCCTTCCCATGGGCCG    150

MaERF1_2        151 GCGTTGGGCTGTTCTACCCGGACGTTCCTCTCCCTTTCAACATGGATGAC    200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2        151 GCGTTGGGCTGTTCTACCCGGACGTTCCTCTCCCTTTCAACATGGATGAC    200

MaERF1_2        201 TCCGAGGAGATGCTGCTGCTCGGAATGCTCGCGGAGGCCTCCGGAAAGGC    250
                    |||||||||||||||||||||||||||||.|||||||||||||||||||
MbERF1_2        201 TCCGAGGAGATGCTGCTGCTCGGAATGCTCTCGGAGGCCTCCGGAAAGGC    250

MaERF1_2        251 GTCGTCCTCGTCGGAGGCCTGCGACCGGAGCGTGATCCGGGCCAAGGAAG    300
                    |||| .||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2        251 GTCGCCCTCGTCGGAGGCCTGCGACCGGAGCGTGATCCGGGCCAAGGAAG    300

MaERF1_2        301 AAGAGGTGGATTCGCGGAGCAAGGCGGCGGATGAGCCGAAGGAGAAGTCG    350
                    |||| .||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2        301 AAGAAGTGGATTCGCGGAGCAAGGCGGCGGATGAGCCGAAGGAGAAGTCG    350

MaERF1_2        351 TACCGGGGGGGTGCGGAAGCGGCCGTGGGGGAAGTTCGCGGCGGAGATCAG    400
                    |||||||||||||||||||||.||||||||||||||||||||||||||||
MbERF1_2        351 TACCGGGGGGGTGCGGAAGCGACCGTGGGGGAAGTTCGCGGCGGAGATCAG    400

MaERF1_2        401 GGACTCGACGCGGCACGGGATACGGGTGTGGCTGGGGACGTTCGACAGCG    450
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2        401 GGACTCGACGCGGCACGGGATACGGGTGTGGCTGGGGACGTTCGACAGCG    450
```

```
MaERF1_2   451 CGGAGGCCGCCGCCCTGGCGTACGACCAGGCCGCCTTCTCGATGAGGGGG   500
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2   451 CGGAGGCCGCCGCCCTGGCGTACGACCAGGCCGCCTTCTCGATGAGGGGG   500

MaERF1_2   501 TCGATGGCGGTGCTCAATTTCCCGGTGGAGCGGGTGCGGGAGTCGTTGAA   550
               ||||||||||||||||||||||||||||||||||||||.|||||||||||
MbERF1_2   501 TCGATGGCGGTGCTCAATTTCCCGGTGGAGCGGGTGCAGGAGTCGTTGAA   550

MaERF1_2   551 CGGCATCAAGTGCTGGAAGGAGGAGGAGAAGGTGTCGCCGGCGGTGGCGC   600
               ||||||||||||||||||||||||||.||.||||||||||||||||||||
MbERF1_2   551 CGGCATCAAGTGCTGGAAGGAGGAGAAGGAGGTGTCGCCGGCGGTGGCGC   600

MaERF1_2   601 TGAAGAGGAGGCACTCCATGAGGAGGAAGTGGATGAACAAGAAAGCAAAG   650
               ||||||||||||||||||||||||||||||||||||||.|||||||||||
MbERF1_2   601 TGAAGAGGAGGCACTCCATGAGGAGGAAGTGGATGAGCAAGAAAGCAAAG   650

MaERF1_2   651 GAGAGTGAGACGAGCAGCAGCAGCAGCAGCAGCGTGGAGAGCGTGCTGGA   700
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2   651 GAGAGTGAGACGAGCAGCAGCAGCAGCAGCAGCGTGGAGAGCGTGCTGGA   700

MaERF1_2   701 GCTGGAGGACTTGGGAACAGAGTATTTGGAGGAGCTTCTGAGAACATCAG   750
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2   701 GCTGGAGGACTTGGGAACAGAGTATTTGGAGGAGCTTCTGAGAACATCAG   750

MaERF1_2   751 AAGTAGCCAACACTTGCTGACTTCTTCCAATCCTTCTCCACCGCCAGTCT   800
               |||||||||.||||||.|||||||||||||||||||||||||.|||||||
MbERF1_2   751 AAGTAGCCGACACTAGCTGACTTCTTCCAATCCTTCTCCAACGCCAGTCT   800

MaERF1_2   801 CCCCTGTTCCTCCTTTTTTCCTAAGGGAAACCCCTCACTTGTTCCTTGTA   850
               ||||||||||||||||||||||..||||||||||||.|||||||||||||
MbERF1_2   801 CCCCTGTTCCTCCTTTTTTCCGGAGGGAAACCCCACACTTGTTCCTTGTA   850

MaERF1_2   851 TTCCTTTCTTGGTTTGTTCTTTCAGTTGTCCAAGTCAGGATGATCTTTTT   900
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_2   851 TTCCTTTCTTGGTTTGTTCTTTCAGTTGTCCAAGTCAGGATGATCTTTTT   900

MaERF1_2   901 TACTTGGCTGTGCTTGGCATG--TGCCATACCAAGATATCTCGATATCTT   948
               |||||||||||||||||||||   |||||.||||||||||||.|||||||
MbERF1_2   901 TACTTGGCTGTGCTTGGCATGGATGCCACACCAAGATATCTTGATATCTT   950

MaERF1_2   949 ATTTCCCTGCTGCAAATCAATATAGCTTTTGATCCTGTAAAA      990
               ||||||||||||||||||||||||||||||||||||||||||
MbERF1_2   951 ATTTCCCTGCTGCAAATCAATATAGCTTTTGATCCTGTAAAA      992
```

534

Pertanika J. Trop. Agric. Sci. 45 (2): 519 - 545 (2022)

```
#=======================================
#
# Aligned_sequences: 2
# 1: MaERF1_3
# 2: MbERF1_3
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 808
# Identity:     793/808 (98.1%)
# Similarity:   793/808 (98.1%)
# Gaps:           2/808 ( 0.2%)
# Score: 3893.0
#
#
#=======================================

MaERF1_3          1 GCCTGAGAACCACCGATCTCCCACCCCACAATTCACGATGGATCCTTCAT     50
                    |||| .||||||||||||||||||||||||||||||||||||||||||||
MbERF1_3          1 GCCTAAGAACCACCGATCTCCCACCCCACAATTCACGATGGATCCTTCAT     50

MaERF1_3         51 ATCTCCAGTCCCAGAGTTACGACGAATTCTCGCCGGAAGATTCCTATCGC    100
                    |||| .||||||||||||||||||||||||||||||||||||||||||||
MbERF1_3         51 ATCTGCAGTCCCAGAGTTACGACGAATTCTCGCCGGAAGATTCCTATCGC    100

MaERF1_3        101 CTCCCCTTCGACGTCAACGACAGCGACGAGATGCTCCTGTTCGACACACT    150
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_3        101 CTCCCCTTCGACGTCAACGACAGCGACGAGATGCTCCTGTTCGACACACT    150

MaERF1_3        151 GGCGGAGGCCACCCCTTCGAACCCGGTCCTGGCAGGGGAGGGTCGACCGA    200
                    |||||||||||||||||.||||||||||||||||||||||||.|||||||
MbERF1_3        151 GGCGGAGGCCACCCCTTCTAACCCGGTCCTGGCAGGGGAGGGCCGACCGA    200

MaERF1_3        201 CGGGCGAGCCGTGCTACCGCGGCGTCCGTAAGCGGCCGTGGGGGAAGTTC    250
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_3        201 CGGGCGAGCCGTGCTACCGCGGCGTCCGTAAGCGGCCGTGGGGGAAGTTC    250

MaERF1_3        251 GCGGCGGAGATAAGGGACTCGACGCGGGGAGGGGCGCGGGTGTGGCTGGG    300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_3        251 GCGGCGGAGATAAGGGACTCGACGCGGGGAGGGGCGCGGGTGTGGCTGGG    300

MaERF1_3        301 GACGTTCGACACCGCGGAGGCCGCCGCCCTGGCGTACGACCAGGCGGCGT    350
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_3        301 GACGTTCGACACCGCGGAGGCCGCCGCCCTGGCGTACGACCAGGCGGCGT    350

MaERF1_3        351 TCTCCATGCGGGGGCGGCTCGCCGTGCTCAACTTCCCAGTGGAGCAGGTG    400
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_3        351 TCTCCATGCGGGGGCGGCTCGCCGTGCTCAACTTCCCAGTGGAGCAGGTG    400

MaERF1_3        401 CAGGAGTCCTTGCAAGAGCTCGAATGGGATAAGGACAACTGCTCCCCCAT    450
                    |||||||||||||||.||||||||||||||||||||||.|||||||||||
MbERF1_3        401 CAGGAGTCCTTGCAGGAGCTCGAATGGGATAAGGATAACTGCTCCCCCAT    450
```

```
MaERF1_3   451 CATGGCACTCAAGAAGAAGCACTCGTTAAGGAGGAGGAGGAGACCTGCAG   500
               |||||||||||||||||||||||| ||||||||||||||||||||||||||
MbERF1_3   451 CATGGCACTCAAGAAGAAGCACTCATTAAGGAGGAGGAGGAGACCTGCAG   500

MaERF1_3   501 TGAGCGGGAAGACCAAGGTGGCACAGAGCAGGATACAGAGTGTCCTGGAA   550
               ||||||||||||||||||||||||||||||| |||||||||||| | |||
MbERF1_3   501 TGAGCGGGAAGACCAAGGTGGCACAGAGCAGGAGACAGAGTGTCCTAGAA   550

MaERF1_3   551 CTGGAGGACTTGGGCACAGATTACTTGGAGGAGTTACTGAGAGTTTCCGA   600
               ||||||||||||| |||||||||||||||||||||||||||||||||||
MbERF1_3   551 CTGGAGGACTTGGGAACAGATTACTTGGAGGAGTTACTGAGAGTTTCCGA   600

MaERF1_3   601 ACTTGCATAA-CTCAGTAAACCTGCTCCCTGCAGCTCAAATCAAACTCCA   649
               |||||||||| ||||||||||||||||||||||||| |||||||||||||
MbERF1_3   601 ACTTGCATAACCTCAGTAAACCTGCTCCCTGCAGCTAAAATCAAACTCCA   650

MaERF1_3   650 TGGAACTCGGATCCAGCTTTCGGTTCCTTCATCATTATTTATTCTGCTTG   699
               |||||||||||||||||||||| |||||||||||||||||||||||||||
MbERF1_3   651 TGGAACTCGGATCCAGCTTTCGATTCCTTCATCATTATTTATTCTGCTTG   700

MaERF1_3   700 CATCATTACTTGGTCCCCCAAAATGATGTAACAGGAAAATGTATGTGTTT   749
               ||||||||||||||||||||| ||||||||||||||||||||||||||||
MbERF1_3   701 CATCATTACTTGGTCCCCCAAAACGATGTAACAGGAAAATGTATGTGTTT   750

MaERF1_3   750 CAGATCCGTTGAATCCATGC-AAAGATGAGCGCGATGGCTTTGCTTGCTT   798
               |||||||||||||||||||| |||||||||||||||||||||||||||||
MbERF1_3   751 CAGATCCGTTGAATCCATGCAAAAGATGAGCGCGATGGCTTTGCTTGCTT   800

MaERF1_3   799 TACACCAA      806
               ||||||||
MbERF1_3   801 TACACCAA      808
```

536

Pertanika J. Trop. Agric. Sci. 45 (2): 519 - 545 (2022)

```
#=======================================
#
# Aligned_sequences: 2
# 1: MaERF1_4
# 2: MbERF1_4
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1054
# Identity:    1032/1054 (97.9%)
# Similarity:  1032/1054 (97.9%)
# Gaps:           1/1054 ( 0.1%)
# Score: 5066.0
#
#
#=======================================

MaERF1_4          1 TGAGGCTCTTATGCCGCGAAACCACACGAGCCGAGCAAGAAGAAGCCTGT     50
                    ||||||||||.||||||||||||||||.|.||||||||||||||||||||
MbERF1_4          1 TGAGGCTCTAATGCCGCGAAACCACAAGGGCCGAGCAAGAAGAAGCCTGT     50

MaERF1_4         51 TTCTCCGTCGATGGATTCTCCAAACCTCTACTTCCGCTGCTCCGAATCCT    100
                    |||||||||||||||||||||||||||||||||.|||.||||||||||||
MbERF1_4         51 TTCTCCGTCGATGGATTCTCCAAACCTCTACTTGCGCAGCTCCGAATCCT    100

MaERF1_4        101 CGGCCGCGTCCACACCCGAATCCCCGGAACCTGCCCCGTGCTCCCGCCTC    150
                    |||||||||||||||||||||||||||.|.||||.|.|||||||||||||
MbERF1_4        101 CGGCCGCGTCCACACCCGAATCCCCGAAGCCTGTCCCGTGCTCCCGCCTC    150

MaERF1_4        151 GACCAACCGCTTCCCTTCGACGTGAACGACGCCGATGAGATGCTCTTGCT    200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4        151 GACCAACCGCTTCCCTTCGACGTGAACGACGCCGATGAGATGCTCTTGCT    200

MaERF1_4        201 GGACATGCTCATCGATGCTCCCGACGTGTCTAACTCTACCATGGCGGCAG    250
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4        201 GGACATGCTCATCGATGCTCCCGACGTGTCTAACTCTACCATGGCGGCAG    250

MaERF1_4        251 AAGAGGTCGGGTCGAGCGTGACGGCGGAGCCCCCGGGGAGCGAGAAGAGC    300
                    |||||||||||||||||||||||||||||||.|||||.||||||||||||
MbERF1_4        251 AAGAGGTCGGGTCGAGCGTGACGGCGGAGCCCTCGGGGGGCGAGAAGAGC    300

MaERF1_4        301 TACAGAGGGGTGCGGAAGCGGCCGTGGGGGAAGTTCGCGGCGGAGATCAG    350
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4        301 TACAGAGGGGTGCGGAAGCGGCCGTGGGGGAAGTTCGCGGCGGAGATCAG    350

MaERF1_4        351 GGACTCGACGCGGCAGGGGGTGAGAGTGTGGCTGGGCACGTTCGACGACG    400
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4        351 GGACTCGACGCGGCAGGGGGTGAGAGTGTGGCTGGGCACGTTCGACGACG    400

MaERF1_4        401 CGGAGGCGGCCGCCTTGGCCTACGACCAGGCGGCATTGGCGATGAGGGGG    450
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4        401 CGGAGGCGGCCGCCTTGGCCTACGACCAGGCGGCATTGGCGATGAGGGGG    450
```

```
MaERF1_4    451 ACGGCGGCGGTGCTCAATTTCCCGGCCGAGCGTGTGCGGGCGTCGCTGCG    500
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4    451 ACGGCGGCGGTGCTCAATTTCCCGGCCGAGCGTGTGCGGGCGTCGCTGCG    500

MaERF1_4    501 GGACCTCGAGCTGGGGGTGGATGGGTGTTCCCCGGTTCTGGCACTGAAGA    550
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4    501 GGACCTCGAGCTGGGGGTGGATGGGTGTTCCCCGGTTCTGGCACTGAAGA    550

MaERF1_4    551 AGAGGCACTGCATCAGGAAGAGGAGGAGGTCAGGGGGCAAGGTAATGGAG    600
                ||||||||||||||||||||||||||||||||||||||||| || |||||
MbERF1_4    551 AGAGGCACTGCATCAGGAAGAGGAGGAGGTCAGGGGGCAAGGAAAGGGAG    600

MaERF1_4    601 AGTGTTGTGGTCTTGGAGGACTTGGGAGCAGAGTACTTGGAGGAACTCTT    650
                || ||||||||||||||||||||||||||||||| |||||||| |||||
MbERF1_4    601 AGAGTTGTGGTCTTGGAGGACTTGGGAGCAGAGTATTTGGAGGAGCTCTT    650

MaERF1_4    651 GAGACTGTCAGAACCTGCAAGTCCTTGGTGATCATCCAATGGTTTTGCTT    700
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4    651 GAGACTGTCAGAACCTGCAAGTCCTTGGTGATCATCCAATGGTTTTGCTT    700

MaERF1_4    701 TCCTGTAGCTTGTTCGTTGTGATGACAAACAGCTTCACAAGTCTAATGAT    750
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4    701 TCCTGTAGCTTGTTCGTTGTGATGACAAACAGCTTCACAAGTCTAATGAT    750

MaERF1_4    751 TTGCTCATTCCCATAAAATCTGGATCCATCTTCTTTCTTGATGCTTCACT    800
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4    751 TTGCTCATTCCCATAAAATCTGGATCCATCTTCTTTCTTGATGCTTCACT    800

MaERF1_4    801 GTATATTAAACCATGGCTGCATCATCATGTGGCCTACACAACGAGCAAAG    850
                |||||| ||||||||||||||||||||||||||||| |||||||||||||
MbERF1_4    801 GTATAGTAAACCATGGCTGCATCATCATGTGGCCTTCACAACGAGCAAAG    850

MaERF1_4    851 ATCT-TCTCTCTCTCTCTCTCAATTTAAGATACATGCTCAGATTACCA    899
                ||||  ||||||||||||||||||||||||||||||||||||||||||
MbERF1_4    851 ATCTCTCTCTCTCTCTCTCTCTCAATTTAAGATACATGCTCAGATTACCA    900

MaERF1_4    900 TGTCAAAAGGTAGGCTATGCCAAAAGAGGATGTCATGTTGCCTTGTTTCA    949
                | |||||||||||||||||||||||||||||||||||||||||| |||||
MbERF1_4    901 TTTCAAAAGGTAGGCTATGCCAAAAGAGGATGTCATGTTGCCTTTTTTCA    950

MaERF1_4    950 ATGAGCTCCATGTATTGCTAGACTCTGTCCAACTGAGTTTACGGCTCATA    999
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_4    951 ATGAGCTCCATGTATTGCTAGACTCTGTCCAACTGAGTTTACGGCTCATA   1000

MaERF1_4   1000 TTGTTTGGATTGGAAGAGTTGATCTGAAACCATCTGAGATATGGGAGTGA   1049
                || |||||||||||||||||||||||||||||||||||| ||||||||||
MbERF1_4   1001 TTATTTGGATTGGAAGAGTTGATCTGAAACCATCTGAGGTATGGGAGTGA   1050

MaERF1_4   1050 GACA   1053
                ||||
MbERF1_4   1051 GACA   1054
```

```
#=======================================
#
# Aligned_sequences: 2
# 1: MaERF1_5
# 2: MbERF1_5
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
#
# Length: 706
# Identity:     685/706 (97.0%)
# Similarity:   685/706 (97.0%)
# Gaps:           6/706 ( 0.8%)
# Score: 3324.0
#
#
#=======================================


MaERF1_5         1 GACCTCCTTCCAAGGTTCCGAATCCTCATCGATATCCACAGCCGGATCGC     50
                   |||||||||||||||||||||||||||||||||.|.||||||||||||||
MbERF1_5         1 GACCTCCTTCCAAGGTTCCGAATCCTCATCGGTGTCCACAGCCGGATCGC     50

MaERF1_5        51 AGGAGGAATCTCTCCCCTTCGACGTGAACGACGCCGGTGAGATGCTCCTG    100
                   ||||||||.|||||||||||||||||||||||||||||||||||||||||
MbERF1_5        51 AGGAGGAGTCTCTCCCCTTCGACGTGAACGACGCCGGTGAGATGCTCCTG    100

MaERF1_5       101 TTCGACATGCTCATCGAGTCCGCCATGACCACGAAGACGTCGACGGGCAA    150
                   ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_5       101 TTCGACATGCTCATCGAGTCCGCCATGACCACGAAGACGTCGACGGGCAA    150

MaERF1_5       151 AGAGGCGGAGTCGAAGGGCCCGACGGCGAGCGGGAAGAGCTACCGAGGGG    200
                   ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_5       151 AGAGGCGGAGTCGAAGGGCCCGACGGCGAGCGGGAAGAGCTACCGAGGGG    200

MaERF1_5       201 TGCGGAGGCGGCCGTGGGGCAAGTTCGCGGCTGAGATCAGGGACTCGACG    250
                   |||||||||||||||||||||||||||||||.||||||||||||||||||
MbERF1_5       201 TGCGGAGGCGGCCGTGGGGCAAGTTCGCGGCGGAGATCAGGGACTCGACG    250

MaERF1_5       251 CGGCAGGGGGTGCGGGTGTGGCTGGGCACGTTCGACAGCGCGGAGGCCGC    300
                   ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_5       251 CGGCAGGGGGTGCGGGTGTGGCTGGGCACGTTCGACAGCGCGGAGGCCGC    300

MaERF1_5       301 CGCCCTGGCCTACGACCAGGCGGCGCTGTCGATGAGGGGGGGCGACGGCGG    350
                   |||||||||||||||||||||||||||||||||||||||||||||||.|
MbERF1_5       301 CGCCCTGGCCTACGACCAGGCGGCGCTGTCGATGAGGGGGGGCGACGGCCG    350

MaERF1_5       351 TGCTCAACTTTCCGGCGGAGCGCGTGCGGGAGTCGCTGCGGGGGCTGGAG    400
                   ||||||||||.|||||||||||||||||||||||||||||.|||||||||
MbERF1_5       351 TGCTCAACTTCCCGGCGGAGCGCGTGCGGGAGTCGCTGCAGGGGCTGGAG    400

MaERF1_5       401 CTGGCGAAGGACGGGTGCTCCCCGGTGGTGGCGCTGAAGAAGAAGCACTG    450
                   ||||||||||||||.|||||||||||||||||||||||||||||||||||
MbERF1_5       401 CTGGCGAAGGACGGCTGCTCCCCGGTGGTGGCGCTGAAGAAGAAGCACTG    450
```

Pertanika J. Trop. Agric. Sci. 45 (2): 519 - 545 (2022)

539

```
MaERF1_5    451 CATGAGGAGGAGGAGGAAGAGAAAGGTGAGGGAGTCGAGTGGGGAGGAGG    500
                |||.|||||||||||||||||||||||||||||||||||||    |||||
MbERF1_5    451 CATCAGGAGGAGGAGGAAGAGAAAGGTGAGGGAGTCGAGTGG---GGAGG    497

MaERF1_5    501 GCGTAGTGGAATTAGAGGA-CTTGGGAGTGGAGTTCTTGGAGGACCTCTT    549
                ||||||||||||||||||| .|||||||||||||||||||||||||||||
MbERF1_5    498 GCGTAGTGGAATTAGAGGATTTTGGGAGTGGAGTTCTTGGAGGACCTCTT    547

MaERF1_5    550 GGGGCTTTCAGGGCTTGCGAGTCAGTGATGACAAGCTCATAGTTTTGCCC    599
                ||||||.||||||||||||||||||||||.||||||||||||||||||||
MbERF1_5    548 GGGGCTATCAGGGCTTGCGAGTCAGTGGTGACAAGCTCATAGTTTTGCCC    597

MaERF1_5    600 AACCTAATGATATTTTAAATATATTAATATGGATATTAAGTTGACTGTCA    649
                ||||||.|||||||||||||||||||||||||||||||||||||||||||
MbERF1_5    598 AACCTTATGATATTTTAAATATATTAATATGGATATTAAGTTGACTGTCA    647

MaERF1_5    650 ATTAGATTTACTGTAATGGACACATGTGCAAGT-TTTTGTATAGTTTTGT    698
                ||||||||||||||||| |||||||||||||| ||||.||||||.|||
MbERF1_5    648 ATTAGATTTACTGTAAT-GACACATGTGCAAGTGTTTTTTATAGTTATGT    696

MaERF1_5    699 TAAGAT      704
                ||||||
MbERF1_5    697 TAAGAT      702
```

```
#=======================================
#
# Aligned_sequences: 2
# 1: MaERF1_6
# 2: MbERF1_6
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 927
# Identity:     899/927 (97.0%)
# Similarity:   899/927 (97.0%)
# Gaps:           8/927 ( 0.9%)
# Score: 4401.5
#
#
#=======================================

MaERF1_6           1 AGCCGTCCTTACGATCAAGCTTAGCAGTTGCACTGATACTACTGAGACAA     50
                     |||||||||||.||||||||||||.|||.|||||||||||||||||||||
MbERF1_6           1 AGCCGTCCTTATGATCAAGCTTAGTAGTAGCACTGATACTACTGAGACAA     50

MaERF1_6          51 GCGGAAGGCAGAAGCAATCTCTGGCTTGTCTTCCTCTTCGATGGATTACT    100
                     |.|||||||||||||||||||.||..||||||||||||||.|||||||||
MbERF1_6          51 GAGGAAGGCAGAAGCAATCCCTATCTTGTCTTCCTCTTCAATGGATTACT    100

MaERF1_6         101 CTCTCTCCTTTCACTCCCATAACCAGGAACACTCATCTGAGTCCTCCACG    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6         101 CTCTCTCCTTTCACTCCCATAACCAGGAACACTCATCTGAGTCCTCCACG    150

MaERF1_6         151 TACTCGCCCAGGTCCTCGGCAACCGACGGCTTCGGGCTCGTCTGCCCTGA    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6         151 TACTCGCCCAGGTCCTCGGCAACCGACGGCTTCGGGCTCGTCTGCCCTGA    200

MaERF1_6         201 CAAGCCCCTTCCGTTCGACGAGAACGACTCCGAGGAGATGCTGCTGCTTA    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6         201 CAAGCCCCTTCCGTTCGACGAGAACGACTCCGAGGAGATGCTGCTGCTTA    250

MaERF1_6         251 GCATGCTCGCAGAGGCCTCAGGCAAGGCGGCGTCGTCGTCCTCGTCGGAG    300
                     |||||||||||||||||||||||||||.||||||||||||||||||||||
MbERF1_6         251 GCATGCTCGCAGAGGCCTCAGGCAAGGCGTCGTCGTCGTCCTCGTCGGAG    300

MaERF1_6         301 GTCCTTGACAGCCGCAGTTCACCCCGACCCAAGGAAGAAGAGGTGGAATC    350
                     |||||||     |.||.||||||||||||||||||||||||||||||||
MbERF1_6         301 GTCCTTG--------ATTTTACCCCGACCCAAGGAAGAAGAGGTGGAATC    342

MaERF1_6         351 GAGAAGCAAGGTGGGTCATGACACAAAGGGAGAGAAGCCCTACCGCGGGG    400
                     ||||||||||||||||||||||||||||||||||||||.|||||||||||
MbERF1_6         343 GAGAAGCAAGGTGGGTCATGACACAAAGGGAGAGAAGTCCTACCGCGGGG    392

MaERF1_6         401 TGAGACGGCGGCCGTGGGGGAAGTTCGCCGCCGAGATAAGAGACTCAACG    450
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6         393 TGAGACGGCGGCCGTGGGGGAAGTTCGCCGCCGAGATAAGAGACTCAACG    442
```

```
MaERF1_6    451 CGGCGCGGGATTCGCGTGTGGCTGGGAACGTTCGACAGCGCGGAGGCAGC    500
                |||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6    443 CGGCGCGGGATTCGCGTGTGGCTGGGAACGTTCGACAGCGCGGAGGCAGC    492

MaERF1_6    501 TGCGCTGGCTTACGACCAGGCGGCGTTCTCGATGCGGGGGACGACGGCGG    550
                |||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6    493 TGCGCTGGCTTACGACCAGGCGGCGTTCTCGATGCGGGGGACGACGGCGG    542

MaERF1_6    551 TGCTCAATTTCCCGGTGGAGAGAGTTCGGGAGTCGCTGCGGGGCGTGAAG    600
                |.||||||||||||||||.|||||||||||||||||||||||||||||||
MbERF1_6    543 TCCTCAATTTCCCGGTGGACAGAGTTCGGGAGTCGCTGCGGGGCGTGAAG    592

MaERF1_6    601 TACGAGGAGGAGGAGATTGGGCTGTCGCCCGTGGTGGCGCTCAAGCGGAG    650
                |||||.||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6    593 TACGCGGAGGAGGAGATTGGGCTGTCGCCCGTGGTGGCGCTCAAGCGGAG    642

MaERF1_6    651 GAATACCCTGAGGAGGAAGTCGACGAGCAAGAAGGCCAAAGGCCGGGAGG    700
                |||||||||||||||||||||||||||||||||||||||||..||||||
MbERF1_6    643 GAATACCCTGAGGAGGAAGTCGACGAGCAAGAAGGCCAAAGGGAGGGAGG    692

MaERF1_6    701 TGAGGACGGCGGAGAGTGTGGTGGAGTTGGAGGACCTGGGAGCAGAGTAC    750
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6    693 TGAGGACGGCGGAGAGTGTGGTGGAGTTGGAGGACCTGGGAGCAGAGTAC    742

MaERF1_6    751 TTGGAGGAGCTCTTGAGCACCTCAGGGTTTGCCAGGCCGTGGTGAACCGC    800
                |||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6    743 TTGGAGGAGCTCTTGAGCACCTCAGGGTTTGCCAGGCCGTGGTGAACCGC    792

MaERF1_6    801 AACTCTCAATCCTCGAGACCATGTTCTCTGTATACCTTTCTTGTTTCCTT    850
                |||||||||||||.||||||.|||||||||||||||||||||||||||||
MbERF1_6    793 AACTCTCAATCCTCAAGACCACGTTCTCTGTATACCTTTCTTGTTTCCTT    842

MaERF1_6    851 TCTTCTTTCCTTCGTTCAATTGTTCCAATCCTGCAGCACAAAGAAGCTCT    900
                ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_6    843 TCTTCTTTCCTTCGTTCAATTGTTCCAATCCTGCAGCACAAAGAAGCTCT    892

MaERF1_6    901 AAGAATTCTACTTCTTTCTCTGTTCCA    927
                ||||||||||||||||.||||||||||
MbERF1_6    893 AAGAATTCTACTTCTTCCTCTGTTCCA    919
```

```
#=======================================
#
# Aligned_sequences: 2
# 1: MaERF1_7
# 2: MbERF1_7
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1417
# Identity:    1379/1417 (97.3%)
# Similarity:  1379/1417 (97.3%)
# Gaps:           3/1417 (  0.2%)
# Score: 6725.0
#
#
#=======================================

MaERF1_7         1 ACTTGCAAGGGGTGAAATCCCAATAACTCAAACAAAAATGCTTTTGATTA      50
                   ||||||||||||||||||||||||.||.|||||||||||||||||||||||
MbERF1_7         1 ACTTGCAAGGGGTGAAATCCCGATTACTCAAACAAAAATGCTTTTGATTA      50

MaERF1_7        51 ATTCTCCTTGATGATAGAAGCCATACCTTGCCTTCCTCAGCTCTTTCACT     100
                   |||||||||||||||||||||||||.||||||||||||||||||||||||||
MbERF1_7        51 ATTCTCCTTGATGATAGAAGCCATGCCTTGCCTTCCTCAGCTCTTTCACT     100

MaERF1_7       101 TTCACACTAGAGTTTGCACAGGTCACCAATGCAGCACTCTAACCCAGCTC     150
                   ||||||||||||||||||||||||||||||||||||.|||||||||||||
MbERF1_7       101 TTCACACTAGAGTTTGCACAGGTCACCAATGCAGCATTCTAACCCAGCTC     150

MaERF1_7       151 TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCGTGTGTGTGTGGTGGCTGC     200
                   |.||||||||||||||||||||||||||||||.|.|||.|||||||||||
MbERF1_7       151 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGAGTGTGGTGGCTGC     200

MaERF1_7       201 AAATACAAGAGGACAGCACAAGAGATCTCCCACCAAAAACTGTCACCCTG     250
                   |||||||||||||||||||||||||||||||||||||||||||||||.|
MbERF1_7       201 AAATACAAGAGGACAGCACAAGAGATCTCCCACCAAAAACTGTCA-CCAG     249

MaERF1_7       251 CAGCGATGGCTTCAACACGGGACATGGAGCCACGAAGTGGCCACCAATGA     300
                   ||||||||  ||||||||||||||||||||||||.||||||||||.|||
MbERF1_7       250 CAGCGAT-GCTTCAACACGGGACATGGAGCCACGACGTGGCCACCACTGA     298

MaERF1_7       301 TGTCACCGTGCTCGTCTCACGGATACTTCACCCGACCTCTGCCGCCGTGC     350
                   |||||||||||||||||||||||||||||||||||||||||||||||||.
MbERF1_7       299 TGTCACCGTGCTCGTCTCACGGATACTTCACCCGACCTCTGCCGCCGTGA     348

MaERF1_7       351 GTGGCTGACCCACGTGCTCCTTTGGCCCGGCACGAACCTTTTCCCGCCAC     400
                   ||||||||.||||||||||||||||||||||||||||||||||||.|||
MbERF1_7       349 GTGGCTGACTCACGTGCTCCTTTGGCCCGGCACGAACCTTTTCCCGTCAC     398

MaERF1_7       401 CCGCAACTCCCAGGTGGCCCCAGTCAATCTATCCATCGATTCCCCCTCTC     450
                   |||||||||||||||||||||||||||||||||||||.||||||||||||
MbERF1_7       399 CCGCAACTCCCAGGTGGCCCCAGTCAATCTATCCATTGATTCCCCCTCTC     448
```

```
MaERF1_7   451 TCGTTCAAGTATAAGAAGGAGCGGGCTTAGATCCTGTCGACTGGACGAGC    500
               ||||||||||||||||||||||||||||||||||||||||||||||.|||
MbERF1_7   449 TCGTTCAAGTATAAGAAGGAGCGGGCTTAGATCCTGTCGACTGGACAAGC    498

MaERF1_7   501 TCGAGCACGAACAAGGAGGTGGGAGACACCCTGATTTCTCTCTCTCCTCA    550
               ||||||||||||||||||.||||||||||||||||||||||||.||||||
MbERF1_7   499 TCGAGCACGAACAAGGCGGTGGGAGACACCCTGATTTCTCTCTTTCCTCA    548

MaERF1_7   551 TCCCTTCCTTTCTCCCCCCCATGGACTACTCCCTCTTCCAGTCGCTACAC    600
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_7   549 TCCCTTCCTTTCTCCCCCCCATGGACTACTCCCTCTTCCAGTCGCTACAC    598

MaERF1_7   601 TCGCCGGAATCTTCCACTGGCTCCGGCGACCCCTTCCCCTGGACCGGCGT    650
               |||||||||||||||||||||||||||||.||||||||||||||||||||
MbERF1_7   599 TCGCCGGAATCTTCCACTGGCTCCGGCAACCCCTTCCCCTGGACCGGCGT    648

MaERF1_7   651 CGGGCTGTTCTACCCGGACGTTCCTGTCCCGTTCGACATGAACGACTCCG    700
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_7   649 CGGGCTGTTCTACCCGGACGTTCCTGTCCCGTTCGACATGAACGACTCCG    698

MaERF1_7   701 AGGAGATGCTCCTCCTCGGAATGCTCGCGGAGGCCTCCGGTAAGGCGTCG    750
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_7   699 AGGAGATGCTCCTCCTCGGAATGCTCGCGGAGGCCTCCGGTAAGGCGTCG    748

MaERF1_7   751 TCCTCGTTAGAGGCCTGCGAGCGCAGCCCAGCCCAGCCCAAGGAGGAAGA    800
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_7   749 TCCTCGTTAGAGGCCTGCGAGCGCAGCCCAGCCCAGCCCAAGGAGGAAGA    798

MaERF1_7   801 GGTGGATTCGCAGAGCAAGGTGGCGGACGATCCCAAGGTGAAGTCGTACC    850
               ||||||||||.||||||||||||||||||||||||||.||||||||||||
MbERF1_7   799 GGTGGATTCGCGGAGCAAGGTGGCGGACGATCCCAAGGAGAAGTCGTACC    848

MaERF1_7   851 GGGGGGTGAGAAAGCGGCCGTGGGGGAAGTTCGCGGCGGAGATCCGGGAC    900
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_7   849 GGGGGGTGAGAAAGCGGCCGTGGGGGAAGTTCGCGGCGGAGATCCGGGAC    898

MaERF1_7   901 TCGACGCGGCACGGCATACGGGTGTGGCTGGGAACGTTCGACAGCGCGGA    950
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_7   899 TCGACGCGGCACGGCATACGGGTGTGGCTGGGAACGTTCGACAGCGCGGA    948

MaERF1_7   951 GGCCGCGGCGCTGGCGTACGACCAGGCCGCCTTCTCGATGCGGGGCTCGA    1000
               ||||||||||||||||||||||||||||||||||||||||||||||||||
MbERF1_7   949 GGCCGCGGCGCTGGCGTACGACCAGGCCGCCTTCTCGATGCGGGGCTCGA    998

MaERF1_7  1001 CGGCGGTGCTCAATTTCCCGGTGGACCGGGTGCGGGAGTCGCTGAACGGC    1050
               |||||||||||||||||||||||||||||||||||||||||.||||||||
MbERF1_7   999 CGGCGGTGCTCAATTTCCCGGTGGACCGGGTGCGGGAGTCACTGAACGGC    1048

MaERF1_7  1051 ATGAAATGCTGGGATGAACAGGAGGAGGAGGGGGTGTCGCCGGTGGTGGT    1100
               |||||||||||||||.||||||||||||.|||||||||||||||||||||
MbERF1_7  1049 ATGAAATGCTGGGAGGAACAGGAGGAGGAGAAGGGGGTGTCGCCGGTGGTGGT  1098
```

544

Pertanika J. Trop. Agric. Sci. 45 (2): 519 - 545 (2022)

```
MaERF1_7    1101 GCTGAAGAGGAAGCACTCCATGAGGAGGAAGTCGATGGGCAAGAAGGCAA  1150
                 |||||||||||||||||||||||||||||||||||||..||||||||||||
MbERF1_7    1099 GCTGAAGAGGAAGCACTCCATGAGGAGGAAGTCGATGACCAAGAAGGCAA  1148

MaERF1_7    1151 AGCAGAGCGAGACGAGCATTCGTAGCGCGGAGAGCGTGTTGGAGCTAGAG  1200
                 |||||||||||||.||||||||||||||||||||||||||||||||||||
MbERF1_7    1149 AGCAGAGCGAGACAAGCATTCGTAGCGCGGAGAGCGTGTTGGAGCTAGAG  1198

MaERF1_7    1201 GACTTAGGAGCAGAGTACTTGGAACAGCTTCTCACAACATCAGAGGTTGC  1250
                 |||||||||||||||||||||||||||||||||||||.|||||||||||||.
MbERF1_7    1199 GACTTAGGAGCAGAGTACTTGGAACAGCTTCTCACTACATCAGAGGTTGT  1248

MaERF1_7    1251 GCCAATCCATGCTCAGTGTTAAGCATCTGTCTTGTGTTTTTTCTGTGGGA  1300
                 ||||||||||||.|||||||||||||||||||||.|||||||||||||||
MbERF1_7    1249 GCCAATCCATGCCCAGTGTTAAGCATCTGTCATGTGTTTTTTCTGTGGGA  1298

MaERF1_7    1301 AATCTCTCCCCTGTTCATCAAATTTGTTTCTTGTTTTGTTCTTCCAGTTG  1350
                 ||||||||.|||||||||||||||||.|||||||||||||||||||||||
MbERF1_7    1299 AATCTCTTCCCTGTTCATCAAATTTCTTTCTTGTTTTGTTCTTCCAGTTG  1348

MaERF1_7    1351 TCCAAG-TAATAAGAACCTCCTTTTTACTTGGCTACGTTTGTGATAGTAA  1399
                 |||||| ||..||||||||||||||||||||||||||||||||||||||||
MbERF1_7    1349 TCCAAGTTACAAAGAACCTCCTTTTTACTTGGCTACGTTTGTGATAGTAA  1398

MaERF1_7    1400 GAGATTTTGAGATCTTA    1416
                 |||||||||||||||||
MbERF1_7    1399 GAGATTTTGAGATCTTA    1415
```