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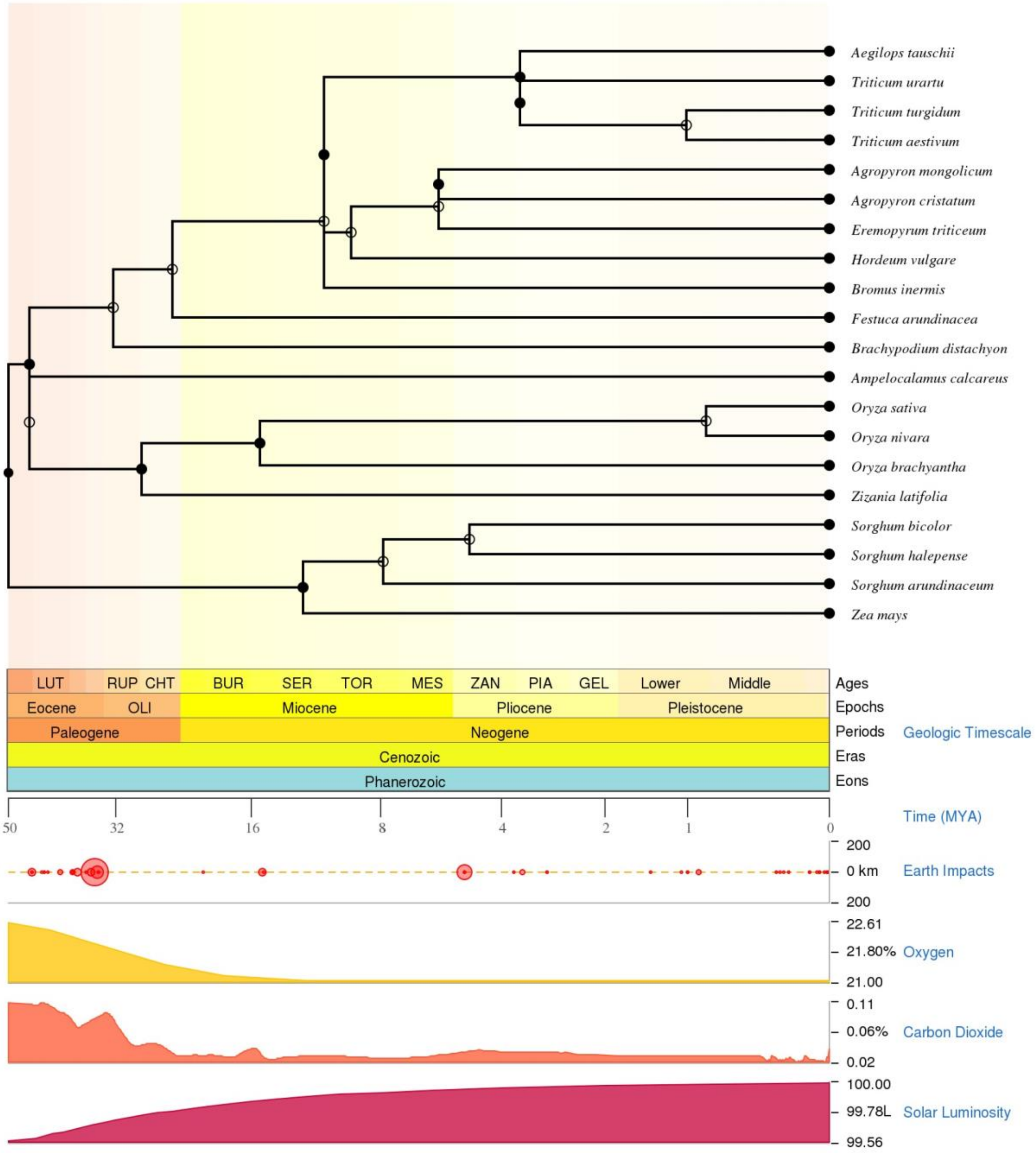
Supplementary 1: The full length or near full-length protein sequences of LEA protein sequences for Poaceae species were obtained in FASTA format from National Center for Biotechnology Information protein database (http://www.ncbi.nlm.nih.gov) used for the analyses.



Supplementary 2: Representation of the relationships and divergence times of the Poaceae species and its evolutionary timescale inferred by the timetree (http://www.timetree.org/) database.

MEME

Multiple Em for Motif Elicitation

For further information on how to interpret these results or to get a copy of the MEME software please access http://meme-suite.org.

If you use MEME in your research, please cite the following paper:
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994. [pdf]

Discovered Motifs | **Motif Locations** | **Inputs & Settings** | **Program information**

Discovered Motifs

	Logo	E-value	Sites	Width	More	Submit/Downl
1.		3.6e-1965	85	31	↧	⇢
2.		1.9e-1546	81	27	↧	⇢
3.		8.1e-1837	100	41	↧	⇢
4.		1.3e-783	75	21	↧	⇢
5.		6.6e-904	70	41	↧	⇢

Stopped because requested number of motifs (5) found.

Motif Locations

● Only Motif Sites ○ Motif Sites+Scanned Sites ○ All Sequences

Name	*p*-value
1. XP_020173182.1_Aegilops_tauschii_tauschii	1.66e-121
2. Q03968.1_Triticum_aestivum	6.19e-119
3. ALD18913.1LEA3_Triticum_turgidum_durum	1.03e-121
4. AAN74637.1_Triticum_aestivum	8.41e-121
5. ACH89913.1_Hordeum_vulgare_vulgare	7.14e-123
6. AEJ88291.1_Agropyron_cristatum	1.17e-108
7. ALD18912.1_Triticum_turgidum_durum	1.19e-125
8. AKC92683.1_Hordeum_vulgare	3.59e-123
9. ACH89911.1_Hordeum_vulgare_vulgare	2.01e-123
10. AAN74639.1_Triticum_aestivum	3.24e-107
11. P14928.1_Hordeum_vulgare_vulgare	1.95e-123
12. ACH89910.1_Hordeum_vulgare_vulgare	1.22e-118

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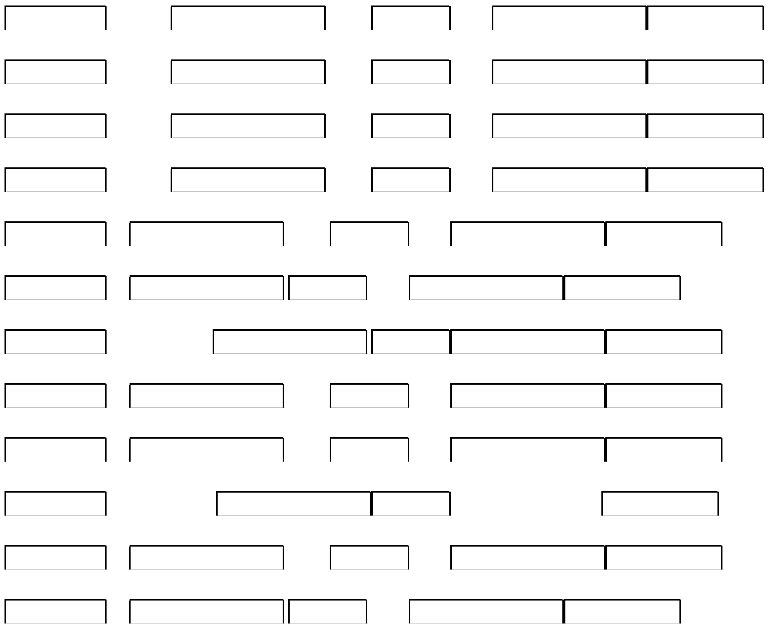

INPUTS & SETTINGS

Sequences

Source	Alphabet	Sequence Count
lea_data.txt	Protein	100

Background

	Name	Freq.	Bg.
A	Alanine	0.210	0.210
C	Cysteine	0.001	0.001
D	Aspartic acid	0.060	0.060
E	Glutamic acid	0.083	0.083
F	Phenylalanine	0.004	0.005

	Name	Freq.	Bg.
G	Glycine	0.093	0.093
H	Histidine	0.013	0.013
I	Isoleucine	0.007	0.008
K	Lysine	0.123	0.123
L	Leucine	0.016	0.016
M	Methionine	0.024	0.024
N	Asparagine	0.023	0.023
P	Proline	0.003	0.003
Q	Glutamine	0.078	0.078
R	Arginine	0.026	0.026
S	Serine	0.052	0.052
T	Threonine	0.127	0.126
V	Valine	0.037	0.037
W	Tryptophan	0.001	0.001
Y	Tyrosine	0.019	0.019

	Name	Freq.	Bg.
A	Alanine	0.210	0.210
C	Cysteine	0.001	0.001
D	Aspartic acid	0.060	0.060
E	Glutamic acid	0.083	0.083
F	Phenylalanine	0.004	0.005
G	Glycine	0.093	0.093
H	Histidine	0.013	0.013
I	Isoleucine	0.007	0.008
K	Lysine	0.123	0.123
L	Leucine	0.016	0.016
M	Methionine	0.024	0.024
N	Asparagine	0.023	0.023
P	Proline	0.003	0.003
Q	Glutamine	0.078	0.078
R	Arginine	0.026	0.026
S	Serine	0.052	0.052
T	Threonine	0.127	0.126
V	Valine	0.037	0.037
W	Tryptophan	0.001	0.001

	Name	Freq.	Bg.
Y	Tyrosine	0.019	0.019

Other Settings

Motif Site Distribution	ZOOPS: Zero or one site per sequence
Site Strand Handling	This alphabet only has one strand
Maximum Number of Motifs	5
Motif E-value Threshold	no limit
Minimum Motif Width	6
Maximum Motif Width	50
Minimum Sites per Motif	2
Maximum Sites per Motif	100

Show Advanced Settings

MEME version
4.12.0 (Release date: Tue Jun 27 16:22:50 2017 -0700)

Reference
Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, pp. 28-36, AAAI Press, Menlo Park, California, 1994.

Command line

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meme lea_data.txt -protein -oc . -nostatus -time 18000 -maxsize 60000 -mod zoops -nmotifs 5 -minw 6 -maxw 50
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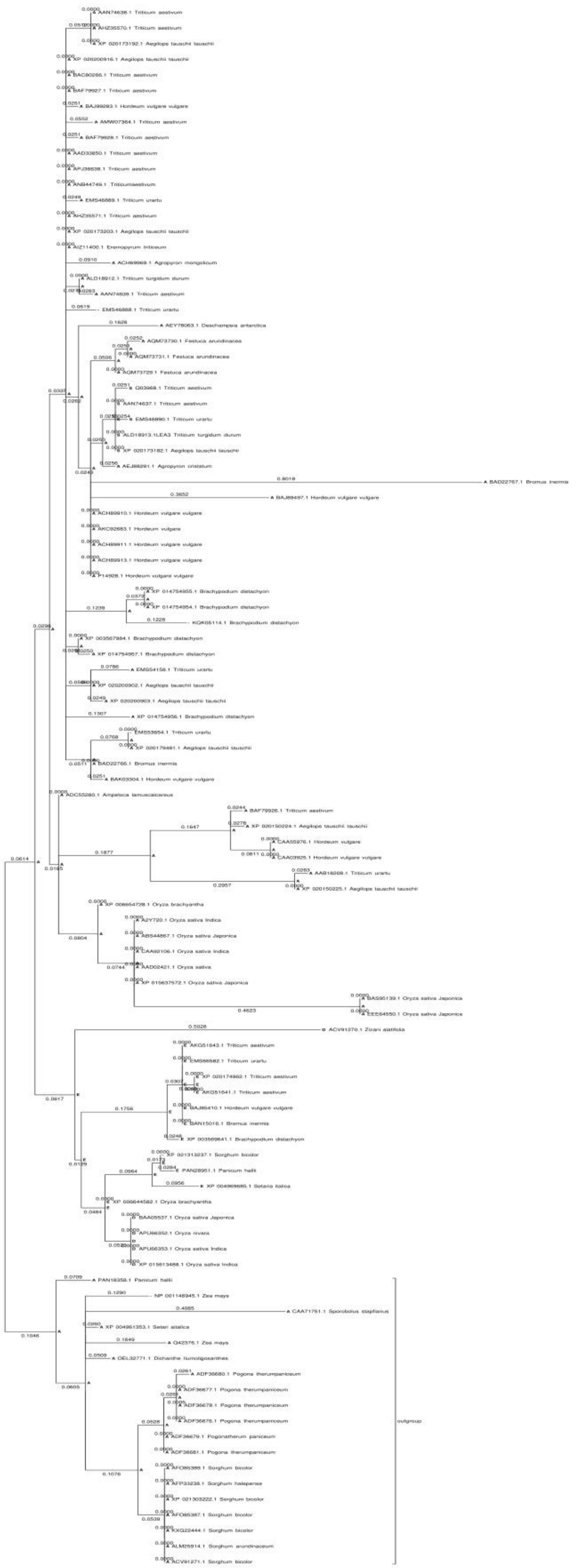
Supplementary 3: LEA protein sequences conserved motif analysis: Relatively short sequences of conserved amino acids (motifs) among the LEA protein sequences were conducted using the MEME/MAST (http://meme-suite.org). Colored blocks presented motifs distinctive for each LEA protein sequences. Each colored block indicates the distribution of distinctive motifs in each sequence. Each block shows the position and strength of a motif site. The height of a block gives an indication of the significance of the site, as taller blocks are more significant. The height is calculated to be proportional to the negative logarithm of the p-value of the site, truncated at the height for a p-value of 1e-10. Equal colors between sequences do not mean sequence similarity.



Supplementary 8: Molecular Phylogenetic analysis by Maximum Likelihood method: The constructed Neighbor joining-specified tree topology was analyzed using the Maximum Likelihood method based on the JTT matrix-based model (Jones *et al.,* 1992). The log likelihood of the tree is (-1178.06). A discrete Gamma distribution was used to model evolutionary rate differences among sites (five categories (+G, parameter = 8.7310)). The rate variation model allowed some sites to be evolutionarily invariable ([+I], 0.00% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). The analysis involved 100 amino acid sequences. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were 38 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar *et al.,* 2016).