Novosibirsk
2021

Evolution of MLO-like proteins in flowering plants

Pozharskiy A.S.[1,2*],
Gritsenko D.A.[1,2]

[1] Institute of Plant Biology and Biotechnology,
Almaty, Kazakhstan
[2] Al-Farabi Kazakh National University,
Almaty, Kazakhstan

*aspozharsky@gmail.com

ӨСІМДІКТЕРДІҢ БИОЛОГИЯСЫ
ЖӘНЕ БИОТЕХНОЛОГИЯСЫ ИНСТИТУТЫ
IPBB

Background

- MLO-like proteins (MLP) are known to present in all land plants
- Some particular MLP confer susceptibility to mildew-like fungi in various plant species
- Thus, MLP are of interest for the breeding of resistant plants
- Phylogeny of MLP remains understudied in global systematic scale

Aims

- Reveal high level phylogenetic groups (clades) of MLP in the wide selection of flowering plants
- Find characteristic protein motifs for these groups

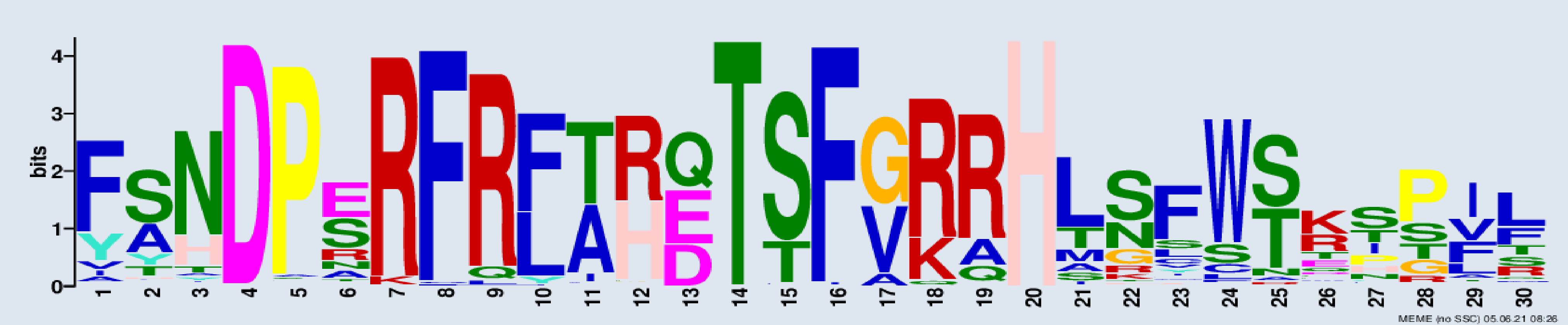
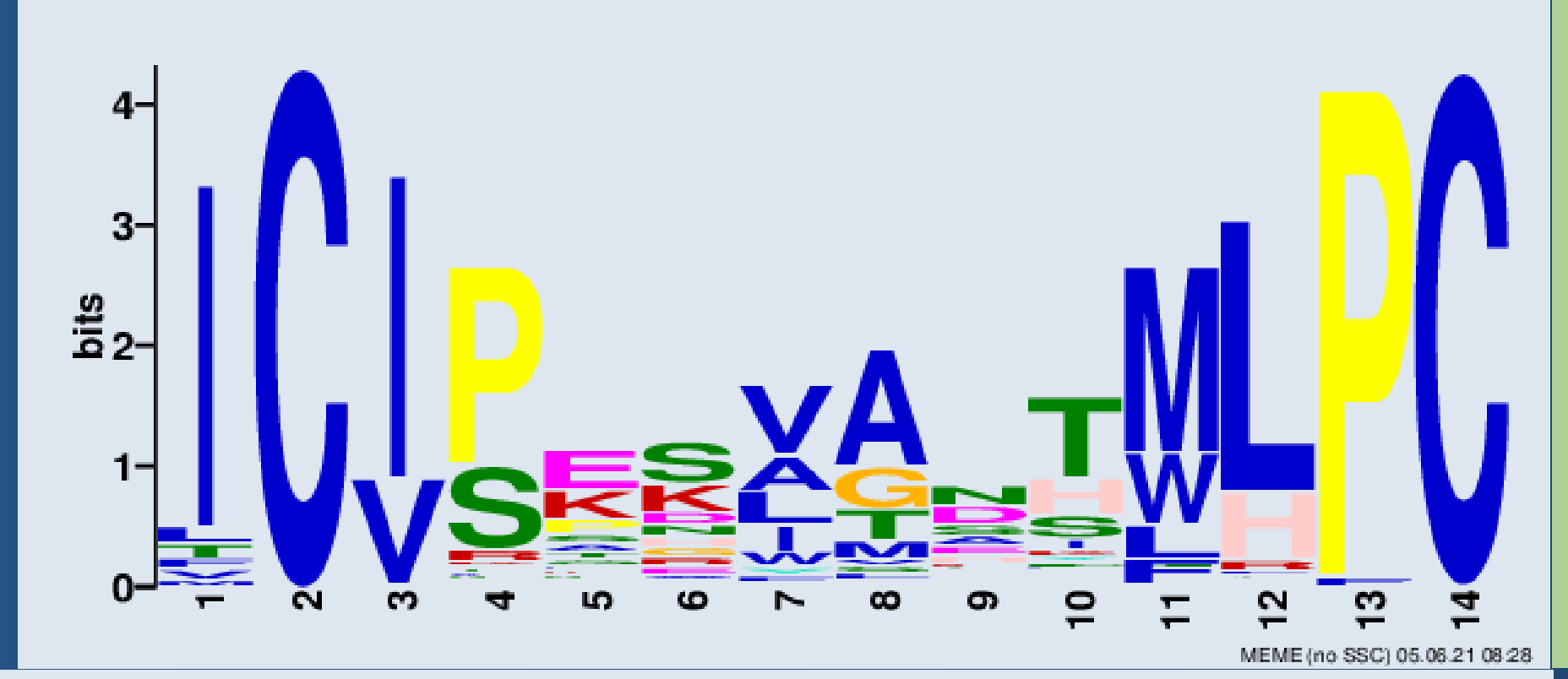
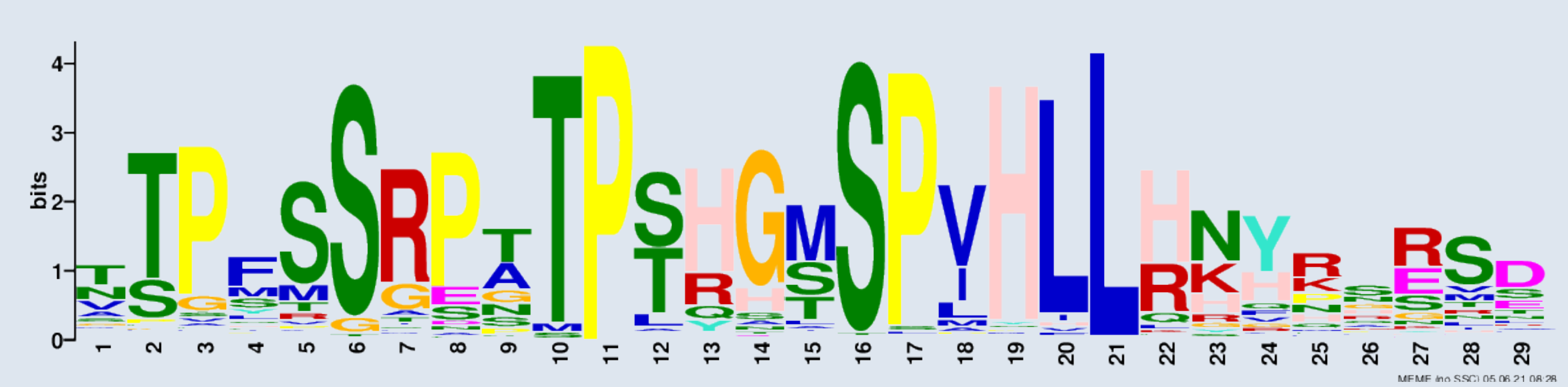
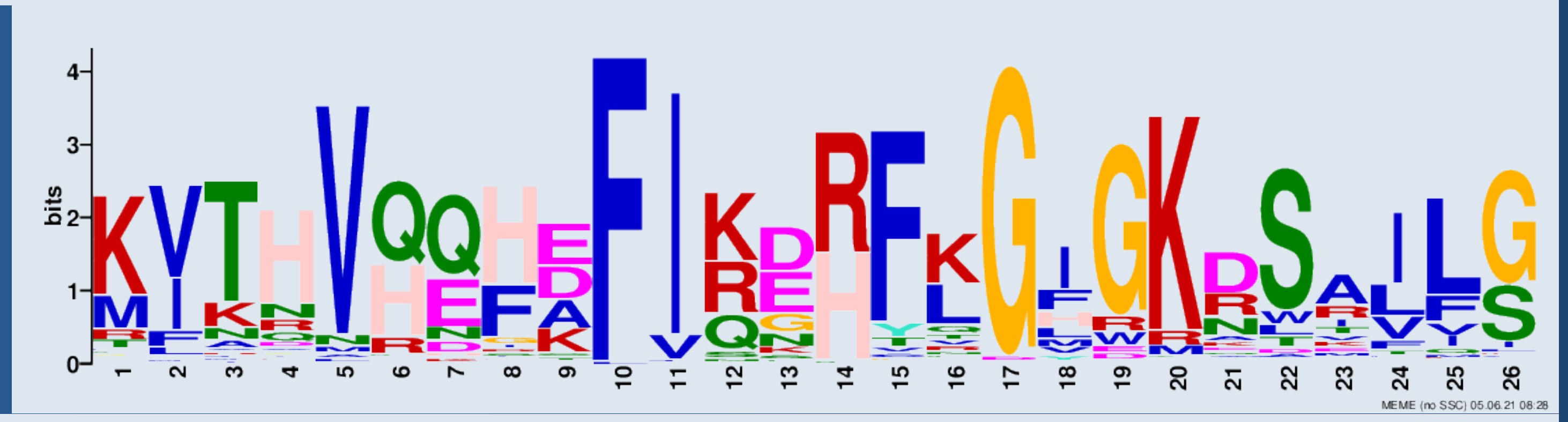
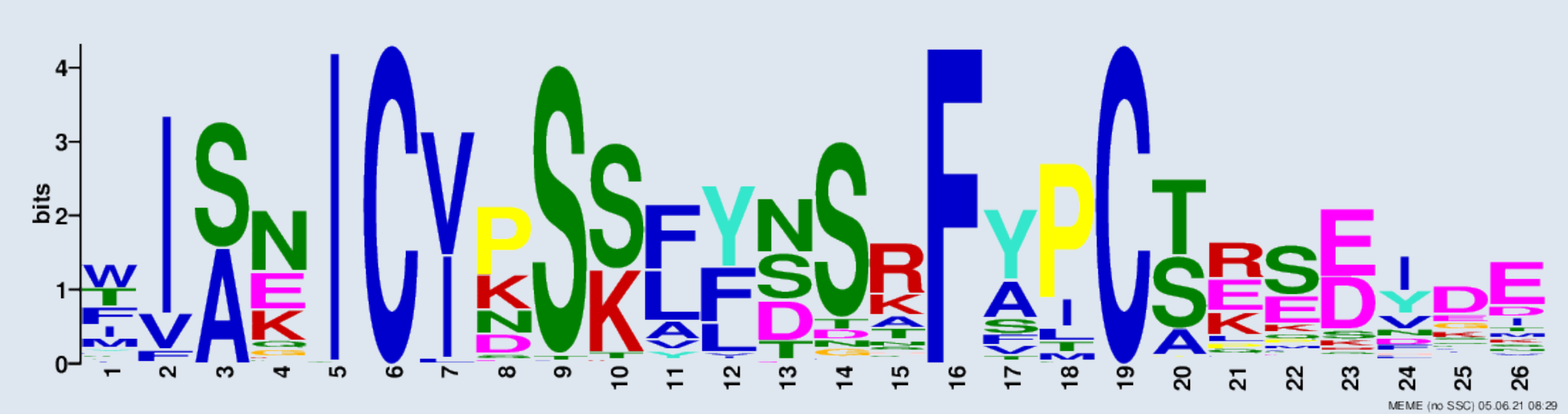
Methods

- **Data acquisition**: UniProt database (https://www.uniprot.org/)
  - Query: “MLO” [ID] AND “Viridiplantae” [OC]
- **Data filtering:**
  - Sequence length between 20th and 80th percentiles and no partial sequences
  - Only angiosperms + gymnosperms as an outgroup
  - Preliminary clustering with CD-HIT: only proteins with 9 and more similar sequences (50% threshold) selected
- **Phylogeny**: MSA with MAFFT, ML tree with FASTTREE, FigTree, MEGA X
- **Motif search:** MEME
- **General software:** R


MSA regions used for building ML tree
MLP – ML tree
Dicotyledons - asterids
Dicotyledons - rosids
Other dycotyledons
Monocotyledons - commenilids
Other monocotyledons
Other angiosperms
Gymnosperms
0
0.5
1
1.5
2
2.
1.1
1.2
1.3
2.1
2.2
3.1
3.2
3.3
3.4
3.5
Cluster 1
Cluster 2
Cluster 3

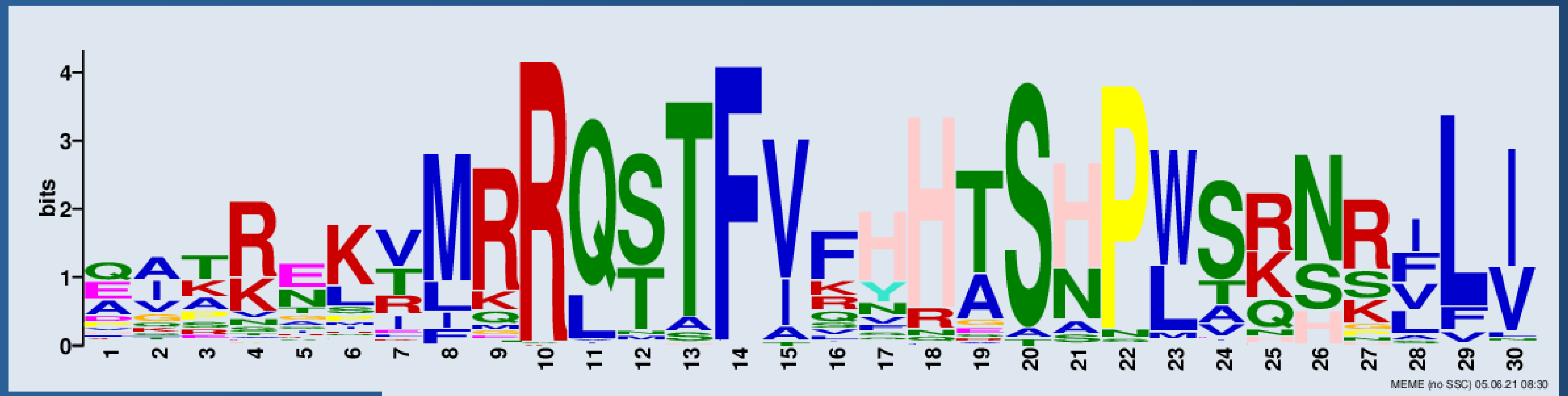
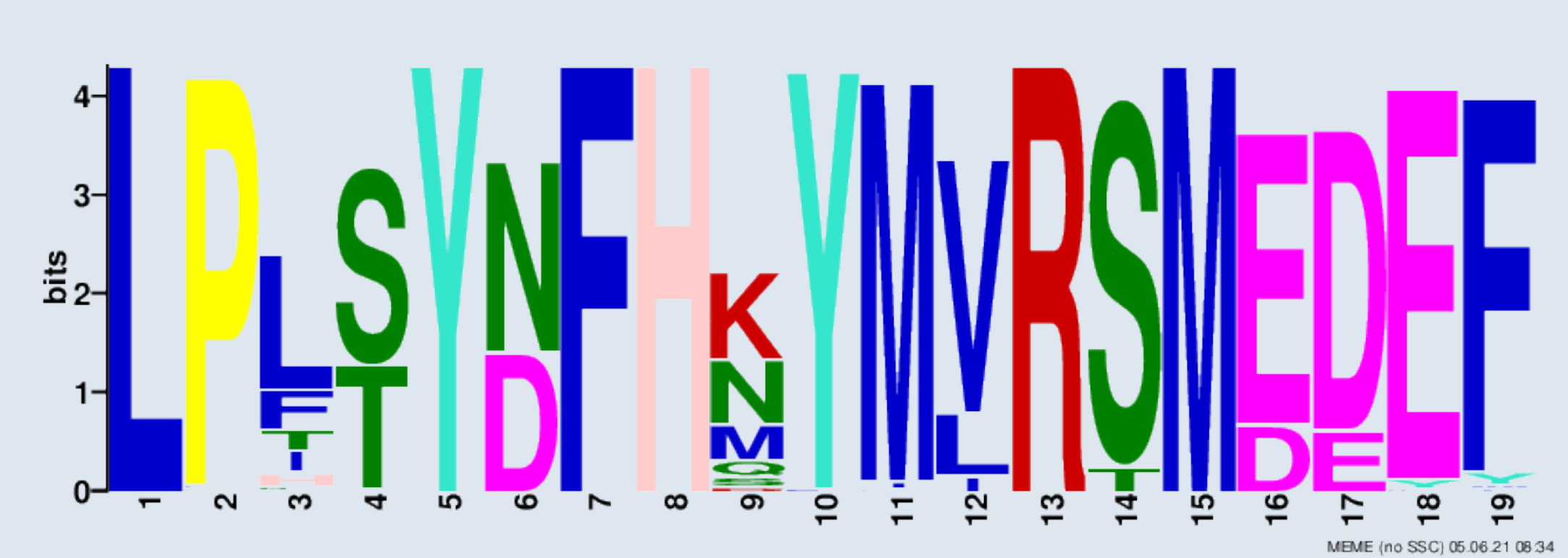
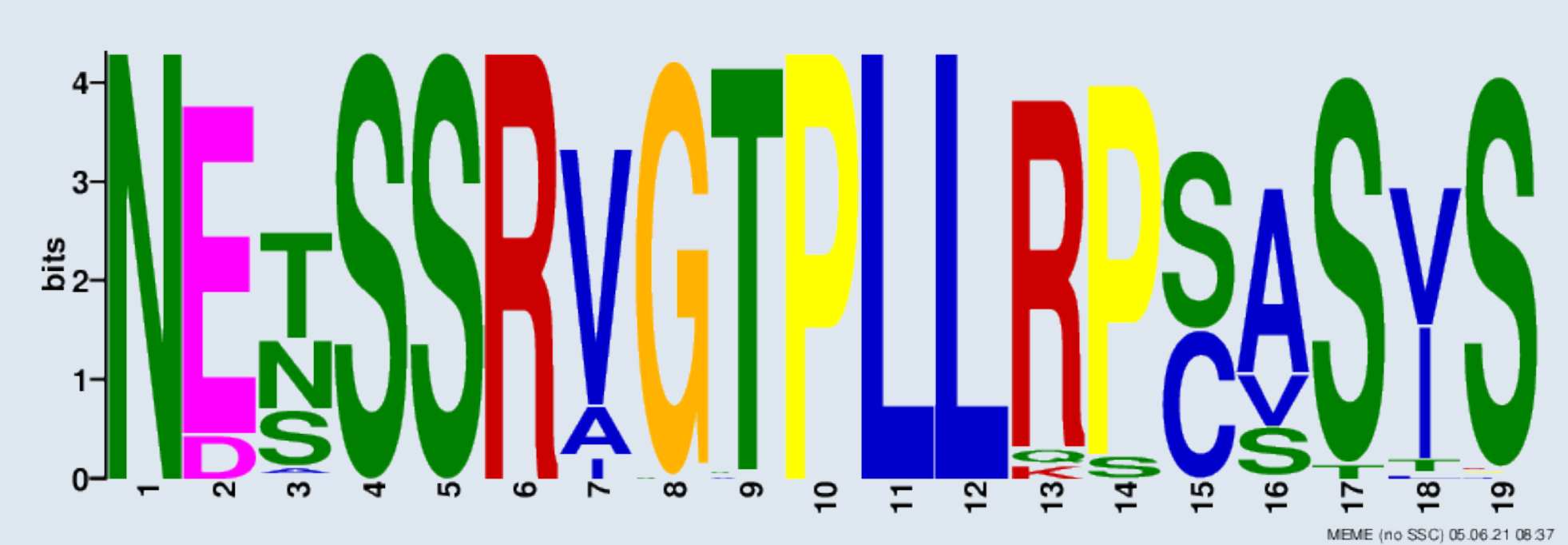
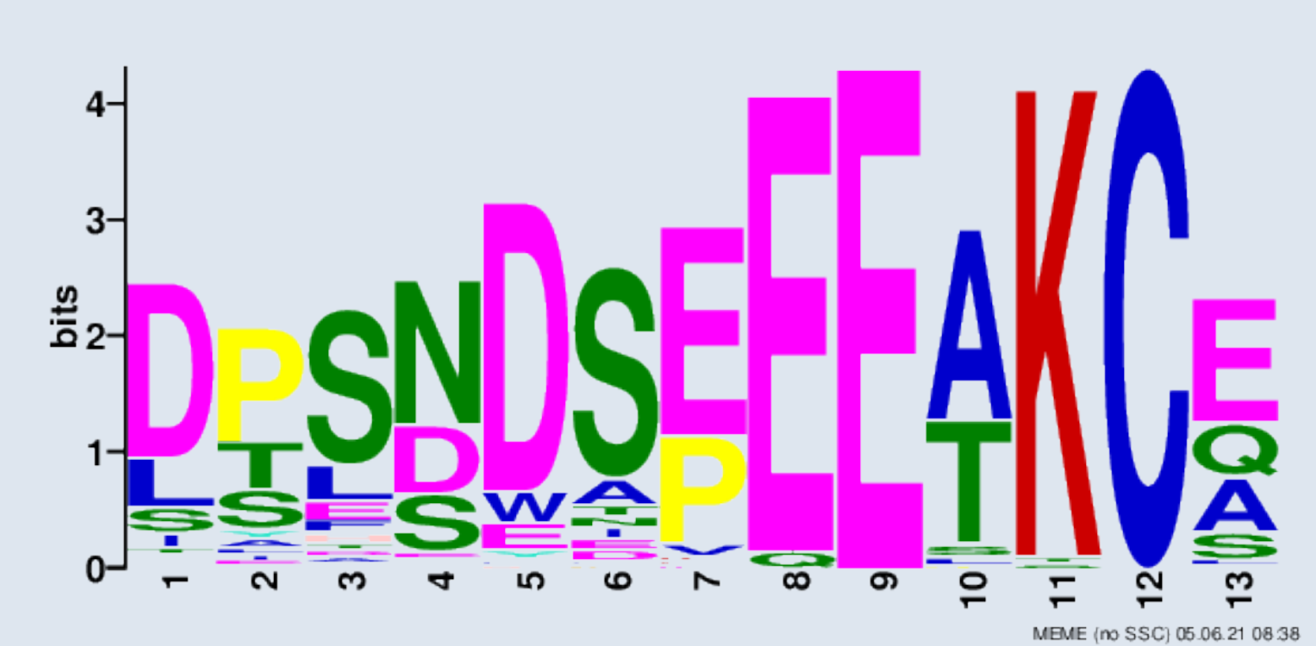
Characteristic motifs in clusters

Frequencies by clusters

	Cluster 1			Cluster 2		Cluster 3				
	1.1	1.2	1.3	2.1	2.2	3.1	3.2	3.3	3.4	3.5
	0.00	0.00	0.00	0.00	0.00	1.00	0.96	0.96	0.98	0.98
	0.05	0.87	0.96	0.00	0.00	0.99	0.97	0.96	0.97	0.99
	0.95	0.96	0.95	0.08	0.00	0.99	0.95	0.93	0.96	0.97
	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.86	0.00	0.94
	0.24	0.97	0.95	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	0.00	0.00	0.00	0.96	0.95	0.00	0.00	0.00	0.00	0.00

Characteristic motifs in clusters (continue)

Frequencies by clusters

	Cluster 1			Cluster 2		Cluster 3				
	1.1	1.2	1.3	2.1	2.2	3.1	3.2	3.3	3.4	3.5
	0.00	0.00	0.00	0.81	0.98	0.00	0.00	0.00	0.00	0.00
	0.00	0.00	0.00	0.00	0.00	0.95	0.97	0.92	0.59	0.61
	0.15	0.00	0.04	0.98	0.99	0.01	0.00	0.21	0.00	0.00
	0.00	0.00	0.00	0.85	0.00	0.00	0.00	0.00	0.00	0.00
	0.00	0.00	0.00	0.73	0.00	0.00	0.00	0.00	0.00	0.00
	0.00	0.00	0.00	0.00	0.01	0.03	0.00	0.00	0.68	0.00

Cluster specific amino acid changes in transmembrane domains (TD 3, 4, 6)

• 1.1	Cluster 1
• 1.2	
• 1.3	
• 2.1	Cluster 2
• 2.2	
• 3.1	Cluster 3
• 3.2	
• 3.3	
• 3.4	
• 3.5	

Conclusions

- Orthologs of MLO-like protein in flowering plants had diverged before and on the early stages of angiosperm evolution
- Some groups of MLP proteins share common motifs across angiosperm species, which can be used for identification of groups of homologs
- Seven MLO transmebrane domains form a conservative core of the protein, yet some domain (3, 4, 6) contain cluster specific amino acid changes with potentially significant functional effect