Screening and Characterization of LIM domain proteins in Cereal Crops

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Background

- LIM domain genes: widely distributed in various living organisms such as humans, animals, and plants.
- LIM domain proteins: believed to play vital role in survival/development of organisms

Introduction

- Two groups within plants: Cysteine-Rich Proteins and Da1/DARs
- CRPs, DA1/DAR proteins further categorized by subfamily: CRPs are WLIM1s, WLIM2s, PLIM1s, and PLIM2s; DA1/DARs are Classes I/II.
- CRPs modulate transcription and pollen development.
- DA1/DARs provide organ formation and response to stress.

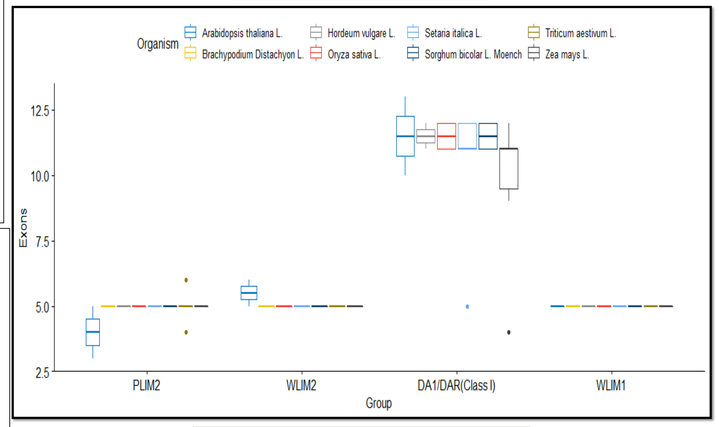
Hypothesis

I hypothesize these proteins are present in cereal crops and can be classified by individual characteristics.

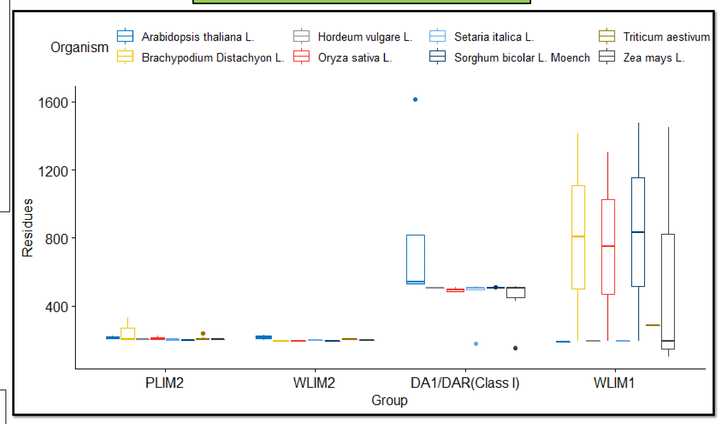
Material and Methods

- To Identify LIM proteins in cereal crops, a seed bank sequence was taken from Pfam.
- Additional protein sequences taken from Arabidopsis, Sunflower, Brassica, Tobacco, and Foxtail Millet were utilized as a query through BLASTp.
- Observed Lim Proteins used for Genome, and Coding Sequence extraction using Phytozome.
- LIM transcripts in cereal crops were aligned using MEGAX, used for phylogenetic analysis.
- Protein characteristics of subfamily, amino acid size, molecular weight, and localization were used to determine protein behavior, structure and functionality.

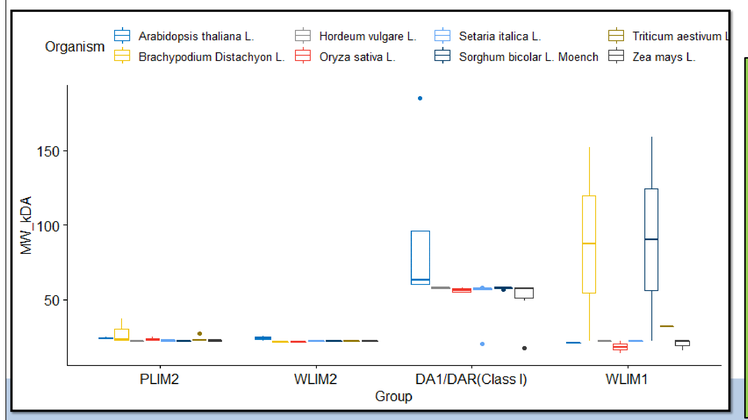
Exons of LIM Domain Proteins Subfamilies [1]



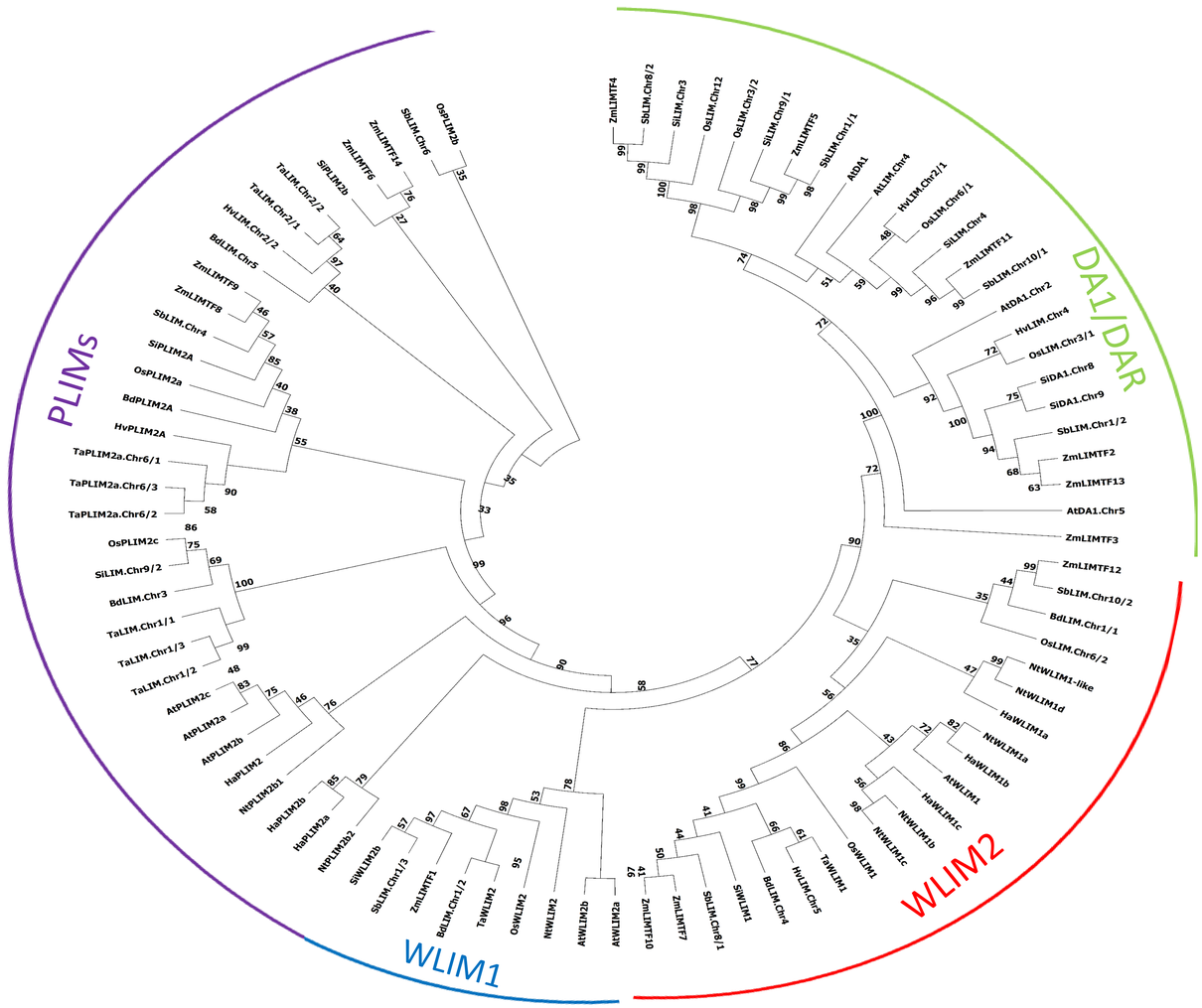
Residue (aa length) of LIM Domain Proteins Subfamilies [2]



Molecular Weight (kDa) of LIM Domain Proteins Subfamilies [3]



Phylogenetic Analysis of LIM domain proteins in Cereal Crops and Model Organisms [4]



-Figure 1,2,3: Comparison of LIM Domain proteins subfamilies and exons, residue, and molecular weight; Arabidopsis: marine blue, Barley: grey , Brachypodium Distachyon: yellow, Foxtail Millet: light blue, Maize: purple, Rice: red, Sorghum: navy blue and Wheat: brown, respectively.
--Figure 4: Maximum- Likelihood and JTT Model, Bootstrap Consensus Tree from 1000 replicates: Phylogenetic Analysis of Arabidopsis, Barley, Brachypodium Distachyon, Foxtail Millet, Maize, Rice, Sorghum, Sunflower, Tobacco, and Wheat.

Number of Lim Proteins in cereal crops and model plants

Plant	Proteins
Oryza sativa L.	10
Zea mays L.	14
Sorghum bicolor L. Moench	9
Hordeum vulgare L.	5
Triticum aestivum L.	10
Arabidopsis thaliana L.	10
Brachypodium Distachyon L.	6
Setaria italica	10
Nicotiana tabacum	9
Helianthus annuus	6

Results/Discussion

- We identified a total of 88 LIM domain proteins within cereal crops and model organisms. This would be 10, 14, 9, 5, 10, 6, 10, 9, and 6 for Rice, Maize, Sorghum, Barley, Wheat, and Brachypodium Distachyon, Foxtail Millet, Tobacco, and Sunflower, respectively.
- These proteins can be grouped based on their respective structure, localization, and molecular weight, amino acid size.
- CRPs: 6 or less exons, DA1/DARs: 5-12 exons
- CRPs (save WLIM1s) are shorter than Da1/DARs
- CRPs: molecular weight 14-37kDas, while DA1/DAR are heavier at 50- 185kDa.
- Majority of CRPs and DA1/DARs localized in nucleus.

Conclusions

- Identified 88 LIM domain proteins: 57 within cereal crops, 31 within model plants (33PLIMs, 9WLIM1s , 17 WLIM2s, 29 DA1/DARs)
- WLIM1s: high HTH-score, compared to other CRP subfamilies
- DA1/DARs: higher number of exons, aa residue, molecular weight (kDa) compared to CRPs

Suggests:
-WLIM1s have higher affinity and significance when binding to promotor sites, hold role in modulation, regulation, activation of transcription or transcription factors
-DA1/DARs more complex than CRPs

References:
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