

Integrated Proteomics and Metabolomics Emphasized Nutritional Benefits Driven by Lentil (Lens culinaris Medik) Seed Germination

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Integrated Proteomics and Metabolomics Emphasized Nutritional Benefits Driven by Lentil (Lens culinaris Medik) Seed Germination.

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Introduction

- 1. Lentils are small, lens-shaped legumes that are a great source of protein, fiber, and various vitamins and minerals, easy to cook and versatile in dishes, and are considered an environmentally friendly and sustainable food source.
- 2. Until now, lentil seed germination has been poorly described. The present work displays an original systems biology approach to address this gap in knowledge.
- 3. This study investigated lentil seeds at different germination stages and temperature conditions through a multi-omics approach, including:
 - Statistical analysis was performed on the proteome and metabolome separately to screen for markers with significant control differences;
 - Functional annotation of lentil protein-coding sequences was done based on homologous alignment against well-annotated plant genomes;
 - Study of physiological and metabolic changes during lentil germination based on annotation enrichment and Multi-Omics Integration (MOI).

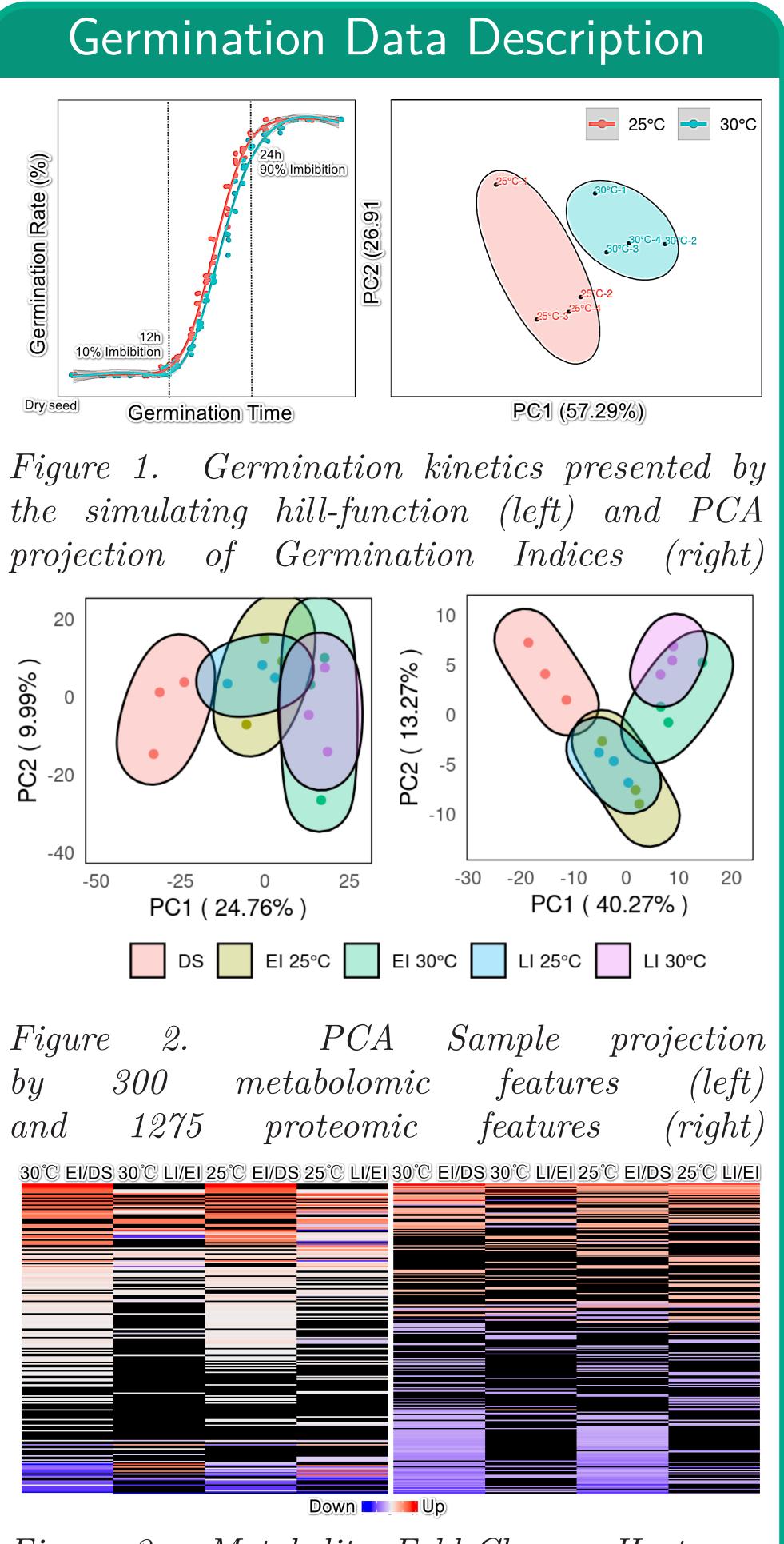


Figure 3. Metabolite Fold-Change Heat-map with total 88 significant features (left) and Protein Fold-Change Heat-map with 136 significant features (right)

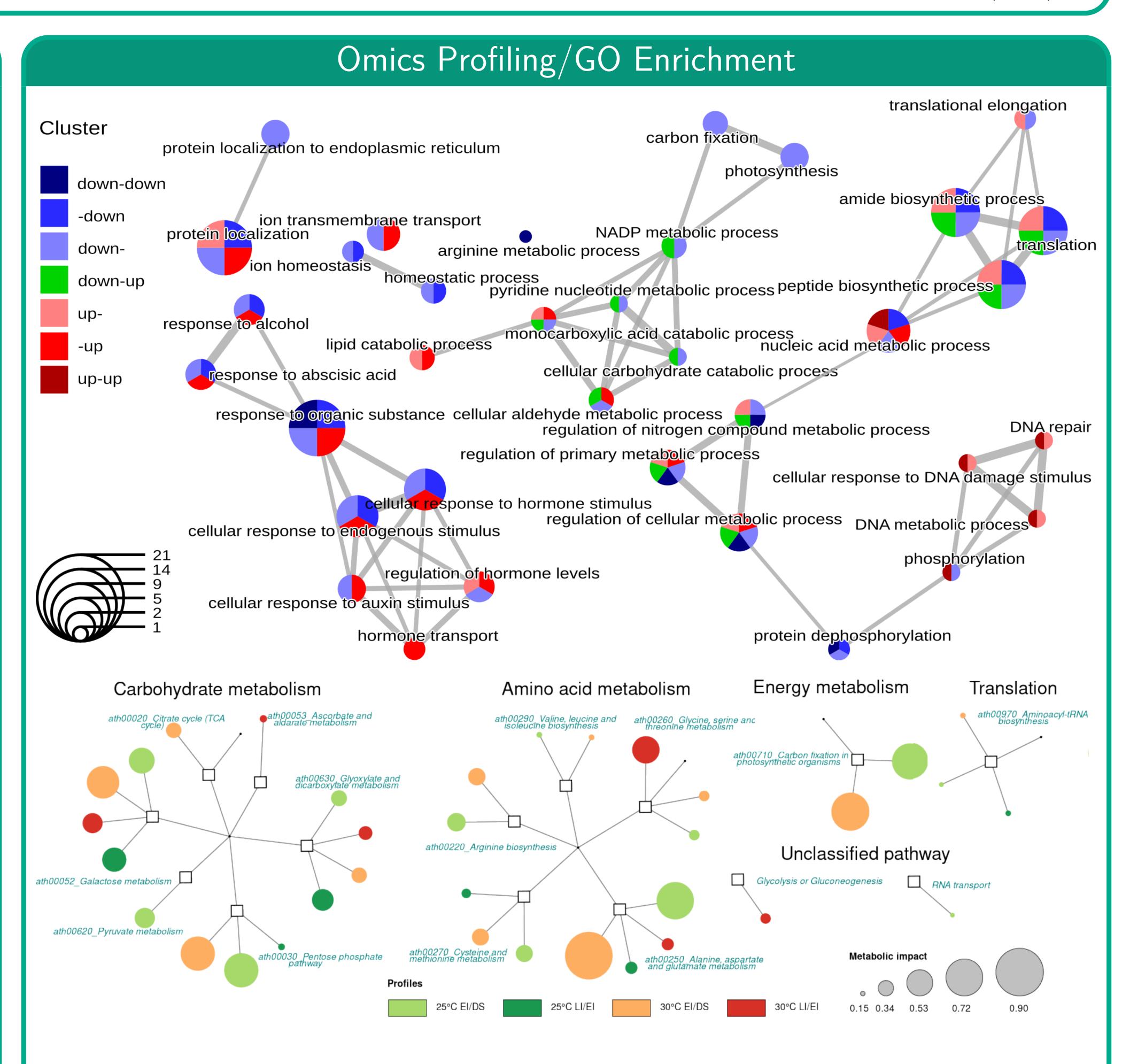


Figure 4. Top Proteomic GO enrichment (In total 1377 biological processes) by statistical profiles (above) and Top KEGG pathway enrichment (In total 85) network from Multi-Omics Integration (below)

Conclusions

- This is the first descriptive analysis about Lentil seed germination by Multi-Omics approach. with no significant differences found in the germination patterns of the two different temperature treatments
- The metabolic dynamics give us the guidance of improving the nutritional quality of Lentil seed as food.
- The biological process revealed the important physiological turn-over during germination process, including central metabolism, hormone signaling, response to abiotic/biotic stress etc.

Future Work

- Adding another omics dimensions (eg. transcriptomics) to reinforce the model interpretability.
- We will access the reproducibility of our results

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