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

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Lentil (Lens culinaris Medik.) is an annual legume rich in protein, fiber, vitamins, and minerals. Germination is a crucial process in the lentil life cycle with potential implications for both agronomy and food processing. However, knowledge about lentil seed germination has been limited. Our study aims to address this gap using a systems biology approach. We investigated lentil seeds at different germination stages (dry seed, 12h imbibition, and 24h imbibition) and two temperature conditions (25°C and 30°C) using physiological germination counting and Multi-Omics Integration (MOI) approaches, including metabolomics and proteomics. We identified differential accumulation of 88 out of 300 metabolites and 136 out of 1275 proteins under different germination/temperature conditions. Due to the lack of complete lentil genomics annotations, we further improved the automatic functional annotation of lentil protein-coding sequences based on homologous alignment against well-annotated plant genomes. Through the integration of Multi-Omics signatures, metabolite/genomic annotations, and pathway analysis, we identified metabolic pathways and biological processes related to protein metabolism, RedOx metabolism, and anti-nutritional compounds. This descriptive analysis using a Multi-Omics approach provides valuable insights into lentil seed germination for the first time. The metabolic dynamics observed in this study can serve as a guide for improving the nutritional quality of germinating lentil seeds as food. Lentil germination has potential implications for food processing and nutrition, and our findings contribute to a better understanding of the underlying molecular processes involved in lentil seed germination.

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Topic: From genes to seed biology, novel issues in molecular mechanisms and beyond