Temporal profiling of the heat-stable proteome during late maturation of Medicago truncatula seeds identifies a restricted subset of late embryogenesis abundant proteins associated with longevity

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Résumé en anglais	Developing seeds accumulate late embryogenesis abundant (LEA) proteins, a family of intrinsically disordered and hydrophilic proteins that confer cellular protection upon stress. Many different LEA proteins exist in seeds, but their relative contribution to seed desiccation tolerance or longevity (duration of survival) is not yet investigated. To address this, a reference map of LEA proteins was established by proteomics on a hydrophilic protein fraction from mature Medicago truncatula seeds and identified 35 polypeptides encoded by 16 LEA genes. Spatial and temporal expression profiles of the LEA polypeptides were obtained during the long maturation phase during which desiccation tolerance and longevity are sequentially acquired until pod abscission and final maturation drying occurs. Five LEA polypeptides, representing 6% of the total LEA intensity, accumulated upon acquisition of desiccation tolerance. The gradual 30-fold increase in longevity correlated with the accumulation of four LEA polypeptides, representing 35% of LEA in mature seeds, and with two chaperone-related polypeptides. The majority of LEA polypeptides increased around pod abscission during final maturation drying. The differential accumulation profiles of the LEA polypeptides suggest different roles in seed physiology, with a small subset of LEA and other proteins with chaperone-like functions correlating with desiccation tolerance and longevity.

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