

Transcriptome and phytohormone changes associated with ethylene-induced onion bulb dormancy

M. Carmen Alamar, Maria Anastasiadi, Rosa Lopez-Cobollo, Mark H. Bennett, Andrew J. Thompson, Colin G. N. Turnbull, Fady Mohareb and Leon A. Terry

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Abstract

Control of dormancy and sprouting in onion bulbs is commercially important for postharvest management. Although ethylene application is sometimes used to extend dormancy, the underlying mechanisms regulating dormancy transition remain unclear. Since the sprout leaves emerge from the bulb baseplate, we used this tissue to assess the impact of ethylene treatment and storage time on the hormone profile and the transcriptome. Reads from 30 libraries were assembled and annotated, with 94,840 unigenes retained after filtering. The *de novo* transcriptome assembly was of high quality and continuity (N50: 1809 bp, GC content: 36.21%), and was used to analyse differential expression and Gene Ontologies. Across two years, applied ethylene resulted in delayed dormancy break and reduced post-dormancy sprout vigour. Ethylene supplementation enhanced endogenous ethylene production and caused a transient climacteric-like increase in respiration. Significant changes in hormone and associated transcript profiles occurred through storage and in response to ethylene. In particular, abscisic acid (ABA) and its metabolite phaseic acid (PA) increased under ethylene during the longer dormancy period; however, cytokinin increases observed during storage appeared largely independent of ethylene treatment. Several hormone-related transcripts showed differential expression over time and/or in response to ethylene. Expression of ethylene biosynthesis (*ACO*), receptor (*EIN4*) and transcription factor (*EIL3*) genes were modified by ethylene, as were ABA biosynthesis genes such *NCED*, and cytokinin biosynthesis genes such as *LOG* and *CKX*. We conclude that ethylene substantially modifies expression of genes in several phytohormone pathways, and some of these changes may underlie the dormancy-extending effects of exogenous ethylene.