

# Transcriptome-wide gene expression plasticity in *Stipa grandis* in response to grazing intensity differences

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## Abstract

Organisms have evolved effective and distinct adaptive strategies to survive. *Stipa grandis* is one of the widespread dominant species on the typical steppe of the Inner Mongolian Plateau, and is regarded as a suitable species for studying the effects of grazing in this region. Although phenotypic (morphological and physiological) variations in *S. grandis* in response to long-term grazing have been identified, the molecular mechanisms underlying adaptations and plastic responses remain largely unknown. Accordingly, we performed a transcriptomic analysis to investigate changes in gene expression of *S. grandis* under four different grazing intensities. A total of 2,357 differentially expressed genes (DEGs) were identified among the tested grazing intensities, suggesting long-term grazing resulted in gene expression plasticity that affected diverse biological processes and metabolic pathways in *S. grandis*. DEGs were identified that indicated modulation of Calvin–Benson cycle and photorespiration metabolic pathways. The key gene expression profiles encoding various proteins (e.g., Ribulose-1,5-bisphosphate carboxylase/oxygenase, fructose-1,6-bisphosphate aldolase, glycolate oxidase etc.) involved in these pathways suggest that they may synergistically respond to grazing to increase the resilience and stress tolerance of *S. grandis*. Our findings provide scientific clues for improving grassland use and protection, and identify important questions to address in future transcriptome studies.

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