Using DNA Metabarcoding to Assess Mowing Impacts on Grassland Arthropod Communities

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BACKGROUND

Extensive grasslands harbour highly diverse arthropod communities that contribute to essential ecosystem functions and provide food for numerous vertebrates.

Mowing is essential for maintaining semi-natural grasslands, but its timing can substantially alter arthropod communities.

Traditional biodiversity monitoring often focuses on selected taxonomic groups, whereas DNA metabarcoding enables the simultaneous detection of a broad range of arthropods, offering a promising approach for assessing community-level responses to grassland management.

AIMS & METHODS

We evaluated the potential of DNA metabarcoding to track seasonal changes in arthropod communities under different mowing regimes.

The study was part of the Interreg Slovenia–Croatia CarEx project focused on managment of extensive grasslands.

Study sites: Kozjansko Regional Park (Slovenia) and Žumberak–Samoborsko gorje Nature Park (Croatia), 2024–2025.
Sampling: Repeated sweep-net sampling per standardized pre-defined protocol across contrasting mowing regimes, including unmown controls.
Laboratory: Non-destructive DNA extraction from bulk arthropod samples, followed by 456-bp COI metabarcoding and Illumina sequencing.
Analysis: Taxonomic composition, alpha diversity and beta diversity.

Test sites



Mowing regime



Sampling



Laboratory work

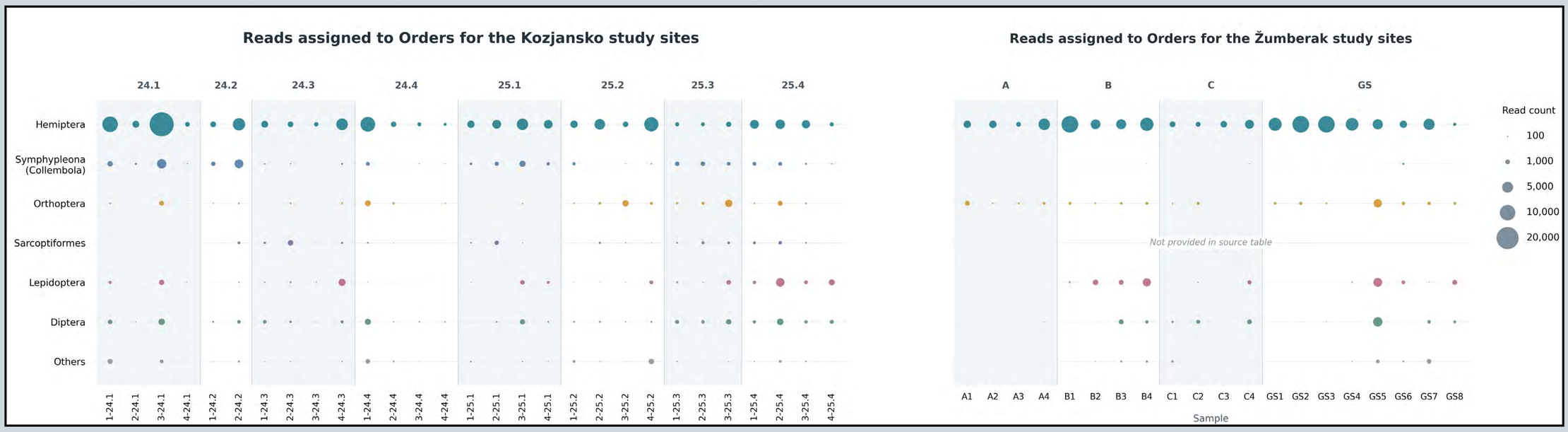


Bioinformatics

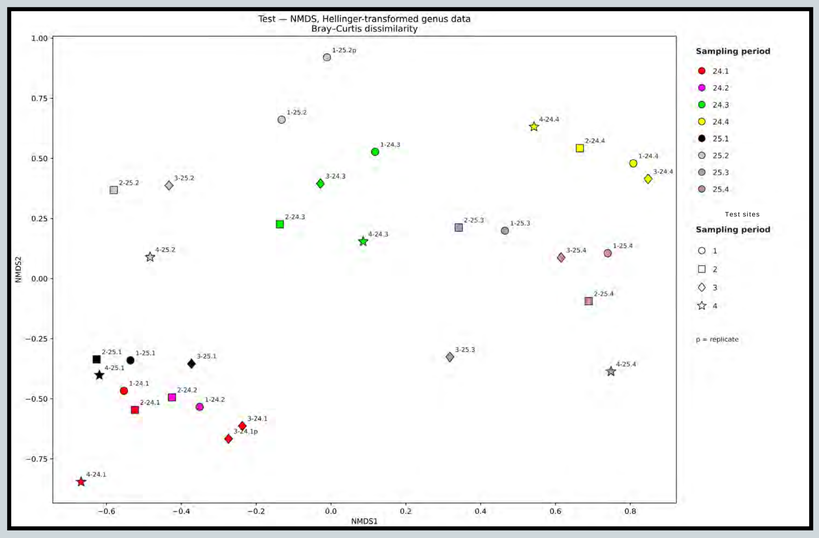


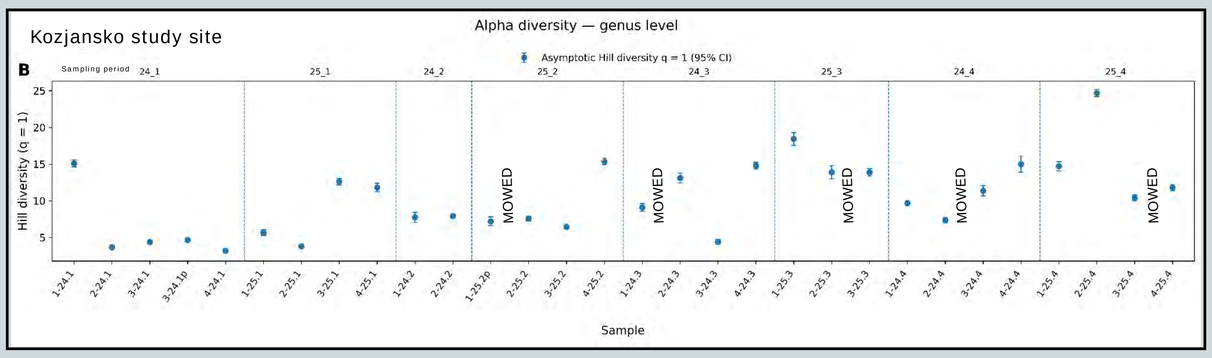
RESULTS

Broad arthropod diversity detected: Despite low sequencing depth (mean: 4,569 reads/sample), 456 Operational Taxonomic Units (OTUs) were assigned to 133 species or genera. Hemiptera dominated the assemblages.

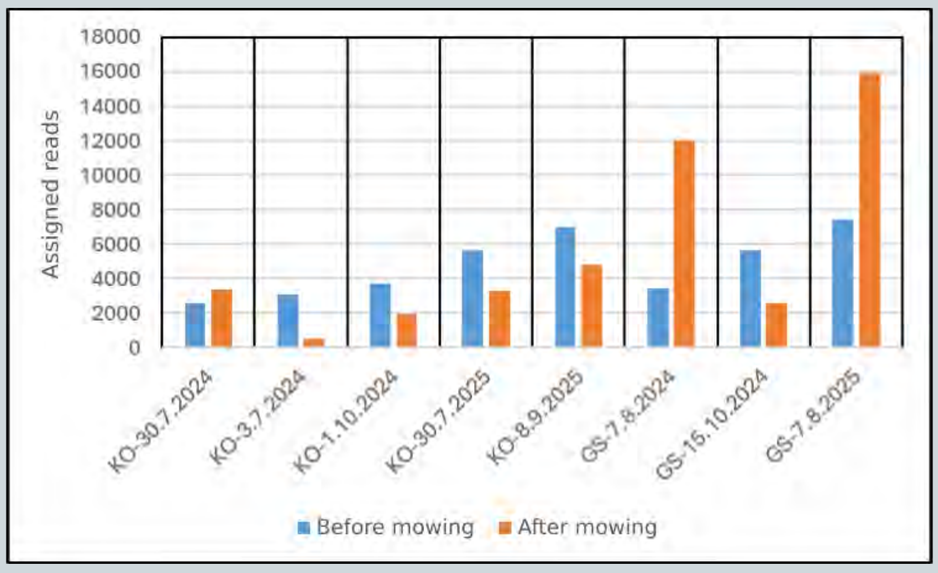


Seasonal changes were best reflected by beta diversity: Alpha diversity metrics show less distinct seasonal patterns. In contrast, beta diversity analyses revealed clearer differences in arthropod community composition across sampling periods.





Mowing effects were most evident in the number of assigned reads: Mowing effects were most evident in the number of reads assigned to metazoan OTUs, which decreased after mowing at most sites.



FUTURE PROSPECTS

(i) Increase sequencing depth to improve the detection of rare taxa and the completeness of community assessments.
(ii) Expand regional reference databases through DNA barcoding of morphologically identified Orthoptera.
(iii) Refine temporal and spatial sampling to better distinguish mowing effects from natural seasonal variation.

ACKNOWLEDGEMENTS

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