

ABSTRACT



Mosses are non-vascular plants that directly absorb atmospheric pollutants, making them powerful indicators of air quality. This study explores how air quality and particulate matter deposition affects moss species diversity in suburban (Rye, NY) and rural (Ithaca, NY) settings. DNA barcoding of the rbcL gene was used to assess sequence-level variation, and Air Quality Index (AQI) data was obtained from monitoring stations near each collection site. Moss samples from high-AQI (low air quality) urban areas had reduced within-group genetic diversity and tighter phylogenetic clustering than those from rural sites. These findings suggest that atmospheric pollution may reduce species diversity and influence adaptive genetic responses in moss populations.

INTRODUCTION

How does air quality, specifically heavy metal deposition, affect moss diversity?

- Atmospheric pollutants pose serious health risks
- Chronic exposure contributes to a variety of health conditions • Traditional air monitoring techniques such as high-volume samplers and mass spectrometry are costly
- Mosses lack protective cuticles and instead absorb solutes directly from the atmosphere
- Moss are sensitive to air quality and capable of accumulating airborne pollutants like heavy métals • Mosses can serve as low-cost indicators of atmospheric
- pollution



The Effect of Atmospheric Pollution on Moss Species Diversity

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RESULTS



Rye, NY (Site A) Moss Sample 1

Ithaca, NY (Site B) Moss Sample 1



Note. AQI data was retrieved from U.S. Environmental Protection Agency.



U.S. Environmental Protection Agency. (2025). Air quality index (AQI) data and weather conditions retrieved via AirNow API. *AirNow*. <u>https://www.airnow.gov</u>





DISCUSSION

- High-AQI (urban) moss populations exhibit reduced genetic diversity and tighter clustering compared to low-AQI (rural) population
- Air pollution likely imposes selective pressures or inhibits gene flow, driving genetic homogeneity in polluted areas
- A subset of urban samples with the highest AQI showed slightly elevated nucleotide diversity, hinting at stressinduced mutations or local adaptation
- Whole-genome and transcriptome analyses are needed to identify adaptive pathways underpinning these patterns
- Small number of sampling sites and no direct measurement of metal concentrations in moss tissues are limitations
- Strong correlation between AQI and moss genetic diversity shows atmospheric pollution as a major driver of genetic variation

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