

Exploring atmospheric microbial communities with autonomous unmanned aerial vehicles

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ABSTRACT

Agricultural ecosystems are shaped by interactions with atmospheric microbial communities (AMCs)—time-stamped consortia of microscopic life forms moving through the atmosphere from near and faraway places. AMCs may participate in a myriad of biological, chemical, and ecological processes in agricultural ecosystems, yet little is known about their structure, dynamics, and function. The ability to characterize, monitor, and forecast the composition and role of AMCs in agricultural ecosystems is important for developing innovative, rational, and informed approaches to managing these habitats. We used state-of-the-art autonomous (self-controlling) unmanned aerial vehicles (UAVs) equipped with unique microbe-sampling devices to collect AMCs tens to hundreds of meters above agricultural fields at Virginia Tech's Kentland Farm. We amplified, cloned, and sequenced ribosomal DNA from five AMCs. A large number of our sequences had close matches to uncultured prokaryotic and eukaryotic microorganisms. One sequence was similar to a bacterium from a cavern in Arizona. We used high-information content fingerprinting (HICF) to monitor population changes in AMCs. HICF profiles frequently matched enterobacteria, with repeated hits to *Pantoea*, which was the best BLAST hit to many of our prokaryotic sequences. Other HICF profiles suggested plant pathogens in the genus *Pseudomonas*. Our work continues to elucidate the potential ecological functions and roles of AMCs in agricultural ecosystems, identify unique phylogenetic properties that may confer adaptation and survival of microorganisms in agricultural ecosystems, assist in predicting the distribution and spread of AMCs over time and space across large-scale biological and meteorological gradients, and forge new discoveries of novel microbes in an under-sampled and relatively unexplored ecological setting.

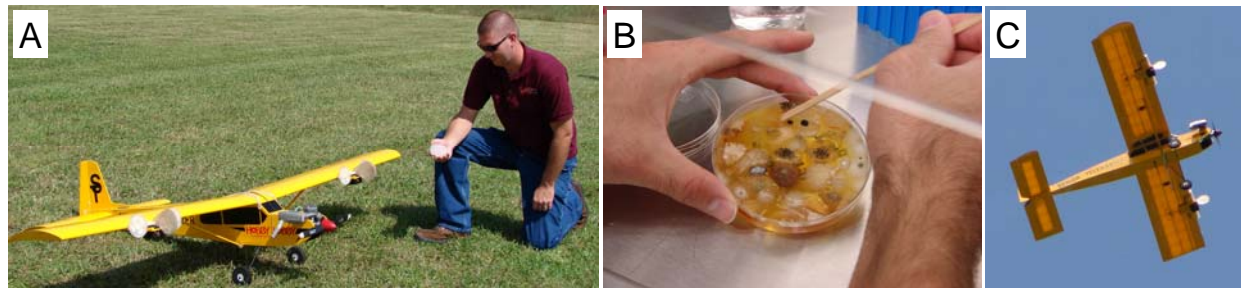


FIGURE 1. Autonomous unmanned aerial vehicles (UAVs) (A) used to collect atmospheric microbial communities (AMCs) (B) tens to hundreds of meters above the surface of the earth. Unique microbe-sampling devices mounted underneath the wings are opened and closed from the ground once the UAV is aloft (A). The UAVs can sample over 150,000 liters of air during a single flight (C).

INTRODUCTION

- The atmosphere is filled with a diverse array of microorganisms traveling from both near and faraway places (2).
- Over 99% of the microorganisms in a given environment are unculturable (1).
- Recent advances in genomics and bioinformatics have revolutionized the way we 'see' complex microbial communities (3-5).
- We have developed cutting-edge autonomous (self-controlling) unmanned aerial vehicles (UAVs) to explore entire communities of microbes in the atmosphere (FIGURE 1, A).

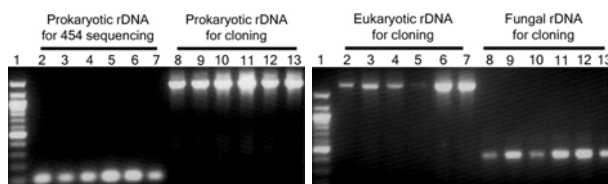


FIGURE 2. Prokaryotic and eukaryotic rDNA PCR amplicons from six different AMCs. Individual AMCs are represented in each lane for each primer pair.

MATERIALS AND METHODS

- We used autonomous UAVs (FIGURE 1, A) to collect atmospheric microbial communities (AMCs) tens to hundreds of meters above agricultural fields at Virginia Tech's Kentland Farm. The UAVs maintained a precise altitude and sampling path during flight (FIGURE 3).
- Genomic DNA was extracted from collection plates (FIGURE 1, B), and 16S/18S rRNA genes were amplified using universal primers (FIGURE 2) (5), cloned, and sequenced. Each individual sequence served as a BLAST query.
- High-information content fingerprinting (6) was used to monitor population dynamics among AMCs.

RESULTS AND DISCUSSION

1. We amplified, cloned, and sequenced ribosomal DNA from five different AMCs collected 100m above the ground (FIGURE 2). A large number of our sequences had close matches to uncultured prokaryotic and eukaryotic microorganisms. One sequence was similar to a bacterium from a cavern in Arizona.
2. High-information content fingerprinting proved useful in providing semi-quantitative interpretations of population changes among individual AMCs. Fragment sizes frequently matched enterobacteria, with repeated hits to *Pantoea*, which was the best BLAST hit to many of our prokaryotic sequences.
3. Our work may help shed light on the ecological functions and roles of AMCs in agricultural ecosystems. Collectively, AMCs may serve as a bioindicator of ecosystem health. Our ongoing studies with autonomous UAVs aim to unleash the new and fascinating field of 'aerogenomics'.

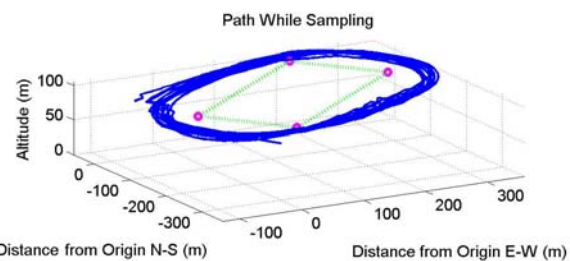


FIGURE 3. The autonomous UAVs maintain a precise altitude and sampling path during aerobiological sampling.

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