Brief report

Dermatophagoides pteronyssinus in ambient air bioaerosols

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Background: House dust mite (HDM) sensitization is a leading cause of allergic rhinitis and asthma worldwide, with *Dermatophagoides pteronyssinus*, *Dermatophagoides farinae*, and *Blomia tropicalis* being the primary allergenic species typically associated with indoor environments. Even effective multicomponent interventions creating an HDM-free indoor environment are often insufficient to prevent allergy, as HDM exposure may also occur outdoors.

Objective: To assess the potential for outdoor HDM exposure, we applied air biomass sequencing and metagenomic techniques to detect HDM DNA in both indoor and outdoor bioaerosols, offering an alternative to conventional dust sampling methods.

Methods: We used 2 data sets in this study: (1) a global data set comprising 1,171 outdoor air samples collected across 33 countries in open air environments and (2) a data set of indoor (n = 161) and outdoor (n = 156) air samples collected across 156 apartments from 106 locations in Singapore. All air samples were collected by drawing 24,000 to 36,000 L of air using SASS3100 air samplers; all samples were processed identically. Species-level taxonomic classification was performed using Kaiju software aligned to the National Center for Biotechnology Information nonredundant database, with a minimum threshold of 40 reads per taxon.

Results: Analysis of 1,171 global outdoor air samples revealed *D pteronyssinus* as the most prevalent HDM species; it was detected in 208 samples, with abundance increasing from temperate toward equatorial regions. In Singaporean households, *D pteronyssinus* was found in 58.4% of indoor samples and 21.2% of nearby outdoor samples, with high median DNA read counts outdoors suggesting that exposure to HDM is not limited to domestic environments. *B tropicalis* and *D farinae* were also detected in Singapore, albeit at lower frequencies.

Conclusion: Our findings highlight the need to expand environmental allergen surveillance beyond household dust to include ambient and outdoor air, particularly in tropical climates. (J Allergy Clin Immunol Global 2026;5:100667.)

Key words: *House dust mite,* Dermatophagoides pteronyssinus*, air microbiome, bioaerosols, metagenomics*

INTRODUCTION

House dust mite (HDM) sensitization is one of the most common allergic responses worldwide, significantly contributing to allergic rhinitis and asthma. The most common species associated with allergic sensitization are *Dermatophagoides pteronyssinus, Dermatophagoides farinae*, and *Blomia tropicalis*.[1] These mites typically thrive in household environments, particularly in bedding, carpets, and upholstered furniture, where they feed on human skin flakes and flourish in warm, humid conditions. The allergens that they produce, mainly through their fecal particles and body fragments, are potent triggers of IgE-mediated immune responses. *D pteronyssinus* is often considered the most medically relevant owing to its widespread distribution in households and high allergenic potential.[2]

Traditionally, HDMs have been regarded as indoor organisms tightly linked to domestic environments, in which conditions favor their proliferation. This view has shaped both public health messaging and allergen avoidance strategies, which focus predominantly on household dust reservoirs. However, even effective multicomponent interventions, such as targeted cleaning strategies, air purification, high-efficiency particulate air (HEPA) vacuuming, and pest control aimed at creating an HDM-free indoor environment, are often insufficient to fully prevent allergic reactions or control severe asthma.[3] Emerging evidence suggests that HDM allergens can be detected in environments beyond the bedroom,[4] raising the possibility of more extensive exposure routes. Expanding our understanding of HDM ecology to include potential outdoor reservoirs is therefore essential, particularly in tropical climates, where year-round warmth and humidity provide conditions that are highly favorable for mite survival and dispersal.

In our study, we aimed to assess the potential for outdoor HDM exposure by direct identification and quantification of the mite-associated biologic material in the air. The uniqueness of our experimental approach lies in the use of ultralow airborne biomass sequencing and metagenomics techniques, which enables identification and classification of HDM-related material in bioaerosols, offering an alternative to traditional sampling of

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Abbreviation used
HDM: House dust mite

settled indoor particles (usually dust[5]). Rather than targeting specific allergenic protein(s), our approach provides a broad and ecologically meaningful assessment of overall allergen exposure potential, reflecting the actual airborne load of HDM-derived particles that individuals inhale. This provides actionable information for managing risk of allergy and asthma in human environments both indoors and outdoors.

In our study, we identified the presence of HDM-specific DNA both indoors and in ambient and outdoor air. Although HDMs are typically associated with indoor household environments, our findings show that potential exposure to HDMs is not limited to domestic spaces, challenging the traditional understanding of HDM ecology and allergen exposure.

RESULTS AND DISCUSSION

Bioaerosol studies predominantly report the prevalence of bacteria and fungi in airborne biomass.[6] In this study, we specifically analyzed a large metagenomic sequencing data set of 1,171 outdoor air samples collected across 33 countries. Sampling prioritized accessibility over a systematic geographic grid, aiming for broad global bioaerosol coverage to detect DNA from the clade Panarthropoda, which includes mites and insects. All air biomass samples were collected using SASS3100 air samplers in open air environments during 2-hour periods (300 L per minute) regardless of season and were processed under standardized operating procedures.[6,7] Libraries of the DNA extracts were prepared with the Accel-NGS 2S Plus DNA Library Kit (Swift Biosciences, Ann Arbor, Mich). Sequencing data were generated on the Illumina HiSeq2500 platform at a DNA read sequencing length of 250-bp paired ends. We generated metagenomic data sets consisting of at least 2 million reads per sample. Species-level taxonomic classification of the metagenomic data in *fastq* format was conducted using Kaiju v. 1.7.2 software[8] aligned against the National Center for Biotechnology Information nonredundant database, with a minimum threshold of 40 reads per taxon. As a result, 346 taxa of the clade Panarthropoda were identified, with a total of 2,133,883 reads assigned to this clade.

The most prevalent (top-ranked) Panarthropoda species identified in our analysis was *D pteronyssinus*, with 226,975 metagenomic DNA reads assigned to this species, accounting for 10.6% of all Panarthropoda-assigned reads. This species was detected in 208 of the 1,171 global air samples. The average number of aligned bases across DNA sequencing reads was 207, indicating high alignment specificity to the reference genomes. In contrast, *D farinae* and *B tropicalis* were found to be exceedingly rare, with only 376 DNA reads from 2 samples and 665 DNA reads from 1 sample identified, respectively.

In the temperate climate (Fig 1 and see Table E1 and Fig E1 in the Online Repository at www.jaci-global.org), the highest abundance of *D pteronyssinus* in bioaerosols was observed in Germany (n = 172), where 13% of samples tested positive, with a median read count of 71. Some samples contained exceptionally high levels of HDM-specific DNA, reaching up to 171,190 reads. A notable presence of HDM was also detected in France (n = 46), where 33% of air samples tested positive, with a median read count of 115 and maximum count of 1,031.

In equatorial and tropical regions (Fig 1 and see Table E1 and Fig E1), *D pteronyssinus* was detected even more frequently: 43% of air samples from Singapore (n = 116), 25% from Malaysia (n = 56), and 20% from Brazil (n = 50) were HDM-positive. The median read counts were 180 (maximum 991) in Singapore, 58 (maximum 1,960) in Malaysia, and 146 (maximum 18,675) in Brazil.

Our air metagenomic data show that *D pteronyssinus* abundance increases from temperate regions toward the equator in terms of both abundance and the proportion of positive air samples (Fig 1, *B*). We also observed prominent seasonal differences: in temperate climates, the proportion of *D pteronyssinus*–positive samples rose from 9.8% in summer to 20.7% in winter, whereas in tropical regions the proportion was even higher (23.8%) (Fig 1, *C* and Table E2 in the Online Repository at www.jaci-global.org). Accordingly, the median DNA read counts among *D pteronyssinus*–positive samples were 70, 73, and 85 in temperate summer, temperate winter, and tropical summer, respectively (Fig 1, *C*). *D pteronyssinus* has previously been reported to exhibit strong seasonal fluctuations in indoor environments and dust samples,[9] with increased loads in summer and decreased loads in winter. In our study, metagenomic analysis indicated that in outdoor environments *D pteronyssinus* is detectable in both summer and winter, with the number of mite-positive samples even higher in winter, suggesting potential overlooked reservoirs of HDM in outdoor environments. However, more rigorous seasonal sampling at the same locations is required to accurately assess the absolute load of *D pteronyssinus*–associated material in the air. In addition, we show that *D pteronyssinus* levels were consistently higher in city settlements than in towns and rural areas (Fig 1, *D*), suggesting the association of HDM with human households and activity.

As Singapore has been identified as one of the locations with the highest levels of HDM, we collected air samples from local households both indoors (n = 161) and outdoors (n = 156). Indoor samples were taken from bedrooms at night (sampling time 11 PM-7AM; sampling rate 50 L per minute), maintaining a consistent sampling window to avoid confounding effects from microbial diel cycles on airborne community structure.[6] Outdoor samples were collected in close proximity to the same households, from areas such as open balconies or window ledges at the same timing. The households were predominantly standard apartments (131 apartments in the Housing and Development Board, 15 apartments in condominiums, and only 10 apartments in landed property) located across 106 locations throughout Singapore, thus providing broad geographic coverage. The vast majority of Singaporean households were naturally ventilated, with 111 reporting daily and nightly use of natural ventilation, whereas only 2 reported never using natural ventilation and keeping their windows or balconies consistently closed. All samples were collected and analyzed using procedures consistent with those used for the global data set described earlier.

DNA from all 3 major HDM species were detected in Singaporean households, with *D pteronyssinus,* which was found in 58.4% of indoor samples, being the most prevalent (Fig 2). *B tropicalis* was identified in 52.8% of households, whereas *D farinae* was detected in only 21.7% of households (Fig 2). The average numbers of aligned bases across DNA sequencing reads were 188 bp for *D pteronyssinus,* 220 bp for B tropicalis, and 175 bp for *D farina.*

Interestingly, a substantial number of air samples collected outdoors in proximity to the tested households were also

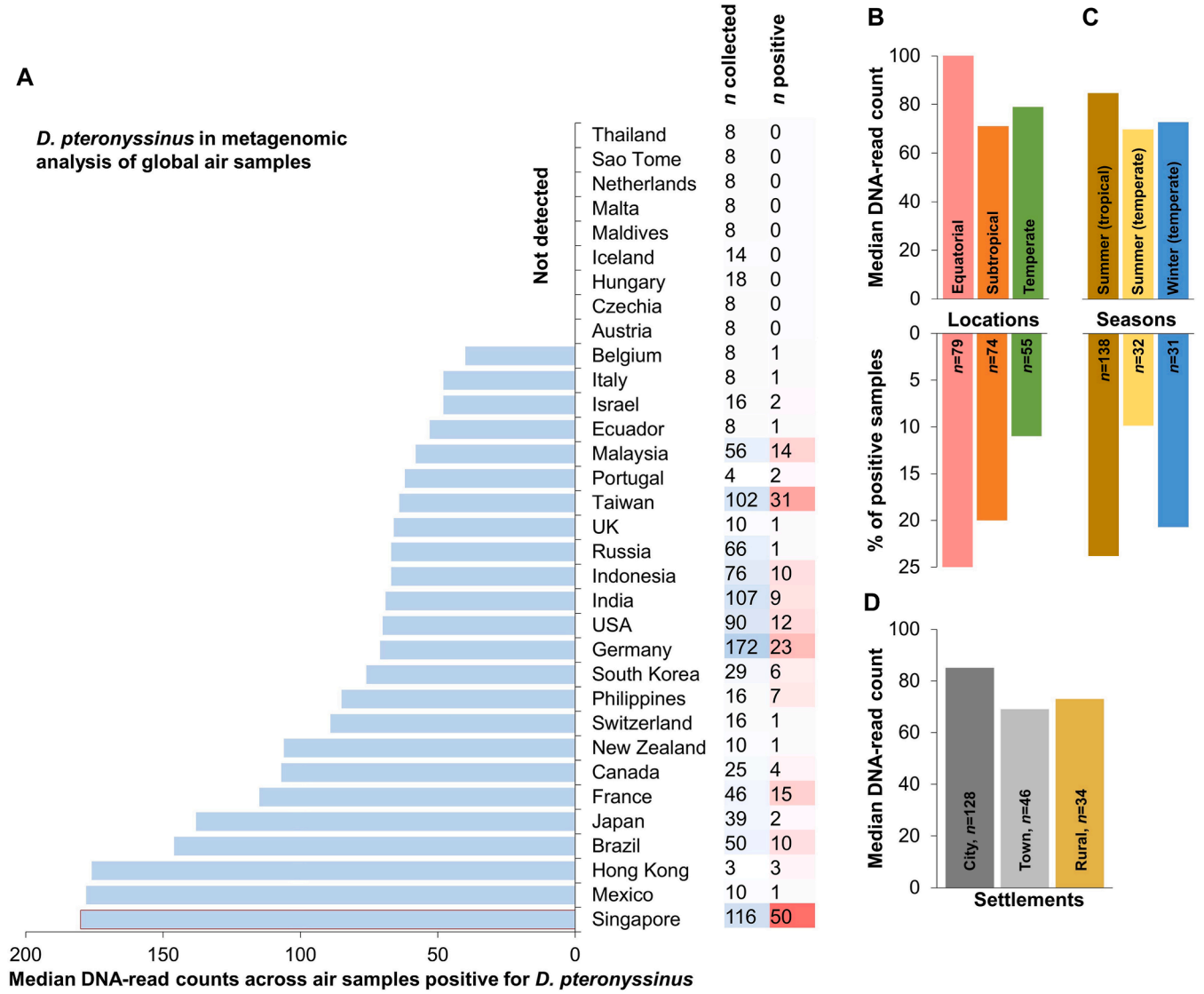

FIG 1. Abundance of *D pteronyssinus* DNA in outdoor air bioaerosols across 33 countries **A,** Sequencing reads were taxonomically assigned using Kaiju against the National Center for Biotechnology Information nonredundant database. Samples with at least 40 reads mapped to the *D pteronyssinus* genome were considered positive. The terms *n collected* and *n positive* indicate the total and positive air sample counts, respectively, per country. **B-D,** Variation in *D pteronyssinus* abundance (median DNA read count) and the proportion (%) of positive air samples across different geographic locations (**B**), seasons (**C**), and settlement types (**D**); *n* denotes the number of positive samples.

HDM-positive: 21.2% tested positive for *D pteronyssinus*, 19.2% for *B tropicalis*, and 8.3% for *D farinae* (Fig 2). Notably, the median DNA read counts in indoor and nearby outdoor samples from HDM-positive households did not differ substantially: for *D pteronyssinus*, there were a median of 186 DNA reads indoors versus 149 outdoors; for *B tropicalis*, there were 113 indoors versus 80 outdoors; and for *D farinae*, there were 76 indoors versus 66 outdoors. Although some resuspension of dust particles from indoor environments is expected owing to natural ventilation in the majority of households, the consistently high median DNA read counts in outdoor mite-positive samples suggest that potential overlooked reservoirs of HDM in outdoor environments cannot be excluded. This is also supported by other research showing that 40.5% of instances of individual HDM (*Dermatophagoides p 1*) exposure during daytime can be attributed to outdoor sources.[3]

The high prevalence of *D pteronyssinus* DNA in both temperate and equatorial and/or tropical bioaerosols aligns with epidemiologic data on HDM sensitization rates reported across different geographic regions. In both Europe and tropical environments, the rate of sensitization to HDM may exceed 80% in atopic individuals.[1,2,10] Global warming, with rising temperatures and humidity, creates conditions favorable for HDM proliferation,[11] potentially expanding their geographic distribution. This is supported by our data showing the abundance of *D pteronyssinus* increasing from temperate climates toward the equator.

The detection of HDM-specific DNA in outdoor air in our study suggests that exposure is not confined to indoor spaces,

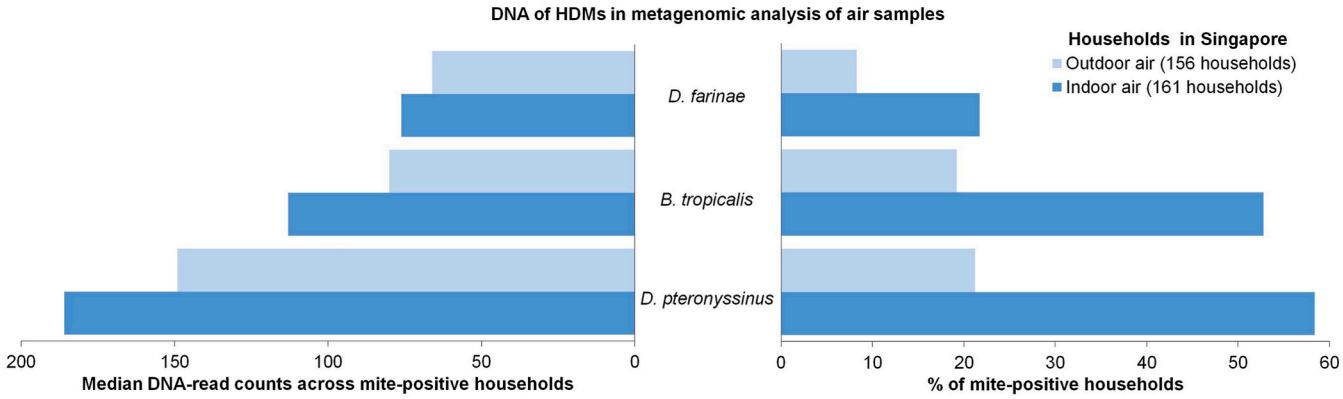

FIG 2. Abundance of DNA from *D pteronyssinus, B tropicalis,* and *D farinae* in bioaerosols collected from and near the households across Singapore. DNA read counts were determined using metagenomic approaches.

potentially explaining early and persistent sensitization (also supported by Hallas[12]). However, further analysis is required to identify specific HDM allergens in outdoor bioaerosols using metagenomic approaches, particularly through the detection of DNA fragments encoding HDM-associated allergenic proteins. Moreover, more systematic global sampling is required to identify potential overlooked reservoirs of HDM outdoors.

Potential sources of HDM DNA in outdoor settings include air exchange between indoor and outdoor spaces; resuspension of dust particles from clothing, bedding, and waste; and human-mediated transport via personal belongings. Additional contributions may arise from waste disposal sites (eg, all Singapore houses equipped with in-house or in-unit chutes for daily waste collection), deposition on outdoor surfaces followed by later resuspension by wind, and long-distance aerosol transport. Our very preliminary results show that HDM taxa can be detected in fruit swab samples as part of the fruit skin microbiome (unpublished data obtained in the year 2025), further supporting the existence of potential outdoor sources of HDM. Identifying such sources could help clarify whether the presence of HDM DNA in ambient air reflects true environmental reservoirs, passive dispersal from indoor environments, or sporadic contamination events. In Singapore, approximately one-third of the HDM-positive households indoors also showed positivity outdoors. Moreover, the observation of higher median DNA read counts in urban settlements with greater human density supports the idea that HDM presence may be associated with human habitation and activity.

Our new experimental approach of direct identification of biologic material originating from HDMs in bioaerosols offers an ecologically valid assessment of potential complex allergen exposure, reflecting the actual airborne burden of HDM-derived particles that individuals are likely to inhale. This provides relevant and actionable information for managing risk of allergy in human environments, including decontamination efforts and household cleaning practices. Our findings also highlight the need to expand environmental allergen surveillance beyond household dust to include ambient air, offering a more comprehensive understanding of exposure risks in the context of climate change, evolving public health challenges, and allergy management.

Data availability statement: The data supporting the findings of this study are available from the corresponding author on reasonable request.

Declaration of the use of generative artificial intelligence. During the preparation of this work the authors used ChatGPT for proofreading to improve grammar and clarity. After using this tool/service, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

DISCLOSURE STATEMENT

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Clinical implications: Using metagenomics techniques, we have demonstrated that HDM DNA is prevalent in outdoor air worldwide, suggesting broader environmental exposure to specific house dust mite species.

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