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AN 'IN SITU' CORING TECHNIQUE FOR ESTIMATING THE POPULATION SIZE OF HOUSE DUST MITES IN THEIR NATURAL HABITAT

by D. B. HAY *

ABSTRACT: An in situ core sampling method was used to obtain absolute population density estimates for the mite, Dermatophagoides pteronyssinus Trouessart (Acari : Pyroglyphidae) in the mattress habitat. At the 95% fiducial limit the numbers of D. pteronyssinus in the top 1.5 cm of substrata were 8,200-26,800 mites m⁻². Mite densities that were calculated from vacuum samples of the same habitat underestimated the abundance of D. pteronyssinus by more than three orders of magnitude. Vacuuming did not detect all mite species inhabiting the mattress, and eggs and immature mites were under-represented in vacuum samples. The importance of absolute population estimates versus relative estimates of abundance and population density indices is discussed, and a number of ways in which the core sampling approach may contribute to future house dust mite research are suggested.

INTRODUCTION

The dust that collects in the human domestic environment provides a habitat for xerophilic fungi and a number of pyroglyphid mites (Acari : Pyroglyphidae) loosely termed "the house dust mites". These mites include members of the genera Dermatophagoides and Euroglyphus that are a cause of asthma, rhinitis and atopic dermatitis in a large proportion of allergic patients (reviewed by FAIN et al., 1990). House dust mites have been a major focus for research since they were first implicated in allergic disease in the mid 1960s (VOORHORST et al., 1964; OSHIMA, 1964), but our grasp of the ecology of these mites has been painstakingly slow to develop in the last three decades (COLLOFF, 1991a). Ironically, the bio-medical emphasis of the research has often obscured progress in house dust ecology; most studies have been biased towards clinical issues (e.g. the quantification of allergens), and

* Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS, UK. 
Present address: Department of Educational Studies, University of Surrey, Guildford, Surrey, GU2 5XH, UK.

sampling has been conducted without reference to mainstream ecological literature.

Ecologists use three broad approaches to estimate population density: a) absolute population density estimates (the number of individuals per unit area of habitat), b) relative density estimates (e.g. the number of individuals encountered per unit sampling effort) and c) population indices (e.g. the assay of waste products). The determination of absolute population size data is by far the most informative method because it allows the comparison of population sizes of different species in a variety of habitats at any sampling time. Furthermore, the mortality factors for a species cannot be determined without absolute figures for the population size.

There are no data on the absolute population density of house dust mites. House dust mite distribution and abundance are regularly assessed from the numbers of mites in vacuumed (or occasionally brushed) samples of dust; either by direct counting (i.e. relative density estimation) or by assay of guanine (a mite excretory product) or mite allergens (i.e. indices of abundance). These approaches are unreliable because the relative mite densities depend upon the suction — strength of the vacuum device used and the depth and structure of the sampled substrata. As a consequence, it is very difficult to compare the relative mite densities reported from different studies, and more fundamentally, comparisons between data obtained for different habitats may not be valid, even within a single sampling program.

Recently, live trapping techniques (e.g., the heat escape technique of Bischoff & Fischer, 1990; and Tovey's mobility test described by Colloff, 1991a) have been developed as alternative sampling methods for use in house dust research. These techniques rely on the use of sticky traps to catch the mites as they approach the surface of their habitat. In general, live trapping is a source of population size estimates, but the data can be used to generate absolute population density estimates if a patch of substratum is sampled repeatedly; the absolute population size can then be estimated because the rate of trapping will decline in successive samples in proportion to the total population density. Alternatively, trapping data can be converted to absolute terms by regression analysis if the absolute population size is determined simultaneously. Similarly, the experimental addition of mites to uninfested patches of habitat can be used to calibrate trap-efficiency. This latter approach has been adopted by Bischoff et al. (1992), and these authors have shown that textiles that would be considered mite-free on the basis of vacuum sampling may in fact harbour considerable numbers of mites. Unfortunately, there are pitfalls to the use of sticky-traps for assessing mite abundance. First, the rate of capture is not independent of behaviour. Second, the nature of the substrata will have a considerable effect on capture success and therefore, comparing data from different habitats will prove difficult. Third, eggs and dead mites cannot be detected.

Another approach is to sample a unit of habitat by coring (counting the number of individuals per unit of habitat i.e. absolute population size data). Core sampling techniques have been used in soil ecology for many decades but to the author's knowledge, this approach sampling has never been applied to the study of house dust mites.

In this report, a coring method for use in house dust mite sampling studies is described. Some preliminary data from a mattress habitat are presented and this includes an estimate of the absolute population size of Dermatophagoides pteronyssinus. As far as the author is aware, this is the first time that an absolute measure of the size of a house dust mite population has been reported for the natural habitat. The results obtained by core sampling are also compared with those of conventional vacuuming sampling techniques.

METHODS

Samples were collected from a double mattress (Fig. 1) on January 14, 1991. Vacuum samples were collected from two areas of the mattress surface (X and Y; Fig. 1) directly into modified, sterile 50 ml Falcon tubes. The tapered base of each tube was removed and replaced with a 24 μm nylon gauze on which the dust was retained. The tubes were fitted
to the hose mouth of a 1000 watt Medivac vacuum cleaner (Medivac PLC, UK) and suction was applied for 2 min as the collection tube was drawn over the mattress surface. Core samples were taken from random locations within each of 27 grid cells drawn over the remaining mattress area (Fig. 1). Plugs of mattress were removed by cutting round an inverted 50 ml Falcon tube (1.8 cm² surface area) with a scalpel blade and the tube was pushed down into the material. At a depth of 1.5 cm, the Falcon tube passed through into the hollow, sprung interior of the mattress and it was withdrawn containing a 2.7 cm³ volume of the fabric. Each core was cut into 3 discs (5 mm deep) and each disk was stored at -20°C for not longer than one month before inspection for mites and other fauna. Briefly, each disc was warmed at 55°C for a minimum of 6 hr in glass Petri dishes containing lactic acid and then carded with a pair of fine forceps. Mites were extracted from the suspension with a Pasteur pipette, mounted in HOYER’s medium (KRANTZ, 1978) and identified by light microscopy using the key of FAIN et al. (1990). The identity of immature pyroglyphids was determined by the criteria of MUMCUOGLU (1976) and eggs were identified by allometry (MUMCUOGLU, 1976; COLLOFF, 1991b).

Damaged specimens were presumed dead and were excluded from further analysis.

Absolute population density estimates for *D. pteronyssinus* were calculated from the core sample data. The frequency distribution of living mites per core was tested for fit the Poisson distribution (a test for randomness) and an expansion of the negative binomial series (overdispersion or clumping). The negative binomial exponent (k) (a measure of the degree of aggregation of mites) was obtained by maximum likelihood estimation. The upper and lower 95% fiducial limits for the total population size were determined by the method of KREBS (1989).

**RESULTS**

Vacuum samples of dust contained living specimens of *D. pteronyssinus*. The population density was 3-46 mites m⁻², assuming that all intact mites were alive at the time of sampling. Similarly, the numbers of live and dead mites was 93-325 *D. pteronyssinus* m⁻².

Mattress cores contained intact specimens of *D. pteronyssinus* (relative dominance = 95 %), *Euroglyphus maynei* (3 %) and *Cheyletus tenuipilis* Fain (2 %). Damaged mites included *C. tenuipilis*, the pyroglyphids *D. pteronyssinus* and *E. maynei*, the stored product mites *Lepidoglyphus destructor* Schrank (Acari : Glycyphagidae) and *Acarus siro* L. (Acari : Acaridae), the follicle mite *Demodex follicorum* Simon (Acari : Demodicidae) and an unidentified species of *Tarsonemus* (Acari : Tarsonemidae). Total mite counts (counts of all specimens alive and dead) per core (2.3 cm³) were from 0 to 97 mites. The highest number of living *D. pteronyssinus* per core was 15 (Fig 2), but the majority of cores (23/27) contained less than 6 live mites. Four cores lacked *D. pteronyssinus*. The mean number of intact mites per core was 3.78 and the sample variance was 11.34 (variance/mean ratio = 3.06). Mites were highly aggregated (variance > mean); the negative binomial exponent (k) was 2.07 (correct to two significant figures). However, there was no evidence to suggest that mites were more abundant at any of the three depths of mattress examined. The 95% fiducial limits for the mean number of living *D. pteronyssinus* in the top 1.5 cm of mattress were 8,200-26,800 m⁻².
FIG. 2 : The frequency distribution of Dermatophagoides pteronyssinus in mattress cores. The data was significantly different from the Poisson distribution (random) but were consistent with an expansion of the negative binomial series ($\chi^2 = 5.97$).

Table 1 shows the population age structure of *D. pteronyssinus* in vacuum and core samples. Statistical comparison of these results would not be valid because of the small number of vacuum samples but these data suggest that vacuuming may underestimate the abundance of smaller instars (larvae and protonymphs) and eggs.

**DISCUSSION**

The discrepancy between vacuum sample estimates of *D. pteronyssinus* abundance (3-46 living mites m$^{-2}$) and the absolute population size of this species (8,200-26,800 m$^{-2}$) is more than three orders of magnitude. Previously, Bischoff and Bronswijk have estimated that vacuuming may sample as little as 5-10 % of the total mite population in a given habitat (reported in Bischoff & Fischer, 1990).

The data presented here suggests that vacuum extraction efficiencies in the region of 0.5-1 % may be closer to reality.

The seasonal fluctuation of mite populations has been thoroughly documented in the literature (e.g. : Arlian *et al.* , 1982; Korsgaard, 1983) but these data have been compiled from vacuum samples of dust and the quantification of mite wastes. Dubabeck (1979) suggests that mites may migrate vertically through their natural substrata in response to changes in microclimate and this phenomenon has been confirmed experimentally by De Boer (1990). Since it is impossible to evaluate the depth from which vacuuming extracts mites, it is also difficult to distinguish the effects of migration from changes in total mite density. It is unlikely that vacuuming samples all mite instars with equal efficiency (see Table 1), and this is a further source of error because a change in population age structure cannot be separated from fluctuations in mite population size. This is particularly significant because changing climatic conditions may cause a shift in population age structure (Suto *et al.*, 1991, reported in Collof, 1991a), presumably because different stages have different environmental tolerance limits; the quiescent protonymph of *D. farinae* for example, is particularly resistant to desiccation (Arlian, 1989) and the eggs of *D. pteronyssinus* may survive periods of environmental conditions that are unfavorable to other life stages (Colloff, 1987).

Although this analysis is based on the study of a single mattress it does highlight gaps in knowledge.

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Table 1 : The population age structure of *Dermatophagoides pteronyssinus*

<table>
<thead>
<tr>
<th>Number of <em>D. pteronyssinus</em> (% of total)</th>
<th>vacuum sampling¹</th>
<th>core sampling²</th>
</tr>
</thead>
<tbody>
<tr>
<td>egg</td>
<td>1 (4)</td>
<td>30 (29)</td>
</tr>
<tr>
<td>larvae</td>
<td>3 (2)</td>
<td>10 (10)</td>
</tr>
<tr>
<td>protonymph</td>
<td>2 (8)</td>
<td>8 (4)</td>
</tr>
<tr>
<td>tritonymph</td>
<td>4 (18)</td>
<td>14 (14)</td>
</tr>
<tr>
<td>adult</td>
<td>14 (58)</td>
<td>40 (39)</td>
</tr>
<tr>
<td>total</td>
<td>24</td>
<td>102</td>
</tr>
</tbody>
</table>

1. Collected by vacuuming a 1.08 m$^2$ of mattress (areas X and Y Fig. 1).  
2. Core samples from areas A1-C5 and E6-G9 (Fig. 1).
of house dust mite ecology and, in particular, emphasises the caution with which vacuum sampling data must be treated. Recent live trapping studies have reached a similar conclusion (e.g. Bischoff et al., 1992). Whether or not it is possible to calibrate dust extraction methods for assessing mite abundance with absolute population size data is a priority for future research.

The core sampling approach has two main drawbacks: it is destructive, and it is labour-intensive. It is unlikely to replace the conventional dust extraction methods. However, the precision afforded by the method should make a considerable contribution to our understanding of mite ecology in the domestic environment.

Inevitably, the emphasis in house dust mite research is the crucial role of these mites in the aetiology of allergic disease. An understanding of house dust mite ecology is a vital component of this research but the house dust habitat is also deserving of ecological study in its own right. The recent origins of the domestic environment, its biotic simplicity and the island-like distribution of habitat patches contribute to make house dust a fascinating model habitat in which to explore some of the central dogmas of ecological theory.

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