



ORIGINAL ARTICLE

OPEN ACCESS

Frequency of *Euroglyphus maynei* sensitization in respiratory allergies: a real-life study with bioinformatic analysis and geographical exploration of allergen prevalence

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Received 8 February 2024; Accepted 23 April 2024

Available online 1 July 2024

KEYWORDS

Dermatophagoidinae;
Dermatophagoides
pteronyssinus;
Dermatophagoides
farinae;
Euroglyphus maynei;
house dust mite;
pyroglyphidae;
pyroglyphinae

ABSTRACT

Background: *Dermatophagoides pteronyssinus* and *Dermatophagoides farinae* belong to the family *Pyroglyphidae* (subfamily: “Dermatophagoidinae”) and have the respective allergenic proteins of Der p1, Der p2, and Der p23 and Der f1 and Der f2. *Euroglyphus maynei*, belongs to the family *Pyroglyphidae* (subfamily: “Pyroglyphinae”) and its main allergenic protein is Eur m1, a source of sensitization. Sensitization to *D. pteronyssinus* and *D. farinae* is assessed through skin tests, while sensitization to *E. maynei* is assessed less frequently.

Objective: This experimental work aims to analyze the prevalence of sensitization to *E. maynei* in patients with respiratory allergies treated at M. Albanesi Allergy and Immunology Unit in Bari, Italy, and the sequence homology of major allergenic proteins of *E. maynei* with *D. farinae* and *D. pteronyssinus* was analyzed.

Methods: In this real-life study, 65 patients were enrolled. In particular, patients with respiratory allergy were subjected to skin prick tests for common respiratory allergens, including *Euroglyphus maynei*. The sequence homology analysis was performed between the major allergenic proteins of *E. maynei* and those of *D. pteronyssinus* and *D. farinae*.

Results: Sensitization to *E. maynei* accounts for 41.5% of patients. All patients with *E. maynei* sensitization had concomitant sensitization to *D. farinae* and *D. pteronyssinus*. The analysis of sequence homology of Der p1 and Der f1 proteins with the sequence of Eur m1 protein demonstrated an identity of 84.4% and 86%, respectively.

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<https://doi.org/10.15586/aei.v52i4.1089>

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Conclusions: Nearly 50% of house dust mites-sensitized patients have a concomitant sensitization to *E. maynei*. The cross-sensitization could be due to Der f1, Der p1, and Eur m1 similarity.
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Introduction

The dust mites *Dermatophagoides pteronyssinus* and *Dermatophagoides farinae* account for about 50% of sensitizations in atopic patients.¹ These mites belong to the family *Pyroglyphidae* (and, in particular, to subfamily: “Dermatophagoidinae”) and have the respective main allergenic proteins of Der p1, Der p2, and Der p23 and Der f1 and Der f2.²⁻⁴ *Euroglyphus maynei*, belonging to the family *Pyroglyphidae* (and, in particular, subfamily: *Pyroglyphinae*), represents another source of sensitization in the context of dust mite allergy.⁵ The main allergenic protein of *E. maynei* is Eur m1.⁶

In this regard, the *D. pteronyssinus*, *D. farinae*, and *E. maynei* (therefore, the main allergenic dust mites) are eight-legged members of the class Arachnida.

The distribution of mites within substrates depends on their avoidance of light whereas their seasonal and geographic distributions depend on their need for adequate humidity.³

Dust mite particles (containing allergens) induce sensitization and atopic symptoms in certain organs by coming into contact with the epithelium of the lower airways, nose, skin, gut, and eyes.

Various mite allergens have important properties such as the following:

- Chitin-cleaving and chitin-binding activity
- Proteolytic activity
- Homology with other invertebrate tropomyosins
- Homology with the lipopolysaccharide-binding component of the Toll-like receptor 4 (TLR4).³

Furthermore, alignment and phylogenetic analyses have demonstrated that *D. pteronyssinus* is evolutionarily closer to *E. maynei*, compared to *D. farinae*, although both *D. pteronyssinus* and *D. farinae* belong to the genus “Dermatophagoides.”⁷

The main allergenic proteins of the above-mentioned dust mites are as follows: for *E. maynei*: Eur m1, Eur m2, Eur m3, and Eur m4; for *D. pteronyssinus*: Der p1, Der p2, Der p3, and Der p4; and for *D. farinae*: Der f1, Der f2, Der f3, and Der f4 (Allergen Nomenclature - WHO/IUIS Allergen Nomenclature Sub-Committee; www.allergen.org).

These proteins can be divided into the following different classes:

- Eur m1, Der p1, and Der f1 belong to the class of “Cysteine protease”
- Eur m2, Der p2, and Der f2 belong to the class of “NPC2 family”
- Eur m3, Der p3, and Der f3 belong to the “Trypsin” class
- Eur m4, Der p4, and Der f4 belong to the “Alpha-amylase” class

It was demonstrated that the allergenic proteins belonging to the Cysteine protease family (Eur m1, Der p1, and Der f1) and the NPC2 family (Eur m2, Der p2, and Der f2) share sequence identity among each class.⁸ In clinical practice, sensitization to *D. pteronyssinus* and *D. farinae* is assessed by skin prick tests. However, sensitization to *E. maynei* is rarely tested and only few reports exist analyzing the prevalence of this sensitization. In particular, a study conducted by Foti et al. on a cohort of 400 patients, of which 159 were atopic (all types of allergies, including respiratory) and 241 non-atopic, residing in Southern Italy, demonstrated that the sensitization toward *E. maynei* was 12.70% (n = 47).⁹ Thus, to date, the percentage of patients sensitized to *E. maynei* is obscure in a more selected cohort of patients (respiratory allergies) as well as the possible cross-reactivity of allergenic proteins of this dust mite to *D. farinae* and *D. pteronyssinus*.¹⁰⁻¹³

Aim

This real-life study proposed to analyze the following:

1. The frequency of sensitization to *E. maynei* in respiratory allergies in a cohort of patients from M. Albanesi Allergy and Immunology Unit in Bari, Italy.
2. The cross-reactivity of allergenic proteins of *E. maynei* with *D. farinae* and *D. pteronyssinus*.

Materials and Methods

In our real-life study conducted in Bari, we chose a sample size of 65 patients (35 men and 30 women). The mean age of the patients in the cohort was 28.74 ± 14.81 years. The patients were not recruited actively but participated voluntarily by presenting themselves at the M. Albanesi Allergy and Immunology Unit over an 8-month period for evaluation of respiratory allergy and skin prick tests. The study concluded at the end of the work period and deemed sufficient to meet our research objectives.

In particular, we analyzed the sequence homology of different mite allergenic proteins. Specifically, of the 65 patients, 58 had rhinitis as clinical manifestation, 32 had conjunctivitis, 19 had cough, and 12 suffered from dyspnea (Figure S1). Hence, a single patient often experienced multiple manifestations simultaneously. Table 1 displays the main sociodemographic characteristics of our patients. Considering that patients frequently experienced multiple manifestations simultaneously, we further analyzed specific combinations of manifestations observed in our study group. The details are divided into the following pairs and triads of symptoms:

- Pairs of symptoms:
 - o Rhinitis and conjunctivitis: found in 29 patients
 - o Rhinitis and cough: found in 20 patients

Table 1 The sociodemographic characteristics of the study sample.

Category	Information
Number of Participants	65 (35 men, 30 women)
Average Age (years)	28.74 ± 14.81
Symptoms	- Rhinitis: 58 patients; - Conjunctivitis: 32 patients; - Cough: 19 patients; - Dyspnea: 12 patients.

- o Rhinitis and dyspnea: found in 12 patients
- o Conjunctivitis and cough: found in 15 patients
- o Conjunctivitis and dyspnea: found in 10 patients
- o Cough and dyspnea: found in 6 patients
- Trios of symptoms:
 - o Rhinitis, conjunctivitis, and cough: found in 14 patients
 - o Rhinitis, conjunctivitis, and dyspnea: found in 10 patients
 - o Rhinitis, cough, and dyspnea: found in 6 patients
 - o Conjunctivitis, cough, and dyspnea: found in 5 patients

These combinations underscore the complexity and variability of patterns of manifestations among patients, highlighting the specific configuration that occurs more frequently.

Finally, in order to apply our results to other countries, we compared climatic data from different cities of the Mediterranean area.

Patient consent to participate

Participants were not actively recruited; they sought routine allergy consultations independently. Thus, no specific recruitment was done for research purposes. Written informed consent was obtained from all the patients.

The data examined in our study were collected retrospectively with skin prick test, an intervention considered standard of care in current allergological practice.

Regarding data handling, patients were asked to provide their consent by signing two specific documents:

- An informed consent form regarding the processing of personal data, in compliance with privacy regulations.
- An informed consent form concerning the medical procedures undertaken, ensuring full understanding and acceptance of the health practices performed. This consent form clearly described the nature and purpose of skin prick tests as well as the associated potential risks and benefits.

Diagnostic procedure

Patients with respiratory allergy were subjected to skin prick tests as described by Albanesi et al.¹⁴ The following allergen extracts were used: Gramineae mix, *Parietaria*

judaica, *Olea* (family Oleaceae), *Cupressus arizonica*, *D. farinae*, *D. pteronyssinus*, *E. maynei*, cat and dog dander, and *Alternaria alternata* (all obtained from Lofarma S.p.A., Milan, Italy). *E. maynei* was provided by Anallergo (Florence, Italy). Histamine was used as a positive control. Skin test positivity was recorded in the patients' medical records along with personal information and clinical history.

Data analysis

For data analysis, we used Matlab, a tool for statistical analysis and numerical computation. In particular, initially we created vectors containing strings of all the information recorded for the patients (allergens, age, residence, and symptoms). Then the latter were combined to create a single matrix containing all the acquired information.

Therefore, by selecting the column of interest, we carried out the data analysis of interest. At the end of this, we were able to draw the related explanatory graphs.

Sequence Homology assessment

We initially used the “UniProt” database of protein sequence and functional information to search for amino acid sequences; then the “Needle” software (<https://needle.software>) was used to make the required comparisons. Using the “Needle” software, the sequence homology analysis was performed between the major allergenic proteins of *E. maynei* (Eur m1) and the allergenic proteins of *D. pteronyssinus* (Der p1 Der p2, Der p3, and Der p23) and *D. farinae* (Der f1 and Der f2).

Bioinformatic analysis

The bioinformatic analysis utilized the Python programming language to calculate the Levenshtein distance, a metric indicating dissimilarity between two sequences. Computed as the difference between the sum of sequence lengths and double the alignment score, the Levenshtein distance represents the minimum number of operations (insertions, deletions, or amino acid substitutions) needed to transform one sequence into another. The Blosum 62 substitution matrix facilitated this calculation, underscoring its effectiveness in assessing sequence similarity.

3D Protein reconstruction

The study employed SWISS-MODEL (a structural bioinformatics web-server) molecular modeling technology for the 3D reconstruction of a specific protein. Based on homology, this method utilizes structural information from the previously solved homologous proteins. The protein sequence was input into SWISS-MODEL, initiating a search for known homologs in structural databases. The software aligned the sequences, constructed the 3D model, optimized it, and validated its quality.

Humidity assessment in Mediterranean cities

The humidity values for Bari, Marseille, Barcelona, Tunis, Beirut, Ceuta, and Zagreb were obtained from the database of the website www.timeanddate.com.

RESULTS

Skin test positivity results

Most of the patients were sensitized to *D. farinae* (46 patients, 70.7%), *D. pteronyssinus* (48 patients, 73.8%), *Cupressus arizonica* (37 patients, 56.9%), grasses (38 patients, 58.4%), and *Olea* (37 patients, 56.9%). Sensitization to *E. maynei* was found in 27 patients (41.5%; **Figure 1A**). All patients with *E. maynei* sensitization had concomitant sensitization to *D. farinae* and *D. pteronyssinus* (**Figure 1B**).

Sequence homology analysis

The analysis of the sequence homology of Der p1 and Der f1 proteins with the sequence of Eur m1 protein demonstrated an identity of 84.4% and 86%, respectively. In contrast, Der p2, Der p3, and Der f2 proteins have sequence identities of 8.1%, 0.7%, and 8.9% with Eur m1 (**Figure 1C**).

Levenshtein distance calculation

The application of the Blosum 62 substitution matrix facilitated the Levenshtein distance calculation, offering quantitative insights into sequence similarity. Low Levenshtein distances indicated high sequence similarity, suggesting minimal changes for conversion, while high distances signified substantial dissimilarity, necessitating significant alterations.

3D Protein reconstruction

In **Figure 2**, 3D reconstructions of Eur m1, Der f1, Der f2, Der p1, Der p2, Der p3, and Der p23 proteins are depicted. This methodology offers a valuable 3D perspective of protein structures, facilitating functional analyses.

DISCUSSION

Our study was the first to analyze the prevalence of *E. maynei* sensitization in a group of patients with respiratory allergy. Indeed, with respect to a previous report, our group of patients was homogeneous from a clinical point of view. In fact, all the patients had respiratory allergies and were residents of Southern Italy. We found that 41.5% of

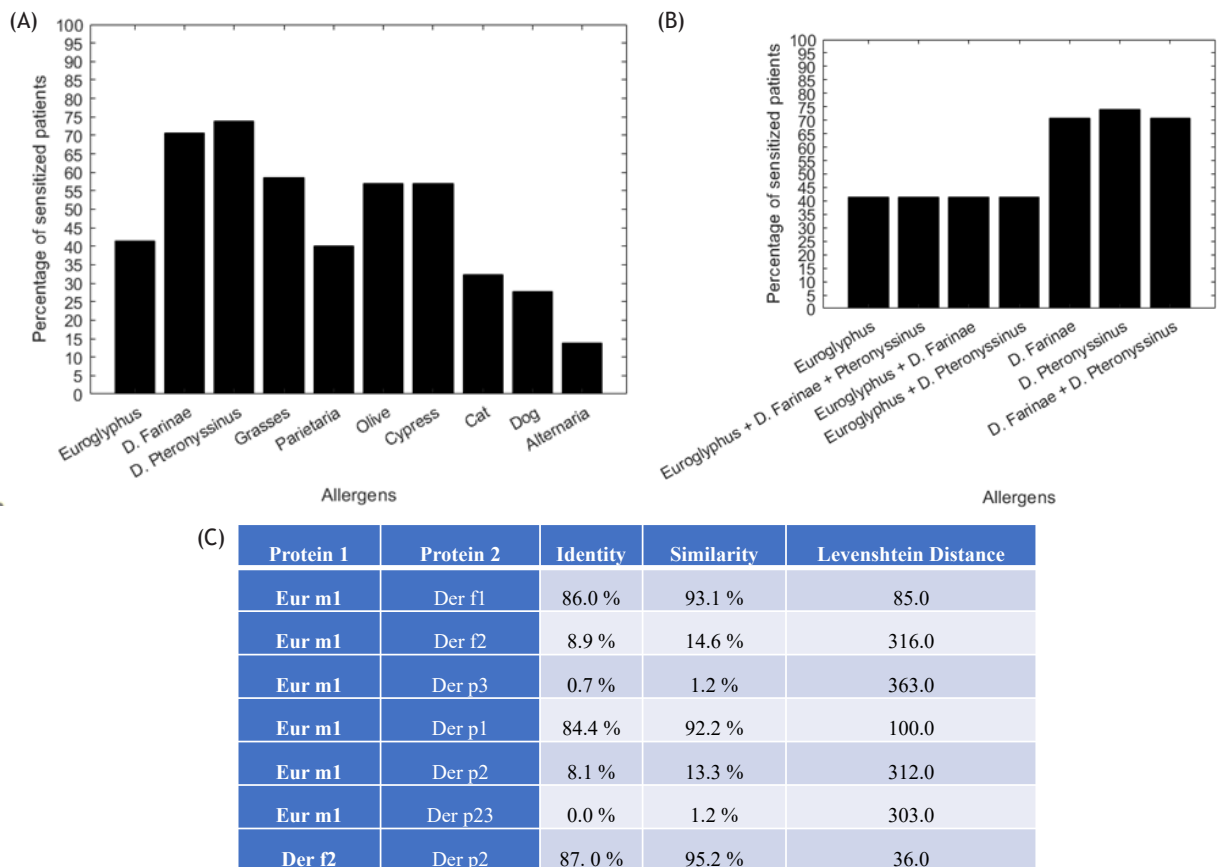


Figure 1 (A) Histogram indicating the percentage of patient sensitization according to all respiratory allergens tested. (B) Histogram indicating the percentage of sensitization of patients according to the respiratory allergens of interest. (C) Table indicating identity, similarity, and Levenshtein distance of allergenic proteins from *E. maynei*, *D. farinae*, and *D. pteronyssinus*.

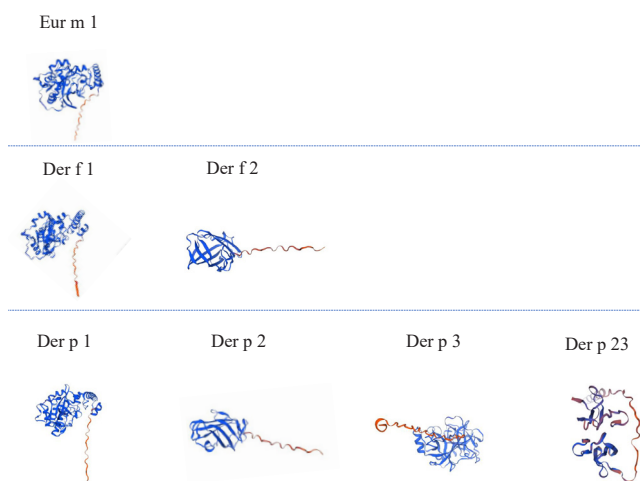


Figure 2 3D reconstruction of Eur m1, Der f1, Der f2, Der p1, Der p2, Der p3, and Der p23.

our total patients were sensitive to *E. maynei*. Notably, this proportion was higher, compared to the studies conducted in the same geographical district.

As a preventive measure, a sequence homology analysis was conducted among the major allergenic proteins of *E. maynei* and *D. pteronyssinus*, and *D. farinae*. In addition to calculating identity and similarity, Levenshtein distances were also computed. The calculated Levenshtein distances played a crucial role in assessing sequence dissimilarity. Sequences with low distances were considered highly similar, sharing common features, while those with high distances were deemed dissimilar, lacking substantial correspondence. The Levenshtein distance metric, by quantifying the "cost" of operations needed for sequence equivalence, provided a valuable tool for understanding sequence relationships.

To identify analogies between proteins, the 3D structures of the proteins were also reconstructed. The study highlighted the importance of SWISS-MODEL molecular modeling technology for 3D protein reconstruction. This approach provided a detailed structural perspective essential for functional analyses. The 3D reconstruction using SWISS-MODEL underscored the need for reliable structural information in bioinformatic studies.

The combined use of Levenshtein distance and 3D reconstruction methodologies offered a comprehensive approach to sequence analysis. While Levenshtein distance assessed sequence dissimilarity, 3D reconstruction provided insights into structural aspects, enhancing the understanding of functional implications.

This was fundamental to understand the proteins that were similar to each other, and therefore the ones that could be cross-reactive: proteins that showed similarities were characterized by recognition of the same immunoglobulin E (IgE) molecule.

Therefore, in order to validate our previous research, observations, and results, we carried out an analysis on a sample of patients belonging to the Albanesi Center for Allergology and Clinical Immunology, Bari, Italy.

Out of 65 patients, precisely 46 patients were deemed positive for *D. farinae*, 48 were positive for

D. Pteronyssinus, and only 27 patients were positive for *E. maynei*. Therefore, we observed that 19 and 21 patients represented, respectively, patients with skin test positivity for *D. farinae* but not for *E. maynei* and skin test positivity for *D. pteronyssinus* but not for *E. maynei*.

In clinical practice, either *D. farinae* and *D. pteronyssinus* are tested or only "mites mix," which generally contains its own extracts of *D. farinae* and *D. pteronyssinus*, is tested. Having found a prevalence of sensitization on *E. maynei*, *D. farinae*, and *D. pteronyssinus*, we proposed that a more precise diagnosis. Therefore, according to our data, we proposed that *E. maynei* should be tested routinely.

Moreover, concomitant sensitization (for more than 40% of patients in our cohort) was observed for *E. maynei*, *D. farinae*, and *D. pteronyssinus*. This might be due to the sequence homology of Der p1 with Eur m1 and homology of Der f1 with Eur m1 (Figure 1C). Thus, the skin test positivity only for *D. farinae* and *D. pteronyssinus* could be due to Der p2 and Der f2 sensitization (Figure 1C). The remaining patients, therefore, are positive only for *D. farinae* and *D. pteronyssinus*, possibly due to Der p2 and Der f2 (Figure 1C). It was pointed out that, as mentioned earlier, Eur m2, Der p2, and Der f2 had a high degree of sequence homology.⁸ In our study, we used the *E. maynei* extract provided by Anallergo (Italy). Up to now, according to the technical data sheet of the product, it was unknown whether both allergenic proteins Eur m1 and Eur m2 were equally present in these diagnostic products. This might explain the absence of *E. maynei* sensitization in some of the house dust mite-sensitized patients (Figure 1B). Thus, a standardization of diagnostic products is required.⁸

From a therapeutic point of view, the positivity toward different mites and the eventual combinations of the same could influence the results of allergen immunotherapy. We demonstrated that the main allergenic protein from *E. maynei*, that is Eur m1, shared more than 95% of sequence homology with Der p1 and Der f1. Interestingly, Der p1 and Der f1 were the main allergens contained in the commercially available immunotherapy preparations. Thus, in a patient with sensitization toward *E. maynei*, *D. farinae*, and *D. pteronyssinus*, an allergen immunotherapy containing Der p1 and Der f1 would guarantee protection toward Eur m1 as well. Therefore, it is important to identify the relevant allergens prevalent in each environment.

These results could also be extended to other geographical sites of the Mediterranean area. Indeed, the optimal humidity proportion for proliferation of mites was above 60%. This value was found in different Mediterranean cities, as shown in Table 2.

As mentioned earlier, in the present study the group of patients was homogenous and relatively small; therefore, it would be important to extend these observations to a larger group of patients from different geographic areas.¹⁵

Finally, it was pointed out that only the positivity or negativity to the allergens tested was considered in a non-quantitative manner in this study.

It would be useful to have a quantitative analysis (size of wheals, number of total IgE, and/or number of specific circulating IgE) in future study. In fact, after having carried out the test on three allergens (*E. maynei*, *D. farinae*, and *D. pteronyssinus*), it would have been appropriate to accurately calculate (and archive) the diameter and surface of

Table 2 The monthly humidity values in 2022 for several major Mediterranean cities.

	Bari	Marseille	Barcelona	Tunis	Beirut	Ceuta	Zagreb
January 2022	71%	74%	71%	75%	59%	71%	81%
February 2022	70%	69%	73%	70%	64%	70%	72%
March 2022	69%	63%	76%	73%	63%	75%	54%
April 2022	65%	65%	67%	63%	65%	69%	66%
May 2022	67%	59%	69%	63%	69%	68%	67%
June 2022	58%	54%	71%	52%	70%	64%	67%
July 2022	57%	52%	67%	56%	71%	72%	60%
August 2022	63%	60%	70%	58%	68%	73%	64%
September 2022	60%	63%	68%	60%	63%	68%	77%
October 2022	79%	76%	79%	67%	60%	79%	83%
November 2022	80%	77%	69%	71%	61%	74%	89%
December 2022	86%	85%	78%	68%	63%	79%	89%

wheals and, perhaps, on the basis of the same, to be able to estimate the number of circulating IgE.

Author contributions

Palazzo Stefano collected and analyzed the data, provided critical reading of the manuscript and wrote the paper; Alessandro Cinquantasei analyzed the data; Concetta De Chirico collected the data and studied the cases clinically; Marco Zurlo helped with the study of the patients; Vincenzo Aresta provided clinical assistance to the patients; Nada Chaoul helped with scientific work and writing of the paper; and Marcello Albanesi provided clinical assistance, conceived the project, analyzed the data, revised the paper, and secured funding. The manuscript was approved by all the authors, who concurred on its submission.

Conflict of interest

The authors declared no competing financial interests.

Availability of data and materials

All data are available upon request.

Funding

The study was funded by Anallergo, Florence, Italy.

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Supplementary

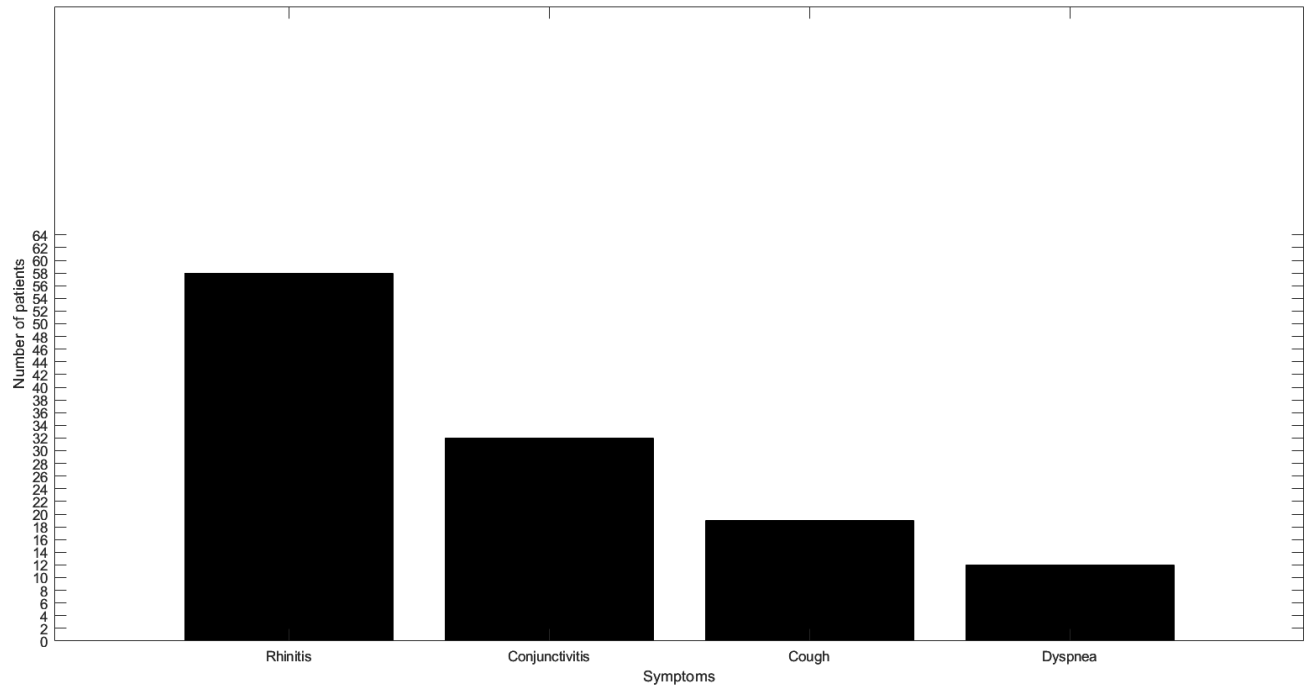


Figure S1 Number of patients included in the study presenting symptoms of rhinitis, conjunctivitis, cough, and dyspnea.