

## A23 Who transmits the most? An analysis of superspreading events of COVID-19 cases in Aveiro region.

Sofia Tedim<sup>1</sup>, Vera Afreixo<sup>1</sup>, Catarina A. Rodrigues<sup>1</sup>, Tiago Pinho-Bandeira<sup>2</sup>, Regina Sá<sup>2</sup>

<sup>1</sup>Department of Mathematics, University of Aveiro (UA), Campus Universitário de Santiago, 3810-193 Aveiro, Portugal.

<sup>2</sup>Public Health Unit, Agrupamento de Centros de Saúde (ACES) Baixo Vouga, Administração Regional de Saúde (ARS) Centro, Av. Dr. Lourenço Peixinho, nº 42, 4º andar, 3804-502 Aveiro/Portugal.

### Introduction

COVID-19 pandemic imposed extraordinary stress on healthcare services worldwide. Lack of effective treatment or large-scale prophylaxis makes outbreak control essential, by breaking transmission chains. The virus has heterogeneous transmission dynamics: while most people do not transmit virus, some cause many secondary cases in transmission clusters called "superspreading events" (SE)[1]. Secondary attack rates (SAR) can be used to quantify the disease's infectiousness and transmissibility. A single person might infect many others either due to having a high viral load and consequently excreting an unusual amount of virus particles or to having many exposed contacts [2]. Social activity and mild symptoms are factors that might influence transmissibility[3-6]. Additionally, certain people, known as super emitters, release more droplets or aerosol particles, by coughing, sneezing or talking [3,4], showing higher SAR. Research on the association of clinical presentation and COVID-19 superspreading events is scarce and controversial. Some studies suggest that asymptomatic patients transmit the virus at a similar rate to symptomatic patients [7], while others identify symptomatic patients as having higher attack rates [4,8,9]. The aim of this study is to describe demographic and clinical characteristics associated with higher SAR in COVID-19 cases in the Aveiro region.

### Methods

A cross-sectional, retrospective study was conducted with all COVID-19 confirmed cases notified to Agrupamento de Centros (ACES) de Saúde Baixo Vouga (Aveiro region) public health authorities from March 8, 2020, until December 29, 2020. Epidemiological link was defined as the most probable infector, or a close contact identified by contact tracing of positive cases. A descriptive model was built to study the factors associated with SE. Subjects identified as outliers for the number of derived contagions in the transmission chain ( $>2$ ) were classified as SE. Outliers were calculated using Tukey's method. To compare the risk factors for being a SE, Odds Ratios (OR) and their 95% confidence intervals (CI95) were estimated. A logistic regression model was calculated using all reported symptoms and age, to explain the outcome, considering adjustment for confounders.

### Results

A total of 12142 cases were included in this analysis. The median number of secondary cases was 0 (IQR 0), ranging from 0-84. The number of source cases considered as SE was 501. Sex, comorbidities, smoking or death were not associated with SE in any model.

In the bivariate analysis, the only age groups that showed a significant association with the main outcome were the 30-39 and 40-49, with an OR 1.83 (CI95 1.11-3.22) and 1.98 (CI95 1.21-3.45), respectively. However, this effect was lost in the multivariate model when adjusting for clinical presentation.

In the bivariate analysis, having any symptom and all singular symptoms excluding dyspnea, diarrhea, amnesia and skin disorders, were associated with the main outcome. In the multivariate analysis, adjusted for age group, only fever (OR 1.82), productive cough (OR 1.64), dry cough (OR 1.63) and myalgias (OR 1.28) presented with significant associations. Final model is in Table 1.

### Discussion

Fever, productive and dry cough, and myalgias are the only symptoms related with an increased transmission. Results for cough are consistent with the available evidence, as this mechanism involves a great amount of expelled particles [3,4]. Fever as a risk factor for SE is a novelty. Active ages (30-49) were expected.

**Keywords:**  
COVID-19, dry cough, fever, Myalgias, productive Cough, superspreading event

**Corresponding author:**  
Ana Sofia Marralheiro Tedim  
[sofiatedim@ua.pt](mailto:sofiatedim@ua.pt)

**Conflict of interest:**  
The authors declare no conflict of interests

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**Table1** - Results for the logistic models.

| Characteristic         | Univariable analysis |                     |         | Multivariable analysis |                     |         |
|------------------------|----------------------|---------------------|---------|------------------------|---------------------|---------|
|                        | OR <sup>1</sup>      | 95% CI <sup>1</sup> | p-value | OR <sup>1</sup>        | 95% CI <sup>1</sup> | p-value |
| Fever (Yes)            | 2.29                 | 1.89, 2.77          | <0.001  | 1.83                   | 1.50, 2.24          | <0.001  |
| Dry cough (Yes)        | 2.03                 | 1.69, 2.44          | <0.001  | 1.74                   | 1.44, 2.10          | <0.001  |
| Productive cough (Yes) | 1.90                 | 1.36, 2.59          | <0.001  | 1.73                   | 1.23, 2.37          | 0.001   |
| Myalgias (Yes)         | 1.98                 | 1.64, 2.38          | <0.001  | 1.50                   | 1.23, 1.82          | <0.001  |

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

ted to be positively associated with superspreading events[2], because of increased social contacts, but when adjusted for symptoms this effect was not seen in our models.

One limitation of this study is that information on clinical presentation was collected at the time of the epidemiological investigation, excluding symptoms that may have developed later in time.

Knowledge on characteristics that increase the risk of superspreading events is useful to promote more precise prevention measures for outbreak control.

#### Ethics committee and informed consent

This study used a secondary data source, containing anonymous information. It was conducted in accordance with the Declaration of Helsinki.

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