Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.


Resarch Article

Multi-household social gatherings contribute to the second SARS-CoV-2 wave in Rhineland-Palatinate, Germany, August to November 2020

Markus Schepersa,∗, Philipp Zangerb,c, Klaus Jahn, Jochem König, Konstantin Strauch, Emilio Gianicolo

a Institute of Medical Biostatistics, Epidemiology and Informatics (IMBEI), University Medical Center, Johannes Gutenberg University, Mainz, Germany
b Federal State Agency for Consumer & Health Protection Rhineland-Palatinate, Koblenz, Germany
c Heidelberg Institute of Global Health (HIGH), University Hospitals, Im Neuenheimer Feld 130.3, 69120 Heidelberg, Germany
d Ministry of Social Affairs, Labour, Health and Demography Rhineland-Palatinate, Mainz, Germany

A R T I C L E   I N F O

Article history:
Accepted 19 January 2022
Available online 23 January 2022

Keywords:
Public health
COVID-19
SARS-CoV-2
descriptive statistics
epidemiology
private households
social gatherings
Germany

S U M M A R Y

Background: Although the private household setting is considered a major driver of viral spread, only little is known about the contextual details of SARS-CoV-2 household transmission, thus hampering political decision-making.

Materials and methods: We analyzed individual case and cluster data from statutory notifications from August to November 2020 in Rhineland-Palatinate - the period preceding the second SARS-CoV-2 wave. We also conducted an in-depth survey on contextual details of household transmission in a representative sample of 149 private household clusters that had occurred during this period.

Results: During the study period, 18,695 PCR-confirmed SARS-CoV-2 cases were notified, 3,642 of which occurred in 911 clusters (private households (67.3%), the workplace (7.8%), elderly homes (1.8%), others (23.2%). Demographically, clustered cases were representative of all notified cases. Two-thirds (77/113, 68%) of sample response clusters involved more than one private household. These caused on average more close contact persons (mean 13.5 ±SD 15.8) and secondary cases (3.9, ±SD 0.4) than clusters involving one household only (5.1 ± 13.8 and 2.9 ± 0.2). About one in six multi-household clusters in the private setting (13/77) followed a social gathering (e.g. birthday party). Breaches of one or more of the three major barrier concepts (mask, ventilation, and distance) were identified in most (10/13) of these social gatherings. SARS-CoV-2 clusters following social gatherings were overrepresented during the second half of the study period.

Conclusion: In times of increasing infectious pressure in a given population, multi-household social gatherings appear to be an important target for reducing SARS-CoV-2 transmission.

© 2022 The British Infection Association. Published by Elsevier Ltd. All rights reserved.

Background

The spreading of SARS-CoV-2 has led to a global pandemic, with a very wide range of country-specific responses and restrictions. A better understanding of transmission patterns is needed for targeting non-pharmaceutical interventions (1). It has been found that SARS-CoV-2 attack rates are highly setting-specific (2) (for the definition of “attack rate” see Box 1). In private households, a systematic review and meta-analysis reports an attack-rate estimate of 16.6% (3). That study also found higher attack rates for symptomatic index cases (compared with asymptomatic ones), for adults (compared with children), for spouses (compared with other family contacts) and for small households (compared with big households). In the very initial stages of the epidemic, a study of the first 30 cases in Korea showed that the attack rate among household contacts is 7.6% (9 out of 119), whereas the overall attack rate is 0.5% (13 infections/transmissions among 2,370 contacts) 13/2370*100=0.548=0.5 (4).

Regarding the attack rate of SARS-CoV-2 within a household, using both serological tests and polymerase chain reaction (PCR) tests, an association between household size and per-person attack rate was found, with estimates of 43.6%, 35.7% and 18.3% for 2-, 3- and 4-person households respectively (5). A study of the social contact patterns relevant for transmission of respiratory infec-
tious diseases in general (with 7,290 participants) across various European countries found that contact patterns were highly assortative, i.e. people predominantly interacted with people of similar age. They also found that contacts at home, school or leisure were more likely to be physical than those at work or while traveling. Furthermore, they expected, probably with the seasonal flu in mind, that the group of 5- to 19-year-olds would suffer the highest incidences during the initial stage of an epidemic (of a disease transmitted via the respiratory or close-contact route) (6).

A recent study based on German data found that social contact data predicted infection dynamics better than population mobility data (7).

Until mid-2021, the Tuesday versions of the Situation Report by the Robert Koch Institute contained a histogram of clustered cases by infection setting. There, the private household context proves as one of the most important transmission settings (Fig. 1).

In the initial stages of the pandemic, the proportion of clusters generated from private households has been approximately one third; a proportion that has meanwhile risen to more than 50%, presumably due to vaccination of the elderly and the decrease probability of outbreaks in old people’s homes.

The main aim of this work is a thorough quantitative and qualitative analysis of infection clusters within the setting of private households. In particular, the main open questions initiating this research project have been:

What are the most common and most striking patterns of transmission of SARS-CoV-2 in the setting of private households?

For instance: Do infections rather happen at social gatherings (like weddings or birthday parties) or during daily life?

How many households are involved in an infection cluster? What about the application of preventive hygiene measures? Are there any temporal changes in the transmission patterns?

**Materials and methods**

In this paper, we restrict ourselves to the state of Rhineland-Palatinate from 17 August – 10 November 2020, the time-period in Germany, from the end of the summer holidays until the beginning of the second infection wave, with relatively few non-pharmaceutical preventive measures in place. During this period, infection incidences were within the contact tracing capacities of the health departments. The latter provided data on household transmission under a minimum of social restrictions.¹

We used two data sets made available by the Federal State Agency for Consumer and Health Protection Rhineland-Palatinate, which is legally in charge of the infectious diseases surveillance system. The first one is a data set of 18,695 individuals who tested positive for SARS-CoV-2 in Rhineland-Palatinate from 17 Aug – 10 Nov 2020. These cases were notified to the competent district public health authority (DPHA) according to place of residence (not according to suspected place of infection), based on case definitions published by Robert Koch-Institute, Berlin, and as set out in the German Infection Protection Act (Infektionsschutzgesetz). As a result of the investigations and contact tracing, the notifying DPHAs assigned 3,642 of these 18,695 subjects (19.4%) to 911 SARS-CoV-2 clusters (second data set). Choosing from a list in the notification software SurvNet@RKI, DPHAs assigned 613 of these 911 clusters (67.3%) with 1,923 cases to the “private household” setting (Table 1).

We developed a questionnaire for the DPHAs to further explore specific infection contexts within the infection setting “private household” in a subsample. For sampling, “private household” clusters were stratified according to quartiles of cluster size and then, for each of 24 DPHAs, up to eight clusters were drawn, i.e. two per quartile (subject to availability). This resulted in a sample of 149 clusters containing 514 cases (Table 1). The questionnaire asked for additional information on clusters such as the number of contact persons of category I (see Box 1 for definitions), the number of households of the contact persons and the number of households of the cluster cases. For those clusters with a social gathering prior to the SARS-CoV-2 outbreak, we included more detailed questions, e.g. on preventive hygiene measures, and allowed DPHAs

---

¹ Non-pharmaceutical measures in place included free testing for returning travelers and registration at restaurants. For more information see [15] and https://www.bundesregierung.de/breg-de/themen/buerokratieabbau/videokonferenz-der-bundeskanzlerin-mit-den-regierungschefinnen-und-regierungschefs-der-laender-am-28-oktober-2020-1805248

---

**Fig. 1.** Plot of COVID-19 cases reported in clusters, by infection setting and week of reporting, Germany, June 2021. Display shows cases from clusters with size ≥ 2. Infection-settings are assigned by District Public Health Agencies from a list of pre-specified categories in the surveillance software and database SurvNet@RKI. Figure shows that clusters from the private household setting (in German “Privater Haushalt”, middle light blue, 2nd category/color from top) contribute substantially to the case load of the “second SARS-CoV-2 wave” before and after introduction of vaccination in December 2020. The latter in turn explains a marked reduction of clusters in elderly homes (German “Alten-Pflegeheim”, middle blue, 3rd category/color from top) in the first half of 2021.

Note: Due to inherent delay, the data of the most recent calendar weeks are incomplete. The inlay displays clustered cases (colored in comparison to all cases in Germany (gray).

(Source: Situation Report of the Robert Koch Institute, https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Situationberichte/jun_2021/2021-06-22-de.pdf?__blob=publicationFile, accessed on 22 June 2021).
to provide further information regarding the event in free-text format. The survey was conducted online, from 18th December 2020 to 28th February 2021, using LimeSurvey.

Statistical analysis

We compared occurrence of cases and clusters of SARS-CoV-2 across cities vs. countryside, their occasion and number of households involved via descriptive statistics (absolute and relative frequencies, mean, standard deviation, standard error, variance, index of dispersion). We calculated Fisher’s exact test in the association between clusters with multiple households and clusters due to social gatherings. To investigate time-dependence, we split the data into two equally long time periods: from 17 August – 30 September 2020 (called period 1) and 1 October – 10 November 2020 (called period 2). The motivation for studying this dissection is that period 1 had stable/constant incidences at a relatively low level, while period 2 was the beginning of the second wave with quickly rising incidences until the beginning of the light lock-down (for the empirical cumulative distribution function, see Fig. 5). We analyzed the data using R version 4.0.2 (8).

Study sample

Regarding the survey, we received 113 responses for the questionnaires on private household clusters (proportion of responses: 75.8%; Table 1). Since any given health department usually either sent responses to all or to none of the assigned questionnaires, our eventual sample of 113 clusters is still stratified according to cluster size, i.e. it has roughly equal numbers of clusters for each quartile of the cluster size.

Ethics

All data presented were collected and analyzed in response to the SARS-CoV-2 pandemic and in accordance with the German Infection Protection Act.

Results

Overdispersion in the distribution of cluster sizes indicates an important role of super-spreading

Considering the number of cases of a cluster, called cluster size (see Fig. 1 and Box 1 for the definition of cluster), the median of the cluster size is 2 (25th-percentile: 2; 75th-percentile: 4; minimum: 2; maximum: 199). The mean of the cluster size is 4.0 and the variance of the cluster size is 63.8. The index of dispersion (variance divided by mean) of the cluster size is 16.0, i.e. the distribution of the cluster size is highly over-dispersed (see Fig. 2). With respect to counting clusters, all clusters with 3 or more cases (49.2% of all clusters) contribute to around 80% of all individual cases with an infection setting (i.e., clustered cases).

Cluster-association of SARS-CoV-2 cases is less likely in the urban context

Comparing city and countryside, the five biggest cities in Rhineland-Palatinate (Mainz, Ludwigshafen, Koblenz, Trier, Kaiserslautern) contribute to 8,286 of all 18,695 reported cases (44.3%), although their population is only approximately 0.7 million out of approximately 4 million people in Rhineland-Palatinate (17.5%). When considering the number of clusters in the comparison between city and countryside, the difference is less pronounced, reflecting that the proportion of cases that have been assigned to a cluster is lower in cities than in the countryside. The cities reported 221 out of 911 clusters (24.3%), containing 858 out of 3642

Table 1

| Categories                        | Cases | Clusters |
|----------------------------------|-------|----------|
| Total                            | 18,695| 911      |
| Observations in clusters         | 3642  | 911      |
| Infection setting of cluster     |       |          |
| - Private household              | 1923  | 613      |
| - Workplace                      | 339   | 71       |
| - Old people’s home              | 269   | 16       |
| - Clubs, activity groups etc.    | 235   | 8        |
| - Remaining                      | 876   | 203      |
| Number sampled of private household stratum | 514 | 149 |
| Response to questionnaires (%) of sampled | 409 | 113 |

* This information refers exclusively to the subsample of cases/clusters that had occurred in the “private household” setting.
Table 2
Impact of social gatherings, daily life and travel on SARS-CoV-2 transmission in the private household setting.

| Clusters a | Total Secondary Cases b | Average cluster size (b + α)/α ± SE | Total close contact persons (only non-missings) c | Total Secondary cases divided by total close contact persons ** |
|------------|-------------------------|------------------------------------|-----------------------------------------------|------------------------------------------------|
| N          | %                       | N                                 | %                                             |                                               |
| Social gathering (always more than one household) | 13 | 11.5 | 60 | 20.3 | 5.6 ± 1.3 | 194 | 58/194 = 0.30 |
| Daily Life | 79 | 69.9 | 172 | 58.1 | 3.2 ± 0.3 | 848 | 172/848 = 0.20 |
| One household | 27 | 34.2 | 45 | 26.2 | 2.7 ± 0.2 | 168 | 45/168 = 0.27 |
| More than one household | 52 | 65.8 | 127 | 73.8 | 3.4 ± 0.4 | 680 | 127/680 = 0.19 |
| Travel-related | 7 | 6.2 | 7 | 2.4 | 2.0 ± 0.2 | 74 | 5/74 = 0.07 |
| One household | 4 | 57.1 | 5 | 71.4 | 2.3 ± 0.3 | 4 | 3/4 = 0.75 |
| More than one household | 3 | 42.9 | 2 | 28.6 | 1.7 ± 0.3 | 70 | 2/70 = 0.03 |
| Unknown | 14 | 12.4 | 57 | 19.3 | 5.1 ± 1.0 | 104 | 47/104 = 0.45 |
| One household | 5 | 35.7 | 19 | 33.3 | 4.8 ± 1.1 | 10 | 9/10 = 0.90 |
| More than one household | 9 | 64.3 | 38 | 66.7 | 5.2 ± 1.5 | 94 | 38/94 = 0.40 |
| Total | 113 | 100 | 296 | 100 | 3.6 ± 0.3 | 1220 | 282/1220 = 0.23 |
| One household | 36 | 31.9 | 69 | 23.3 | 2.9 ± 0.2 | 182 | 57/182 = 0.31 |
| More than one household | 77 | 68.1 | 227 | 76.7 | 3.9 ± 0.4 | 1038 | 225/1038 = 0.22 |

* For simplicity, we assumed that there was exactly one primary case in each cluster, i.e., for each cluster, we subtracted one from the cluster size.
** Estimating the attack rate. Among social gatherings and travel-related, there were 2 clusters each with missing number of contact persons not considered. Among unknown sub-category, there were 3 clusters with missing number of contact persons not considered.

notified cases with cluster information (23.6%). 59 out of all 911 clusters (6.5%) involved more than one district.

Private households are the most common setting producing SARS-CoV-2 clusters

The clear majority of 1923 out of 3642 cases with cluster information (52.8%) belonging to 613 out of 911 clusters (67.3%) occurred in the infection setting private household (see Table 1). This observation prompted our closer study of this setting.

Clusters are representative for all cases

We checked that in terms of age and gender the clustered cases are representative for the overall set of reported cases, with the clustered data having a slightly higher fraction of females (50.7% vs 48.8%) and with similar estimates for age (40.6 years vs 40.2 years).

Multi-household ‘social gatherings’ neglecting hygiene drive large SARS-CoV-2 clusters

Within the study sample of the private setting, 77 out of 113 sample response clusters (68.1%) involved more than one household and caused 227 out of 296 secondary cases (76.7%). For these sample response clusters that involved two or more households the average cluster size (3.9 ± 0.4) was higher than in those clusters within one household (2.9 ± 0.2). This difference was mostly due to large clusters following 13 multi-household social gatherings (cluster size 5.6 ± 1.3) (see Table 2). At the same time, most of the large outbreaks in the private household (≥ 10 cases) occurred following multi-household ‘social gatherings’ (Fig. 2b). Indeed, clusters due to social gatherings more frequently involved multiple households than clusters from daily life (according to Fisher’s exact test, p = 0.009, see Table 2). Eight of these 13 clusters (multi-household social gatherings) could be further classified as private meeting (dinner, barbeque, coffee and cake, etc.), three were birthday parties with six, three and two cases respectively, and two were weddings with six and two cases, respectively. In 10 of 13 ‘social gatherings’, face masks were not used; 12 took place in closed rooms; in nine events no social distancing was applied and in four events rooms were not ventilated (for all remaining clusters the corresponding information is unknown).

There were five of 13 clusters where the index case was symptomatic at the event, six clusters where the index case was asymptomatic at the event, two clusters where this information was not available (Table 3).

Variation in burden on tracing capacity (i.e. number of contact persons)

The mean number of category I contact persons of all 113 sample response clusters in the private setting overall is 11.73 (median 6) compared to 17.64 (median 18) for social gatherings, 14.80 (median 3) for travel, and 11.01 (median 5) for clusters with transmission occurring during daily private life (see Figs. 3 and 4).

Multi-household ‘social gatherings’ contributed to the second wave of the SARS-CoV-2 epidemic in Rhineland-Palatinate, autumn 2020

With respect to all clusters in Rhineland-Palatinate, we observed that period 1 contains 170 clusters with 688 cases (average cluster size: 4.0), while period 2 contains 741 clusters with 2954 cases (average cluster size: 4.0).
### Table 3

Overview of the 13 clusters with ‘social gathering’.

| Event description | Cluster size: number of cases (including primary case) | Number of category-I contact persons (total) | Number of category-I contact persons present at social gathering |
|-------------------|-------------------------------------------------------|---------------------------------------------|---------------------------------------------------------------|
| Private party with guests from surrounding villages | 18 | 25 | 13 |
| Meeting in a pub (couple with a daughter, considered as index cases, had contact to 9 other people, 6 of which were tested positive/turned into cases later, some of these visited the pub again 2 days later and it turned out that they infected people at other tables, i.e. people they did not even know) and contacts at work (7 contacts, 2 of which tested positive later on) | 11 | 17 | 8 |
| Barbeque party in a garage | 7 | 7 | 7 |
| Children’s birthday party | 6 | 36 | 15 |
| 25th wedding anniversary celebration | 6 | 21 | 11 |
| Party | 6 | 7 | 3 |
| All cases took part in a family gathering/celebration, where a person was symptomatic: parents, son and daughter-in-law turned into cases. | 4 | 31 | 12 |
| Birthday and Halloween party | 3 | 18 | 18 |
| Private gathering/meal | 3 | 2 | 2 |
| Mother and daughter tested positive, source of infection unknown. 3 days prior to that, daughter invited another family for dinner (gathering of 8 people). At this dinner, another person was infected who had 7 contacts at her sports club and 3 colleagues at work. Mother had contact to another household with 4 persons, but no one was infected there. Meeting for coffee and cake | 2 | 2 | - (unknown) |
| Wedding | 2 | - | 1 |
| Birthday party with 6 guests, later contacts at physiotherapy and several sports clubs | 2 | 6 | 6 |
| **Total** | **73** | **194** | **105** |

**Fig. 4.** Number of households of category-I contact persons in 113 sample response clusters within the private household setting, Rhineland-Palatinate, August to November 2020.

**Fig. 5.** Cumulative incidence of 113 sample response clusters within the private household setting, Rhineland-Palatinate, August to November 2020.

In the study sample, 26 clusters with 88 cases were recorded in period 1 and 87 clusters with 321 cases in period 2 (see Table 4). Clusters with social gatherings and with unknown sub-category were over-represented in period 2 (data not shown).

**Discussion**

The goal of this work was to more specifically characterize transmission clusters of SARS-CoV-2 infections occurring in the private household-setting, accounting for a substantial and largely unexplored fraction of all infections. We analyzed data from statutory notifications on individual cases and clusters collected by the district public health authorities (DPHAs) from 17 August to 10 November 2020. In order to obtain additional details that are not routinely reported, e.g. regarding number of households involved, number of contact persons and hygiene measures, we have sent a
questionnaire to the reporting DPHAs for a representative subset of clusters that had occurred in the private household-setting.

While 75% of all clusters in the overall sample of clusters contain up to four cases, our results show that there is a high variance and dispersion of the cluster size, with a maximum reaching 199 cases, thus suggesting the presence of super-spreading events. This finding could be replicated for the subsample of clusters occurring in private households. We also observe a relatively higher proportion of infection cases in the five biggest cities in Rhineland-Palatinate than would be expected according to the population, which could simply reflect higher reported incidences in bigger cities. Conversely, we have found on average larger clusters in countryside regions. Possible reasons for this observation are that contacts of a person might be more easily traceable in the countryside and that capacities of DPHAs in the bigger cities are demanded to a larger degree during the pandemic; admittedly, this reasoning is of speculative nature and beyond the scope of this work.

The demographic structure of clusters showed no remarkable difference when compared to that of the overall set of reported cases. Thus, clustering did not favor persons of younger or older ages. In addition, the distribution of the clusters indicates that the size of those occurring in the household setting is very similar to that of all clusters (see Fig. 2a and b).

We found, that most of the clusters in the private setting (68%) involved more than one household. This empirical finding also fits to results obtained by simulation (9) and a report (10) containing the observation that a substantial fraction of transmissions occurs between households (i.e. meetings where more than one household is involved). The authors found that transmissions within households and transmissions between households are the strongest drivers of the epidemic and that their contribution to the infection numbers is roughly equal. With our data, we cannot directly confirm or reject their simulation results, as we do not see how many of the infections that happened in a cluster with more than one household actually occurred within a single household during the temporal evolution of the cluster. However, we observed that clusters with more than one household clearly contribute the biggest share to the total number of cases in our sample. We observed that the number of cases in daily life within a single household, number of cases in daily life with more than one household and number of cases with social gatherings behave like ¾: ¾: ¾.

Considering that a certain part of the infection events of the latter two categories can in fact be accounted to have occurred within a single household, our results appear to be in accordance with the above-mentioned results obtained by performing simulations (10).

We observed an increased cluster size in association with social gatherings which is line with one recent study that found birth-days, which likely correspond to social gatherings and celebrations, are associated with increased rates of diagnosed SARS-CoV-2 infection (11). Furthermore, the DPHAs reported that during social gatherings in the private setting, preventive hygiene measures were commonly violated. This is in line with findings of a study regarding the effectiveness of masks and hand hygiene in the context of influenza (11) and the aforementioned observation that birthdays are associated with increased rates of SARS-CoV-2 infection (12).

Finally, after splitting the data according to time period, we observed an increase in the number of clusters, while the average cluster size remained constant. Private household clusters with social gathering and with unknown sub-category were over-represented in period 2, thus supporting that such activities have contributed to the evolution of the second infection wave in autumn 2020.

**Strengths and limitations**

1. We observed a good response rate to our survey given the high work load of the health departments during the epidemic. Specific obstacles when conducting the survey were: the lack of an available contact person at some health departments, invalid or inconsistent identification codes of clusters, and some contact persons at the health departments not filling in the questionnaire themselves, so they could not respond to later (follow-up clarification) questions.

2. The fraction of cases assigned to a cluster, and hence with an assigned infection setting, is less than 20% and could be distorted. Some infection settings like buses and public transport are more difficult to trace and hence, may be underrepresented. Conversely infections within a family or household are more easily traceable (13). Furthermore, people may give false reports, or not recall all potential contacts. Symptom-free cases complicate matters further, since they might not be detected at all, thus forming part of the number of non-reported cases (14) (15).

3. Sometimes it is difficult to infer whether two infected individuals were exposed to the same source of infection or whether one of them infected the other (16).

4. The fraction of cases in a particular infection setting (e.g. private households) varies considerably during the epidemic, maybe also in response to political interventions and regulations (17).

5. We assume that the test strategy and testing conditions (e.g. number of tests) remained roughly constant throughout the study period (15) (14).

In conclusion, even though there does not seem to be a single measure to stop the spread of SARS-CoV-2 due to the diver-
sity of the transmission contexts, it might be worthwhile to pay more attention to social gatherings that include members of multiple households. Besides restricting such meetings as one potential anti-epidemic measure, adherence to standard hygiene measures might be a way to keep up some social interaction during the SARS-CoV-2 pandemic.

Acknowledgments

We thank Thomas Stelzer for conducting the database queries in SurvNet@RKI, Susanne Blomenkamp for implementing the sur-

Box 1. Definitions of terms and concepts used in this article.

A **cluster** is a collection of two or more persons that tested positive for SARS-CoV-2-RNA and are suspected to have some underlying causal transmission tree based on links on the level(s) “person, place and/or time”. A **cluster-file** is a collection of cases assigned to an underlying transmission tree by the investigating District Public Health Authority (DPHA).

We say that a cluster occurred in the **infection setting of ‘private households’** if it was assigned the label ‘private household’ by the investigating DPHA, based on preset categories in the software SurvNet@RKI.

**Index or index case:** the case or cases that brings awareness of a cluster to the DPHA and prompts the setup of a cluster file in the database.

**Primary case:** the case in a cluster that is considered its root or origin, i.e. the first case in a distinct chain of transmissions. It is not necessarily the index case, since cases further downstream the chain of infection may be initially detected. Note that the status of primary case may be revised during the course of investigations by the DPHA.

**Category I contact person:** less than 1.5 m distance for 15min or more or exposition in a closed room with a high load of infectious aerosol for at least 30min. At the time of data collection, category I contact persons had to record symptoms for 14 days during quarantine at home and, in case of symptoms, notify the DPHA for immediate PCR-testing. Note that a category I contact person testing positive and thus turning into a case will still be included in the total number of category I contact persons of a given cluster.

The **attack rate** is defined as the quotient of the number of new infections among the contacts of an index case divided by the total number of contacts of the index case.

**Super-spreading** denotes the phenomenon that a few individuals infect a very large number of people, thereby driving the infection dynamics.

References

1. Haag N, Geyrhofer L, Londel A, Derive E, Desvars-Larrive A, Loreto V, et al. Ranking the effectiveness of worldwide COVID-19 government interventions. *Nature human behaviour* 2020;4(12):1303–12.

2. Thompson HA, Mousa A, Dighe A, Fu H, Arnedo-Pena A, Barrett P, et al. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) setting-specific transmission rates: a systematic review and meta-analysis. *Clinical Infectious Diseases* 2021;73(3):e754–ee64.

3. Madewell ZJ, Yang Y, Longini IM, Halloran ME, Dean NE. Household transmission of SARS-CoV-2: a systematic review and meta-analysis. *JAMA network open* 2020;3(12):e2031755-e.

4. Choe YJ. Coronavirus Disease-19: Summary of 2,370 Contact Investigations of the First 30 Cases in the Republic of Korea. *Osong Public Health Res Perspect* 2020;11(2):81–4 PubMed PMID: 32257773. PubMed Central PMCID: PMC7104686. eng.

5. Streeck H, Schulte B, Kümmerer BM, Richter E, Hölter T, Fuhrmann C, et al. Infection fatality rate of SARS-CoV2 in a super-spreading event in Germany. *Nature communications* 2020;11(1):1–12.

6. Mossong J, Hens N, Jit M, Beutels P, Auranen K, Mikolajczyk R, et al. Social contacts and mixing patterns relevant to the spread of infectious diseases. *PLoS medicine* 2008;5(3):e74.

7. Tomori DV, Rübsamen N, Berger T, Scholz S, Walde J, Wittenberg I, et al. Individual social contact data and population mobility data as early markers of SARS-CoV-2 transmission dynamics during the first wave in Germany—an analysis based on the COVIMOD study. *BMC medicine* 2021;19(1):1–13.

8. R: A Language and Environment for Statistical Computing. *R Core Team* 2020.

9. Müller SA, Balmer M, Charlton W, Ewert R, Neumann A, Rakow C, et al. Predicting the effects of COVID-19 related interventions in urban settings by combining activity-based modelling, agent-based simulation, and mobile phone data. *PLoS one* 2021;16(10):e0259037.

10. Müller SA, Charlton W, Conrad ND, Ewert R, Jefferies D, Rakow C, et al. MODUSCOVID Bericht vom 19.03. 2021. 2021.

11. Suess T, Remschmidt C, Schnik SB, Schweiger B, Nitsche A, Schroeder K, et al. The role of face masks and hand hygiene in the prevention of influenza transmission in households: results from a cluster randomised trial; Berlin, Germany, 2009-2011. *BMC infectious diseases* 2012;12:1–16.

12. Whaley CM, Cantor J, Perá M, Jena AB. Assessing the association between social gatherings and COVID-19 risk using birthdays. *JAMA internal medicine* 2021;181(8):1090–9.

13. SARS-CoV-2 RC. 2-Nationale Teststrategie–wer wird in Deutschland auf das Vorliegen einer SARS-CoV–2 Infektion getestet. 2020.

14. Guzzetta Giorgio, Minosse Claudia, et al. Household transmission and disease transmissibility of a large HAV outbreak in Lazio, Italy, 2016–2017. *Epidemics* 2019;29:100351.

15. Epidemiologisches Bulletin 15/2021. RKI 2021.

16. Guzzetta Giorgio, Minosse Claudia, et al. Household transmission and disease transmissibility of a large HAV outbreak in Lazio, Italy, 2016-17 Epidemics. Guzzetta Giorgio, Minosse Claudia, Pisapia Raffaella, Giombini Emanuela, Mammone Alessia, Vairo Francesco, et al., editors. Elsevier; 2019.

17. RKI. Epidemiologisches Bulletin 17 September 2020 - Infektionsumfeld von Covid-19 Ausbrüchen in Deutschland. 2020.