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Outbreak of COVID-19 in Germany resulting from a single travel-associated primary case

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Outbreak of COVID-19 in Germany resulting from a single travel-associated primary case

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Abstract

Background:

In December 2019, a newly identified coronavirus (SARS-CoV-2) emerged in Wuhan, China, causing respiratory disease (COVID-19) presenting with fever, cough and frequently pneumonia. WHO has set the strategic objective to interrupt virus spread of SARS-CoV-2 worldwide. An outbreak in Bavaria, Germany, starting end of January 2020, gave the opportunity to study transmission events, incubation period, and attack rates.

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Conclusions:

While our cases present with predominately mild, non-specific symptoms, infectiousness before or on the day of symptom onset or during prodromal phase is substantial. Additionally, the incubation period is often very short, false-negative tests may occur. Although the outbreak was apparently controlled, successful long-term and global containment of COVID-19 may be difficult to achieve.

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Background

On December 31, 2019, Chinese officials reported a cluster of cases of pneumonia in Wuhan, China. A newly discovered coronavirus (SARS-CoV-2) was identified to be responsible for the ensuing outbreak.[1] As of March 1, 2020, over 87,000 confirmed cases of coronavirus disease 2019 (COVID-19) have been reported, 7,169 of which occurred outside of China in 58 countries.[2]

As of March 1, 2020, the World Health Organization (WHO) adheres to the strategic objective to 'interrupt human-to-human transmission including reducing secondary infections among close contacts and health care workers, preventing transmission amplification events, and preventing further international spread'.[2] The International Health Regulations (IHR) Emergency Committee stated in its most recent declaration that it 'believes that it is still possible to interrupt virus spread, provided that countries put in place strong measures to detect disease early, isolate and treat cases [and] trace contacts'.[3] China has implemented unprecedented measures to curb the epidemic, including cordoning off entire cities, and implementing rigorous contact restrictions.[4] In the meantime, countries outside of China attempt to contain the spread of the virus upon detection of travel-associated cases.

On January 27, 2020, the Bavarian Health and Food Safety Authority (LGL), Germany, was informed of the first human case of infection with SARS-CoV-2 in a German national who works for a company in the greater Munich area. The primary case in this satellite outbreak of COVID-19 is a person from Shanghai, China, who had contact to their own parents from Wuhan before visiting Germany for a business meeting in the above-mentioned company. Between January 27 and February 11, a total of 16 COVID-19 cases were identified in this cluster.

Management and investigation of the outbreak was immediately initiated on January 27 in order to identify further cases and contact persons, understand transmission events, and thus identify factors relevant for successful containment.

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Methods

Contact classification

On January 27, 2020, all employees of the affected company were informed about the potential risk of COVID-19 infection. International public health authorities were informed via the Early Warning and Response System (EWRS) or IHR National Focal points. Employees were actively queried for any contacts to the first two known cases. New cases were asked about professional and private contacts. Contact persons were classified as high-risk contacts if they had cumulative face-to-face contact to a laboratory-confirmed case for at least 15 minutes, had direct contact to secretions or body fluids of a confirmed case, or, in the case of health care workers, had worked within 2 meters of the confirmed case without personal protective equipment. All other contacts were classified as low-risk contacts.

Contact management

High-risk contacts were ordered to stay in home quarantine for 14 days after the last known contact to a confirmed case. Their health status was monitored daily. Laboratory testing was conducted in the beginning and end of home quarantine periods, irrespective of the presence of symptoms. Low-risk contacts were asked to self-monitor their health status and report any symptoms. In high- and low-risk contacts, laboratory testing was triggered upon onset of any symptoms.

Case interviews

Case interviews were conducted in a two-stage procedure. In a first stage, confirmed cases or the cases' household members were interviewed to determine date of symptom onset, links between cases, contact persons during the incubation period and contact classification. In a second stage, in-depth interviews with 10 cases were conducted by a team of two professionals (one physician and one epidemiologist) using a semi-structured questionnaire. Additional topics included characteristics of symptoms and details on type, setting and environment of contact to other cases and high-risk contacts. The in-depth interview with the primary case from Shanghai, China, was conducted twice (January 30 and 31, 2020) and supported by a Chinese native speaker. We defined fever and/or cough as specific symptoms, a prodromal phase (with non-specific symptoms) was defined as presence of symptoms other than fever and cough for at least one day prior to the beginning of the specific illness phase.

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Attack rate among contact persons

To calculate attack rates among contacts or contact persons, respectively, we considered four distinct groups: (1) a household cluster with one household member being a case, cohorted together in one room, (2) other household contacts, (3) non-household high-risk contacts, (4) known low-risk contact persons.

Laboratory testing

Laboratory testing involved two swabs (nasopharyngeal and oropharyngeal, pooled) that were stored in viral transport medium and cooled. RNA was extracted using the QiAamp Bio Robot Kit (Qiagen, Hilden, Germany) on a Hamilton Microlab Star as recommended by the manufacturer. Real-time reverse transcription PCR was performed with the QuantiTect Virus + Rox Vial Kit (Qiagen, Hilden, Germany) on the Bio-Rad CFX96 Touch™ Real-Time PCR Detection System. Primer and probes were used as described by Corman et al.[5] and provided by Tib-Molbiol, Berlin Germany. The reference laboratory worked exactly as described in Corman et al.[5] Whole genome sequencing involved Roche KAPA HyperPlus library preparation and sequencing on Illumina NextSeq and MiSeq instruments as well as RT-PCR product sequencing on Oxford Nanopore MinION using the primers described in Corman et al.[6] Case #1 was sequenced on all three platforms, cases#2-7 were sequenced on Illumina NextSeq, both with and without RT-PCR product sequencing with primers as in Corman et al.[6] Cases #8-11 and #14 were sequenced on Oxford Nanopore MinION. Sequence gaps were filled by Sanger sequencing.

Ethics statement

The outbreak investigation was conducted as part of the authoritative, official tasks of the county health departments as well as the state health department of the Bavarian Health and Food Safety Authority, supported by the Robert Koch Institute. As conducted in response to a public health emergency, this study was exempt from institutional review board approval.

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Results

SARS-CoV-2 importation to Germany

The primary case (case #0) stated that their parents, who normally live in Wuhan, had arrived for a visit in Shanghai on January 16. Both parents recalled cold-like symptoms the week before, and one parent showed fatigue and loss of appetite while visiting. The primary case, an employee of the Chinese branch of the German company, travelled from Shanghai to Munich by airplane on January 19, 2020, in order to facilitate workshops and attend meetings in the company building. On the day after arrival (January 20, 2020), the person felt chest and back aches – which they reported to be unusual – and took a single dose of medicine containing paracetamol (acetaminophen). Furthermore, the person reported fatigue during the whole stay in Germany and attributed the symptom to jetlag. After an overnight flight back to Shanghai on January 22/23, the person felt feverish. With a self-measured temperature of 38.6°C and cough on January 24, the person visited a physician's office on January 25. The case was tested positive for SARS-CoV-2 on January 26 and was hospitalized the next day. The clinical situation in both parents also deteriorated during the primary case's stay in Germany and both were laboratory-confirmed with COVID-19 later. The German company was informed of the primary case's infection in the morning of January 27, 2020, and immediately informed its employees as well as the local health authority.

Initial case identification and containment measures

The initial testing by RT-PCR of high-risk contacts between January 27-29 identified cases #1-#4 as first generation cases (**Figure1**).[7] All confirmed cases were immediately hospitalized and isolated. Their immediate contacts, including persons with contact 2 days before symptom onset, were traced. A 14-day home quarantine was ordered for all newly identified high-risk contacts, starting at the day of the last contact to a case during the potential infectious period. Contacts were actively followed-up on a daily basis. All high-risk contacts were instructed to minimize contact to other persons including household members in home quarantine. The affected company site was closed on the company's own initiative until February 11, 2020, and on-site disinfection measures were applied.

Onward transmission of SARS-CoV-2

As of February 19, 2020, sixteen subsequent cases have been identified, four female and 12 male (**Figure 1**). All cases had been registered as high-risk contacts of the primary case or subsequent cases, before being identified. The median age of all 16 cases was 35 years (range 2-58 years).

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Ten cases (#1-5, #7, #8, #10, #13, #16) plus the primary case (#0) are employees of the company. A Chinese colleague (case #13) of the primary case accompanied the primary case in multiple activities while in Germany. Case #13 travelled back to China with the primary case, developed symptoms on January 27, and tested SARS-CoV-2-positive a few days later.

Case #1 was an employee who attended a 1-hour business meeting with the primary case and two other colleagues on January 20, 2020. The meeting took place in a small room (~12 m^2); case #1 sat next to the primary case, the two other colleagues on the opposite side of the table. The two other colleagues never tested positive during follow-up as high-risk cases.

Case #1 had another brief contact with the primary case on January 21, and developed a sore throat on January 23. During the following weekend (Jan 25/26), this person developed cold-like symptoms with fever up to 39°C and mild productive cough. On January 27, the person felt well enough to go to work. There, case #1 learned about the primary case's infection and got tested positive on the same day.

Case #2 was not aware of any direct person-to-person contact with case #0, however virus sequence analysis supports the assumption that the Chinese index case transmitted the virus to #2. Case #3 had daily contact with case #1 from January 21 to 24. Already coughing, #1 and #3 worked simultaneously for a short period of time on the same computer on January 24. Only one day later, case #3 had a private meeting with case #12, sitting next to them for approximately 90 minutes. Afterwards they spent the rest of the evening together at case #3´s home, joined by case #3´s partner, who never tested positive upon follow-up as high-risk contacts. Case #12 departed for vacation to Spain three days later (January 28). After Spanish authorities were informed, the case was isolated in hospital on January 30 and diagnosed with COVID-19.

Case #4 had contact with the primary case on January 20, 21, and 22. Case #4 reported chills on January 24. The case had subsequent mild symptoms with slight malaise, slight nose and sinus congestion and was isolated on January 28. Case #5 met case #4 on January 22. Their only encounter was a canteen visit, sitting back to back, when case #5 turned to case #4 to borrow the saltshaker from the other table. The encounter was two days prior to symptoms onset in case #4. In spite of this early time before symptoms onset, transmission is confirmed by virus sequence analysis (**Table 3**), suggesting pre-symptomatic transmission. A nonsynonymous nucleotide substitution (G6446A) was found in virus from cases #4 and #5 but in no other case detected up to this point (cases #1-#3). Later cases with available specimens, all containing this same substitution, were all traced to case #5. No specimen was available for sequencing for case #12, #13, #15 and #16. The possibility that #4 could have been infected by #5 was excluded by detailed sequence analysis (*Wölfel et al. 2020, submitted*). Case #4 had the novel G6446A virus detected in throat swab, and the original 6446G virus detected in sputum, while case #5 had a homogenous virus population containing the novel G6446A substitution in the throat swab.

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The household of case #5 consists in total of five members, who were all hospitalized together after case #5 was confirmed positive. In addition to case #5, three members developed symptoms and were also tested SARS-CoV-2-positive, while one remained without symptoms and never tested positive based on RT-PCR. Case #9 became symptomatic last, the virus showing an additional C22323T substitution. This same mutation was found as a minority virus population of approximately 4% reads also in the sputum of case #11, but in none of the other household members. Case #11 had become symptomatic four days before case #9.

Case #7 met case #5 for a 1.5h meeting with approximately 1.5m distance on January 24, the day of symptoms onset in case #5. Symptoms in case #7 started four days later, on January 28, when the case had a 1h meeting with case #10. Case #8 and case #5 had regular daily meetings at work, also between January 22 and 24. Case #8 as well as case #10 were identified when a large number of employees, both high- and low-risk contacts, were invited to be sampled at the company during the three days following the initial discovery of the cluster (January 29-31). Retrospectively, during detailed interviews both recalled mild unspecific symptoms prior to testing, but not at the day of testing.

Case #14 is a household member of case #7 and both spent multiple days together after #7 was sent to home quarantine. Case #15 is a household member of case #2 and is asymptomatic. Cases #15 and #16 were initially tested negative between January 29 and 31 at the company and tested positive when the test was repeated at the end of the follow-up period. Retrospectively, case #16 had experienced a short period of very mild rhinorrhoea from February 4, and had not perceived this as a relevant symptom. Two possible transmission options could have occurred for case #16, one involving case #7 and the other involving case #8. Case #16 had participated in the same meeting in which case #10 likely got infected from case #7 on January 28. Case #16 had also met case #8 in a meeting with distance >1m on the day of symptoms onset also on January 28. Transmission history cannot be resolved because viral sequences in cases #7, #8 and #10 are identical and no sequence is available for case #16.

Contact tracing involved the international flights from Munich to Shanghai (Chinese primary case #0: January 22, 2020) and from Munich to Tenerife (case in Spain #12: January 28, 2020). Extensive contact tracing and notification via IHR focal points resulted in identification of case #12 by Spanish authorities. At the time of writing (March 3, 2020), no further cases have been identified amongst these or other contacts.

Characterization of transmission events

All cases but #15 were symptomatic, even if very mild (**Table 1**). However, no transmission originated from the asymptomatic case. Pre-symptomatic transmission was the only possible

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explanation for the transmission from case #4 to case #5. The cases involved in this transmission event had symptom onset on the identical day. On enquiry, case #4 affirmed having had slight otalgia the day before. Four cases likely transmitted the infection on the day of symptoms onset (**Table 1**). Transmission during the prodromal phase of the illness occurred from the primary case to cases #1, #2 and #4, as well as from case #3 to case #12. The incubation period ranged from a minimum of one day to seven days. When using the most likely duration (or in case of two equally likely durations, the mean duration) of the incubation periods, the median is 4.0 days. The median serial interval is 4.0 days as well.

Contacts traced and attack rates

After the infection of the index case was confirmed, high-risk contacts were identified and put under home quarantine (updated with identification of every new case). As of February 19, 2020, 241 high-risk contacts were identified. These also include 24 household contacts. One household consisting of 5 persons (cases #5, #6, #9, #11) stayed together during home quarantine first as well as in isolation in hospital later. Next to the first identified case (#5) in the household cluster, 3 persons subsequently became cases, resulting in an attack rate of 75% (95% confidence interval (CI): 19-99%; **Figure 3; Table 2**). Among the other high-risk contacts who were quarantined at home and became cases, 20 household contacts were identified that lived with the cases during the time of home quarantine until the cases were isolated in hospital. Among those household members, 2 further cases were identified, resulting in an attack rate of 10% (95%CI, 1.2-32%). Because these 20 household contacts had 80 contact days, this attack rate can be attributed to a household contact period of 4 days on average. In total, 217 further high-risk contact persons with 11 transmissions were identified among local employees of the affected company as well as other social contacts, except household contacts. The resulting attack rate is 5.1% (95% CI, 2.6-8.9%). No cases occurred among the 108 identified low-risk contacts.

Genome mutations

Over the four generations of transmission in this outbreak, the virus acquired two mutations in total, both of them non-silent (**Table 3**). The G6446A exchange leads to a valin to isoleucine exchange in the Betacoronavirus-specific marker (ßSM) domain in non-structural protein 3. No structure and function is known for this domain in SARS-coronavirus.[8] The C22323T exchange causes a serine to phenylalanine exchange in the spike protein S1 domain, which is outside the receptor binding domain. [9] The directly-observed substitution rate was two substitutions per 29903 nucleotides per 11 days, equaling 2.2E10E-3 substitutions per site, per year.

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Discussion

The present cluster constitutes the first documented chain of multiple human-to-human transmissions of SARS-CoV-2 outside Asia. Due to the particular setting centred around a business company with encounters tractable through electronic calendars, the timing and setting of most contacts were well defined. The sensitizing and close monitoring of subjects may have triggered sensitive reporting of prodromal symptoms. This may explain a rather short median incubation period of 4 days in our study, substantially shorter than the 5.2 days calculated from data of the first 425 confirmed cases in China[10] but similar to the recent findings of Guan and colleagues.[11] In comparison, for SARS the incubation period was 6.37 days with a range of 1-14 days.[12]

The short incubation period corresponds to transmission early in the course of disease, which is corroborated by studies of viral shedding in the same patients (*Wölfel et al. 2020, submitted*). High-level replication with frequent virus isolation from the pharynx stands in contrast to the SARS virus (genetically similar to the SARS-CoV-2 virus) that was shed at lower concentrations from the upper respiratory tract and was effectively transmitted roughly a week after symptoms onset.[10] This delayed shedding in SARS caused substantial problems with the sensitivity of RT-PCR based on upper respiratory tract swabs. It is evident from our study that RT-PCR on throat swabs can discover asymptomatic or oligosymptomatic persons that shed the virus. Overall, it appears that throat swabs are an appropriate diagnostic sample to detect SARS-CoV-2 infection.

The present investigation enables us to determine secondary attack rates based on closely monitored high-risk contacts. The attack rate thereby decreases with the intensity of contact. While among members of the cohorted household the attack rate was 75%, it was 10% among household contacts that were only together until isolation of the case. Among 217 non-household high-risk contacts that were cumulatively followed because of direct contact with a confirmed case, 11 were infected. The resulting secondary attack rate of 5% looks like a low figure, indicating limited spread in the here-investigated cluster. However, more effective spread of the virus might have been prevented by the proactive quarantine of high-risk contacts later identified as cases while still being pre- or mildly symptomatic as well as the pro-active closure of the affected company. Transmission originating from persons with more distinct respiratory symptoms might have resulted in a higher number of secondary cases.

At the time of writing, none of the cases are in severe condition, although two cases have developed signs of pneumonia later in the course of disease (*Wölfel et al. 2020, submitted*). However, it should be taken into account that the outbreak occurred in a population of work-age, generally healthy individuals. The overall clinical picture possibly would have been different in a population including elderly and/or individuals with underlying chronic diseases. Another limitation that should be acknowledged is that conceivably not all infectious encounters could be

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reconstructed. Since the company held larger business and social events during the exposure period, it is possible that an infectious case might have met a successor case so briefly that neither of the two remembered the encounter. Some critical transmission events were nevertheless confirmed by viral sequencing and population analysis. The contact investigation and interviews followed a general hypothesis of direct human-to-human transmission, and we believe that the concurring epidemiological and genetic results in reconstructing the transmission network support this assumption. Although we acknowledge the possibility of indirect (fomite) transmission (which might be an explanation of the infection of case #5 by case #4 and possibly of case #2 by case #0), it seems that its role is minor.

In conclusion, while COVID-19 cases present partially with mild, non-specific symptoms in our outbreak, infectiousness before symptoms onset, on the day of symptom onset as well as during mild prodromal symptoms is substantial and poses a huge challenge on the implementation of public health measures. Additionally, the incubation period is often very short and false negative tests may occur. Thus, although the outbreak was apparently controlled, successful long-term and global containment of COVID-19 may be difficult to achieve.

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Contributions

Initials	Contribution
MMB	*Writing, literature search, figures, study design, data collection, data analysis, data interpretation*
UB	*Writing, literature search, figures, study design, data collection, data analysis, data interpretation*
VMC	*Data collection, data analysis, data interpretation, writing*
MH	*Data collection, writing, review of manuscript*
KK	*Data collection, data analysis, data interpretation, review of manuscript*
DVM	*Data collection, data analysis, data interpretation, review of manuscript*
SB	*Data collection, data analysis, data interpretation, review of manuscript*
TW	*Data analysis, review of manuscript*
NA	*Data collection, review of manuscript*
RK	*Data collection, , writing, review of manuscript*
UE	*Data collection, , review of manuscript*
BT	*Data collection, , review of manuscript*
DA	*Data collection, review of manuscript*
KB	*Data collection, review of manuscript*
VF	*Data collection, review of manuscript*
AB	*Data collection, review of manuscript*
SH	*Data collection, review of manuscript*
SI	*Data collection, review of manuscript*
BW	*Data collection, review of manuscript*
AG	*Data collection, review of manuscript*
KP	*Data collection, data analysis, data interpretation, review of manuscript*
NM	*Data collection, data analysis, data interpretation, review of manuscript*
NZ	*Data collection, review of manuscript*
TSB	*Data collection, review of manuscript*
WC	*Data collection, review of manuscript*
AR	*Data collection, review of manuscript*
MadH	*Data collection, figures, review of manuscript*
UR	*Data collection, review of manuscript*
OH	*Data collection, review of manuscript*
JS	*Data collection, analysis, interpretation, review of manuscript*
TV	*Data collection, analysis, interpretation, review of manuscript*
BM	*Data collection, analysis, interpretation, review of manuscript*
RW	*Data collection, review of manuscript*
MA	*Data collection, review of manuscript*
MW	*Data collection, review of manuscript*
UP	*Data collection, review of manuscript*
BL	*Review of manuscript*
WH	*Data interpretation, supervision, review of manuscript*
AS	*Data collection, analysis, interpretation, supervision, review of manuscript*
CD	*Writing, data collection, analysis, interpretation; supervision*
AZ	*Supervision, review of manuscript*

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Table 1: Characteristics of laboratory confirmed cases in COVID-19 outbreak in Bavaria, Germany, in January/February 2020

Case no	Date of symptom onset (DSO)	Likely infected through… (predecessor)	Likely (possible) date of infection	Incubation period (days)	Transmission forward to successor case				Self-reported symptoms
					asymptomatic	pre-symptomatic	at day of symptom onset	in the prodromal phase	
#1	23 Jan 2020	Primary case	20 Jan or 21 Jan	2 or 3 (assumed 2.5)	no	no	#1 → #3	no	Sore throat after DSO: cold-like symptoms, fatigue, chills, fever, cough, headache, joint pain, muscle pain shortness of breath, diarrhoea
#2	25 Jan 2020	Primary case	Unknown (20-22 Jan)	3-5 (assumed 4)	unknown	unknown	unknown	unknown	Cold-like symptoms, mild headache after DSO: mild earache, chills, fatigue, mild sore throat, blocked nose, loose stool, shortness of breath
#3	25 Jan 2020	#1	24 Jan (21-23 Jan)	1 or 2 (assumed 1)	no	no	#3 → #12	#3 → #12	Fatigue, blocked nose, sinus congestion, headache, swollen lymph nodes after DSO: chest pain, cough, loose stool,
#4	24 Jan 2020	Primary case	20 Jan (21-22 Jan)	2, 3 or 4 (assumed 4)	no	#4 → #5	no	no	chills after DSO: fatigue, blocked nose, sinus congestion
#5	24 Jan 2020	#4	22 Jan	2	no	no	#5 → #8 #5 → #7 #5 → #11 #5 → #6	no	Fever, limb pain, nausea, vomiting, cough, fever after DSO: fatigue, loss of appetite, chest pain
#6	29 Jan 2020	#5	unknown	unknown	n.a.	n.a.	n.a.	n.a.	Fever, vomiting, nausea
#7	28 Jan 2020	#5	24 Jan	4	no	no	#7 → #10 #7 → #14 (#7 → #16, *option 1)*	no	Cough, blocked nose after DSO: fatigue, headache, fever, nosebleed, pneumonia

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#8	28 Jan 2020	#5	24 Jan (22-23 Jan)	4	no	no	(#8 → #16, *option 2*)	(#8 → #16, *option 2*)	Neck pain after DSO: headache, fatigue
#9	31 Jan 2020	#11	unknown	unknown	n.a.	n.a.	n.a.	n.a.	Fever, cough, vomiting, diarrhoea
#10	30 Jan 2020	#7	28 Jan (27 Jan)	2	n.a.	n.a.	n.a.	n.a.	Shortness of breath, after DSO: cold-like-symptoms, night sweat, cough, pneumonia
#11	27 Jan 2020	#5	unknown	unknown	unknown	unknown	unknown	unknown	Fever, limb pain, nausea, vomiting, back pain, fatigue
#12 (case diagnosed in Spain)	30 Jan 2020	#3	25 Jan	5	n.a.	n.a.	n.a.	n.a.	Blocked nose
#13 (2nd Chinese case)	27 Feb 2020	Primary case	20-23 Jan	4-7 (assumed 5.5)	n.a.	n.a.	n.a.	n.a.	Cough, general symptoms
#14	3 Feb 2020	#7	28-31 Jan	3-6 (assumed 4.5)	n.a.	n.a.	n.a.	n.a.	Fever after DSO: mild cough, fatigue, mild headache, loose stool
#15	---	#2	23-28 Jan	unknown	n.a.	n.a.	n.a.	n.a.	Asymptomatic
#16	4 Feb 2020	#7 or #8	28 Jan	7	n.a.	n.a.	n.a.	n.a.	Blocked nose

n.a. = not applicable; DSO = date of symptom onset

Definition of "Transmission forward to successor case": asymptomatic = transmission through a case who never developed any symptoms during infection; pre-symptomatic = transmission through a case who developed symptoms only after the transmission to another person; at day of symptom onset = transmission through a case at the date of symptom onset, including both specific (fever and cough) and unspecific symptoms; in the prodromal phase = transmission through a case during the phase where only unspecific symptoms (other than fever, cough) were present

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Table 2: Attack rates among high-risk contacts in Bavarian COVID-19 outbreak in January/February 2020

Type of contact	Number of contact persons	Number of cases originating from these contacts	Attack rate	95% confidence interval
Household contacts				
common household isolation	4	3	75%	19%-99%
together until isolation of case	20	2	10%	1,2%-32%
Other high risk contacts				
close unprotected contact (contact persons)	217	11	5%	2,6%-8,9%
close unprotected contact (case-contact pairs)	249	11	4%	2,2%-7,8%
Low-risk contacts				
distant unprotected contact	108	0	0%	0%-3,4%

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Table 3: Genome single nucleotide polymorphisms as opposed to reference sequence

Position[1]	**241**	**3037**	**6446**	**8981**	**22323**	**23403**
Gene	**non-coding**	**ORF1ab**	**ORF1ab**	**ORF1ab**	**S**	**S**
Nucleotide in reference	C	C	G	C	C	A
Case #1	T	T	G	C	C	G (D>G)
Case #2	T	T	G	C	C	G (D>G)
Case #3	T	T	G	C	C	G (D>G)
Case #4	T	T	A (V>I)/G	Y (for T, A>V)	C	G (D>G)
Case #5	T	T	A (V>I)	C	C	G (D>G)
Case #6	T	T	A (V>I)	C	C	G (D>G)
Case #7	T	T	A (V>I)	C	C	G (D>G)
Case #8	T	T	A (V>I)	C	C	G (D>G)
Case #9	T	T	A (V>I)	C	T (S>F)	G (D>G)
Case #10	T	T	A (V>I)	C	C	G (D>G)
Case #11	T	T	A (V>I)	C	C	G (D>G)
Case #14	T	T	A (V>I)	C	C	G (D>G)

[1]Positions relative to EPI_ISL_402125 (the Genome with closest similarity presently available on GISAID). Information in parenthesis are amino acid exchanges in case of non-silent mutations.

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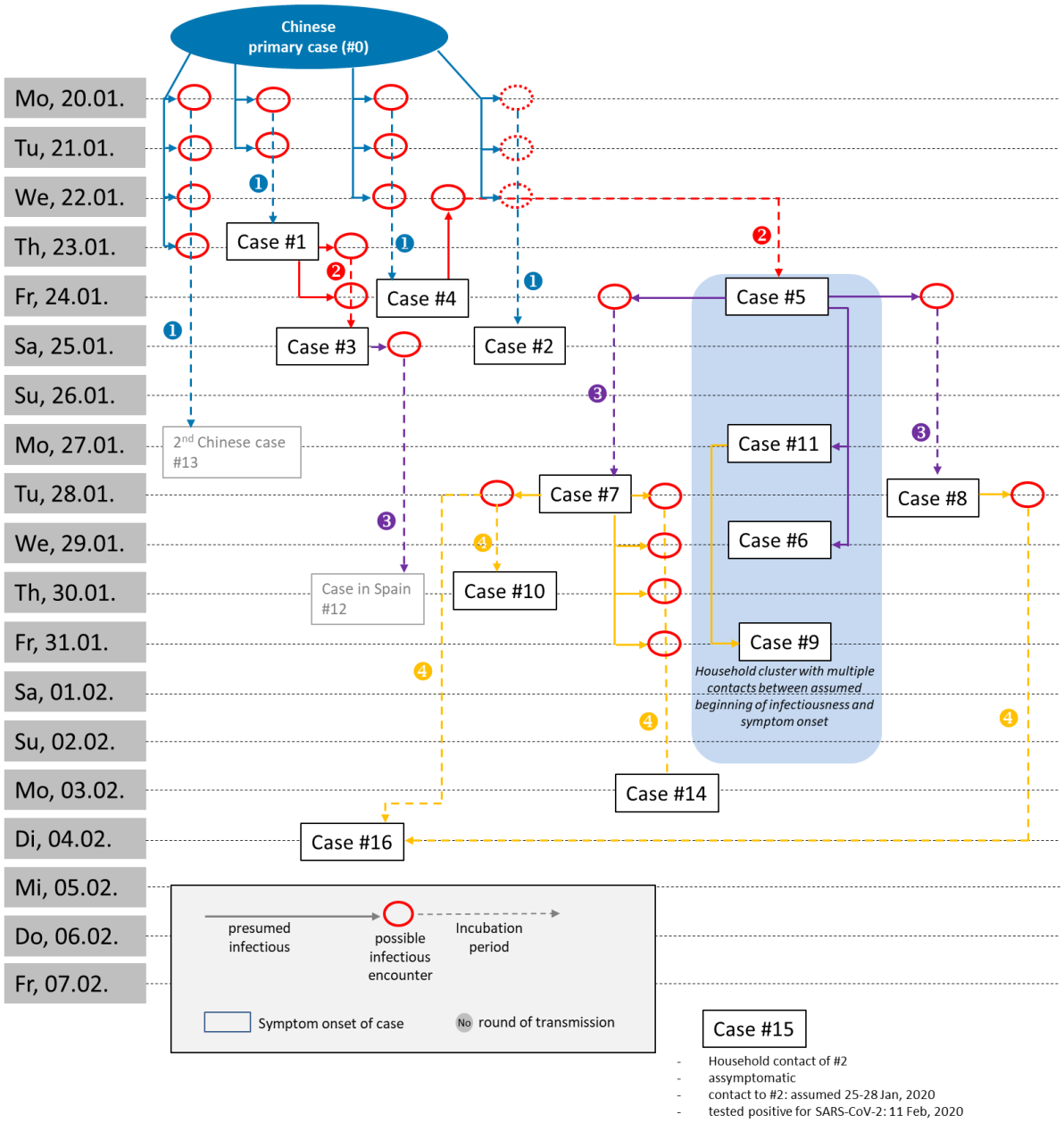
Figure 1: Transmission chain of COVID-19 satellite outbreak in Bavaria, Germany, in January/February 2020.



Legend to figure 1:

Boxes denote the day of symptom onset of cases, transmission rounds (arrows) are numbered and displayed in different colours. Circles indicate the encounter when transmission likely occurred, transmission from primary case to case #2 is confirmed by whole genome sequencing, however, no specific encounter could be identified (encounter circle is dotted). Potential pre-symptomatic infectious encounters are only included if no other encounter could be identified. Dotted arrows indicate the incubation period (transmission event until presentation of first symptoms), solid arrows lead from source cases to likely infectious encounters with recipient cases. For cases the infectious period was assumed to start 2 days prior to onset of symptoms.

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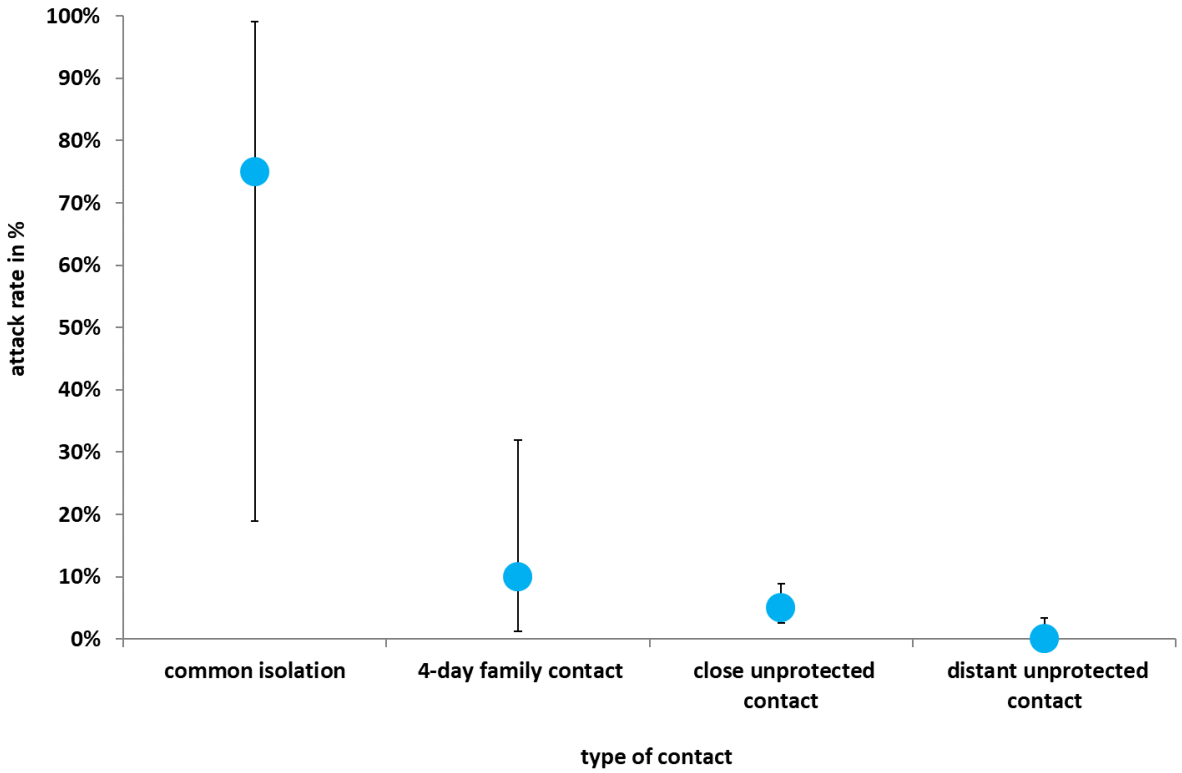
Figure 2: Attack rates (and 95% confidence intervals) among different groups of high-risk contacts and low-risk contacts identified in COVID-19 outbreak in Bavaria, Germany, January/February 2020.



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