

# Transmission of SARS-CoV-2 into and within immigrant households: nationwide registry study from Norway

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## ABSTRACT

**Background** Minority groups and immigrants have been hit disproportionately hard by COVID-19 in many developed countries, including Norway.

**Methods** Using individual-level registry data of all Norwegian residents, we compared infections across all multiperson households. A household with at least one member born abroad was defined as an immigrant household. In households where at least one person tested positive for SARS-CoV-2 from 1 August 2020 to 1 May 2021, we calculated secondary attack rates (SARs) as the per cent of other household members testing positive within 14 days. Logistic regression was used to adjust for sex, age, household composition and geography.

**Results** Among all multiperson households in Norway (n=1 422 411), at least one member had been infected in 3.7% of the 343 017 immigrant households and 1.4% in the 1 079 394 households with only Norwegian-born members. SARs were higher in immigrant (32%) than Norwegian-born households (20%). SARs differed considerably by region, and were particularly high in households from West Asia, Eastern Europe, Africa and Eastern Europe, also after adjustment for sex and age of the secondary case, household composition and geography.

**Conclusion** SARS-CoV-2 is more frequently introduced into multiperson immigrant households than into households with only Norwegian-born members, and transmission within the household occurs more frequently in immigrant households. The results are likely related to living conditions, family composition or differences in social interaction, emphasising the need to prevent introduction of SARS-CoV-2 into these vulnerable households.

## INTRODUCTION

Ethnic minority groups originating from West-Asia and Africa have been hit harder by COVID-19 than others in many European and North American countries.<sup>1–3</sup> Norway is no exception, as immigrants from West-Asia and Africa, among others, have suffered more infections and hospitalisations than non-immigrants.<sup>4 5</sup> While some of the over-representation can be attributed to socioeconomic deprivation, substantial over-representation prevails after adjustment for demographic, socioeconomic, household and medical factors.<sup>1–6</sup> More knowledge is needed to design and implement measures that can break the chains of transmission.

Households are one of the most important arenas for transmission of SARS-CoV-2.<sup>3 7 8</sup> Little is known at the population level about characteristics of households more susceptible to infection and of households with more intra-household transmission.

Using individual-level data for all residents in Norway, our aim was to analyse transmissions of SARS-CoV-2 into and within all multiperson households by the region of origin of the household members.

## METHODS

### Data

As part of the legally mandated responsibilities of The Norwegian Institute of Public Health during epidemics, a new emergency preparedness register, labelled BeredtC19, covering all residents of Norway, was established in cooperation with the Norwegian Directorate of Health in April 2020.<sup>9</sup> The purpose of the register is to provide rapid knowledge on the pandemic and the effect of the measures taken to contain the spread of the virus. The register includes daily updated information from the Norwegian Surveillance System for Communicable Diseases (MSIS), updated information from the Population Registry and members of each household from Statistics Norway. All laboratories in Norway conducting PCR tests for SARS-CoV-2 notify MSIS about the test result, the date of testing and the identity of the person tested. The time from sampling to results, which may influence secondary transmissions, has typically been less than 1 or 2 days.<sup>10</sup> Information was linked at the individual level using the unique personal identification number (encrypted version) provided to every Norwegian resident at birth or on immigration.

We used the individual-level data in BeredtC19 for all residents of Norway, with vital demographic statistics (sex, year of birth, household members and so on), and PCR tests for SARS-CoV-2. Testing capacity was restricted before the summer of 2020, and we have thus limited the analysis to the period from 1 August 2020 when testing was encouraged and free.

### Population, definitions and time of follow-up

Our population included all residents of Norway at the beginning of 2020 (5.4 million), implying that non-residents (like tourists, temporary workers and asylum applicants) were not available. A household



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comprises every resident of one dwelling (excluding institutions), typically one family living in the same housing unit at the same address. We restricted the analyses to individuals who were living in households with at least two members.

A household with at least one member born abroad was classified as an immigrant household. We further divided households into seven regional entities: Africa, Americas/Oceania, East Asia, Eastern Europe, New EU-members, West Asia and Western Europe (online supplemental S-Figure 1). To be able to make non-overlapping household definitions, we put immigrant households with members born in more than one region (in addition to Norway), in a separate category ('multiple countries of origin').

We focused on households with at least one member with a positive PCR-test for SARS-CoV-2 between 1 August 2020 and 1 May 2021, with follow-up time to 15 May 2021. The first member of a household who tested positive in a PCR test was defined as index case.

Following the literature, secondary attack rates (SARs) were calculated as the share of household members (excluding the index case in both the numerator and denominator) with a positive test within 14 days after the sampling date of the index case (SAR14).<sup>11</sup> SAR14 was calculated for the overall sample, as well as by the households' region of origin.

## Analyses

We described characteristics of households with an index case and compared them to the overall population of multiperson households. We then calculated the per cent of households with secondary infection, and calculated SAR14 for immigrant and non-immigrant households separately, both aggregated and by region. To gauge robustness, we ran a separate regression analysis with a different immigrant definition (online supplemental S-Table 1), and ran analyses including households with more than one index person ('co-indexes') (online supplemental S-Table 2). To check that as good as all secondary cases were captured by 14 days, we also calculated SAR from 1 through 30 days after date of index case; to check that results were not driven by frequency of testing, we calculated the per cent of household members who had been tested from 1 through 30 days after date of index case; and to check that results were not driven by variation in increasing vaccination during the spring of 2021, we calculated SAR14 by calendar month. 95% CIs were calculated using the Wilson method. To explore robustness of SAR14 by region to compositional differences (sex, age, household composition and geography), we ran a logistic regression model on the sample of all non-index household members, with secondary infection by 14 days as the outcome variable. All variables were included as categorical variables, that is, sex (male/female), age (0–9, 10–19, 20–29, 30–39, 40–49, 50–59, 60–69 and 70 or above), household members (two, three, four, five, six and seven or more), presence of both at least one household member below the age of 20 and at least one household member above the age of 60 (yes/no) and county of residence (the 11 administrative counties of Norway). The statistical software used was Stata MP V.16.

## RESULTS

### Background statistics

Among multiperson households in Norway (n=1 422 411), immigrant households (n=343 017) comprised more members on average (3.2) than households with only Norwegian-born members (2.8); see online supplemental S-Table 3. The per cent of households that included members both below 20 and above

60 years of age was also higher (3.6% vs 1.7%). Members of immigrant households were on average younger (33) than households with only Norwegian-born members (40), and particularly so for households with members born in Africa (28) and West Asia (30) (online supplemental S-Table 3).

The share of households with at least one member hospitalised or dead from COVID-19 was higher in immigrant (0.4% households with hospitalised member, 0.02% households with dead member) than Norwegian-born households (0.1%, 0.01%) (online supplemental S-Table 3). Households from West Asia were among the most severely hit, with 1.1% having at least one member hospitalised and 0.06% having at least one dead member.

In 57% of immigrant households, at least one member had been tested, while this was the case in 49% of households with only Norwegian-born members. Testing was most frequent in households from West Asia (63%) and Africa (62%).

### Transmissions into households

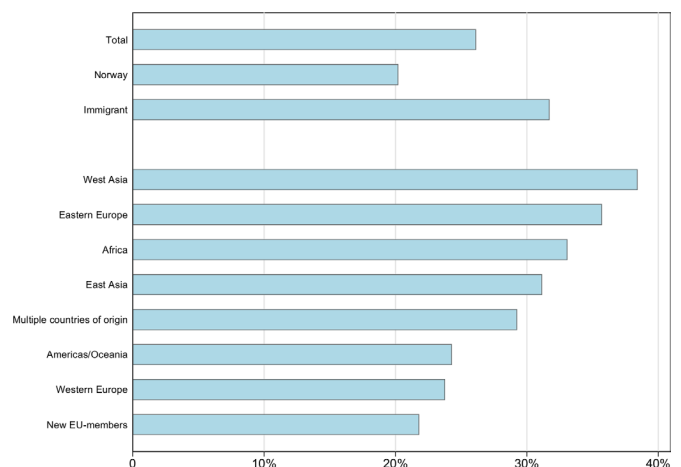
The share of all immigrant households (tested or not) with at least one member infected was 3.7%, compared with 1.4% in households with only Norwegian-born members; see online supplemental S-Table 3. There was substantial variation across regions, with at least one member having been positive in 7.6% of West Asian and 6.9% of African households.

The high infection rates are not likely to be a result of more testing in immigrant households, as the share of the tested households that tested positive is also higher in immigrant households.<sup>12</sup>

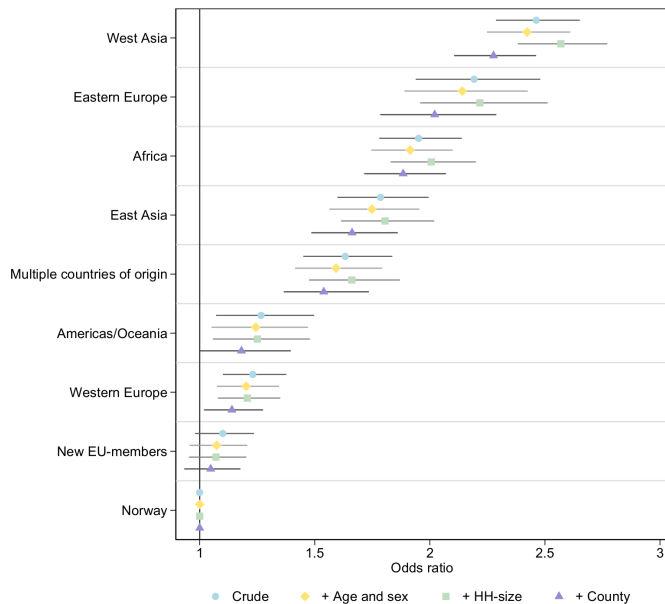
### Transmissions within households

Among the households with an index case, 42% of immigrant households and 29% of households with only Norwegian-born members had at least one secondary member infected by 14 days (online supplemental S-Figure 2). After introduction of the virus into the household, more than 50% of households from West Asia had at least one more member infected within 14 days.

SARs (SAR14) were also higher in immigrant (32%) than Norwegian-born households (20%); see figure 1. Results differed considerably by region, with the highest SAR14 in households from West Asia (38%), Eastern Europe (36%), Africa (33%) and East Asia (31%). Results from the logistic regression model (figure 2; online supplemental S-Table 4) show that the elevated



**Figure 1** Secondary attack rate (SAR14). Note: It shows the percentages of household members that tested positive within 14 days after the index person tested positive, by region of birth.



**Figure 2** Logistic regression. Note: Logistic regression showing the OR of being infected within 14 days after index person tested positive, using households with only Norwegian-born as baseline. Crude models contain no confounders, +Age and sex adjusts for age in categories and dichotomous sex, +HHsize additionally accounts for the number of persons in each household and whether the household is generational and +County additionally adjusts for the county of residence. All models contain SEs clustered on the household. Markers shows the estimated OR with the corresponding 95% CI.

secondary transmissions by 14 days in immigrant households changed little when adjusting for age, sex and household size. When also adjusting for county of residence, the difference between Norwegian-born and immigrants decreased slightly for all regions, suggesting that immigrant households may have elevated SAR<sub>14</sub> partly because they live in high-prevalence Norwegian counties.

In our preferred specification, co-index households are excluded from the sample; retaining these households in the estimation sample produces very similar results (online supplemental S-Table 2). The share of household members tested within 14 days after the index case is high for all groups, although the testing rates in immigrant households were slightly below that of Norwegian-born households up to about 9 days after index positivity, and thereafter higher (online supplemental S-Figure 3). SAR<sub>14</sub> tended to increase over calendar time, but it remained about 10 percentage points higher in immigrant than Norwegian-born households in all calendar months (online supplemental S-Table 5).

## DISCUSSION

### Principal findings

Studying all residents in Norway living in multiperson households, we find that registered transmission of SARS-CoV-2 from 1 August 2020 to 1 May 2021 is substantially higher both into and within immigrant households than households with only Norwegian-born members.

Immigrant households were more than two times as likely to have a member infected with SARS-CoV-2 than households with only Norwegian-born members. Once a household member was infected, the SAR by 14 days was more than 50% higher in immigrant households than in households with only Norwegian-born

members. Results differed considerably by region of origin, with households from West Asia hit particularly hard. Main results were not altered by adjusting for age, sex, household composition and county of residence, nor by using different immigrant definitions (online supplemental S-Table 1) or including households with co-indexes (online supplemental S-Table 2).

### Related studies

Though there are many studies showing higher infection rates among ethnic minority and immigrant groups originating from West-Asia and Africa also after adjusting for demographic, socio-economic, household and medical factors,<sup>1-6</sup> we are not aware of any previous study of transmissions into and within immigrant households. Previous studies of household SAR do not focus on differences in transmission across region of origin, and results on intra-household transmissions of SARS-CoV-2 are inconclusive, as the studies are few and small, with different designs, and report widely varying SARs.<sup>8 13-21</sup> We observed an overall SAR in line with previous studies, for example, in three systematic reviews Madewell *et al* reported household SAR of 17%,<sup>13</sup> Fung *et al* of 17%<sup>14</sup> and Lei *et al* of 27%,<sup>15</sup> neither providing information about ethnic groups or immigrants.

### Interpretations

Norway has based much of its pandemic response on a strategy of coordinated control measures. In the study period, this has included testing everyone after travel abroad and everyone with known exposure or minor symptoms, isolation of positive cases, careful contact tracing and quarantine and testing through the incubation period.

PCR testing has been widely available in Norway, and from August 2020 anyone wanting a test could have one for free by contacting their local municipal test-station. In our data, the frequency of testing in immigrants has exceeded slightly that of Norwegian-born, but higher test frequency among immigrants is unlikely to influence our results as their positivity rate is also higher.

We found substantial differences in the share of infected households and in SARs by household region of origin. The more than two times as high transmission rate into immigrant households than households with only Norwegian-born members, could be related to the immigrant households being significantly larger with accompanying higher aggregated risk of one of the members being infected. Moreover, immigrants tend to live in urban areas that have had higher infection rates,<sup>5</sup> and more often work in high-risk occupations,<sup>22</sup> which may also explain some of the higher introduction rates into these households. The government has prioritised vaccine distribution in Norway to areas with high infection rates and a high percentage of multiperson immigrant households. As this went into effect from March 2021, and were reinforced from June 2021, we may start to see declining differences in transmission into (and within) households by immigrant and non-immigrant descent. Differences in social contact patterns, travelling and occupational risks have also been suggested as possible partial explanations.<sup>3 4 22</sup>

A consensus statement from SAGE in the UK concludes that households are important drivers of COVID-19 transmission.<sup>3</sup> The paper is based on five published studies. All five studies found that household composition is crucial in understanding spread with a larger risk associated with larger multigenerational households. While they support the idea that household composition may explain additional risk for some ethnic groups, they

do not explain the total additional risk seen in some parts of the population.

We also found substantial differences in secondary transmissions within households by region. This may be related to the composition of the households, and we observe, for example, that the share of immigrant households with members both below 20 and above 60 years of age is more than two times as high in immigrant households than in households with only Norwegian-born members. Nafilyan *et al*<sup>6</sup> find that part of the ethnic inequalities in mortality can be explained by living in a multigenerational household, and Telle *et al*<sup>11</sup> have shown that SAR is high from young children to their care givers. Also, older people may develop more symptoms and have a higher viral load, which may enhance intra-household spread. We observe households originating from the regions with highest intra-household SAR, are also those with most members and with both young and old members in the same household. However, in logistic regression models, we find that the elevated secondary transmission in immigrant households persists after adjustment for household size and presence of both young and old members (figure 2; online supplemental S-Table 4).

Not only household size, but also housing space may contribute to the spread of the virus.<sup>4</sup> Norwegian advice has been that when isolating at home, cases should have as little contact with other family members as possible and their own bathroom and meals brought to them. This is harder in large families sharing smaller living spaces. In Norway, alternative housing to separate infected from non-infected household members has only been offered and accepted to a limited extent. Measures that make alternative housing more appealing, for instance moving the whole household to a larger dwelling, may be considered.

Early testing of the index is important to break the chain of intra-household transmission, but so is also testing of the rest of the household. Small delays in such testing for possible secondary cases may affect intra-household secondary transmissions considerably.<sup>10</sup> Our data suggest that testing of immigrant households is somewhat delayed in the first week after index is positive (online supplemental S-Figure 3), and the possible consequences of this deserve further research. We do not know why the testing is delayed, but possible reasons could be differences in health literacy and language difficulties.

The effect of strict travel control measures in preventing virus introduction into immigrant household is also worthy of more research. These should be contrasted with local measures aimed at, for example, increasing trust between immigrant communities and health authorities or restricting the size of social gatherings. Moreover, the municipal contact tracing teams should have access to professional interpreters in the communication with immigrant households.

One possible explanation for the higher intra-household secondary transmission in immigrant households compared with households with only Norwegian-born members has been that the share of more easily transmittable virus variants is higher in these households. Between 1 August 2020 and 1 May 2021, the difference in SAR<sub>14</sub> between immigrant and Norwegian-born households varied between 7 and 14 percentage points (online supplemental S-Table 5). Prior to the first confirmed case of the alpha variant in Norway in December 2020,<sup>23</sup> the monthly difference varied between 9 and 12 percentage points. Hence, circulation of new variants is not likely to explain the higher SAR in immigrant families.

## Potential limitations

We did not have data to confirm that the secondary cases were in fact transmissions from the index case. It is possible that both the index case and the secondary cases had a common external source, or that they were infected by different external sources. Better knowledge of actual directions of transmission within families would improve our ability to evaluate this, for example, by judgements by healthcare personnel following each family or by genomic characterisation of the viruses. However, several transmissions into the same household have been unlikely in Norway as the incidence rate of SARS-CoV-2 has been low throughout the pandemic. Still, immigrants more often live in urban areas with higher infection rates, and more often work in high-risk occupations, possibly making several introduction events into immigrant households marginally more likely than for households with only Norwegian-born members.

A clear advantage of our registry-based study to most other studies is that we do not have attrition: we observe every household, and we can observe all household members in the follow-up period, regardless of motivation to participate in a study or not. Indeed, our data stem from a real-world situation, where detection of secondary cases relates to a combination of the actual transmission of the virus and the behavioural responses to disease and the actual testing regime.<sup>11</sup>

## Conclusions

By looking at register data of all Norwegian residents living in multiperson households, we see that households with immigrants are both more vulnerable to virus introduction into the household and to subsequent transmission within the household. More knowledge is needed to find the specific measures that can break the chains of transmissions into and within households, especially immigrant households that are hit particularly hard by COVID-19.

### What is already known on this subject

- ▶ We know that ethnic minority groups have been hit disproportionately hard by COVID-19, but less is known about why this is so.
- ▶ We do not know whether there is more transmission into immigrant household or whether there is higher intra-household transmission in immigrant households.

### What this study adds

- ▶ We find that the transmission of SARS-CoV-2 is both more frequent into, and within, multiperson immigrant households compared with multiperson households with only Norwegian-born members.
- ▶ For some immigrant groups, the share of household members testing positive within 14 days after the index case is almost two times as high as for households with only Norwegian-born members.
- ▶ Adjusting for age, sex, household composition and county of residence does not substantially alter the results.

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**Contributors** FM had access to all of the data in the study, takes full responsibility for the integrity of the data and the accuracy of the data analysis, and serves as a guarantor for the overall content. RKH and AAG coded the initial dataset. FM and KET performed the statistical analyses and drafted the manuscript with SBJ and OK. All authors contributed with acquisition of data, conceptual design, analyses and interpretation of results. All authors contributed to writing the article or critically revising it for important intellectual content. All authors gave final approval for the version to be submitted.

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**Patient consent for publication** Not applicable.

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**Data availability statement** No data are available. The individual-level data used in this study are not publicly available due to privacy laws. However, the individual-level data in the registries compiled in BeredC19 are accessible to authorised researchers after ethical approval and application to helsedata.no administered by the Norwegian Directorate of eHealth. Stata do-files are available upon request.

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#### REFERENCES

- Mackey K, Ayers CK, Kondo KK, *et al.* Racial and Ethnic Disparities in COVID-19-Related Infections, Hospitalizations, and Deaths: A Systematic Review. *Ann Intern Med* 2021;174:362–73.
- Mathur R, Rentsch CT, Morton CE, *et al.* Ethnic differences in SARS-CoV-2 infection and COVID-19-related hospitalisation, intensive care unit admission, and death in 17 million adults in England: an observational cohort study using the OpenSAFELY platform. *Lancet* 2021;397:1711–24.
- SAGE. Housing, household transmission and ethnicity: for SAGE meeting 26 November 2020. Available: <https://www.gov.uk/government/publications/housing-household-transmission-and-ethnicity-26-november-2020>
- Labberton AS, Godøy A, Elgersma IH. SARS-CoV-2 infections and hospitalizations among immigrants in Norway – significance of occupation, household crowding, education, household income and medical risk. A nationwide register study. *medRxiv* 2021.
- Indseth T, Elgersma IH, Strand BH, *et al.* Covid-19 blant personer født utenfor Norge, justert for yrke, trangboddhet, medisinsk risikogruppe, utdanning og inntekt, Rapport 2021 [Covid-19 among persons born outside Norway, adjusted for occupation, Household crowding, medical risk group, education and income, Report 2021]. Oslo: Folkehelseinstituttet, 2021.
- Nafilyan V, Islam N, Ayoubkhani D, *et al.* Ethnicity, household composition and COVID-19 mortality: a national linked data study. *J R Soc Med* 2021;114:182–211.
- Thompson HA, Mousa A, Dighe A, *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:ciab100.
- Tian T, Huo X. Secondary attack rates of COVID-19 in diverse contact settings, a meta-analysis. *J Infect Dev Ctries* 2020;14:1361–7.
- Norwegian Institute of Public Health. The Norwegian emergency preparedness register (BEREDT C19), 2020. Available: <https://www.fhi.no/sv/smittsomme-sykdommer/corona/norsk-beredskapsregister-for-covid-19/>
- Kretzschmar ME, Rozhnova G, Bootsma MCJ, *et al.* Impact of delays on effectiveness of contact tracing strategies for COVID-19: a modelling study. *Lancet Public Health* 2020;5:e452–9.
- Telle K, Jørgensen SB, Hart R, *et al.* Secondary attack rates of COVID-19 in Norwegian families: a nation-wide register-based study. *Eur J Epidemiol* 2021;36:741–8.
- Methi F, Hart RK, Godoy AA. Transmission of SARS-CoV-2 into and within immigrant households. Nation-wide registry-study from Norway. *medRxiv* 2021.
- Madewell ZJ, Yang Y, Longini IM, *et al.* Household transmission of SARS-CoV-2: a systematic review and meta-analysis. *JAMA Netw Open* 2020;3:e2031756.
- Fung HF, Martinez L, Alarid-Escudero F, *et al.* The household secondary attack rate of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2): a rapid review. *Clin Infect Dis* 2021;73:138–45.
- Lei H, Xu X, Xiao S, *et al.* Household transmission of COVID-19—a systematic review and meta-analysis. *J Infect* 2020;81:979–97.
- ECDC. *European Centre for Disease Prevention and Control. COVID-19 in children and the role of school settings in transmission - first update.* 23. Stockholm, 2020.
- Grijalva CG, Rolfes MA, Zhu Y, *et al.* Transmission of SARS-CoV-2 Infections in households - Tennessee and Wisconsin, April–September 2020. *MMWR Morb Mortal Wkly Rep* 2020;69:1631.
- Kim J, Choe YJ, Lee J, *et al.* Role of children in household transmission of COVID-19. *Arch Dis Child* 2021;106:709–11.
- Park YJ, Choe YJ, Park O, *et al.* Contact tracing during coronavirus disease outbreak, South Korea, 2020. *Emerg Infect Dis* 2020;26:2465–8.
- Kuvelker K, Zhou F, Blomberg B. High attack rates of SARS-CoV-2 infection through household-transmission: a prospective study. *medRxiv* 2020.
- Viner RM, Mytton OT, Bonell C, *et al.* Susceptibility to SARS-CoV-2 infection among children and adolescents compared with adults: a systematic review and meta-analysis. *JAMA Pediatr* 2021;175:143–56.
- Kjøllesdal M, Magnusson K. Occupational risk of COVID-19 by country of birth. A register-based study. *J Public Health* 2021;49.
- Norwegian Institute of Public Health. Weekly reports of the COVID-19 situation in Norway. Week 51, 2020. Available: <https://www.fhi.no/contentassets/8a971e7b0a3c4a06dbf381ab52e6157/vedlegg/andre-halvar-2020/2020.12.23-ukerapport-uke-51.pdf>