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The association of combinations of social factors and SARs-CoV-2 infection: A retrospective population-based cohort study in Ontario, 2020–2021

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ABSTRACT

Objective: The COVID-19 pandemic highlighted and exacerbated health inequities worldwide. While several studies have examined the impact of individual social factors on COVID infection, our objective was to examine how interactions of social factors were associated with the risk of testing positive for SARS-CoV-2 during the first two years of the pandemic.

Study design and setting: We conducted an observational cohort study using linked health administrative data for Ontarians tested for SARS-CoV-2 between January 1st, 2020, and December 31st, 2021. We constructed multivariable models to examine the association between SARS-CoV-2 positivity and key variables including immigration status (immigrants vs. other Ontarians), and neighbourhood variables for household size, income, essential worker status, and visible minority status. We report main and interaction effects using odds ratios and predicted probabilities, with age and sex controlled in all models.

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Results: Of 6,575,523 Ontarians in the cohort, 88.5 % tested negative, and 11.5 % tested positive for SARS-CoV-2. In all models, immigrants and those living in neighbourhoods with large average household sizes had greater odds of testing positive for SARS-CoV-2. The strength of these associations increased with increasing levels of neighbourhood marginalization for income, essential worker proportion and visible minority proportion. We observed little change in the probability of testing positive across neighbourhood income quintiles among other Ontarians who live in neighbourhoods with smaller households, but a large change in probability among other Ontarians who live in neighbourhoods with larger households.
Conclusion: Our study found that SARS-CoV-2 positivity was greater among people with certain combinations of social factors, but in all cases the probability of testing positive was consistently greater for immigrants than for other Ontarians. Examining interactions of social factors can provide a more nuanced and more comprehensive understanding of health inequity than examining factors separately.

1. Introduction

Social factors are associated with disproportionate disease burden and unequal health outcomes [1,2], including infection rates [3], prevalences of chronic conditions [4], and mortality [5,6]. The COVID-19 pandemic both highlighted and exacerbated such health inequities, with studies in high-income countries such as the United States, United Kingdom and Canada showing that certain social factors – most prominently those related to race, ethnicity and socioeconomic status – were strongly associated with the risk of SARS-CoV-2 infection [7–16]. In Ontario, both individual-level (e.g., immigration status) and neighbourhood-level (e.g., living in a low-income neighbourhood) factors were independently associated with SARS-CoV-2 positivity [17–21]. For example, Sundaram et al. [17] showed that several area-based social factors, including neighbourhood household size, and proportion of essential workers, increased the odds of testing positive for SARS-CoV-2 in Ontario [17]. Udell et al. [19] found that the introduction of public health measures mitigated the association between clinical risk factors and the odds of SARS-CoV-2 infection in areas with lower, but not greater, ethnic or racial diversity [19]. Mishra et al. [22] identified correlations between several different social determinants with SARS-CoV-2 infection in Toronto, Ontario. However, these studies mostly examined these social factors as independent risks without interaction terms that could reflect more complex relationships between these determinants [17,19,22]. Since social factors do not operate in isolation, studies may have missed the burden of COVID-19 on specific communities.

In this study, our objective was to examine how the interaction of social factors were associated with risk of testing positive for SARS-CoV-2 during the first two years of the COVID-19 pandemic. We used linked health administrative data to identify SARS-CoV-2 testing patterns for over 6.5 million people in Ontario, Canada's most populous province. We identified key individual- and neighbourhood-level variables and analyzed how the interactions of these variables cumulatively affected COVID positivity. We hypothesized that there is a synergistic effect of acquiring SARS-CoV-2 faced by some populations as a result of particular combinations of social factors.

2. Materials and methods

2.1. Study design, setting, and population

We conducted a retrospective cohort study using Ontario's health administrative data. Ontario has a single-payer health care system which provides universal access to physician and hospital services [23]. Our cohort included all Ontarians alive and eligible for provincial health care on January 1, 2020, who received SARS-CoV-2 polymerase chain reaction (PCR) testing between January 1, 2020, and December 31, 2021. Individuals were excluded if their date of death, date of birth, or sex, were invalid, if they were over 105 years old, had not been in contact with the health care system for seven years before index date, or were not eligible for the Ontario Health Insurance Plan (OHIP).

2.2. Data sources, outcomes, and variables

This study used the linked health administrative databases at ICES (ices.on.ca), an independent, non-profit research institute. ICES has legal status under Ontario's health information privacy law that allows it to collect and analyze health care and demographic data, without consent, for health system evaluation and improvement. These datasets were linked using unique encoded identifiers and analyzed at ICES.

Our outcome of interest was testing positive for COVID-19. We used the COVID-19 Integrated Testing Data database to identify individuals in our cohort who received SARS-CoV-2 PCR testing between January 1, 2020, and December 31, 2021, after which date the Ontario government implemented restrictions on publicly-funded PCR testing eligibility due to capacity constraints arising from the large number of individuals infected during the Omicron variant wave. Individuals were categorized as testing positive if they had at least one positive test during the study period. Individuals were categorized as testing negative if they had at least one negative test and no positive tests during the study period. For each individual, the index date was the first positive test among the test positive group, and the first negative test among the test negative group, regardless of the number of subsequent tests during the study window. Individuals with indeterminate, pending, cancelled, or rejected test results were excluded from analyses.

We determined age and sex (ICES does not contain records of gender) from the Registered Persons Database (RPDB). We used the Immigration Refugee Citizenship Canada Permanent Residents database (CIC_IRCC) to identify people who immigrated to Ontario after 1985. We categorized individuals as immigrants or other Ontarians. We used the Postal Code Conversion File and Canada Census (adapted from Statistics Canada, 2016 Census of Population) to obtain neighbourhood-level (i.e., census dissemination area) variables for average household size (categorized as small vs. large (0–3 vs. 3.1+ individuals respectively)), income quintiles, essential worker quintile, and visible minority quintile, as well as apartment building density grouping, uncoupled quintile, and limited educational attainment quintile (see Table A2). We used Census Metropolitan Areas to categorize rurality [24]. We used the Ontario Drug Benefit Claims database to identify individuals who filled a prescription in the two years prior to their index date as those receiving social assistance under a variety of prescription drug benefits programs. We categorized individuals as seniors (eligible due to ≥65 years old), people on the Ontario Disability Support Program (ODSP), people receiving benefits through other assistance programs, and those with no ODB claim record. We ascertained all variables on the index test date. Data sources and variable definitions are found in Appendix 1, Tables A1 and A2.

2.3. Statistical analysis

We used standardized differences to compare baseline characteristics between individuals who tested positive for SARS-CoV-2 to those who tested negative. We considered any standardized difference greater than 0.10 to be important [25].

For our multivariable models, we prioritized for selection variables that have previously been identified as strongly associated with SARS-CoV-2 infection among tested Ontario residents [17,19,22] and that in our cohort also had important standardized differences between individuals who tested positive vs. negative. We used multivariable logistic regression to examine the association of (i) five of these variables (immigration status, and neighbourhood variables for average household size, income quintile, essential worker quintile, and visible minority quintile) and (ii) their two-way interactions with testing positive for SARS-CoV-2 infection. First, we constructed a base model which included immigration status and average neighbourhood household size. As model interpretability decreases with the number of variables included, we adjusted the main effects for age and sex in all models and excluded interactions with age and sex. To balance the number of variables modelled with model interpretability, we then constructed three separate models by adding one additional neighbourhood variable to the base model: income quintile (model 1); essential worker quintile (model 2); and visible minority quintile (model 3). We present adjusted model outputs for testing positive for SARS-CoV-2 as odds ratios (OR) for each covariate, and predicted probabilities (PP) (for females aged 40 years) with 95 % confidence intervals (CI) for combinations (interactions) of model covariates.

All analyses were conducted in SAS -Enterprise Guide version 8.3 [26].

2.4. Ethics approval

Section 45 of Ontario's Personal Health Information Protection Act authorizes ICES (a prescribed entity) to collect personal health information for the purpose of analysis or gathering statistical information with respect to the management, evaluation, or monitoring of the allocation of resources, or planning for the health system [27]. The methods used in this project followed all relevant requirements and did not require review by a Research Ethics Board.

3. Results

There were 6,575,523 individuals who underwent SARS-CoV-2 PCR testing during the study period. Of these, 5,816,476, (88.5 %) tested negative, and 759,047 (11.5 %) tested positive for SARS-CoV-2 (Fig. 1).

Table 1 shows the comparison of baseline characteristics among those who tested positive vs. negative (additional characteristics not included in subsequent analyses are presented in supplemental Table 1). Among those who tested positive, the largest groups were those who were 20–34 years old, immigrants, or lived in neighbourhoods with large average household size (3.1+ individuals) or the highest proportions of visible minorities. Those who tested negative were more likely to be 0–4 or 65–84 years old, other Ontarians, or lived in neighbourhoods with small household sizes (0–2.4 individuals), the highest income quintile, or lowest visible minority quintiles. The distributions of male vs. female sex and essential worker quintiles were similar among the test positive and test negative groups (standardized differences <0.10).

Table 2 presents the adjusted main effects odds ratios (OR) and 95 % confidence intervals (CI) for testing positive for SARS-CoV-2 for each variable in each multivariable model. In all models, immigrants and those living in neighbourhoods with large average household sizes had greater odds of testing positive. For each of the three models, we observed significant gradients of increasing odds of testing positive across the neighbourhood quintiles, from highest to lowest income quintile (model 1), and from lowest to highest essential worker quintile (model 2) and visible minority quintile (model 3).

Fig. 2 panels a-c depict the predicted probabilities (CI 95 %) of the interaction effects for the combinations of variables in each of the 3 models, ordered from least to greatest probability. Visualizing these interactions reveals that there are also variations *within* the different

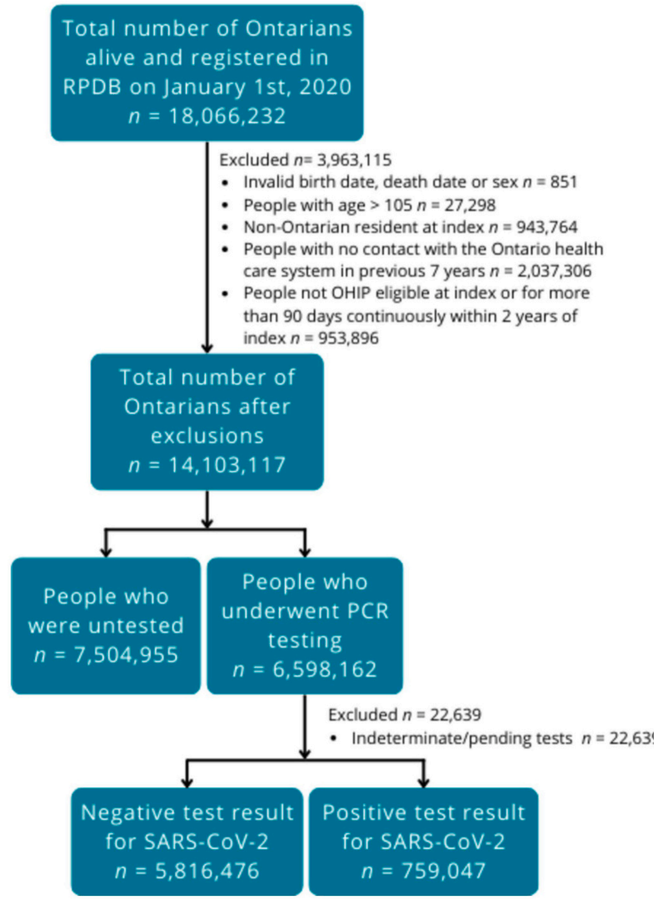


Fig. 1. Flow chart of inclusion and exclusion for cohort construction.

values. For example, in each panel (a to c) there are low probability clusters of other Ontarians living in neighbourhoods with small households across all quintiles, but in panel c, this cluster is more dispersed across visible minority quintiles.

Fig. 3 shows the predicted probabilities of testing positive for SARS-CoV-2 for the interactions of all three variables in each of the three models (see Supplemental Table 2 for additional details). In each panel, the probabilities of testing positive for SARS-CoV-2 remain consistently greater among immigrants (blue markers) than those for other Ontarians (red markers). Similarly, for almost all variable combinations, the probabilities of testing positive for SARS-CoV-2 is greater for residents in neighbourhoods with larger households (triangles) than those in neighbourhoods with smaller households (circles).

However, the interaction effects of these variables are evident in the slopes of the lines in each model. For example, in panels a and b, there is little change in the probability of testing positive for SARS-CoV-2 among other Ontarians in small household neighbourhoods across quintiles of neighbourhood income and essential worker proportion, whereas for all other combinations (other Ontarians in large household neighbourhoods, immigrants in small household neighbourhoods, and immigrants in large household neighbourhoods), there was a significant increase in the probability of testing positive for SARS-CoV-2 as neighbourhood income quintile decreased or neighbourhood essential worker quintile increased. In contrast, panel c shows that the effect of neighbourhood household size on the probability of testing positive for SARS-CoV-2 is less pronounced with increasing quintiles of neighbourhood visible minority among immigrants and other Ontarians in large households but more pronounced for other Ontarians in small households.

Table 1
Individual- and neighbourhood-level characteristics of the study cohort used in subsequent analyses. See Appendix 1 Table E1 and E2 and Supplemental Table 1 for more details and a complete list of variables.

Variable	Tested positive (n = 759,047 n, column %)	Tested negative (n = 5,816,476 n, column %)	Standardized difference
Individual-level variables			
Sex			
Female	388,850 (51.2)	3,101,438 (53.3)	0.04
Male	370,197 (48.8)	2,715,038 (46.7)	0.04
Age (years)			
0–4	18,058 (2.4)	257,197 (4.4)	0.11
5–19	122,089 (16.1)	1,007,459 (17.3)	0.03
20–34	211,966 (27.9)	1,234,828 (21.2)	0.16
35–49	172,570 (22.7)	1,165,480 (20.0)	0.07
50–64	147,267 (19.4)	1,154,638 (19.9)	0.01
65–74	44,315 (5.8)	526,281 (9.0)	0.12
75–84	23,476 (3.1)	293,311 (5.0)	0.10
85+	19,306 (2.5)	177,282 (3.0)	0.03
Immigration status			
Other Ontarians	542,463 (71.5)	4,885,140 (84.0)	0.30
Immigrants	216,584 (28.5)	931,336 (16.0)	0.30
Neighbourhood-level variables			
Income quintile			
Quintile 1 (low)	164,383 (21.7)	1,054,575 (18.1)	0.09
Quintile 2	152,179 (20.0)	1,085,682 (18.7)	0.04
Quintile 3	158,224 (20.8)	1,159,372 (19.9)	0.02
Quintile 4	148,355 (19.5)	1,220,849 (21.0)	0.04
Quintile 5 (high)	133,587 (17.6)	1,279,625 (22.0)	0.11
Missing	2319 (0.3)	16,373 (0.3)	0.00
Average household size (number of persons)			
0–2.1	109,183 (14.4)	1,061,041 (18.2)	0.11
2.2–2.4	101,396 (13.4)	1,022,981 (17.6)	0.12
2.5–2.6	87,218 (11.5)	818,711 (14.1)	0.08
2.7–3.0	185,439 (24.4)	1,410,544 (24.3)	0.00
3.1–5.7	271,417 (35.8)	1,472,623 (25.3)	0.23
Missing	4394 (0.6)	30,576 (0.5)	0.01
Essential worker quintile			
Quintile 1 (least)	141,186 (18.6)	1,301,721 (22.4)	0.09
Quintile 2	168,100 (22.2)	1,322,696 (22.7)	0.01
Quintile 3	150,944 (19.9)	1,151,828 (19.8)	0.00
Quintile 4	150,169 (19.8)	1,069,870 (18.4)	0.04
Quintile 5 (most)	144,567 (19.1)	942,343 (16.2)	0.08
Missing	4081 (0.5)	28,018 (0.5)	0.01
Visible minority quintile			
Quintile 1 (least)	66,629 (8.8)	927,295 (15.9)	0.22
Quintile 2	87,297 (11.5)	1,033,038 (17.8)	0.18
Quintile 3	120,193 (15.8)	1,120,538 (19.3)	0.09
Quintile 4	181,440 (23.9)	1,288,909 (22.2)	0.04
Quintile 5 (most)	299,422 (39.4)	1,418,863 (24.4)	0.33
Missing	4066 (0.5)	27,833 (0.5)	0.01

Table 2
Adjusted odds ratios and 95 % confidence intervals for main effects of associations between independent social variables and SARS-CoV-2 infection. All models adjusted for sex, age, and all listed covariates.

Variable	Adjusted odds ratio of testing positive for SARS-CoV-2 (95 % CI)
Base model	
Immigration status (immigrants vs. other Ontarians)	1.97 (1.96–1.98)
Average neighbourhood household size (>3 vs. 0–3)	1.45 (1.44–1.45)
Neighbourhood income quintile model (model 1)	
Immigration status (immigrants vs. other Ontarians s)	1.85 (1.84–1.86)
Average neighbourhood household size (>3 vs. 0–3)	1.58 (1.57–1.59)
Income quintile 1 (lowest) (vs. quintile 5 (high))	1.60 (1.59–1.61)
Income quintile 2 (vs. quintile 5 (high))	1.40 (1.39–1.41)
Income quintile 3 (vs. quintile 5 (high))	1.29 (1.28–1.30)
Income quintile 4 (vs. quintile 5 (high))	1.13 (1.12–1.14)
Neighbourhood essential worker quintile model (model 2)	
Immigration status (immigrants vs. other Ontarians)	1.95 (1.94–1.97)
Average neighbourhood household size (>3 vs. 0–3)	1.49 (1.48–1.50)
Essential worker quintile 2 (vs. quintile 1 (low))	1.14 (1.13–1.15)
Essential worker quintile 3 (vs. quintile 1 (low))	1.25 (1.24–1.26)
Essential worker quintile 4 (vs. quintile 1 (low))	1.35 (1.34–1.36)
Essential worker quintile 5 (highest) (vs. quintile 1 (low))	1.48 (1.47–1.49)
Neighbourhood visible minority quintile model (model 3)	
Immigration status (immigrants vs. other Ontarians)	1.62 (1.61–1.63)
Average neighbourhood household size (>3 vs. 0–3)	1.13 (1.13–1.14)
Visible minority quintile 2 (vs. quintile 1 (low))	1.16 (1.15–1.18)
Visible minority quintile 3 (vs. quintile 1 (low))	1.41 (1.40–1.43)
Visible minority quintile 4 (vs. quintile 1 (low))	1.72 (1.71–1.74)
Visible minority quintile 5 (highest) (vs. quintile 1 (low))	2.26 (2.24–2.29)

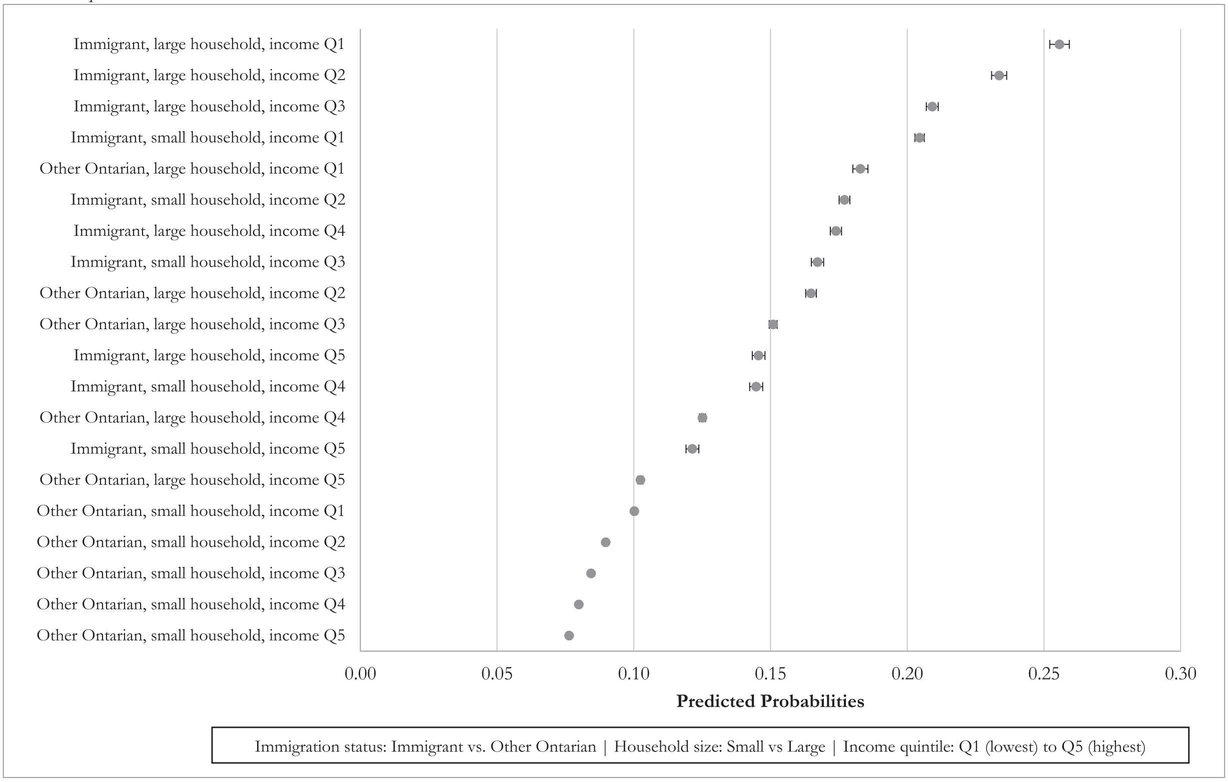
4. Discussion and conclusions

4.1. Discussion

In this study, we examined the association between social factors and SARS-CoV-2 positivity among Ontarians during the first two years of the COVID-19 pandemic. As expected, we found certain social factors were strongly associated with having a positive SARS-CoV-2 test, but further identified significant interactions among these factors that increased the probability of testing positive. In particular, we found that being an immigrant (with arrival in Ontario after 1985) made a greater contribution to testing positive for SARS-CoV-2 across all social profiles. While our findings confirm those of other studies demonstrating that several individual-level and area-based social factors are strongly associated with SARS-CoV-2 infection [7–11,13–20,28,29], our study suggests that earlier studies may have missed the impact of the combined effects of these factors on certain populations, and thus the existence of particular health inequities.

Udell et al. [19] examined the effect of several clinical and social variables on SARS-CoV-2 infection among Ontarians between April and June 2020. As we also observed, they found greater odds of infection among immigrants and people living in neighbourhoods with lower income and greater racial or ethnic diversity. Udell et al. also found that, among those living in more racially or ethnically diverse communities, there was a gradient of significant, increasing odds of testing positive for SARS-CoV-2 as the number of clinical and social risk factors increased, which was not observed in less ethnically diverse communities. This study agrees with our own findings of the heterogeneity of SARS-CoV-2 infection risk and the heightened impact of factors related to greater diversity, such as immigration status. Mishra et al. [22] found significant inequity among people testing positive for SARS-CoV-2 from January to November 2020, with the number of cases in areas with lower income, more recent immigrants, more people of visible minority or more

a. Income quintile model



b. Essential worker quintile model

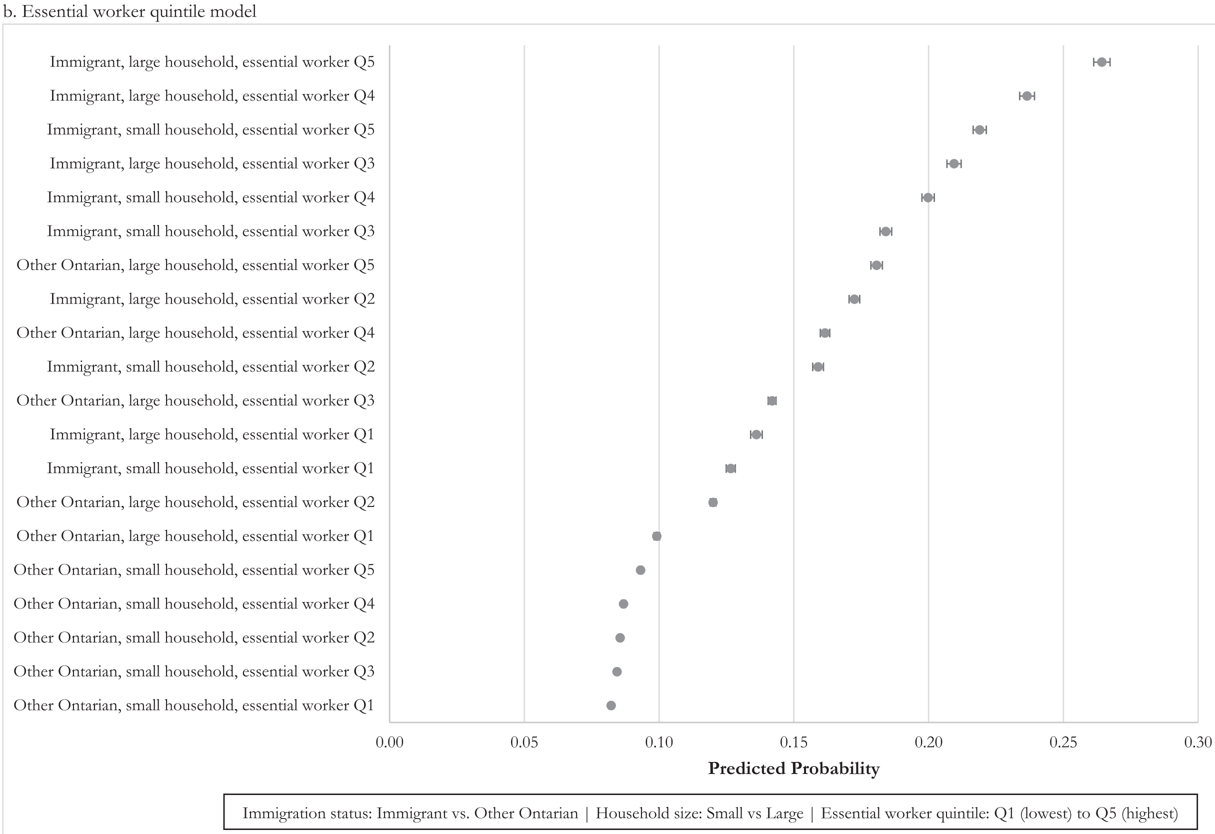


Fig. 2. Forest plots of predicted probabilities and 95 % confidence intervals for three models for SARS-CoV-2 test positivity, presented from lowest to highest predicted probabilities compared to the reference group. All models adjusted for age and sex with baseline values of 40 years and female and all listed covariates. Exact predicted probability values and confidence intervals can be found in Supplemental Table 2.
a. Income quintile model.
b. Essential worker quintile model.
c. Visible minority quintile.

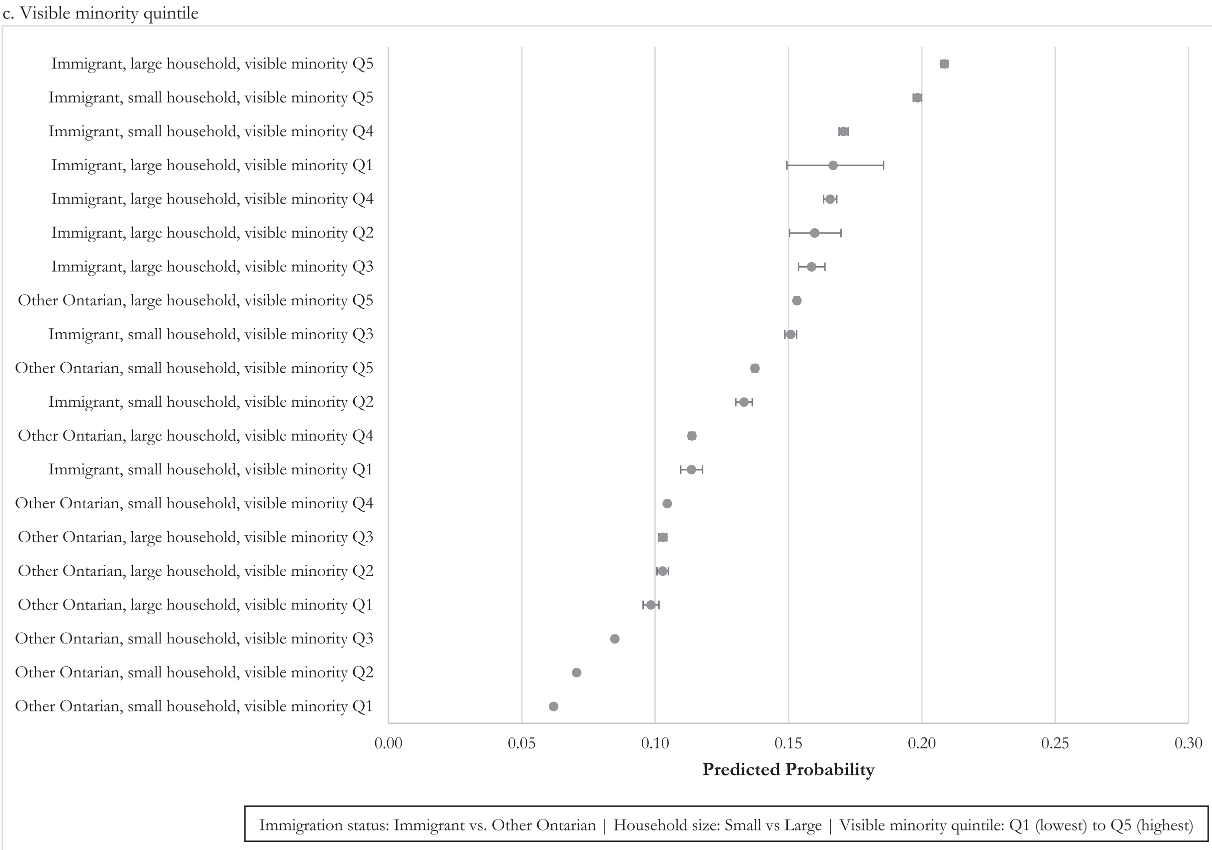


Fig. 2. (*continued*).

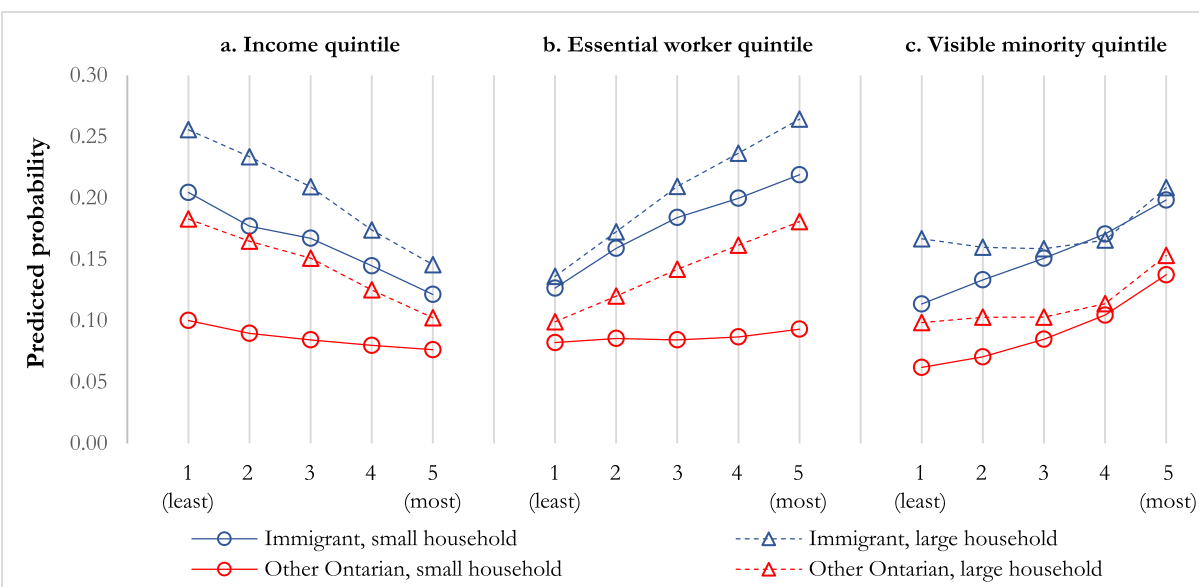


Fig. 3. Scatter plot of predicted probability of SARS-CoV-2 infection for each of the three models (a. income quintile, b. essential worker quintile, c. visible minority quintile), including average neighbourhood household size and immigration status. All models adjusted for age and sex with baseline values of 40 years and female.

essential workers increasing over time. While they did not examine the combined effects of neighbourhood determinants, this study confirms the effects that different social factors had during the COVID-19 pandemic.

By extending the work of other scholars, our study provides new insights into the populations that experienced greater risk of infection during the COVID-19 pandemic. For example, while the strength of the associations varied, both our study and that of Sundaram et al. [17] found a significant increase in the age- and sex-adjusted odds of SARS-CoV-2 positivity among Ontarians in neighbourhood quintiles with larger compared to smaller average household sizes, the highest compared to lowest proportion of essential workers, and the highest compared to lowest proportion of people of visible minority. Our study, however, also found that these effects were amplified among people living in neighbourhoods with *both* larger households and lower income, *both* larger households and higher proportion of essential workers, and *both* larger households and higher proportion of people of visibility minority. In addition, we found that these differences were further amplified among immigrants compared to other Ontarians. Factors such as the overrepresentation of recent immigrants in jobs requiring extensive interaction with the public [30], and among those experiencing barriers in access to health care [31] may contribute to the increase in COVID-19 positivity in this population.

Our study confirms that multivariable regression models of main effects can be helpful in describing the prevalence and impact of different social factors on health outcomes and identifying where people may be experiencing health inequities. However, the methods used in our study (and those of others) are limited in the number of interacting variables they can analyze simultaneously. As a result, we had to make decisions about which social factors warranted inclusion in the models, which meant that we could not look at the effects of other variables, such as age and sex/gender, that are known to significantly influence health outcomes [32,33]. We selected variables based on their association with SARS-CoV-2 positivity, or based on existing literature, meaning we might not have identified variables having strong effects within the strata of other variables. Machine learning methods, which can examine complex interactions across multiple variables more readily than conventional analysis, have been developed that may be better suited for complex analyses in population health [34–36], e.g., decision tree methods such as classification and regression trees (CART) [37,38], chi-square automatic interaction detection (CHAID) [39–41], and random forests [31,32,39]. While machine learning models can often better model complex interactions, interpreting them can be difficult. Several tools have been developed, such as Shapley Additive Explanations (SHAP) [42], that can aid in part in adding explainability to machine learning models and provide a means to examine interactions in more detail.

4.2. Limitations

While this study was conducted using population-level health administrative data for 6.5 million Ontarians, with the statistical power to look at several social variables, there are limitations. First, the analysis is limited to the variables that are available in routinely collected health administrative databases. This means that important individual social variables, such as self-reported race, ethnicity and gender, are missing from our analyses, and others are inferred by using neighbourhood-level proxies (e.g., income, household size). Second, the CIC_IRCC dataset only contains immigrants from 1985 or later who landed in Ontario and therefore does not include those who may have landed in another province and subsequently moved to Ontario; however, this number is estimated to be less than 10 % [43]. Further, as at the time of submission the IRCC data was updated only for immigrants arriving until September 2020, our analyses miss attributing immigrant status to the estimated 93,000 immigrants who arrived between October 1. 2020 and December 31, 2021. Given the disproportionate effect of immigration status on SARS-CoV-2 positivity, we anticipate this attribution would have a small impact on our effect estimates. Third, immigrants are a heterogeneous population thus our dichotomization of immigrants vs. other Ontarians may mask important differences within the immigrant category. Fourth, we restricted our study to the period from the start of the pandemic to December 2021 to exclude from our analysis (i) the massive wave of infections from the Omicron variant that resulted in group prioritization for PCR testing, and (ii) the period after COVID-19 vaccination became widely available to the general public, regardless of age. The changing nature of COVID-19 variants, vaccine uptake, and public health policies over the course of the pandemic may have resulted in different outcomes for SARS-CoV-2 positivity. While COVID-19 testing was available in Ontario during the study period, there were significant inequities in access to testing [44,45]. As such, our estimates may be conservative if the risk of SARS-CoV-2 infection is greater among marginalized groups who did not access testing. Finally, we recongize the potential for bias, including Type I (false positive) and Type II (false negative) errors, in SARS-CoV-2 test results, which may have impacted the data quality.

4.3. Conclusion

Our findings demonstrate that examining interactions of social variables, rather than independently assessing their associations, produces a clearer picture of the heterogeneous SARS-CoV-2 risks faced by groups at different levels of marginalization. Employing more advanced statistical techniques such as machine learning models with explainability tools may prove fruitful for developing a more comprehensive understanding of these relationships, as these approaches can examine complex interactions across multiple variables more readily than conventional analysis [42]. Future work should build on these findings to test more specific hypotheses pertaining to how different combinations of social variables relate to SARS-CoV-2 infection, and the implications these might have for pandemic response.

5. Data sharing

The data set from this study is held securely in coded form at ICES. Although legal data-sharing agreements between ICES and data providers prohibit ICES from making the data set publicly available, access may be granted to those who meet prespecified criteria for confidential access, available at https://www.ices.on/ca/DAS (email: das@ices.on.ca). The full data set creation plan and underlying analytic code are available from the authors upon request, with the understanding that the computer programs may rely upon coding templates or macros that are unique to ICES and are therefore either inaccessible or may require modification.

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This document used data adapted from the Statistics Canada Postal Code[OM] Conversion File, which is based on data licensed from Canada Post Corporation, and/or data adapted from the Ontario Ministry of Health Postal Code Conversion File, which contains data copied under license from ©Canada Post Corporation and Statistics Canada. Parts of this material are based on data and/or information compiled and provided by the MOH, the Canadian Institute for Health Information (CIHI), Immigration, Refugees and Citizenship Canada (IRCC), Statistics Canada: Family, Labour, Education, and Ethno-cultural diversity datasets (From the 2016 Census database), and IQVIA Solutions Canada Inc. The analyses, conclusions, opinions and statements expressed herein are solely those of the authors and do not reflect those of the funding or data sources; no endorsement is intended or should be inferred.

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CRediT authorship contribution statement

Sydney Persaud: Methodology, Project administration, Visualization, Writing – original draft. **Michael Fitzgerald:** Conceptualization, Funding acquisition, Methodology, Visualization, Writing – original draft. **Steven Hawken:** Conceptualization, Funding acquisition, Methodology, Writing – review & editing. **Peter Tanuseputro:** Conceptualization, Funding acquisition, Methodology, Writing – review & editing. **Lisa Boucher:** Methodology, Writing – original draft. **William Petrcich:** Data curation, Formal analysis, Methodology, Software, Validation, Writing – review & editing. **Martin Wellman:** Conceptualization, Methodology, Writing – review & editing. **Colleen Webber:** Conceptualization, Methodology, Writing – review & editing. **Esther Shoemaker:** Conceptualization, Writing – review & editing. **Robin Ducharme:** Conceptualization, Writing – review & editing. **Simone Dahrouge:** Conceptualization, Writing – review & editing. **Daniel Myran:** Conceptualization, Writing – review & editing. **Ahmed M. Bayoumi:** Conceptualization, Writing – review & editing. **Susitha Wanigaratne:** Conceptualization, Writing – review & editing. **Gary Bloch:** Conceptualization, Writing – review & editing. **David Ponka:** Conceptualization, Writing – review & editing. **Brendan T. Smith:** Conceptualization, Writing – review & editing. **Aisha Lofters:** Conceptualization, Writing – review & editing. **Austin Zygmunt:** Conceptualization, Writing – review & editing. **Krystal Kehoe MacLeod:** Conceptualization, Writing – review & editing. **Luke A. Turcotte:** Conceptualization, Software, Writing – review & editing. **Beate Sander:** Conceptualization, Writing – review & editing. **Michelle Howard:** Conceptualization, Writing – review & editing. **Sarah Funnell:** Conceptualization, Writing – review & editing. **Jennifer Rayner:** Conceptualization, Writing – review & editing. **Kurtis Kitagawa:** Conceptualization, Writing – review & editing. **Sureya Ibrahim:** Conceptualization, Writing – review & editing. **Claire E. Kendall:** Conceptualization, Funding acquisition, Methodology, Supervision, Writing – review & editing.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Claire E. Kendall reports financial support was provided by Canadian Institutes of Health Research. Dr. Bayoumi was supported by the Baxter and Alma Ricard Chair in Inner City Health at Unity Health Toronto and the University of Toronto. Dr. Claire Kendall was supported by a Clinical Research Chair in Strengthening Primary Care for Integrated Health Equity and the University of Ottawa. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A

Table A1
Data sources: Description of ICES databases.

Database	Description and uses
Registered Persons Database (RPDB)	This is an ICES-derived database that contains demographic information on all individuals who have ever held an Ontario health card, including their date of birth, date of death (where applicable), sex, and OHIP eligibility start and end dates.
COVID-19 Integrated Testing Data (C19INTGR)	The COVID19 Integrated Testing Database (C19INTGR) is an ICES-generated dataset that contains SARS-CoV-2 testing results from the Ontario Laboratory Information System (OLIS). It also includes testing data from the COVID-19 Diagnostic Network, and the Public Health Case and Contact Management Solution.
Census data (CENSUS)	The Canadian Census contains social data based on a population survey (Census of Population) that include aggregate demographic information such as age, sex, marital status, employment, and income for all persons and housing units within each dissemination area in Canada. Statistics Canada conducts a Census every five years. It takes account of all Canadian citizens (by birth and by naturalization), landed immigrants, and non-permanent residents together with family members living with them. Dissemination areas include between 400 and 700 persons and the data can be aggregated upward to various geographic levels.
Postal Code Conversion File (PCCF)	The Postal Code Conversion File (PCCF) is used to link postal codes to standard geographic areas (such as dissemination areas, census tracts, and census subdivisions).
Ontario Drug Benefit Claims database (ODB)	Prescription claims by individuals aged 65 or older or by those who receive income assistance (Ontario Works), disability payments (Ontario Disability Support Program), or provincially-subsidized catastrophic drug coverage (Trillium).
Immigration, Refugees, and Citizenship Canada Permanent Residents Database (CIC_IRCC)	Provides demographic, socioeconomic and country of origin information on permanent and temporary residents of Canada.

Table A2
Description of categories and/or definition of all variables used.

Variable	Values & definitions	Source
Individual-level variables		
Sex	Categories Male Female	RPDB
Age	Categories 0–4 years 5–19 years 20–34 years 35–49 years 50–64 years 65–74 years 75–84 years 85+ years	RPDB
Immigration status	Categories Other Ontarians (comprising Canadian-born individuals, those who immigrated before 1985, and may include more recent immigrants who landed in a province or territory other than Ontario) Immigrant (those who immigrated from 1985 until present, and landed in Ontario)	CIC_IRCC
Prescription drug benefits through social assistance	Database Categories OHIP + Seniors Ontario Disability Support Program (ODSP) Ontario Works Low Income Seniors Congregate living (Long Term Care and Homes for Special Care) Trillium Other Categorization approach hierarchy: ODSP > Ontario Works > Low income seniors > Congregate living > Trillium > Seniors > OHIP + > Others Project Categories People 65 or older (ODB eligible) Under 65 and in ODSP Under 65 and in any other ODB program (not ODSP or non-ODB Meds Check) No plan/record	ODB
Neighbourhood-level variables		
Neighbourhood income quintile	This variable is defined as median household income and is categorized into Quintiles 1 (Low) to 5 (high)	RPDB
Average household size	This variable is defined as the average number of persons in private households, calculated at the Dissemination Area (DA) level using the 2016 Census data. DAs across the province were ranked by average number of persons per household into 5 categories (quintiles), such that each group contained approximately one-fifth of the DAs. 1 (0–2.1) 2 (2.2–2.4) 3 (2.5–2.6) 4 (2.7–3.0) 5 (3.1–5.7) This variable was dichotomized for the regression models as 0–3.0 (smaller) and 3.1+ (larger).	CENSUS
Apartment building density grouping	This variable was calculated at the DA level using 2016 Census data. This variable will be computed by identifying the number of individuals reporting living in an “apartment in a building that has five or more storeys” or “apartment in a building that has fewer than five storeys” and dividing this value by the total number of individuals having answered questions about occupied private dwellings by structural type of dwelling. This yielded a percentage of dwellings in each DA considered to be apartment buildings. DAs across the province were then ranked by these percentages into three groups with cut-offs at the 60th and 80th percentiles, due to a zero-inflated distribution of DAs. 1 (0 %–7.3 %) 2 (7.3 %–37.7 %) 3 (37.7 %–104 %)	CENSUS
Uncoupled quintile	This variable was calculated at the DA level using 2016 Census data. “Uncoupled” individuals are individuals who, in the 2016 Census, reported having the following relationship statuses (wording from 2016 Census): never married (persons who have never legally married and are not living with a person as a couple); separated (persons who are married but who are no longer living with their spouse [for reasons other than, for example, illness, work or school], have not obtained a divorce and are not living with a person as a couple; divorced (persons who have obtained a legal divorce, have not remarried and are not living with a person as a couple); and widowed (persons who have lost their married spouse through death, have not remarried and are not living with a person as a couple). The number of individuals fulfilling this description in a given DA was divided by the total number of individuals with marital status in the DA, yielding a percentage figure for each DA. DAs across the province were then ranked by these percentages into quintiles, with the lowest 1/5 of DAs comprising the first quintile, and so on. 1 (11.2 %–33.7 %) 2 (33.7 %–38.4 %) 3 (38.4 %–43.6 %)	CENSUS

(continued on next page)

Table A2 (*continued*)

Variable	Values & definitions	Source
	4 (43.6 %–51.0 %) 5 (51.0 %–94.6 %)	
Essential work quintile	This variable was calculated at the DA level, using 2016 Census data. For each DA, we calculated the number of individuals ≥15 years old that were working in one of the following Census-defined work categories: Sales and service occupations; trades, transport and equipment operators and related occupations; natural resources, agriculture and related production occupations; and occupations in manufacturing and utilities. DAs across the province were then ranked by these percentages into quintiles, with the lowest 1/5 of DAs comprising the first quintile, and so on. 1 (0 %–32.5 %) 2 (32.5 %–42.3 %) 3 (42.3 %–49.8 %) 4 (50.0 %–57.5 %) 5 (57.5 %–114.3 %)	CENSUS
Limited educational attainment quintile	This variable was calculated at the DA level using 2016 Census data. This variable will be computed by identifying the number of adults aged 25–64 reporting having "no certificate, diploma, or degree" and dividing this value by the total number of individuals aged 25–64 having answered questions about their highest certificate, diploma or degree. This yielded a percentage of individuals in each DA considered to have no certificate, diploma, or degree. DAs across the province were then ranked by these percentages. 1 (0.0 %–4.1 %) 2 (4.1 %–7.5 %) 3 (7.5 %–11.4 %) 4 (11.4 %–17.1 %) 5 (17.1 %–94.3 %)	CENSUS
Visible minority quintile	This variable was calculated at the DA level, using 2016 Census data. An individual was marked as "self-identify as a visible minority" if they reported being one or more of the following (wording from the 2016 Census): "South Asian (e.g., East Indian, Pakistani, Sri Lankan, etc.), Chinese, Black, Filipino, Latin American, Arab, Southeast Asian (e.g., Vietnamese, Cambodian, Laotian, Thai, etc.), West Asian (e.g., Iranian, Afghan, etc.), Korean, Japanese, or Other—specify". DAs across the province will then be ranked by these percentages into quintiles, with the lowest 1/5 of DAs comprising the first quintile, and so on. 1 (0.0 %–2.2 %) 2 (2.2 %–7.5 %) 3 (7.5 %–18.7 %) 4 (18.7 %–43.5 %) 5 (43.5 %–102 %)	CENSUS
Rurality (Using Census Metropolitan Areas (CMAs)	Categories 1,500,000 + 500,000-1,499,999 100,000-499,999 10,000-99,999 <10,000 (Rural/ Small town)	RPDB / PCCF/ CENSUS

Note: Quintiles represent categorization of the population so that each group (quintile) contains a fifth of the geographic units.

Appendix B. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dialog.2024.100197.

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