

Learnings from the Australian first few X household transmission project for COVID-19



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Summary

Background First Few “X” (FFX) studies provide a platform to collect the required epidemiological, clinical and virological data to help address emerging information needs about the COVID-19 pandemic.

Methods We adapted the WHO FFX protocol for COVID-19 to understand severity and household transmission dynamics in the early stages of the pandemic in Australia. Implementation strategies were developed for participating sites; all household members were followed for 14 days from case identification. Household contacts completed symptom diaries and had multiple respiratory swabs taken irrespective of symptoms. We modelled the spread of COVID-19 within households using a susceptible-exposed-infectious-recovered-type model, and calculated the household secondary attack rate and key epidemiological parameters.

Findings 96 households with 101 cases and 286 household contacts were recruited into the study between April–October 2020. Forty household contacts tested positive for SARS-CoV-2 in the study follow-up period. Our model estimated the household secondary attack rate to be 15% (95% CI 8–25%), which scaled up with increasing household size. Our findings suggest children were less infectious than their adult counterparts but were also more susceptible to infection.

Interpretation Our study provides important baseline data characterising the transmission of early SARS-CoV-2 strains from children and adults in Australia, against which properties of variants of concern can be benchmarked. We encountered many challenges with respect to logistics, ethics, governance and data management. Continued efforts to invest in preparedness research will help to test, refine and further develop Australian FFX study protocols in advance of future outbreaks.

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Introduction

The global spread of the severe acute respiratory virus 2 (SARS-CoV-2) virus which causes coronavirus disease 2019 (COVID-19) was deemed a pandemic in March 2020.¹ The emergence and global spread of SARS-CoV-2 was initially characterised by uncertainty over key epidemiological, clinical and virological characteristics of the pathogen, particularly, its ability to spread between humans and cause disease in a susceptible population.

First Few “X” (FFX) studies provide a platform to explore transmission dynamics and infection-severity of

Research in context

Evidence before this study

The emergence of SARS-CoV-2 was initially characterised by uncertainty over key epidemiological, clinical and virological characteristics of the pathogen. In early 2020, we conducted a prospective household transmission study of confirmed cases of COVID-19 and their household contacts to understand severity and household transmission dynamics in Australia and add to the emerging evidence base for decision making. A large body of literature including systematic reviews and meta-analyses of severity and transmission dynamics of SARS-CoV-2 in households is now available, although estimates vary by setting.

Added value of this study

This is the first multi-jurisdictional prospective household transmission study of its kind for SARS-CoV-2 in Australia. Australia experienced low epidemic activity during the study period in 2020 due to robust public health and social measures including extensive PCR testing of symptomatic persons and isolation of all known contacts of confirmed cases. Hence, we describe the transmission dynamics in our cohort, i.e. in a low incidence setting and provide estimates of the household secondary attack rate, the relative susceptibility of children compared to adults, and transmission from children compared to adults.

Implications of all the available evidence

Our findings describe the epidemiology of COVID-19 in Australian households in 2020, and demonstrate the effectiveness of public health measures to limit transmission in this setting. Comparisons to other household transmission studies must be interpreted in light of the local epidemiology and context including study design, and sampling methods. Additional research is needed to incorporate genomic and serological data to further study transmission dynamics in our cohort. Continued development of the FFX study platform in Australia will enable integration into surveillance systems and help inform targeted public health responses to future infectious disease emergencies.

SARS-CoV-2 across demographic subgroups through the collection of epidemiological, clinical and virological data from confirmed cases and close contacts in well-defined settings. These data can help address emerging information needs about the pandemic.^{2–4}

Australia's first epidemic wave in 2020 was driven by returned international travellers and subsequent local transmission in major urban centres across the country. Public health and social measures were introduced to control the escalating epidemic, which included: international and state border closures, expanded case management and contact tracing, and

social measures such as density quotients in workplaces and public venues and lockdowns. Mandatory quarantine for returned international travellers was also introduced to reduce the risk of further importation. These measures drove incident cases in Australia to very low levels, and effective elimination (sustained periods of zero case incidence) was achieved in many states and territories by May 2020. A national strategy was set to pursue no community transmission of COVID-19 in the absence of widespread vaccine coverage.⁵

Breaches from the compulsory quarantine system for returned international travellers led to intermittent periods of local transmission in Australia, particularly in mid-2020 and the early stages of 2021. Australia's second most populous state, Victoria, experienced a second epidemic wave of activity from late May 2020 to November 2020 with a peak of 700 cases per day and approximately 20,000 cases in total (see Supplementary Figure 3). In contrast New South Wales, Australia's most populous state sustained lower case levels over the same period (see Supplementary Figure 4).

All Australian states and territories now have established community transmission of SARS-CoV-2 in the context of high vaccination rates and opening of international borders. As of December 13th 2021 (prior to the Omicron wave), there have been 228,930 laboratory confirmed cases of COVID-19 in Australia and 2104 deaths. Of these cases, 220,083 were locally acquired and the majority were confirmed since June 2021.^{6,7}

In February 2020, the eight Australian state and territory health departments together with the Commonwealth Department of Health and researchers from the Australian Partnership for Preparedness Research on Infectious Disease Emergencies (APPRISE) developed a national plan to implement the WHO FFX study protocol for COVID-19 in Australia with a specific focus on households.^{8,9} The Australian FFX Household transmission project aimed to inform understanding of local COVID-19 epidemiology in the early epidemic phases, and provide evidence for the development of guidelines and policy in specifically directing Australia's ongoing public health response. The findings from this investigation are described here.

Methods

Study design, ascertainment and eligibility

We adapted the WHO UNITY FFX transmission study protocol for COVID-19, focusing on the household components. Households were defined as two or more people living together in a domestic residence or a dwelling or group of dwellings with a shared space. Residential institutions were not included. We aimed to recruit 200 households into the project across participating sites between April–October 2020, prior to the emergence of any variants of concern (Supplementary Figures 2–5).³

Participating sites primed for recruitment included New South Wales (NSW; capital Sydney), Victoria (VIC; capital Melbourne), Western Australia (WA; capital Perth), South Australia (SA; capital Adelaide) and Queensland (QLD; capital Brisbane).

We separated the study into two components: public health (epidemiological data and viral swab collection as part of enhanced public health unit surveillance activities), and; additional research components (sequencing of positive samples and serology collection and analysis, not presented here), as detailed in Supplementary Table 1.

Laboratory confirmed index cases were recruited from the NSW, WA, and QLD state public health units where they were the first case identified in the household according to public health investigations and contact tracing. We recruited co-primary index cases where two household members tested positive within a 24-h period and there was at least one other household member who was PCR-negative at baseline. In addition, we enriched for paediatric index cases by recruiting from positive cases who presented to the Royal Children's Hospital Respiratory Infection Clinic (RCH) in VIC for testing.

All locally acquired cases were eligible for recruitment regardless of local source of infection provided they lived within an appropriate geographical area for logistics (i.e., metropolitan areas), and were not in mandated 14-day quarantine. All household members of eligible cases were required to provide their consent to participate. Hospitalised index cases were eligible for recruitment as we assumed that household contacts were exposed by the time hospitalisation of the index case has occurred. Households were excluded when all household members were infected at the time of the initial visit, making the direction of transmission events unclear and unobservable.

Epidemiological data were collected from confirmed cases and household contacts as close as possible to laboratory confirmation (day 0/baseline) of the index case, including health status interviews on days 7,14 and where available day 28. The questionnaires collected details on participant demographics, symptoms and vaccine and medical history (details provided in Supplementary Table 2). Household contacts also completed daily symptom diaries (via SMS) and provided specimens in line with Public Health Laboratory Network advice at baseline, days 7,14 and where available day 28. Respiratory swabs were professionally or self-collected depending on study site and were tested by polymerase chain reaction (PCR) in the state of collection.¹⁰ Households were cleared from the project at day 14 if all household contacts were symptom free and tested negative for COVID-19 at previous study timepoints (baseline and days 7/14). Index/primary cases did not complete symptom diaries or provide further swabs during their involvement in the study.

Deidentified data were collected and managed using REDCap electronic data capture tools hosted at The University of Melbourne. Ethics approval was not required for the FFX public health components being led through state and territory health departments as the project was recognised as an enhanced national public health surveillance activity. Ethics approval for the FFX project at the RCH site was obtained through the Murdoch Children's Research Institute Ethics Committee (ref: 63666).

Analysis

Descriptive analyses were performed to explore the characteristics of initially confirmed cases and their household contacts.

The household secondary attack rate (HSAR) was defined as the proportion of household contacts that were eventually infected in their study follow-up. We assumed that household contacts tested positive for COVID-19 by PCR if and only if they had COVID-19 (i.e., the false positive rate is zero). We classified all further detected cases within households as secondary cases and assumed that the primary case was the source of infection.

We characterised and modelled disease spread within households using an SEIR-type compartmental mathematical model previously developed for pandemic influenza,^{11–13} and adapted it for COVID-19 according to early evidence about the incubation period and the generation interval.¹⁴ The model allows for pre- and asymptomatic infection status, and is age-structured allowing for age-specific contact rates.¹⁵ Adults were defined as 18 years old or older, and children were defined as less than 18 years old. The rate of transmission was allowed to scale depending on the household size. Model parameters were estimated using a bespoke Markov chain Monte Carlo method;^{14–15} additional model details are outlined in the Supplementary Technical Appendix. Median posterior estimates and 95% credible intervals (CrI) are reported.

Statistical analysis was also conducted to support the choice of variables considered in the mathematical model, identify other variables that may be able to inform the mathematical model, and to align with global FFX and UNITY studies. We used logistic regression models to investigate the association between the HSAR and case- and household-level covariates. Multi-level mixed-effects logistic regression models were used to account for multiple observations per household in the contact-level HSAR analysis. The covariates used in these models are detailed in Supplementary Table 3. Households with co-primary cases were excluded from the statistical HSAR analysis but are included in the household model analysis.

Alpha was set to 0.05, and covariates that had a *p*-value of <0.2 in univariate regression analysis were

included in the multivariable models for the different variable levels. Adjusted odds ratios, adjusted marginal estimates of the HSAR, and associated 95% confidence intervals (95% CIs) were produced for each included covariate.

Data cleaning and descriptive analyses were performed in R, (<https://www.r-project.org/>).¹⁶ Statistical HSAR analyses were performed in Stata version 16.0 (StataCorp LLC, College Station, Texas).¹⁷ All modelling and parameter estimation was performed using Julia 1.6.0 (<https://julialang.org>).¹⁸

Role of the funding source

The public health components of the Australian FFX Household Transmission Project were funded by the Australian Government Department of Health, and were administered through APPRISE. The Australian Government Department of Health had no role in data collection, analysis, interpretation and writing of the article. The funding agency reviewed the manuscript prior to submission.

Results

Characteristics of FFX study population

We recruited 96 households with 101 confirmed index cases (due to co-primary cases) and 286 associated household contacts between April 2020 and October 2020. Three households had a false positive index case and were subsequently removed. Four households had incomplete study data. Supplementary Figure 2 shows recruitment into our study over time in relation to the number of locally acquired cases in Australia and in states that contributed data (Supplementary Figures 3–5).

FFX cases had a median age of 29 years (Interquartile range 15–42) and there were slightly more female cases than males. Thirty-five of the confirmed cases were children (<18 years old). Further case and contact participant characteristics can be seen in Table 1. The median household size was 4 (IQR 3–5) and ranged from 2–10 persons (Supplementary Figure 6).

Household transmission dynamics – mathematical modelling

Of the 286 household contacts recruited into the study, 40 tested positive for SARS-CoV-2 by PCR, with the majority (36/40, 90%) being detected and confirmed by the Day 7 timepoint. The modelling analysis is based on households with sufficient data (92 households comprising of 230 adults and 140 children). Of the included households, 68 had a single case only and experienced no secondary transmission. Final size distributions (i.e., the total number of individuals with laboratory-confirmed infections within a household over the period of monitoring) are shown in Supplementary Figure 1.

	Confirmed cases (n = 101, from 96 households)	Household contacts (n = 286)
Age, years		
Mean (SD)	28.0 (18.3)	28.0 (19.3)
Median (IQR)	29.0 (15.0–42.0)	26.0 (11.0–44.0)
Age group, No. (%)		
<12	21.0 (20.8)	73.0 (25.5)
12–17	14.0 (13.9)	40.0 (14.0)
18–49	55.0 (54.5)	122.0 (42.7)
50+	11.0 (10.9)	51.0 (17.8)
Sex, No. (%)		
Male	48.0 (47.5)	141.0 (49.5)
Female	53.0 (52.5)	144.0 (50.5)
Other	0 (0)	0 (0)
Received influenza vaccination in previous 12 months, No. (%)		
Yes	55.0 (54.5)	131.0 (46.0)
No	45.0 (44.6)	151.0 (53.0)
Unknown	1.0 (1.0)	3.0 (1.0)
Ever had pneumococcal vaccine, No. (%)		
Yes	21.0 (20.8)	82.0 (28.8)
No	62.0 (61.4)	145.0 (50.9)
Unknown	18.0 (17.8)	58.0 (20.4)
Pre-existing health conditions, No. (%)		
Has pre-existing health conditions	27.0 (26.7)	87.0 (30.5)
Has no pre-existing health conditions	74.0 (73.3)	198.0 (69.5)
Asthma	8.0 (7.9)	32.0 (11.2)
Chronic respiratory condition (excluding asthma)	1.0 (1.0)	0 (0)
Cardiac disease	1.0 (1.0)	4.0 (1.4)
Immunosuppressive condition/therapy	0 (0)	1.0 (0.4)
Diabetes	3.0 (3.0)	8.0 (2.8)
Obese	1.0 (1.0)	5.0 (1.8)
Renal disease	1.0 (1.0)	1.0 (0.4)
Other condition(s)	14.0 (13.9)	41.0 (14.4)

Table 1: Characteristics of included case and household contact participants in the FFX project.

Abbreviations: IQR = Interquartile range.

Posterior distributions for the household secondary attack rate (HSAR) unstratified and stratified by household size, N (HSAR_N), are shown in Figure 1. In both panels of this figure, HSAR is calculated as an average over the households in the dataset to account for the age-structured mixing and difference in adult-child transmissibility/susceptibility. The HSAR was estimated to be 15% (95%CrI 8–25%, Figure 1a) which increases with household size (Figure 1b).

Adults had a higher likelihood of showing symptoms than children (Supplementary Figure 9). There is some evidence to suggest children are more susceptible than

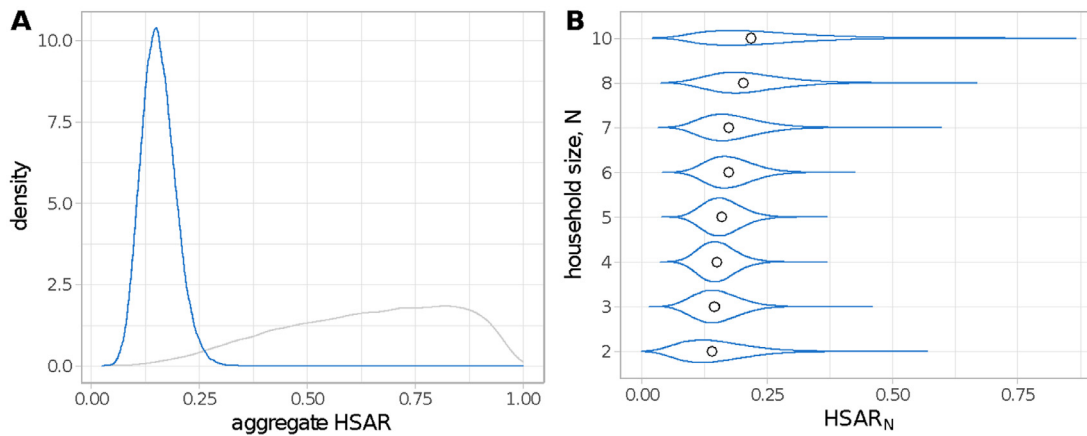


Figure 1. Posterior distributions for (A) the household secondary attack rate (HSAR) and (B) the household secondary attack rate conditional on household size N ($HSAR_N$) shown in blue. The grey curve shows the prior distribution. In (B) the dots represent the median of the distributions. $HSAR$ and $HSAR_N$ are calculated as averages over the households in the study and over all ages. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

adults – the median posterior estimate of the relative susceptibility of children compared to adults was 1.26 (95%CrI 0.75–2.08) as seen in Figure 2A – the median posterior estimate of relative transmissibility compared to adults was 0.52 (95%CrI 0.23–1.06), seen in Figure 2B, suggests that children were also less infectious than their adult counterparts.

Household transmission dynamics – statistical analysis

Using the contact-level mixed-effects logistic regression model and excluding households with co-primary cases, the $HSAR$ estimate was found to be 12% (95%CI

7–17%). Details of the multivariable logistic regression models at the various factor-levels are presented in Supplementary Table 4. The odds ratio estimate for household size was 1.31 (95%CI 0.97–1.77, $p=0.080$), representing an average 31% increase in the odds of secondary infection within the household for each one person increase in household size. There is some evidence to suggest that $HSAR$ is associated with the relationship between cases and their contacts – parents/guardians/carers and siblings had lower odds of being a secondary case when children were the primary case. The other covariates included in the multivariable models were not found to be associated with the $HSAR$.

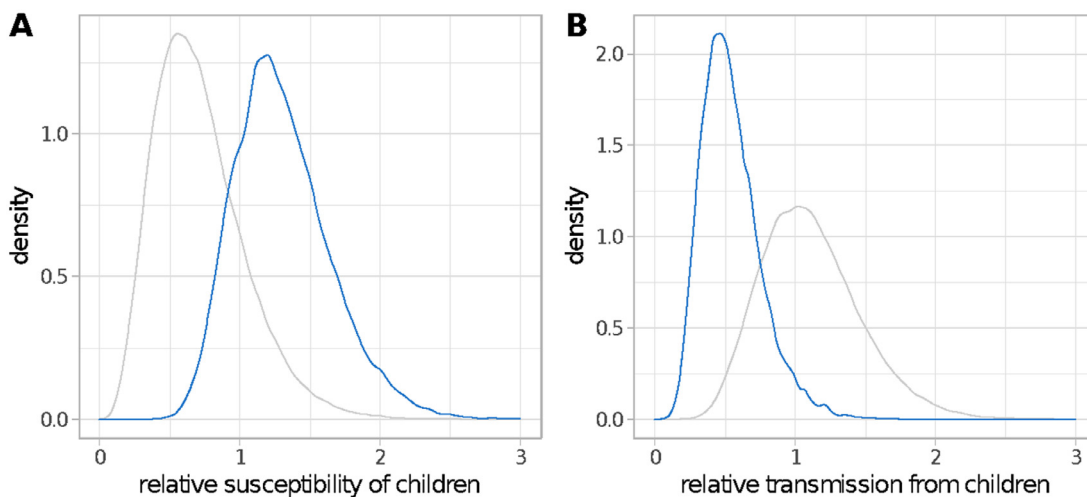


Figure 2. Posterior distributions (blue lines) for the relative susceptibility (A) and transmissibility (B) from children compared to adults, shown in blue. Prior distributions are shown in grey. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Severity

Four confirmed cases were hospitalised during their follow-up period (Case hospitalisation rate, 2.8% (4/141), 95%CI 0.9–7.5%) and no deaths were reported in our cohort.

Overall, 31.9% (45/141) of confirmed cases were asymptomatic (95%CI 24–40%). 10/101 (9.9%) were asymptomatic primary cases at baseline and 35/40 (87.5%) secondary cases were asymptomatic during their follow-up. Symptoms experienced by household contacts by COVID-19 status can be seen in Supplementary Figure 7.

Discussion

This is the first multi-jurisdictional household transmission study of its kind for SARS-CoV-2 in Australia. We demonstrate that the HSAR increases with household size. Our findings suggest that children were relatively more susceptible to infection compared to adults when exposed and were also less infectious than their adult counterparts.

The mathematical model captures the complex dynamics of transmission in households. Thus, we believe these results to be more robust than those produced by the statistical models. Associations in the statistical modelling need to be taken with caution due to the small sample size and our underlying assumption that all cases we observe in our households are attributed to the primary case – an assumption that is not required in the mathematical model. However, the statistical model results are important as they are broadly consistent with the results from the robust mathematical modelling approach, and represent the standard analytic method that is used to analyse such household transmission studies. They are presented here such that results from our cohort may be fairly compared to other international studies – our HSAR estimate is consistent with estimates from two systematic review and meta-analyses of household transmission.^{19,20} We note that our results differ from similar household transmission studies including studies based on the WHO UNITY protocols, such as the FFX study conducted in the UK, which estimated a higher base HSAR that decreased with increasing household size.^{21–31} Other studies using population surveillance data, which represent transmission within a broader range of settings have estimated lower relative susceptibility to SARS-CoV-2 infection for children compared to adults.^{32,33}

It can be difficult to make direct comparisons between studies that are conducted in different countries and settings due to the unique features of local epidemics and adaptations required for implementation.³⁴ Studies should be interpreted in light of the local epidemiology and context—considerations should be made for the surveillance and contact tracing capacity, local incidence of COVID-19 cases during study implementation, predominant circulating SARS-CoV-2 variant, the

timing and duration of the study, and study design including case ascertainment strategies and specimen sampling methods. Characteristics of individuals affected by COVID-19 and recruited into the study such as socioeconomic status, occupation and size of recruited households may also be significantly different across these studies, and therefore may influence aggregate outcomes. Additionally, differences in public health interventions such as: test, trace and isolate capacity and practices; behavioural and distancing measures; mobility restrictions; communication campaigns; and varying degrees of community engagement and cohesion in response, could also help to explain how estimates may vary across countries and settings.

We note ascertainment and recruitment bias in our study cohort that may contribute to some of the differences we observe to other studies – we excluded households where all members of these households were already infected at baseline. This was more likely to exclude smaller households than larger households for participation, and subsequently may have resulted in the HSAR for smaller households being underestimated. Our modelling outputs are therefore influenced more strongly by larger households, particularly three large outbreaks in households with more than five household members. These may be outliers and as such the observed effect could disappear if more data had been collected including from smaller households who experienced rapid transmission making them ineligible for recruitment. Additional sources of data could help us understand the extent to which our results are influenced by our inherent study biases and if our HSAR estimate is an underestimate, or if it is rather a feature of Australia's unique epidemiology, i.e. transmission in a low incidence setting with stringent public health and social measures to reduce within-household and community transmission.

We did not observe longer chains of infection in households that had detected secondary transmission. As a result, there were insufficient data to confidently estimate other quantities of interest such as the incubation period, and the pre-symptomatic and symptomatic infectious periods. Although some households experienced larger absolute numbers of cases, in the majority of such households most individuals were already infected at the recruitment baseline or initial swabbing time point (90% of secondary cases were positive by day 7 testing). These outcomes were expected especially as public health units provided extensive advice to reduce the probability of additional spread within the household, including advice on mask use, and how to isolate from each other in their homes. Whilst not the case in this cohort, some cases were removed from their household to further mitigate the risk of spread if their home environment was not suitable for quarantine.

We conducted sensitivity analyses to consider how the arbitrary age cut-off of 18 years to define adults and

children and the use of our contact matrices were impacting our results. We explored age cut-offs of 8, 13 and 16 years of age. We found that the estimated HSAR was not sensitive to changes in the age cut-off (Supplementary Figure 9). There are small differences in the probability of symptom onset for the different age cut-offs (Supplementary Figure 10), although these appear to be centred on the same values. The age cut-off of 16 yielded posterior estimates for the probability of symptom onset that were very similar. Sensitivity to the contact matrix was also investigated by running the inference with and without it. Very little change was observed in the posteriors indicating there was no sensitivity to the contact matrix being used – this is likely a result of the large number of households who experienced no secondary transmission.

Our study has several strengths. We provide insights into household transmission with testing of known household contacts regardless of symptoms in a sustained low incidence setting, where there is more certainty about the source of SARS-CoV-2 transmission being from within the household, rather than the community, compared to a higher incidence setting. The pre-existing relationship between public health departments and APPRISE researchers was an enabling factor to provide capacity for the implementation of the study, as Australian health departments were prioritising hospital preparedness and scaling up testing and contact tracing in early 2020 when this study commenced. Our study enriched for paediatric cases through recruitment at the RCH site—children were generally not index cases at the other sites, and as such this recruitment strategy provided us with unique insights into household transmission from children in the Australian context. Operationally, our data fields were aligned with the National Notifiable Diseases Surveillance Scheme to harmonise with enhanced surveillance efforts and reduce duplication of data collection where possible. Our bespoke REDCap database provided a central repository to analyse FFX data as a national dataset. Analysis and reporting of FFX data was performed in real time to key national and international stakeholders including, the Communicable Diseases Network Australia (CDNA), WHO Headquarters and the WHO Western Pacific Regional Office.

The lack of an Australian specific protocol with a pre-determined implementation strategy led to issues with logistics, and made it difficult to obtain the relevant ethics and governance approvals for all associated research components. We originally anticipated a 6–8 week window of intense recruitment in line with a short and sharp epidemic in early 2020. Strong social and public health control measures including border closures and mandated hotel quarantine reduced case numbers and subsequently the number of eligible cases and households. Two of our sites (QLD and SA) had sustained zero community transmission of COVID-19

by the time they were ready to recruit in April 2020 and WA achieved this in May 2020 after only recruiting four households. We were able to recruit more as epidemic activity increased in VIC and NSW in mid-2020, but case ascertainment in Victoria was limited due to recruitment being limited to the paediatric hospital site. These factors prolonged the duration of our study and may have further contributed to our ascertainment bias.

Future research will also involve further collection and analysis of associated genomic and serological data in the FFX research components to better understand and confirm the transmission dynamics in our cohort. Genomic data can help confirm our classification of individuals as we assumed additional cases in the household were attributed to the index case. Serological data may identify historic infections in individuals who continue to present as PCR positive but are non-infectious. Serological data may also be important to identify previously undetected infections in household members especially as the rate of false negatives from PCR may not be insignificant.³⁵ Together these can provide more accurate data to classify household members and subsequently inform attack rate calculations.

Our study provides important baseline data characterising the transmission of early SARS-CoV-2 strains from children and adults in the Australian context, against which properties of emerging variants of concern such as the Alpha and Delta strains can be benchmarked.^{36–39} We plan to follow our recruited FFX households longitudinally to continue to develop our understanding of household transmission and immunity in the context of emerging variants of concern and hybrid immunity from both vaccination and previous infection. This study will be conducted as Australia's vaccination program continues and throughout the eventual establishment of community transmission of SARS-CoV-2 in Australia. Research is also currently underway to formally evaluate the implementation of our FFX study to help consolidate on lessons learnt and inform preparedness efforts for future FFX studies in Australia for COVID-19 or other infectious disease emergencies.

Conclusion

The Australian FFX project for COVID-19 has been useful to provide valuable insight into the epidemiology of SARS-CoV-2 in Australia despite encountering many challenges in the planning and implementation phases with respect to logistics, ethics, governance and data management. Continued efforts to invest in preparedness research will help to test, refine and further develop Australian FFX study protocols in advance of future outbreaks of concern and ensure they are embedded in pandemic response plans.^{40,41} Being able to rapidly activate and provide high-quality information in real-time will be useful for epidemic situational

assessment and modelling studies in response to future outbreaks of concern, to ensure a more proportionate, equitable and targeted public health response and help reduce disease impact.

Contributors

Adrian J Marcato – study design, project administration, data cleaning, data analysis, writing – original draft, writing – review and editing, approval of manuscript
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 Niamh Meagher – study design, data analysis, writing – review and editing, and approval of manuscript
 The Australian FFX Household Transmission Project Group – study design, project administration, data collection, supervision, review of manuscript
 David J Price – study design, data analysis, writing – review and editing, and approval of manuscript
 Jodie McVernon – study design, funding acquisition, supervision, writing – review and editing, and approval of manuscript
 All authors have accessed and verified the underlying data and were responsible for the decision to submit the manuscript.

Data sharing statement

Data release from the Australian FFX Project is subject to approval by the FFX Project Data Governance Committee. Please contact the authors for additional information.

Declaration of interests

JMcV reports receiving funding from the Australian Government Department of Health Office of Health Protection, Australian Government Department of Foreign Affairs and Trade, the National Health and Medical Research Council (Australia) and the World Health Organization (WPRO and Geneva offices). JMcV was an invited expert member of the Australian Health Protection Principal Committee (AHPPC), Communicable Diseases Network of Australia COVID-19 working group and had an unpaid role with the key health policy committee advising National Cabinet on Australia's COVID-19 response. All other authors declare no competing interests.

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Supplementary materials

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