

## Household COVID-19 Prevalence

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Dear Editor,

We read with the greatest interest the study of Rosenberg & al. about household covid-19 prevalence [1]. We found interesting that the secondary rate of infections, when excluding first-reported cases, was no more than 38 %. Intuitively, this rate might appear lower than expected, considering the high level of promiscuity in households and the absence of index patients quarantine. However, two other Chinese study reported the very same rates of infection among households [2,3]. Moreover, a French study determined the seroprevalence among schoolmates in a college, which is also a situation at high risk of transmission. The seroprevalence rate was 41% [4]. Taken together, these results raise the possibility that some people may have an innate resistance against SARS-cov2 infection, hindering cell penetration and replication in target cells. Such a phenomenon has been demonstrated for other viruses. For HIV-1, about 1% of the Caucasian population shows inborn resistance to infection with CCR5-tropic HIV-1, thanks to a specific deletion in the CCR5 gene, the co-receptor of HIV-1 [5].

We thus urge researchers and geneticists to assess whether some individuals could have innate resistance to SARS-cov2 infection. Such data would be essential to inform epidemiological models [6] that aim to predict the threshold of infected people required to reach herd immunity. Moreover, genome-wide association studies in “resistant” individuals could provide further insight into the mechanisms allowing the virus to replicate in humans, thus paving the way towards new treatment opportunities.

## References:

1. Rosenberg ES, Dufort EM, Blog DS, et al. COVID-19 Testing, Epidemic Features, Hospital Outcomes, and Household Prevalence, New York State—March 2020. *Clin Infect Dis*. Available at: <https://academic.oup.com/cid/advance-article/doi/10.1093/cid/ciaa549/5831986>. Accessed 12 May 2020.
2. Li W, Zhang B, Lu J, et al. The characteristics of household transmission of COVID-19. *Clin Infect Dis* **2020**;
3. Wang Z, Ma W, Zheng X, Wu G, Zhang R. Household transmission of SARS-CoV-2. *J Infect* **2020**;
4. Fontanet A, Tondeur L, Madec Y, et al. Cluster of COVID-19 in northern France: A retrospective closed cohort study. *medRxiv* **2020**; :2020.04.18.20071134.
5. Liu R, Paxton WA, Choe S, et al. Homozygous Defect in HIV-1 Coreceptor Accounts for Resistance of Some Multiply-Exposed Individuals to HIV-1 Infection. *Cell* **1996**; 86:367–377.
6. Friston KJ, Parr T, Zeidman P, et al. Dynamic causal modelling of COVID-19. *arXiv:200404463 [q-bio]* **2020**; Available at: <http://arxiv.org/abs/2004.04463>. Accessed 12 May 2020.