SUPPLEMENT

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Supplementary Data 1: SARS-CoV-2 serological testing

A SARS-CoV-2 serological test was offered to all the members of each household. Venous blood samples were collected between July 21, 2020 and October 19, 2020 in the 5 referral Hospitals. The sera were stored at -20°C, sent and tested in Rennes referral hospital laboratory. SARS-CoV-2 nucleoprotein antibodies were tested using Elecsys SARS-CoV-2 assay (Roche, Meylan, France). This automated electro-chemiluminescent assay (ECLIA) was performed on a Cobas system. It detects all antibodies directed against the SARS-CoV-2 nucleoprotein.

Supplementary Data 2: Statistical analyses

The statistical units were the households. All the items of the questionnaire were mandatory. There were therefore no missing data. Continuous variables were described using medians and range. Comparison of characteristics across case and control households was performed using the non-parametric Wilcoxon test. Categorical variables were described using frequencies (%). Comparisons of characteristics, features related to SARS-CoV-2 exposure and seropositivity across case and control households were performed using Fisher's exact test, or ridit scores for ordered qualitative variables.

The association between case households and the exposure in the main analysis, i.e. the level of household exposure to SARS-CoV-2, was based on odds-ratio and 95% confidence interval (OR, 95%CI) estimation. Given our definitions for case and control households, our comparison enabled us to draw conclusions on the association between chilblains occurring during lockdown and household exposure to SARS-CoV-2. Since chilblains have been mostly reported among young adults, age was suspected of being a factor in their development. Age categories were formed based on the quartiles of age distribution across individuals with chilblains. Case households were allocated to the age category of the individual member with chilblains. In case households including several individuals with chilblains, one was chosen randomly. Control households were allocated to the age category of their youngest individual. A stratified univariate logistic regression analysis was conducted and separate ORs between chilblains and exposure to SARS-CoV-2 were computed for each age category. As there was no heterogeneity across the ORs obtained from the 4 age strata, subsequent analyses were conducted on the overall population. A logistic regression analysis was conducted and crude ORs as well as age-adjusted ORs between chilblains and exposure to SARS-CoV-2 were computed. As a sensitivity analysis, we adjusted for the minimum age in

each case and control household, and used a spline function (a piecewise polynomial function, 3 degrees and 3 knots) to fit the curve to the data. The analysis was also stratified and adjusted for the number of individuals confined together (3 levels: 2, 3-4, 5 and more members), since this could impact the estimate of the viral exposure level.

Statistical tests were 2-tailed, and results were deemed statistically significant at $P < .05$. The analyses were conducted using SAS version 9.4 software (SAS Institute, Cary N.C., USA).

Supplementary Table 1. Algorithm used to determine exposure to SARS-CoV-2 for individuals and households

A/ First step: individual risk of promoting SARS-CoV-2 circulation at home for any household member

Category	Variable name	Significance	Code Value
Symptoms	[S]	Presence of anosmia or ageusia	2
		Presence of other symptoms[a] without anosmia or ageusia	1
		No symptom	0
SARS-CoV-2 RT-PCR test	[V]	Positive	2
		Negative or not performed	0
Contact with a person diagnosed with COVID-19	[C]	Prolonged contact without protection[b]	2
		Other type of contact[c]	1
		None	0
Activities outside the home	[A]	Regular	1
		Not regular, or none	0

[a] fever, asthenia, rhinitis, sore throat, cough, dyspnea

[b] without protective mask or physical distance (less than one meter)

[c] protected (mask or physical distance) or short-lived

Combinations used to determine the individual risk of promoting SARS-CoV-2 circulation at home for any household member [IR]:

[S]= 2	*and*	[V]= any	*and*	[C]= any	*and*	[A]= any	→	[IR]= "High"
[S]= any	*and*	[V]= 2	*and*	[C]= any	*and*	[A]= any	→	[IR]= "High"
[S]= any	*and*	[V]= any	*and*	[C]= 2	*and*	[A]= any	→	[IR]= "High"
[S]= 1	*and*	[V]= 0	*and*	[C]= 0 *or* 1	*and*	[A]= any	→	[IR]= "Intermediate"
[S]= 0 *or* 1	*and*	[V]= 0	*and*	[C]= 1	*and*	[A]= any	→	[IR]= "Intermediate"
[S]= 0 *or* 1	*and*	[V]= 0	*and*	[C]= 0 *or* 1	*and*	[A]= 1	→	[IR]= "Intermediate"
[S]= 0	*and*	[V]= 0	*and*	[C]= 0	*and*	[A]= 0	→	[IR]= "Low"

B/ Second step: household exposure to SARS-CoV-2

Algorithm for determining household exposure to SARS CoV-2 [HE], from the individual risks of the household members

At least one household member with [IR]= "High"	→	[HE]= "High"
All household members with [IR] "Low"	→	[HE]= "Low"
Other combinations of household members' [IR]	→	[HE]= "Intermediate"

Supplementary Table 2. Bias analysis for household exposure to SARS-CoV-2 misclassification

Different scenarios of misclassification were simulated to quantify the effect of misclassification on the study results. For example, a false positive rate of 20% means that 20% of case households have been misclassified as having a high or intermediate level of exposure to SARS-CoV-2 rather than an intermediate or low level of exposure. The association between chilblains and household exposure to SARS-CoV-2 remained significant in all these scenarios.

	Differential misclassification		**Non-differential misclassification**
	Among case households	**Among control households**	**Among case and control households**
False positive rate= 20%	2.78 (1.06-7.29)	8.54 (3.04-24.04)	4.36 (1.58-12.02)
False negative rate= 20%	9.19 (3.39-24.85)	2.66 (1.07-6.60)	4.48 (1.78-11.25)

Supplementary Figure 1. Forest plot of the analyses estimating the association between chilblains and exposure to SARS-CoV-2 within households

The analyses were stratified and adjusted for the number of persons confined together.