

Social Connectedness and Disease Transmission: Social Organization, Cohesion, Village Context, and Infection Risk in Rural Ecuador

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Social networks are typically seen as conduits for the spread of disease and disease risk factors. However, social relationships also reduce the incidence of chronic disease and potentially infectious diseases. Seldom are these opposing effects considered simultaneously. We have shown how and why diarrheal disease spreads more slowly to and in rural Ecuadorian villages that are more remote from the area's population center. Reduced contact with outside individuals partially accounts for remote villages' relatively lower prevalence of diarrheal disease. But equally or more important is the greater density of social ties between individuals in remote communities, which facilitates the spread of individual and collective practices that reduce the transmission of diarrheal disease. (*Am J Public Health.* 2012;102:2233–2239. doi:10.2105/AJPH.2012.300795)

Studies of the transmission of infectious diseases^{1,2} often use social networks as maps of direct contact that facilitate person-to-person transmission of pathogens. From this perspective, relationships are increasingly associated with greater individual-level risk.³ The social cohesion and organization embodied in networks is, however, also critical to the functioning of communities,^{4–6} but researchers typically neglect the influence of these factors on community-level infectious disease risk.

Social relationships have long been employed as contacts in transmission models^{1,7–9} and as protective factors for chronic disease.^{10,11} However, outside the literature on sexually transmitted diseases^{12,13} there are few examples of the protective role of social relationships in the epidemiology of infectious diseases.¹⁴ Yet individuals in strongly connected, socially cohesive communities are more likely to perceive economic and social interests as shared. Consequently, they may be more motivated and better organized to pursue collective goals such as building and maintaining effective water and sanitary infrastructure.¹⁵

This means that understanding infectious disease risk at the community level requires understanding not only how certain social networks may spread disease but also how other social networks may influence the infrastructure and behavior that can prevent population-level exposure. We examined 2

types of social networks from the same set of villages to test the hypothesis that increased social network connectedness predicts diminished risk of diarrheal illness, using a sample of 18 villages in rural, northern coastal Ecuador. Figure 1 illustrates our conceptual model.

We sought to measure specific risk and protective effects of social relationships via survey and social network analysis methods. In the first part of the analysis, we examined the association of village social networks and different routes of exposure to self-reported illness. In the remainder of the analysis, we attempted to explain these associations in terms of factors that affect village social networks (e.g., remoteness) and the mechanisms by which increased social cohesion is linked to diminished illness risk (e.g., improved water sanitation, education).

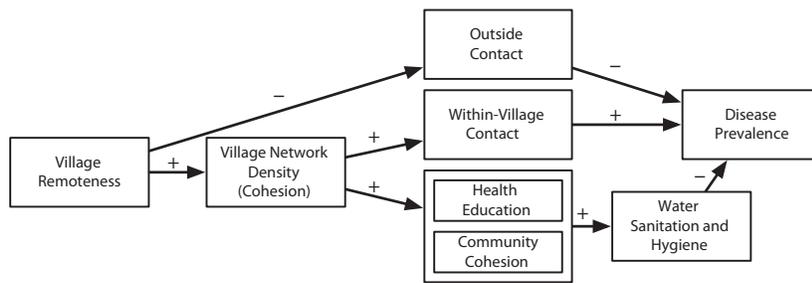
A road was recently built that connects some of these villages to the nearest large town, which has about 5000 inhabitants. Consequently, these villages now vary in their remoteness, measured by distance and time of travel to this trading center. Our previous analysis suggested that increasing remoteness is associated with increasing average degree in village social networks and that increasing average degree is associated with decreased prevalence of diarrheal disease.¹⁶ Additionally, the connectivity of villages to communities in and outside the study region decreases with remoteness.¹⁷

Consequently, less remote villages have more transient inhabitants and are more socially fragmented and therefore may be less able to build and maintain the water and sanitation infrastructure and promote hygiene practices than are more remote villages. We explicitly tested the relationships among these components, as described in Figure 1.

We defined a contact network as a network comprising relationships that are likely to facilitate transmission of pathogens, that is, a structure of connections through which an individual, denoted “ego,” may infect or be infected by his or her network neighbors, denoted “alters.” This network contains all the pathways an infection may follow through the community via direct human contact. In contrast to contact networks, we defined links in sociality networks as connections between people that represent specific types of social engagement. Connections in sociality networks can correspond to casual acquaintance, close friendship and trust, or economic exchange. The presence or absence of these relationships affects infection risk because they often determine whether communities have effective sanitary infrastructure and health services. In this way, more network connections (e.g., friends) may indicate protective social support, instead of increasing exposure, as in a contact-only network.¹⁸

COMMUNITY SOCIAL STRUCTURE AND RISK

Understanding how sociality networks influence infection risk in these villages required us to answer the question of how social organization and action can inhibit or enhance pathogen transmission via the environment. Figure 1 illustrates the mechanism by which we posit that this occurs. Poor quality sanitary infrastructure is a leading cause of infection by enteric pathogens such as cholera,^{19–21} and such infrastructure is usually a public good



Note. Solid arrows illustrate the hypothesized pathway by which remoteness affects risk of infection. Plus or minus signs indicate the directionality of the relationship.

FIGURE 1—Postulated conceptual model: effects of social relationships on disease outcomes, Esmeraldas, Ecuador, 2007.

that requires ongoing funding and management by the community. Transmission of many enteric pathogens is often conceptualized as person-to-environment-to-person, with water acting as the environmental reservoir.²² Greater community cohesion may facilitate better overall water quality through the support of community education programs that impart knowledge of household sanitary practices, such as water filtration, and social organization that produces infrastructural improvements, such as sewage treatment. Alternatively, improved water quality or sanitation may result from the establishment of social norms and the reinforcement of those norms. If this is true, we would expect to find that the average number of social network connections in a village and risk of infection by enteric pathogens are inversely related.

For example, if ego has many relationships (i.e., has high degree) in her or his village sociality network and belongs to a community organization focused on improving local water quality, it may help reduce the entire village's exposure to pathogens. Although these social relationships can also be transmission pathways, the salutary effects of ego's social engagement may preempt transmission via those connections by reducing village-wide exposure to enteric pathogens in the first place.

MEASURING EFFECTS OF SOCIALITY AND CONTACT NETWORKS ON RISK

We analyzed our illness data with respect to 2 networks. The first network comprised individuals, excluding ego's household members,

with whom ego reported having spent time in the previous week. This is called the "passing time network." We used this inclusive definition of contact because a wide range of casual and close contacts can transmit gastrointestinal pathogens.²³ In addition to being conceptualized as a contact network, the passing time network may represent sociality in a village. This definition of a sociality relationship highlights many connections between people in the community, without capturing fine-grained social structures. If a widespread, but not necessarily strong, level of attachment to the community is sufficient to stimulate social organization and diffuse information that can reduce infection risk, we would expect that greater average degree in the passing time network would predict diminished risk.

An alternate approach is to constrain membership in the sociality network to relationships corresponding to the question "Outside of members of your household, with whom can you talk about important matters?" This is the second network we used in our analysis, which we call the "important matters network." This network typically contains fewer individuals than does the passing time network, but it may better expose the essential structure of the community. If attachment to the community stronger than that implied by the passing time network is necessary to reduce illness risk, relationships in the important matters network should be better predictors of risk than should those in the passing time network. By comparing results from both networks, we were better able to understand how the nature of relationships in the sociality network affected risk.

Our analysis of sociality conceptualizes risk in terms of the network's village-level features and ego's position in this village-wide network. By contrast, the analysis of contact focuses on ego's risk of infection by ill individuals in his or her household and contact network. This approach, therefore, allowed us to examine the separate effects of the contact and sociological aspects of social relationships on disease outcomes.

METHODS

We collected our data in 18 villages in the northern coastal Ecuadorian province of Esmeraldas. These villages are situated along 3 rivers: Cayapas, Santiago, and Ónzole, all of which drain toward Borbón, which is the major population center of the region. In 1996, a new paved road was built westward from Borbón to the coast, and in 2001 a road connecting Borbón to the Andes was completed. A network of smaller roads linking villages to the main road is under continual construction. These villages vary by remoteness, a function of time and cost of travel to Borbón (for a map of the study region, see Eisenberg et al.¹⁷). Remoteness influences social relationships and network structure, migration into and out of the region, and other factors that affect both social network characteristics and exposure to infectious diseases.

Recent Infectious Illness as Outcome Measure

Our outcome measure is ego's self-reported diarrheal disease or fever in the week before the survey. Diarrheal illness is defined as having 3 or more liquid stools in 1 day.²⁴ Our initial analyses performed with each outcome in a separate model yielded broadly similar risk factors, so we combined these 2 categories of illness into a single binary response variable. The outcome variable was "1" if the individual had experienced either diarrhea or fever, indicating the individual had recently experienced illness that was likely of infectious origin.

Measuring Community Cohesion and Household Attachment

We took several approaches to measuring social cohesion and organization, utilizing data on the structure of community social networks,

education, and participation in community organizations.

We measured the average number of relationships in the sociality network for individuals aged 13 years and older. As the number of connections per person grows, the cohesion of the community is expected to grow as well.^{16,25} Unless otherwise noted, we measured this quantity in 1-unit increments.

Because the effects of social connectedness in villages affect household hygiene and water quality, we expected to see the salutary effects of cohesion at the household level. Because of this, we measured the effect of sociality (passing time or important matters) network degree on risk using the sociality degree of the most connected individual in ego's household, which we defined as ego's household degree. We standardized each village's distribution of household degree to have mean zero and unit variance, and we have presented household degree in SD units from village mean household degree. This allowed us to measure the effect of ego's household social connectedness relative to the average household in her or his village. We performed data processing with Python 2.7 and social network analysis using *igraph* 0.5.4 for Python (<http://igraph.sf.net>).

Other Covariates

Village remoteness is a composite of time and cost of travel to Borbón, the commercial center in the region. We normalized this scale so that the closest village had a remoteness value of zero and the most remote village had remoteness equal to 1. For additional information on the construction of this scale, see Eisenberg et al.¹⁷ Contact network exposure is the number of alters in an ego's contact (passing time) network that reported symptoms in the previous week. Household exposure is the number of individuals in an ego's household reporting symptoms in the previous week.

We also included several measures of village and household sanitation and hygiene: (1) observed hygiene is the average of 23 indicators of household cleanliness across all households in the village, (2) improved sanitation is the proportion of households in the village with a septic tank or a latrine, (3) improved water source measures the proportion of households using piped water or collected rainwater, and (4) water treatment measures the proportion of

households in the community reporting that they used some kind of water treatment. For values of these measures by village, see Table C (available as a supplement to the online version of this article at <http://www.ajph.org>).

In addition to these factors, we accounted for individual and village demographics, contact with individuals outside the village, household wealth, and education. For information on the calculation of these covariates, see the supplementary materials (available as a supplement to the online version of this article at <http://www.ajph.org>).

Modeling Risk for Individuals Nested in Communities

Because we conceptualized individual outcomes as being influenced by potentially unobserved village-level factors, we expected that responses in a village would be correlated.

We dealt with this correlation in all regression models by using mixed-effects logistic regression models with village-level random intercepts and estimates of individual-level fixed effects for all covariates over all villages.^{26,27} We fitted all mixed-effects logistic regression models to data using the *lme4* package in R 2.15 (<http://lme4.r-forge.r-project.org>).

Indirect Effects of Village-Level Characteristics on Individual Risk

Village remoteness and sociality networks do not directly affect disease but instead act through (or are mediated by) more immediate factors (e.g., sanitation), as illustrated by Figure 1. Because quantifying such indirect effects through the difference of regression coefficients²⁸ is not readily extended to binary response variables, we used an alternate approach. We estimated the indirect effect as the difference between the total association of remoteness with illness and the residual direct association of remoteness and illness, adjusted for the proximal variable. These are quantified by the ratios of the expected probability of illness for individuals in far versus near villages, with and without the mediator in the model.

We assessed statistical significance of this effect using a nonparametric bootstrap; we set the threshold for statistical significance at $P < .05$. Positive values of indirect effect indicate mediation and can be interpreted as the change in the risk ratio comparing far and near

villages when the mediator is taken into account. We repeated this analysis to estimate the mediation of average village-level degree. For a detailed discussion of this analysis, see the supplementary materials (available as a supplement to the online version of this article at <http://www.ajph.org>).

RESULTS

Our data set consisted of 3413 cases obtained in a census with a greater than 95% response rate in the 18 villages in our analysis. To facilitate comparisons between different models using the Akaike information criterion, we included in our analysis only the 2912 (85%) individuals with complete observations for all social network, illness, and sanitation variables. Village-level descriptive statistics for remoteness, illness, water sanitation, water quality, and household hygiene appear in Table 1, with villages listed in order of increasing remoteness. Descriptive characteristics of the important matters and passing time networks for each village include average degree and the global clustering coefficient (Table A, available as a supplement to the online version of this article at <http://www.ajph.org>).

Additional village-level descriptive statistics on organization membership, education, and wealth are available in Table B (available as a supplement to the online version of this article at <http://www.ajph.org>).

We used logistic regression models to examine the effects of exposures (contact outside villages, in households, and in social networks), household and village-level social network characteristics (degree), village-wide socioeconomic status (wealth, education), and social capital (membership in community organizations) on illness (whether a person had fever or diarrhea; Table 2). Model 1 (Akaike information criterion = 2110) shows risk associated with routes of exposure, adjusted for age and village size. This model shows that (1) a 10% increase in the proportion of households with visitors from outside the community in the week before the survey predicted an increased risk of illness (odds ratio [OR] = 1.11; 95% confidence interval [CI] = 1.00, 1.25), (2) a 1-person increase in the number of ill individuals in ego's household predicted increased risk

TABLE 1—Descriptive Characteristics of Villages: Effects of Social Relationships on Disease Outcomes, Esmeraldas, Ecuador, 2007

Village	Remoteness		Sample Size, No.	Fever or Diarrheal Disease, Cases/100	Households With Water Treatment, %	Households With Improved Sanitation, %	Households With Improved Water Source, %	Observed Household Hygiene Index, Mean
	Continuous	Category						
1	0.06	Close	158	14	25.00	43.00	43.00	0.64
2	0.07	Close	642	15	74.00	33.00	49.00	0.70
3	0.13	Close	407	13	18.00	55.00	59.00	0.69
4	0.20	Medium	110	11	14.00	61.00	7.00	0.69
5	0.20	Medium	41	14	0.00	64.00	15.00	0.63
6	0.20	Medium	30	23	93.00	11.00	2.00	0.53
7	0.25	Medium	49	8	33.00	100.00	0.00	0.79
8	0.25	Medium	37	30	72.00	55.00	100.00	0.51
9	0.31	Medium	101	12	0.00	15.00	0.00	0.45
10	0.40	Medium	64	15	0.00	26.00	100.00	0.68
11	0.57	Medium	89	18	23.00	50.00	77.00	0.71
12	0.62	Medium	119	19	19.00	7.00	19.00	0.31
13	0.71	Far	62	10	13.00	52.00	48.00	0.38
14	0.78	Far	185	8	33.00	55.00	55.00	0.71
15	0.80	Far	71	0	15.00	86.00	99.00	0.74
16	0.83	Far	285	8	0.00	41.00	82.00	0.73
17	0.96	Far	324	6	13.00	56.00	64.00	0.73
18	1.00	Far	138	14	5.00	50.00	28.00	0.68
Total	2912	12.3	30.00	45.40	52.40	0.66

of illness (OR = 1.59; 95% CI = 1.40, 1.78), and (3) a 1-person increase in the size of ego's household was associated with diminished risk (OR = 0.86; 95% CI = 0.81, 0.91). Model 1 also shows no significant change in risk associated with a 1-individual increase in the number of ill alters in ego's community contact network (OR = 0.91; 95% CI = 0.74, 1.11).

For both networks, a 1-unit increase in average village-level degree, adjusted for household and village-level network characteristics, was associated with diminished risk when household degree was fixed at its village mean (passing time: OR = 0.89; 95% CI = 0.81, 0.98; important matters: OR = 0.83; 95% CI = 0.72, 0.95). This translated into an adjusted reduction in risk of 45% or 48% between the least connected and most connected villages for the important matters and passing time networks, respectively. This protective effect remained unchanged in the absence of controls for the number of ill contacts in the community.

The statistically significant interaction in model 3 between village average and household important matters degree (OR = 1.17;

95% CI = 1.02, 1.34) suggests that the protective effect of village-level average degree applied to households with degree less than 0.6 SD above the village mean. Above this level, the associations become nonsignificant, and our data cannot resolve the relationship. This indicates that in villages with high average degree, individuals were always protected regardless of the degree of their household. But in villages where average degree was lower, household degree became protective. This relationship is analogous to herd immunity obtained through high vaccine coverage. (For further discussion of this interaction see the supplement to the online version of this article at <http://www.ajph.org>.)

As with average degree, residence in the most versus the least remote village in our sample was associated with a large decrease in ego's unadjusted risk of infectious illness (OR = 0.49; 95% CI = 0.29, 0.84). As shown in Table 3, this effect can be explained by 4 statistically significant village-level mediators ($P < .05$): the percentage of households with an outside visitor in the previous week (indirect effect = 0.058; $P = .013$), improved sanitation

(indirect effect = 0.040; $P = .011$), improved water treatment (indirect effect = 0.072; $P = .035$), and ego's household size (indirect effect = 0.014; $P = .007$). We also included average degree in the passing time network (indirect effect = 0.045; $P = .051$) as a mediator, as it has a strong theoretical link with remoteness and was close to our cutoff for statistical significance.

To assess whether these 5 variables could fully explain the association between remoteness and illness, we fit a logistic regression model predicting ego's illness as a function of remoteness, household size, village average passing time degree, and improved sanitation and water treatment. In this model, the relationship between remoteness and illness was no longer significant, and the point estimate was closer to the null (OR = 0.75; 95% CI = 0.37, 1.53), suggesting that these variables explain much of the variability in risk associated with remoteness and are likely important mediators linking remoteness to illness.

The analysis of indirect effects thus far suggests that remoteness influences risk through village networks and more proximal

TABLE 2—Multivariate Models for Risk of Disease in Previous Week: Effects of Social Relationships on Disease Outcomes, Esmeraldas, Ecuador, 2007

Sociality Network Type	Model 1, None, OR (95% CI)	Model 2, Passing Time, OR (95% CI)	Model 3, Important Matters, OR (95% CI)
Demographics			
Age, decades	0.90*** (0.84, 0.96)	0.90*** (0.84, 0.96)	0.90*** (0.85, 0.96)
Village size	1.11*** (1.03, 1.19)	1.05* (0.99, 1.10)	1.04* (0.99, 1.10)
Ownership of material goods by household	0.86 (0.35, 2.12)	0.90 (0.37, 2.20)	0.86 (0.36, 2.09)
Outside contact, %			
Households with outside visitor	1.12* (1.00, 1.25)	1.10 (0.99, 1.22)	1.08 (0.97, 1.21)
Households with outside trip	1.03 (0.91, 1.16)	1.03 (0.92, 1.15)	0.96 (0.86, 1.08)
Food-sharing exposure	0.84 (0.45, 1.56)	0.84 (0.45, 1.55)	0.89 (0.48, 1.66)
In-household exposure			
No. infected in household	1.59*** (1.41, 1.79)	1.55*** (1.37, 1.74)	1.54*** (1.36, 1.73)
Mean-centered household size	0.86*** (0.81, 0.90)	0.86*** (0.82, 0.91)	0.87*** (0.82, 0.92)
Contact network exposure			
No. infected alters in passing time network	0.91 (0.74, 1.11)	0.97 (0.80, 1.19)	0.95 (0.78, 1.16)
Sociality network			
Household degree		0.64 (0.37, 1.10)	0.59** (0.40, 0.85)
Average degree		0.89** (0.81, 0.98)	0.83** (0.72, 0.95)
Average degree × household degree		1.06 (0.96, 1.17)	1.17** (1.04, 1.32)
Graph clustering		1.18 (0.94, 1.48)	1.12 (0.89, 1.42)
Goodness of fit			
Log-likelihood	-1045	-1038	-1037
Akaike information criterion	2110	2107	2103

Note. CI = confidence interval; OR = odds ratio.
* $P \leq .05$; ** $P \leq .01$; *** $P \leq .005$.

water and sanitation factors. Further analysis showed that village-level social networks may also exert influence on risk through a number of mechanisms. Improved community sanitation was the strongest mediator of the effect of both average important matters and passing time degree (important matters: indirect effect = 0.133; $P = .003$; passing time: indirect effect = 0.146; $P \leq .001$), whereas community water treatment (indirect effect = 0.168; $P = .006$) is the strongest mediator of passing time degree. Observed hygiene (indirect effect = 0.072; $P = .002$) and average village education (indirect effect = 0.017; $P = .027$) also mediated passing time degree. Additionally, household ownership mediated the relationship between both important matters and passing time degree and risk (important matters: indirect effect = 0.010; $P = .015$; passing time: indirect effect = 0.031; $P = .009$).

After adjusting for these mediator variables, we found that the effect of living in the village

with the highest versus lowest average passing time degree (OR = 0.83; 95% CI = 0.35, 1.98) was nonsignificant and slightly closer to the null, whereas the relationship between average important matters degree (OR = 0.47; 95% CI = 0.26, 0.87) and illness was essentially unchanged. This finding suggests that the relationship between degree in the passing time network and risk can be largely explained by community sanitation, community water, observed hygiene, and household ownership. The relationship between degree and illness in the important matters network was not explained by these variables: our measures of nonnetwork protective factors may not be sensitive to all the pathways by which important matters network degree was associated with decreased risk.

DISCUSSION

Highly connected social networks are usually represented as efficient transmission

systems.³ By contrast, we have shown how greater connectivity at the village level may inhibit the prevalence of self-reported diarrheal disease and fever. When controlling for sources of exposure to illness, our analysis shows that increasing village-wide average degree is associated with decreasing risk for all households in the passing time network and for households of average degree or above in all village important matters networks.

Our analysis also connects social network, water sanitation, and hygiene factors to the social and environmental context in which the village is situated, that is, its remoteness. The processes of environmental change reflected by a village's remoteness occur over a long time. As a result, analyzing a cross-sectional slice of a group of villages in the same region that are at different stages of social and environmental transformation provides insight into the effects of these long-term processes.

We postulated that remoteness would affect risk through contact networks and village cohesion.¹⁷ To test this, we analyzed the protective effects of local social networks as indirect effects of remoteness. Results from this analysis agree with that theory, showing that more remote villages experience decreased risk not only because of a lower rate of contact with individuals from outside but also because the average individual in them has more relationships in the village passing time network and lives in a larger household than does a comparable person in a less remote village. Further mediation analysis suggests that villages with high average degree experience decreased risk of illness through improved water quality and sanitation.

The finding that individuals in larger households experienced decreased risk may be explained by the fact that increasing household size explains some of the protective effects of remoteness. Larger households may indicate more traditional, cohesive communities. This would be consistent with our finding that the protective effect of remoteness manifested at least partly through increased social cohesion.

The finding that household wealth explains some of the relationship between average degree and risk for both the important matters and passing time networks highlights the potential for social capital and household ownership to be mutually reinforcing. However,

TABLE 3—Indirect Effects of Remoteness and Village-Level Average Degree on Risk of Illness: Effects of Social Relationships on Disease Outcomes, Esmeraldas, Ecuador, 2007

Pathogen Exposure	Remoteness, Indirect Effect (95% CI)	Average Passing Time Degree, Indirect Effect (95% CI)	Average Important Matters Degree, Indirect Effect (95% CI)
Outside contact, %			
Households with outside visitor	0.058** (0.008, 0.099)		
Households with outside trip	0.002 (-0.081, 0.121)		
In-household exposure, mean-centered household size	0.014** (0.004, 0.041)		
Wealth, ownership of material goods by household	0.006 (-0.015, 0.019)	0.031*** (0.005, 0.067)	0.010** (0.001, 0.032)
Sociality network			
Average degree, important matters	0.078 (-0.067, 0.352)		
Average degree, passing time	0.045* (-0.011, 0.184)		
Mean village years of education	-0.019 (-0.087, 0.050)	0.017** (0.000, 0.042)	0.020 (-0.041, 0.115)
Participation in community organizations			
Mean no. of organization memberships in village	-0.041 (-0.136, 0.026)	-0.039 (-0.039, 0.151)	-0.028 (-0.116, 0.093)
Max no. of organization memberships in household	0.000 (-0.003, 0.011)	0.002 (0.006, 0.012)	0.005 (-0.016, 0.016)
Water quality and sanitation			
Observed hygiene index	0.006 (-0.010, 0.019)	0.072*** (0.020, 0.142)	0.095 (-0.079, 0.377)
Community improved sanitation	0.040* (0.006, 0.094)	0.146*** (0.058, 0.443)	0.133** (0.033, 0.310)
Community water treatment	0.072* (-0.008, 0.203)	0.168** (0.029, 0.362)	0.004 (-0.009, 0.037)
Community water source	-0.019 (-0.076, 0.031)	-0.007 (-0.025, 0.010)	0.007 (-0.043, 0.076)

Note. CI = confidence interval. Positive values indicate mediation. Relative strengths of mediation may be interpreted in terms of differences between values of indirect effect for different mediators of the same distal variable, e.g., remoteness.

* $P \leq .05$; ** $P \leq .01$; *** $P \leq .005$. P values reflect proportion of bootstrapped values of indirect effect.

household ownership was not an independent predictor of risk of illness when we adjusted for village-level attributes associated with remoteness, and the size of this mediation effect relative to measures of water sanitation quality was small, indicating that these effects do not confound the relationship between social cohesion and risk.

Our conceptual model (Figure 1) posited that village remoteness was related to reduced risk through increasing village social organization and cohesion. We postulated that strong social organization supports infrastructure and behavior that decrease disease prevalence. Because we conceptualized sanitation and hygiene as village-level constructs, the relatively small number of villages in our sample made it difficult to directly test the hypothesis that water sanitation and hygiene are outcomes of village-level social cohesion. However, ethnographic observations and interviews in these villages have shown how these effects might be produced. For example, we have observed that remote villages tend to have higher and more frequent participation in meetings designed to disseminate health information, whereas

factionalism in villages along the road reduces the likelihood that all community members will participate in the same meeting.

Although we have identified 7 factors mediating distal risk factors and disease, additional mechanisms clearly relate remoteness to risk. However, we have demonstrated that relationships in social networks can protect against waterborne disease and that there are important mechanisms by which these relationships may decrease risk; the scope of this analysis was not to rule out all alternative mechanisms linking remoteness to risk.

In addition to the protective effects of social organization we have outlined, we found that migration between villages, measured by the proportion of households with a visitor from outside the village in the previous week, predicts increased risk of infection. This confirms previous findings from these villages.¹⁷

Networks of social relationships can reduce the individual-level risk of illness from infectious diseases by mitigating population-level exposures, thereby preempting person-to-person transmission over these networks.

These results expand on the theory that social

connectedness and support are important predictors of chronic illness and mortality^{29,30} as well as risk of tuberculosis and HIV infection.³¹

Infectious disease epidemiologists and social scientists should incorporate these insights into mechanistic models that can explain outbreak and epidemic time series in terms of both the contact and sociality functions of networks. Such models can provide a more nuanced analysis of the relative contributions of social organization and contact to the risk of infectious diseases. ■

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Contributors

J. L. Zelner and J. N. S. Eisenberg designed the study, analyzed the data, and interpreted the results. J. Trostle designed the study and interpreted the results. J. E. Goldstick contributed analytic tools and analyzed the data. W. Cevallos performed field research. All authors contributed to the writing of the article.

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Human Participant Protection

Institutional review boards at the University of California Berkeley, University of Michigan, Trinity College, and Universidad San Francisco de Quito approved all protocols.

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