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Raising the Level of Analysis of Food-Borne Outbreaks:

Food-Sharing Networks in Rural Coastal Ecuador

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Abstract

Objectives—Consuming contaminated food is a well-documented individual-level risk factor for diarrheal disease. The sharing of food also influences the distribution of diarrheal disease risk through a community and region. Understanding this social process at a population level is therefore an important dimension of risk not captured by standard individual-level analyses. We examined social networks related to food-sharing in rural villages at 2 scales: within a village, examining whether connections within these networks clustered or were uniformly spread; and among villages, looking at whether food-sharing networks differed according to the village's remoteness from a population center.

Methods—We surveyed 2129 individuals aged 13 years and older in 2003–2004, within a representative (block-randomized) sample of 21 rural villages in Esmeraldas province, northern coastal Ecuador. We calculated degree (number of social contacts) for a social network defined by sharing food.

Results—Networks of households sharing food differ according to remoteness from a metropolitan center. On average, residents living in “far villages” had 2 more social contacts than those in “close villages,” and 12 more years of residence in their village. Estimates of transmissibility (a measure of outbreak potential) based on network structure varied as much as 2-fold across these villages.

Conclusions—Food-sharing practices link particular households in rural villages and have implications for the spread of food-borne pathogens. The food-sharing networks in remote rural villages are heterogeneous and clustered, consistent with contemporary theories about disease transmitters. Network-based measures may offer tools for predicting patterns of disease outbreaks, as well as guidance for interventions.

Food has been strongly implicated in the transmission of diarrheal diseases, especially in developing countries.^{1,2} Yet while authors have focused on the risk that agricultural practices in developing countries may pose for developed ones,^{3,4} they have paid little attention to the types of food distribution practices that might expose people in developing countries to outbreaks of diarrhea-causing pathogens. In cultures with extensive sharing of food across

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households, the secondary spread of diarrhea from food-borne pathogens can be important in disease transmission. Even in the United States, where the “Oswego church supper” outbreak investigation of the 1940s is still a staple of epidemiologic training,⁵ little time has been spent understanding the food-sharing practices that can lead to this type of contamination event, or that may cause it to disseminate through secondary transmission.

How might social networks based on food-sharing affect disease transmission within and across villages, as opposed to industrialized settings? Social networks have attracted increasing attention from epidemiologists in the past 2 decades.⁶⁻⁹ These networks have been shown to play critical roles in the transmission of sexually transmitted infections,¹⁰ HIV,¹¹ tuberculosis,¹² influenza,¹³ *Staphylococcus aureus*,¹⁴ and obesity.¹⁵ A recent simulation study of social networks¹⁶ concluded that an individual’s position in a network predicts time to infection and risk of infection. Network attributes have also been explored in predicting disease transmission across population centers such as towns and villages.¹³ These studies suggest that social networks add useful information beyond the standard paradigm of individual risk factors.

In sexually transmitted diseases, core group members contribute a disproportionate share of infection.^{17,18} Recent evidence suggests that this process is not limited to sexually transmitted diseases, but occurs in a wide variety of communicable diseases.¹⁹ Are food-sharing networks also clustered so that a relatively few number of individuals—comprising a core group—account for a majority of such connections?

To assess this question, we collected data on social network structures in 21 villages in rural Ecuador, where a paved road has been constructed in an area where there had previously been no roads. This road has opened the region to new forms of production (especially logging and plantation agriculture), greatly increased population movement and migration rates, and increased household reliance on purchased foods rather than subsistence farming and hunting. However, the road does not yet reach all villages, so its effects are differentially felt in the region. In a previous paper, we examined the relationship between physical and social space in 9 of the 21 study villages, and found evidence that social network and geographic measures are correlated and have independent associations with diarrheal disease.²⁰ In the present paper, we extend this analysis to all 21 villages, focusing on network structure and its relationship to remoteness and disease transmissibility. We examine the relationship between remoteness of villages from a population center and the extent of clustering in food-sharing social networks, and the effects that these different network structures might have on transmissibility of food-borne pathogens. Lloyd-Smith et al¹⁹ speculated that the clustering of transmission in outbreaks reflects greater connectedness (via social networks) among some individuals than others, thus increasing their potential to spread disease compared with more isolated individuals. We report here on a transmission network consisting of people (outside the household) with whom one prepared or shared food in the past 7 days.

METHODS

Setting

We studied 21 villages in the northern coastal Ecuadorian province of Esmeraldas. These villages are located along 3 rivers, the Cayapas, Santiago, and Onzole, all draining towards the town of Borbón, the main population center of the region (eFigure, available with the online version of this article). According to the 2001 Ecuadorian national census, almost 55% of the canton self-identifies as Afro-Ecuadorian and 13% as Chachi, the predominant indigenous group in Ecuador.²¹ The remainder self-identify as mestizos (people of mixed origin), mulattos (mixture of white and black), or white. These categorizations help somewhat in measuring extent of immigration, since recent immigrants tend to be mestizo or white. The region is described in detail elsewhere.²²⁻²⁴

The new paved road from Borbón was completed westward to the coast in 1996, and was linked eastward to the Andes in 2001. Secondary and tertiary roads from this highway are steadily being built, mostly for logging. At the time these data were collected, 4 of our 21 study villages were accessible by roads. The villages were selected using block randomization to ensure representation of the entire geographic area of the canton.

Following consent by village leaders, we recruited all households within each village and obtained consent. Field work protocols and informed consent documents were approved by Institutional Review Boards at all cooperating institutions.

Network Survey and Census

All field surveys were translated, back-translated, and tested before fieldwork began. Network and census data were collected in 2 three-month summer research periods between June 2003 and September 2004. Nine of the 21 villages (numbers 3–11) were surveyed in 2003, and the rest in 2004.

To establish the universe of available persons for the social network study, a census of each village was done before each network survey. Key informants from each household provided name and age information for each village resident eating and sleeping in that household.

The sociometric surveys included questions about 2 types of affective networks, as well as 5 types of potential transmission networks. Only the food-related network is reported here. The degree of social connectedness for each individual was defined as the number of names provided to the interviewer in response to the question, “In the past week, outside your household, with whom did you participate in activities having to do with food, like preparing or sharing it?” Data were checked for logical errors and a 10% random sample of the surveys was re-entered to check quality.

Basic demographic data included age, ethnicity, duration of residence, birthplace, education, recent movement within and outside the study area, and contact with people outside the village.

Outcome Measure

We chose number of contacts (referred to as “degree” in network analyses) as our primary network measure. Number of contacts is easy to measure, makes intuitive sense, and has been shown to be as accurate as other measures of individuals’ importance in a population (known as *centrality*) in predicting risk of infection.^{16,25}

We used number of contacts to calculate transmissibility, T , defined as the average probability that an infectious individual will transmit the disease to a susceptible individual with whom they are connected in a network.²⁶ The minimum T necessary to have the disease spread throughout the network is a function of mean number of contacts (D or “degree”) and mean degree-squared:

$$T_{\min} = \frac{\text{mean}(D)}{\text{mean}(D^2) - \text{mean}(D)}$$

where D is the number of contacts in the network and $T_{\min}$ represents the minimum transmissibility of a pathogen necessary for it to spread in a network.

Remoteness Index

We developed a remoteness index by determining travel time and total cost of travel to Borbón for each village (through interviews with bus and canoe operators within the region) and combining these into a single metric. Because this metric is the result of 2 values each standardized to a 0–1 scale, the possible range of the remoteness index is from 0 (the town of Borbón itself) to 2 (the value a village far from Borbón would have if all other villages had an index of 0).²⁷ Villages were also classified into 3 groups—close, medium, and far from Borbón—based on their remoteness metric, with cut points derived from the distribution of the data so as to avoid a small change in units causing a change in category. “Close” villages were defined as having a remoteness value of less than 0.03; “medium” was defined as a value between 0.03 and 0.13; and “far” was defined as a greater than 0.13.

Analysis

UCINET v. 6²⁸ was used to calculate network parameters and network figures, and Stata 9.0 (StataCorp, College Station, TX) was used for statistical analyses.

We examined the clustering of first degree network connections (those reachable in one step from any individual) to examine whether the data are more consistent with a relatively clustered distribution (characterized as a negative binomial)—where few individuals have a disproportionate share of social connections—or with a relatively even distribution (characterized as Poisson) of the number of connections among subjects. The negative binomial distribution allows individuals to have distinct underlying rates of connections; the Poisson distribution assumes all individuals have the same underlying rate of connections. The dispersion parameter of the negative binomial distribution (k) measures aggregation of individuals within populations. There are many possible ways to measure network aggregation, but our choice of the negative binomial and of k allows us to maintain a focus on number of contacts and its relationship to transmissibility and epidemic potential.²⁶

For logistical reasons, data collection was spread over 2 summers. Because of these differences between years of survey administration, analysis was also stratified by year. A proportion of the interviewer team changed between the 2 years. Despite extensive training, there was some evidence that interviewers’ assessment of network contacts varied within each year. To assess whether this variability contributed substantially to aggregation, we reanalyzed adjusting for interviewer (by including a categorical variable for interviewer in a negative binomial regression model) and found no difference. We therefore report the unadjusted analyses.

We examined the marginal distribution of each individual’s number of contacts, and stratified this distribution by village to see whether it changed with community level factors, namely remoteness. For each analysis, both the Poisson and negative binomial distribution were fit to the data. A likelihood ratio test was used to evaluate the relative fit (a small P value would indicate that the negative binomial fit significantly better). For all analyses, we included only subjects aged 13 years and older to increase comparability of demographic variables such as education and length of residence. We subsequently examined trends of mean number of contacts and aggregation versus remoteness at the village level. To assess these trends in this relatively small sample of villages, we performed a stratified permutation test (stratified by year). The test statistic of interest was the F-statistic on the coefficient of distance, corresponding to a regression of rate on distance and year. Each point was weighted in the regression by the number of observations in that village to derive the estimate.

RESULTS

Survey response rates exceeded 80% in all villages. Table 1 presents some basic demographic information by village for people aged 13 years and older, including the number surveyed, remoteness index, remoteness category, mean number of contacts, years lived in village, and percent born in village. The village remoteness value ranged from 0.012 to 0.198. Some attributes varied little across the villages: 46% were female overall, 91% were Afro-Ecuadorian and the mean age was 34.9 years (SD = 18.4). Other attributes varied considerably across villages: the percent born in the village ranged from 0% (village 6) to 79% (villages 11 and 20); the mean length of residence ranged from 7.2 years (village 6) to 33 years (village 16); and the mean duration of education ranged from 3.1 year (village 18) to 6.0 years (village 2). Linear regression analyses comparing these demographic variables to “remoteness” estimated that the number of years in the village was 12 years greater on average for “far” villages compared with “close” villages; and the percent born in the village was 40% higher for “far” compared with “close” villages. In contrast, remoteness was not linearly related to mean age, mean education, ethnicity, or sex ratio (eTable, available with the online version of this article).

The mean number of contacts in the food-sharing network also varied considerably among the villages, ranging from 0.02 (village 6) to 4.8 (village 11) contacts per person. The mean number of contacts for the food-sharing network was 2.6 contacts in year 1 and 1.7 in year 2. Sex was associated with number of contacts: females had an average of 2.6 contacts in year 1 and 3.4 contacts in year 2, while males had an average of 1.0 contacts in year 1 and 2.0 contacts in year 2.

The food-sharing network showed substantial aggregation in each year, with the negative binomial distribution providing a better fit than the Poisson distribution; the dispersion parameter k was estimated at 0.87 for year 1 and 0.45 for year 2. To examine whether mean number of contacts and aggregation varied by remoteness, we plotted them for each community in each study year (Fig. 1). The plots show the heterogeneity in number of contacts (range 1.5–4.8 in year 1 and 0.2–4.0 in year 2) and aggregation (range 0.6–2.3 in year 1 and 0.4–1.5 in year 2) among these rural villages. The permutation regression (stratified by year) of mean number of contacts versus remoteness had a P value of 0.035. The slope of the relationship between number of contacts and remoteness was 1.7 (95% confidence interval = 0.28–3.18), suggesting almost 2 more connections per person in the food-sharing network for the farthest village compared with the closest. Figure 2 is an alternative way to represent aggregation, categorizing remoteness into far, medium, and close. Within each year we graphed the percent of contacts versus the percent of people after ranking by the number of contacts. This approach shows how the distribution of contacts, on average, is distributed across these 3 groups. Data from the food-sharing network suggest that close villages are more aggregated than medium or far ones. For example, in year 2, the top 20% of people in far villages comprise 62% of food-sharing contacts, while in close villages the top 20% of people comprised 82% of contacts. For year 1, the difference in aggregation between far and close villages was much smaller (the top 20% of people in far villages comprised 44% of food-sharing contacts, while the top 20% in near villages comprised 54% of food-sharing contacts).

Figure 3 graphically represents the different densities and sex-distribution of food network structures in 2 villages (numbers 3 and 9) of similar size (152 and 175 interviewed inhabitants aged 13 and older) surveyed in year 1. Village 3 is classified as “close” and village 9 as “far.” Individuals not sharing food (called “isolates”) are represented without any connecting lines; they comprised 51% of village 3 and 30% of village 9.

Estimates of transmissibility varied as much as 2-fold across villages. To illustrate the relationship between network structure and transmissibility, the food-sharing network in the

“close” village shown in Figure 3A has an epidemic threshold $T_{\min}$ of about 0.25 (per network contact), while the food-sharing network in the “far” village with higher mean number of contacts shown in Figure 3B has an epidemic threshold $T_{\min} = 0.17$.

DISCUSSION

Theorists are exploring the potential relevance of various types of social networks to health.^{9,11} *Sociocentric* networks describe all possible contacts among all members of a given population. Such networks are difficult to assess because they require a population census. Egocentric networks start from a single individual and branch out to include that individual's contacts.⁶ Many contemporary theories about the relevance of social networks to disease transmission are based in single sites and egocentric networks. In contrast, collecting data from complete populations over multiple sites allowed us to assess variability in network structures and to correlate network characteristics with other population attributes.

We used the techniques of sociocentric network measurement to describe all possible food-preparation and food-sharing contacts among members of each village. We found that the extent of interconnection among people preparing and sharing food varied considerably. Rural villages that might at first glance look similar can have important differences in sociodemographic composition and network densities. The remoteness of villages from a population center was associated with network degree in both survey years, and the aggregation of the food-sharing network was more marked in villages surveyed in year 2 than in year 1. This suggests that differentiating only between “rural” and “urban” patterns of disease transmission may fail to capture considerable heterogeneity among rural villages.²⁹

It could be argued that remoteness is merely a proxy for village demographic characteristics such as duration of residence or percent born in the village. However, our definition of remoteness combines temporal and economic measures of distance, and therefore is not influenced by the possible effects of village origin and duration of residence. Instead, these are consequences of remoteness, as measured here. We would argue that proximity to Borbón and to the road influence factors such as availability of wage labor, ease of transport, and ease of land settlement by new immigrants, and these in turn influence the proportion of residents born in the village as well as mean duration of residence. Therefore these sociodemographic aspects are mediators rather than confounders, and remoteness is the salient determinant of number of contacts.

Why do close villages tend to have lower numbers of contacts in the food-sharing network? Some close villages (eg, numbers 3 and 6) are growing along the new road. Because of extensive immigration, these villages tend to have a more mixed ethnic population with shorter mean duration of residence than more distant villages. This may constrain the number of social ties and food-sharing practices among residents. The more distant villages (eg, numbers 9 and 11) are demographically more homogeneous, with more social ties within them. Villages 16 and 21 have lower mean number of contacts and appear somewhat different from the other villages classified as “far”: they have greater ethnic diversity and a lower proportion of locally-born inhabitants.

The distribution of social network contacts within these villages varies by remoteness and appears consistent with contemporary theories about the clustering, rather than uniformity, of disease transmitters. Lloyd-Smith et al¹⁹ suggested that some 20% of individuals can be expected to account for some 80% of transmission events. We found a similar distribution in our network study, especially in year 2 when 20% of individuals in close villages accounted for 82% of the contacts in the food-sharing network. Might these persons be “superspreaders” if they were to become infected?

To emphasize the public health significance of network structure, a recent paper by Meyers et al.²⁶ provides analytic methods for connecting the attributes of a network (specifically the distribution of number of contacts) to the potential for outbreaks and epidemics in that network based on infection of particular nodes. Transmissibility is a function of 2 characteristics of these networks: mean number of contacts and extent of clustering as defined by number of contacts squared. This links network structure to the potential public health impact of altering such networks, such as that occurring through the social changes in our study area. For example, if food sharing were the dominant mode of transmission, a food-borne pathogen would be almost a third less likely to become epidemic in village 3 (Fig. 3A) compared with village 9 (Fig. 3B).

The design of this study did not allow us to quantify the extent of intervillage food sharing, but ethnographic evidence has shown that visitors from nearby villages attend village celebrations, with some of them bringing food and almost all consuming food during the celebration in the host village. We would require additional data before we could take advantage of existing spatial analysis tools to examine regional food and disease distribution.³⁰⁻³¹

We found systematic differences in mean village number of contacts between the 2 years of network survey administration. The survey was done over 2 summers. In addition to interviewer bias, which is possible, the differences between years 1 and 2 might reflect fewer villages in the “far” category in year 1, and a lower mean remoteness index of these far villages in year 1. It is also possible that degree varies by year based on geographic variables, since 2 different regions were interviewed in the 2 summers. We were unable to address this issue because of logistical constraints.

Distribution of contact patterns within a social network has implications for the epidemiology of diseases characterized by rare but explosive outbreaks.^{19,32} Contact patterns may also help in the design of intervention strategies, where one must consider the trade-offs between targeted and complete coverage.³³⁻³⁵ For example, an intervention to reduce enteric diseases might effectively target women active in food-sharing networks. Understanding these specific patterns can help in developing an appropriately complex model that shows which people in which networks might be relevant to transmission, and which interventions will be most effective in the control of infectious diseases, such as those causing diarrhea.

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FIGURE 1.

A, Dispersion parameter (aggregation, measuring the amount of clustering in the network). B, Mean degree by remoteness for 20 villages. (Village 6 not shown because of the high proportion (82%) of isolates.) Data are represented by circles (year 1) and triangles (year 2). The solid line represents the linear fit for year 1 data, and the dashed line represents the linear fit for year 2 data.

FIGURE 2.

Cumulative percent of contacts by cumulative percent of people in close (solid line), medium (dashed line), and far (dotted line) villages in: A, year 1; and B, year 2.

FIGURE 3.

Representations of food-sharing networks for individuals >12 years of age in village 3 (A), a close village with low mean number of contacts; and village 9 (B), a far village with high mean number of contacts. Males are triangles and females are circles. Lines represent food-sharing connections between village inhabitants. Individuals with no food-sharing connections (isolates) are displayed on the margins of the network.

TABLE 1
Descriptive Statistics on Residents (aged 13 yrs and older) by Village

Village	Remoteness			Mean No. Contacts	Years in Village Mean (SD)	Origin (%)
	No.	Index	Category			
Year 1						
3	152	0.012	Close	1.5	11.0 (15.1)	16
5	425	0.015	Close	2.7	20.6 (16.6)	45
4	256	0.027	Close	1.9	21.2 (19.3)	47
8	86	0.040	Medium	3.3	22.3 (21.0)	35
6	34	0.049	Medium	0.2	7.2 (5.4)	0
7	56	0.049	Medium	1.6	23.6 (16.8)	45
10	84	0.122	Medium	4.0	25.9 (17.2)	75
9	175	0.152	Far	3.0	32.1 (22.3)	75
11	122	0.155	Far	4.8	27.9 (19.7)	79
Total year 1	1390			2.6	21.9 (19.1)	49
Year 2						
12	27	0.022	Close	0.2	17.7 (17.3)	15
1	28	0.040	Medium	0.7	21.5 (22.7)	61
2	52	0.040	Medium	1.1	23.3 (14.9)	56
13	35	0.061	Medium	1.8	25.4 (19.1)	37
15	41	0.080	Medium	0.9	18.1 (14.4)	22
18	43	0.113	Medium	4.0	11.2 (10.2)	19
16	49	0.140	Far	1.0	32.9 (18.1)	51
20	47	0.155	Far	1.8	27.0 (16.8)	79
19	121	0.165	Far	2.9	27.2 (16.1)	69
14	9	0.173	Far	2.5	31.9 (25.0)	67
17	233	0.190	Far	1.4	27.6 (16.4)	60
21	54	0.198	Far	0.8	22.0 (13.6)	54
Total year 2	739			1.7	24.7 (16.9)	54
Years 1 and 2	2129			2.3	22.9 (18.4)	51