

LIVESTOCK MANAGEMENT, HUMAN HEALTH AND WELFARE IN AGRICULTURAL
HOUSEHOLDS

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LIVESTOCK MANAGEMENT, HUMAN HEALTH AND WELFARE IN AGRICULTURAL HOUSEHOLDS

Abstract

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Farm-households face substantial livestock as well as human health risk. Biotechnology adoption for disease control and other management practices can affect livestock disease outcomes and welfare of a farm-household; while financial technology adoption can help in alleviating credit constraints through facilitation of formal and informal transactions and smooth consumption during income shocks. The second and third chapters of the dissertation examine the relationships between livestock management practices and household welfare, while the fourth chapter examines the impact of mobile money technology on risk-sharing during illness periods.

The second chapter models the relationships between communal grazing, disease transmission risk and antimicrobial use, and derives testable hypothesis about these relationships. Regression results suggest that history of disease and communal grazing are associated with higher subjective disease risk and greater antimicrobial use. The implications of these results are discussed in light of the potential for higher inter-herd disease transmission rates among

communal grazers and potential contributions to antimicrobial resistance due to antimicrobial use.

The third chapter examines the relationships between livestock disease outcomes and vaccinations and herd restocking decisions. The main findings are: (i) herd owners restock in response to livestock death, but replacement is less than one-for-one, and herd owners tend to replace cattle lost to disease-related death with sheep and goats; (ii) restocking is a contributor to higher livestock disease death and abortions, presumably through inter-herd disease transmission; (iii) vaccinations reduce disease deaths, implying that vaccination availability and use may improve herd and household welfare.

The fourth chapter explores the effects of mobile money technology adoption on consumption smoothing and healthcare use in the face of a negative health shock. Results suggest that mobile money, through increased informal lending, helps households utilize more healthcare services in terms of visits to a clinic, consultation and medication expenditures, in comparison with the non-users of this technology. This better utilization of healthcare services may result in better health and poverty reduction in a meaningful way. These effects can be explained by the decrease in transaction costs related to borrowing and lending and ease of risk sharing due to the use of this technology.

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Dedication

Dedicated to Nasra and Zia,
for everything they have done for me.

CHAPTER ONE: INTRODUCTION

Negative livestock and human health events are costly for agricultural households of east Africa. Technology adoption and other risk management practices can affect economic outcomes and well-being of these households. The second and third chapters of this dissertation examine the relationships between livestock management practices, disease-control technology adoption, disease risk and costs and benefits associated with these management decisions. The fourth chapter examines the role of adoption of a financial innovation (mobile money technology) on consumption smoothing and healthcare utilization in livestock-dependent households of east Africa. Since livestock health and productivity affects livelihoods and nutrition in agricultural households, second and third chapters of this dissertation have important policy implications in terms of livestock management, disease transmission and poverty alleviation. The fourth chapter has important implications on how financial innovations and inclusion can help poor households insure themselves against negative income shocks.

The second chapter of this dissertation examines the relationships between communal grazing, disease risk, and antimicrobial use in Maasai, Chagga and Arusha households in northern Tanzania. Households can invest in disease prevention and treatment, but livestock disease risk is also affected by grazing practices that result in inter-herd contact and disease transmission in regions with endemic communicable diseases. We develop a theoretical model of the economic connection between communal grazing, disease transmission risk, risk perceptions, and antimicrobial use, and derive testable hypotheses about these connections. Since communal grazing may relate to higher inter-herd contact and consequently higher disease transmission risk, it may lead to higher antimicrobial use as well. Furthermore, history of disease in the herd

may affect the perception of disease risk and therefore may relate to higher antimicrobial use. Regression results corroborate these aforementioned hypotheses. The implications of these results are discussed in light of the potential for relatively high inter-herd disease transmission rates among communal grazers and potential contributions to antimicrobial resistance due to antimicrobial use.

The third chapter of my dissertation carries the work done in the second chapter forward by shifting the focus a bit and examining how ex-ante livestock disease risk mitigation and ex-post risk management activities are related with livestock disease outcomes. This article specifically focuses on livestock death due to disease and abortion incidence as illness outcomes, and management in the form of vaccination for illness prevention and animal replacement decisions for herd maintenance and accumulation. To examine these relationships, we develop a theoretical model of livestock management decisions in the context of herd disease challenge, and derive a set of testable hypotheses relating to the objectives above. A system of econometric regression equations is developed and used to test the hypotheses about livestock introduction and vaccination, and their impact on livestock abortions and disease-related deaths. Because livestock health management practices are theoretically responsive to disease and illness risk through herd owner disease management incentives, management activities and disease outcomes are jointly determined. Therefore, a simultaneous system of regression equations is applied, with careful treatment of the endogeneity of management decisions.

We find that restocking is both a response and contributor to livestock death. Herd owners restock in response to disease and drought-related deaths, but replacement is less than one-for-one. The magnitude of replacement is smaller than the size of negative asset shocks, which may indicate households' partial ability to insure against disastrous events. Further, we find that

restocking is not just costly in terms of replacement costs but is also a contributor to higher livestock disease deaths and abortions, presumably as an inter-herd disease transmission mechanism. Finally, we find that vaccinations reduce disease death rates, suggesting that vaccination availability and use may improve herd and household welfare.

The fourth chapter is devoted to how financial technologies, like mobile money technology (MMT), can help households overcome credit constraints and help in risk sharing during negative income shocks. We find that risk sharing effects of MMT are concentrated on healthcare expenditures and utilization of formal healthcare services, in comparison with the non-users of this technology. Since non-health consumption seems to be insured against negative health shocks and risk sharing effects are concentrated on health consumption for MMT users, this may imply that households need money for healthcare use in the very short-run in the face of illness and are able to adjust other expenditures over the quarter. This better utilization of formal healthcare services may result in better health and poverty reduction. These effects can be explained by the decrease in transaction costs related to borrowing and lending and ease of risk sharing due to the use of this technology.

CHAPTER TWO: RELATIONSHIPS BETWEEN LIVESTOCK GRAZING PRACTICES,
DISEASE RISK, AND ANTIMICROBIAL USE AMONG EAST AFRICAN
AGROPASTORALS

Abstract

Livestock health is economically important for agropastoral households whose wealth is held partly as livestock. Households can invest in disease prevention and treatment, but livestock disease risk is also affected by grazing practices that result in inter-herd contact and disease transmission in regions with endemic communicable diseases. This paper examines the relationships between communal grazing and antimicrobial use in Maasai, Chagga and Arusha households in northern Tanzania. We develop a theoretical model of the economic connection between communal grazing, disease transmission risk, risk perceptions, and antimicrobial use, and derive testable hypotheses about these connections. Regression results suggest that history of disease and communal grazing are associated with higher subjective disease risk and greater antimicrobial use. We discuss the implications of these results in light of the potential for relatively high inter-herd disease transmission rates among communal grazers and potential contributions to antimicrobial resistance due to antimicrobial use.

Introduction

Communicable livestock disease is costly for livestock-dependent households and communities in the tropics, and can be especially important for the economic well-being of low-income rural households for whom livestock represents a primary household asset. Livestock disease results in loss of wealth and income through livestock mortality and decrease in livestock productivity (Lybbert et al. 2004; Marsh et al. 2016). It also poses a threat to human health through loss of animal-based protein intake, zoonosis and food-borne illnesses (Narrod et al. 2012; Mosites et al. 2015; Caudell et al. 2017b).

Livestock disease burden can be mitigated by reducing disease transmission risk, by reducing animal susceptibility, and through treatment. Disease transmission risk is dependent on general animal husbandry such as grazing and feeding practices that affect the frequency and nature of inter-herd contact (Bronsvort et al. 2004; Rufael et al. 2008; Schoonman and Swai 2010). Illness in the face of transmission risk can be avoided or mitigated by modern vaccination strategies, antibiotic use, traditional medicine, and other treatment methods. These targeted avoidance and treatment investments by herd owners are mediated through perceptions and understanding of disease transmission risk and the relative benefits and costs of avoidance and treatment options. Thus, general livestock husbandry and targeted disease management decisions can be related to, and through, livestock health.

In East Africa and other parts of the world, there is substantial variation in livestock feeding and grazing practices depending on localized environmental factors, land tenure, and cultural norms (Nugent and Sanchez 1993; Davies and Hatfield 2007). In areas with sufficient rainfall and forage availability and relatively limited grazing land, fodder is often brought to livestock and grazing is more limited (Keyyu et al. 2006; Caudell et al. 2017a). In more arid environments,

extensive grazing is widely practiced, and in Tanzania in particular, communal and transhumant grazing practices are common. These types of grazing practices may lead to higher rates of inter-herd contact and disease transmission than under other management practices (Hutchings and Harris 1997; Keyyu et al. 2006; Bohm et al. 2009) such as “zero grazing” common among the Chagga and some peri-urban Arusha households (Caudell et al. 2017b).

Antimicrobials are an important health intervention widely used in livestock and poultry management even in remote, rural communities as a prophylaxis, as treatment for microbial and protozoal infections, and in some (primarily commercial) settings for growth augmentation (Page and Gautier 2012; Perry et al. 2013). As with other management inputs, the extent of antimicrobial use is driven in part by the perceived value of the input, and is likely to be used more where the threat and incidence of diseases thought to be treatable with antimicrobials is high (Gustafson and Bowen 1997). Antimicrobial use can also reduce the extent of pathogen shedding and the likelihood of transmission to other animals, but may also lead to development of antibiotic resistance within the microbiome.

Thus, communal grazing is potentially related to disease risk through higher rates of direct and indirect inter-herd contact than private grazing or zero-grazing. Higher objective risk may then be associated with higher perceived disease risk. Therapeutic antimicrobial use may increase in response to actual incidence of disease (and therefore disease risk), and prophylactic antimicrobial use would be positively correlated with perceived disease risk. The perceived marginal value of antimicrobials could be higher where actual or perceived risk is high, potentially leading to higher antimicrobial use.

The objective of this paper is to examine the relationships between livestock grazing practices, past disease outcomes, and demand for antimicrobials among agro-pastoralists of

northern Tanzania. We develop a theoretical model that elucidates basic connections between grazing practices, past and current disease incidence, and antimicrobial use. We then estimate these relationships by using data from surveys of agricultural households around ecologically heterogeneous regions of Mount Meru and Mount Kilimanjaro. This heterogeneity in ecology leads to widely different grazing practices, from communal grazing to zero-grazing in the region, and allows us to examine how grazing patterns are related to antimicrobial use. There are some changes in the grazing patterns of the Maasai with the seasons, but the inhabitants on the slopes of Mount Meru and Mount Kilimanjaro tend to keep their animals confined, with fodder delivered to the animals. This zero-grazing behavior is relatively stable over all seasons in a year (Caudell et al. 2017b).

Communal land tenure and use and transhumant grazing can provide vital benefits in spatiotemporally variable climates (Nugent and Sanchez 1993; Agrawal 2001; Davies and Hatfield 2007; Ostrom 2015). That said, overgrazing has long been recognized as a potential problem of communal grazing land ownership, although the details of the social contract over communal grazing can be important mitigating factors (Ciriacy-Wantrup and Bishop 1975; Runge 1981; Swallow and Bromley 1995). Additionally, communal grazing and transhumant management practices may increase disease transmission risk (Sanderson et al. 2000) and impose disease risk on other grazers that may not be fully accounted for in the private decision calculus of an individual herd owner. The consequence is that disease transmission mitigation practices and safeguards are likely to be under-applied, and disease transmission may be higher than socially optimal (Brito et al. 1991; Philipson 2000; Hennessy et al. 2005).

The historic value of antimicrobials for global health outcomes is hard to overstate (Gustafson and Bowen 1997; Kingston 2000). But antimicrobial resistance is becoming a major

public health concern globally, and the use of veterinary antimicrobials in agriculture sectors may be an important contributor (Carlet et al. 2012; Van Boeckel et al. 2015). To the extent that antimicrobial use or misuse can impose external costs on other herd owners through antimicrobial resistance, herd owners may tend to overuse or misuse antimicrobials from a social economic efficiency perspective (Althouse et al. 2010), which may exacerbate the emergence and prevalence of antimicrobial resistance (Laximinarayan and Brown 2001; Secchi and Babcock 2002).

The externalities described above – higher potential inter-herd disease transmission from communal grazing, reduced pathogen shedding due to effective antimicrobials and reduced effectiveness from antimicrobial resistance – interact in complex ways. While our data do not allow us to tease out the externalities associated with these dimensions of grazing and antimicrobial use, we are able to examine the relationships between communal grazing, reported livestock illness, and antimicrobial use, and therefore contribute to an understanding of the incentives surrounding antimicrobial use for livestock in agropastoral settings.

We contribute to the literature in several ways. We extend the analysis of Caudell et al. (2017b) who treat communal grazing as a component of Maasai ethnicity, and account for the fact that grazing decisions of households may be jointly (endogenously) determined along with antimicrobial use in response to disease risk. Moreover, we extend Caudell et al. (2017b) by conceptualizing how past disease incidence contributes to current antimicrobial use, perhaps through its impact on perceived risk. In doing so, we also contribute to the literature on subjective risk assessment generally. Subjective inference about disease risk is often based on sparse information from direct observation, indirect covariates, and broader belief contexts, and plays an important role in the perceived marginal value of risk-reducing management practices

(Tversky and Kahneman 1973; Johnson et al. 1993; Mittal and Ross 1998; Cole et al. 2003; McNamara et al. 2006; Clark 2013). Although the role of perceptions in avoidance behavior has been well documented in economics (Courant and Porter 1981; Crocker et al. 1991; Dickie and Gerking 1996), the evidence of the impact of disease risk perceptions on disease mitigation and control strategies such as vaccination and antimicrobial use is scant.

A Model of Communal Grazing, Disease Prevalence and Antimicrobial Use

We examine how grazing patterns and past disease history relate to antimicrobial use. Grazing patterns and fodder collection practices chosen by livestock owners depend on relative forage availability, water availability, and land tenure characteristics, and other factors (Coppolillo 2000; Pringle and Landsberg 2004; Caudell et al. 2017b).¹ While grazing practices change somewhat over grazing seasons, the basic pattern of less travel and herd interaction in higher rainfall regions versus more travel and more herd interaction with more arid conditions is a relatively stable, long-term phenomenon (Bollig, 2006). In contrast, decisions about and variation in antimicrobial use can likely be more easily altered in the short-run, depending on the real and perceived disease risk a herd owner faces. These differences allow us to divide the decision process into two stages; the communal grazing decision as a stable, quasi-fixed management practice, and antimicrobial use as a variable input with more flexibility in response to disease risk and outcomes.

Based on this decision environment, we consider a two-stage expected profit (net income) maximization model, with stages distinguished by a long-term grazing decision and a short-term

¹ Formally, the Tanzanian Government owns all land in the country, but allocates use rights among villages and other private entities. Common grazing land is widely available, and pastoral land tenure in Tanzania is better described as a common property system than private property (Smith *et al.*, 2001).

antimicrobial use decision.² In the first stage, the farmer chooses the proportion of the household herd to graze on common grazing land (the grazing rate). In the second stage, the farmer chooses antimicrobial use to maximize expected short-run profits based on preventive and therapeutic antimicrobial goals, the disease environment, and grazing practices. Expected profit to the household from livestock is

$$\pi = v(g; \tilde{g})(1 - \gamma(g; \tilde{g}, \tilde{a}, \rho)\alpha(a; \tilde{a})) - ca.$$

The function $v(g; \tilde{g})$ is the potential value to a household of livestock production in the absence of disease. The household communal grazing rate is g , and communal grazing by other households is \tilde{g} . $v(g; \tilde{g})$ increases at a decreasing rate with the communal grazing rate g and decreases with the communal grazing rate of other households ($v_g > 0, v_{gg} < 0, v_{g\tilde{g}} < 0$, where subscripts represent partial derivatives throughout).

The term $(1 - \gamma(g; \tilde{g}, \tilde{a}, \rho)\alpha(a; \tilde{a}))$ is the fraction of potential livestock value realized given disease losses. The function $\gamma(g; \tilde{g}, \tilde{a}, \rho) \in (0,1)$ is the fraction of livestock value lost to disease in the absence of private (own-herd) antimicrobial use, where ρ is the background (environmental) disease prevalence. Regional antimicrobial use by others (\tilde{a}) can reduce private infection risk to the herd, and communal grazing rates by others (\tilde{g}) can increase infection risk ($\gamma_g > 0, \gamma_{\tilde{g}} > 0, \gamma_{\tilde{a}} < 0, \gamma_{\rho} > 0$). In addition, the marginal losses from grazing increase with the grazing rates of other households, and background disease prevalence ($\gamma_{g\tilde{g}} > 0, \gamma_{g\rho} > 0$). The function $\alpha(a; \tilde{a}) \in (0,1)$ is the reduction in the loss rate from private antimicrobial use. Antimicrobial use reduces losses at a decreasing rate ($\alpha_a < 0, \alpha_{aa} > 0$), and the marginal

² Our focus on expected profit maximization is consistent with an assumption that herd owners are risk neutral or that there is separation between consumption and production (Singh et al. 1986; Lopez (1986); De Janvry *et al.*, 1991). Allowing for risk-aversion would not affect the qualitative hypotheses we develop with our model.

effectiveness of a declines with regional antimicrobial use, \tilde{a} due to its impact on antimicrobial resistance ($\alpha_a < 0, \alpha_{aa} > 0, \alpha_{a\tilde{a}} > 0$). Thus, regional antimicrobial use has two competing impacts: reductions in disease transmission due to its effect of reducing transmission of antimicrobial-susceptible pathogens, and increases in losses from the transmission of antimicrobial resistant pathogens.

The marginal cost of antimicrobial use is c . Additional grazing costs are suppressed for clarity. Other exogenous factors may drive the value of production, e.g., market prices, livestock characteristics, total forage usage, and other inputs, grazing impacts on disease, and antimicrobial use effectiveness. These are omitted above for clarity but discussed below as they apply to the empirical analysis.

In summary, net returns from livestock ownership are $v(1 - \gamma\alpha)$ minus private antimicrobial costs ca . The function γ embodies the harm from disease and is a function of grazing and antimicrobial use. Communal grazing has two effects: it increases the value of livestock by providing food for the animals, but may decrease the value of livestock through disease morbidity and mortality. Regional and private antimicrobial use mitigates disease losses, but antimicrobial use also may reduce its effectiveness through resistance.

Expected net returns are solved by backward induction by choosing antimicrobial use subject to grazing practices, and grazing practices conditional on expected optimal antimicrobial use. The first-order condition for the second stage (antimicrobial use) decision is

$$\pi_a = -v\gamma\alpha_a - c = 0.$$

The first-order condition gives a standard result of private marginal benefit of antimicrobial use equal to marginal cost of antimicrobial use and, assuming the Implicit Function theorem holds, antimicrobial demand is $a^* = a(g, \rho, \tilde{a}, \tilde{g}, c)$. The marginal rate of substitution between a

and g is

$$\frac{\partial a}{\partial g} = -\frac{\partial \pi_a / \partial g}{\partial \pi_a / \partial a} = -\frac{\alpha_a (v_g \gamma + v \gamma_g)}{v \gamma \alpha_{aa}} > 0.$$

From this relationship we have our first hypothesis:

***Hypothesis 1:** More antimicrobials are used by households that graze more on communal grazing lands.*

Optimal antimicrobial use in relation to the baseline disease risk, conditional on the grazing rate is

$$\frac{\partial a^*}{\partial \rho} = -\frac{\partial \pi_a / \partial \rho}{\partial \pi_a / \partial a} = -\frac{\gamma_\rho \alpha_a}{\gamma \alpha_{aa}} > 0,$$

implying a second hypothesis:

***Hypothesis 2:** A higher background disease prevalence is associated with higher antimicrobial use.*

The first stage first-order condition for grazing is (after applying the envelope theorem based on the first-order condition for antimicrobial demand) is

$$\frac{\partial \pi}{\partial g} = v_g (1 - \gamma \alpha) - v \gamma_g \alpha = 0,$$

which indicates that the marginal value of grazing is equal to the marginal cost of disease exposure due to grazing, accounting for optimal response to antimicrobial use. Communal grazing demand is $g^* = g(\rho, \tilde{a}, \tilde{g}, c)$, which includes the same arguments as a^* (except g itself).

Losses from livestock illness are represented by $l^* = v(g^*)(\gamma(g^*; \tilde{g}, \tilde{a}, \rho) \alpha(a^*; \tilde{a}))$, and dependent on (endogenous) grazing and antimicrobial use. Losses increase with increase at the

margin from communal grazing by $\frac{\partial l^*}{\partial g^*} = v_g \gamma \alpha + v \gamma_g \alpha$ and decrease at the margin from antimicrobial use by $\frac{\partial l^*}{\partial a^*} = v \gamma \alpha_a$ (evaluated g^* and a^* in both cases).

From a social welfare perspective, private decisions about communal grazing and antimicrobial use have impacts beyond the household through \tilde{g} and \tilde{a} . To examine the implications of these inter-household impacts, assume there are $N+1$ identical households as described above, and define $\tilde{g} = \sum_{j=1}^N g = Ng$ and $\tilde{a} = \sum_{j=1}^N a = Na$. In other words, the sum of other households' communal grazing and antimicrobial use increase or decrease the morbidity and mortality losses to a household. Given that $\tilde{a} = \sum_{i=1}^N a$, a one unit increase in one household's use of antibiotics adds one unit to \tilde{a} , so the net externality of a household's antibiotic use on all N other households at the margin is

$$E_a = N \frac{\partial \pi^*}{\partial \tilde{a}} = -Nv(\alpha \gamma_{\tilde{a}} + \gamma \alpha_{\tilde{a}}),$$

where $\pi^* = \pi(\rho, c, \tilde{g}, \tilde{a})$ is the indirect profit function.³ The net marginal external cost of antibiotic use across N identical users is $E_{\tilde{a}} = NE_a$.

The marginal externality of one household grazing on communal land due to contributions to disease incidence is similarly

$$E_g = N \frac{\partial \pi^*}{\partial \tilde{g}} = N(v_{\tilde{g}}(1 - \gamma \alpha) - v(\alpha \gamma_{\tilde{g}} + \gamma \alpha_a \alpha_{\tilde{g}}^*)),$$

and the communitywide externality is $E_{\tilde{g}} = NE_g$. Note that the externality in this case has three parts: a) the negative effect on grazing productivity, b) increased transmission risk due to grazing itself, and c) increased antimicrobial resistance from the induced increase in antimicrobial use in response to higher transmission and disease risk from grazing.

³ The indirect effects through the choice variables a and g cancel out per the Envelope Theorem.

Data and Econometric Methods

To test hypotheses 1 and 2 above, we run regressions to represent communal grazing and demand for antimicrobials, and a third regression to estimate the relationship between grazing, antimicrobial use, and livestock illness:

$$\begin{aligned}g^* &= g(c, \rho, \tilde{a}, \tilde{g}) = g(\mathbf{X}) \\a^* &= a(g, c, \rho, \tilde{a}, \tilde{g}) = a(g^*, \mathbf{X}) \\l^* &= l(g, c, \rho, \tilde{a}, \tilde{g}) = l(g^*, a^*, \mathbf{X}).\end{aligned}$$

Because the characteristics of our data define the specific estimation strategies we use, we first describe our data, and then describe our regression estimation procedures.

Data collection was performed by Washington State University, with a protocol approved by the Tanzania National Institute for Medical Research. Data were collected from 416 households in 13 villages, and the dataset is made up of one record (observation) per household (Caudell et al., 2017b). There are three main ethnic groups that inhabit the area of study, which ranges between Mount Meru and Mount Kilimanjaro in North Central Tanzania, and West to the Ngorogoro area (figure 2.1). The Arusha and Chagga populate the slopes of Mt. Meru and Mt. Kilimanjaro, respectively, while the Maasai mostly live in the surrounding steppe. Some Arusha live in lower lying areas interspersed among Maasai to the West of Arusha Town in Monduli District. The Chagga generally live in the higher rain fed, green regions around Mount Kilimanjaro, and their herds are generally small (mean herd size = 8.9) and more confined. The Maasai mostly live in the more arid lowland steppe plains. Their herds are relatively large (mean herd size = 345.5), and they mainly rely on communal grazing to feed their animals, given the predominant land tenure system in Tanzania. The green regions around Mount Meru are mostly inhabited by the Arusha. Again, with greater forage around the farms, they typically rely less on communal grazing than the Maasai.

Table 2.1 describes each of the variables used in the analysis, and table 2.2 provides summary statistics. *Antimicrobial use* (represented by a in our theoretical model) provides information about antimicrobial inventories on-hand in each household, which are used to develop an antimicrobial use index. The index indicates the presence of syringes/needles for antimicrobial injection and number of types of antimicrobials on-hand in a household at the time of survey enumeration.⁴ The largest number for any household was 7, and the lowest was 0, therefore, our index ranges from 0 to 7. As such, our antimicrobial use data are treated as count data in our analysis (refer to figure 2.2). The average index value of antimicrobials on hand in a household is 1.69 (standard deviation 1.63) (table 2.2). One hundred fifty-seven out of the 382 households did not have any antimicrobials/syringes in their inventory. Virtually none of the Chagga households held antimicrobials or syringes, and virtually all Maasai households held some, while Arusha households varied more in their antimicrobial holdings.

Communal grazing (represented by g in our theoretical model) is the fraction of animals in a household's herd that are regularly grazed outside the household or compound, therefore g ranges in the unit interval.

We hypothesize that background disease prevalence, measured imperfectly in our data through recent history of local livestock illness, affects antimicrobial use through its impact on herd owner risk perceptions (Pingali and Carlson, 1985; Dickie and Gerking, 1996; McNamara et al., 2006; Clark, 2013). *Current illness* is the number of animals reported sick during the time of the survey, and is a proxy for current and expected illness outcomes (represented by $\nu\gamma\alpha$ in the model). *Prior illness* is the number of animals reported sick in the past year prior to current

⁴ The inventories included four types of antibiotics (Oxytetracycline, Penicillin, Streptomycin and Sulfa and Tylosin), acaricides, anti-protozoal drugs and syringes and needles that indicated self-use. The most commonly found drug in the inventories was Oxytetracycline.

illnesses. Figure 2.2 contains histograms of *current illness*, *prior illness*, *antimicrobial use* and *communal grazing*.

Sheep/goats, and *cattle* herd size are important control variables in the analysis. They relate to total herd livestock value (v) and, in conjunction with grazing rates, determine the number of animals grazed on communal land. The Chagga and Arusha who inhabit Mt. Meru and Mt. Kilimanjaro often practice zero-grazing because the rainfall in these regions is plentiful and land is limited, while the Maasai generally use communal grazing, and live in more arid conditions. About 50 per cent of the sample consists of Maasai households and the other 48 per cent of the sample is made up of Chagga and Arusha. About 2 percent of the sample households belong to other ethnicities.

Other variables that we hypothesize may explain the differences in the *antimicrobial use* include total household *income*, *household size*, and method of consultation regarding livestock health. The household *income* variable is measured in Tanzanian Shillings (10,000s). Crop inventory, and sale were converted into monetized value, and added to the cash income to indicate total household wealth. Cash income is a good indicator of wealth for Chagga and Arusha, but Maasai may have less cash income, and more crop income. Therefore, recent sale prices of the produce were multiplied by crop stored and sold quantities to estimate cash value of the crops.

The variable *Govt. Vet.* is an indicator variable equal to 1 if a household uses a professional veterinarian for livestock health consultation, and zero if a household uses traditional methods or over-the-counter antimicrobials. *Distance to urban* is the natural logarithm of distance between the household and an urban center, and *Distance to market* is the logarithm of distance between the household and a market. We include these variables as proxies to control for access to

antimicrobials, livestock health services, and both livestock and human population density.

Empirical Model

We developed two econometric models to test our hypotheses: (a) a model of communal grazing rates conditional on household characteristics, and (b) an instrumental variables model of antimicrobial use conditional on grazing patterns, prior livestock disease, and household characteristics. A third regression model is used to estimate the relationship between livestock illness rates, communal grazing and antimicrobial use.

A fractional Probit regression is used to model the grazing practices of the households because the dependent variable, *communal grazing* (g), is the proportion of a herd grazed bounded by zero and one (see figure 2.2).⁵ Following Papke and Woolridge (1996), the conditional expectation of the grazing rate is

$$E(g_i|\mathbf{X}_i) = \Phi(\mathbf{X}_i\boldsymbol{\beta}) + \eta_i,$$

where $\Phi(\mathbf{X})$ is a standard normal cumulative distribution function and \mathbf{X} includes rainfall, ethnicity dummy variables and other available exogenous controls that may explain grazing patterns, and η_i is a random disturbance. The fractional Probit model is estimated via quasi-maximum likelihood using the Stata[®] 14 *fracreg* routine.

Antimicrobial use is count data, with a high proportion of zeros. A zero-inflated Poisson model is used for estimation using Stata[®] 14 *zip* routine. This specification implicitly assumes that the decision to use antibiotics is not systematically different from the decision about how much or how many antimicrobials to use. The first stage in the econometric model characterizes

⁵ Fractional probit or logit regressions are used when the dependent variable is a proportion bounded by zero and one.

the probability of a household having no antimicrobials on hand ($a = 0$). Following Greene (2011), $\text{Prob}[a = 0|g, \mathbf{X}] = F(a|g, \mathbf{X})$. The probability of nonzero antimicrobials on hand is $\text{Prob}[a = j|\mathbf{X}, a > 0] = (1 - F(a|g, \mathbf{X})) = \frac{\exp(-\lambda)\lambda^j}{j!}$; where $\lambda = \lambda(g, \mathbf{X})$ and is the conditional mean of the Poisson process. Hence,

$$E[a|g, \mathbf{X}] = F * 0 + (1 - F(a|g, \mathbf{X})) * E[a|g, \mathbf{X}, a > 0] = (1 - F(a|g, \mathbf{X}))\lambda.$$

F is estimated as a logit such that $\text{prob}[q = 1|g, \mathbf{X}] = \frac{\exp(\mathbf{X}'\boldsymbol{\delta})}{1 + \exp(\mathbf{X}'\boldsymbol{\delta})}$, which results in the following probability regression that can be estimated using maximum likelihood, motivated in Greene (2011):

$$E(q = 1|g, \mathbf{X}) = F_l(\mathbf{X}'\boldsymbol{\delta}) + \mu_l,$$

where μ_l captures producer heterogeneity. \mathbf{X} constitutes all the factors described in the theoretical model, and g is the grazing rate. The second stage (the Poisson process) can be estimated using the canonical formulation motivated by Cameron and Trivedi (1986),

$$\ln(\lambda_i) = \mathbf{X}'_i\boldsymbol{\delta} + \varepsilon_i,$$

where ε_i captures unobserved heterogeneity among households in the data sample.

Our theoretical model treats *communal grazing* (g) as a quasi-fixed choice variable and is endogenous in the intermediate run, depending on several factors including land grazing characteristics and land tenure. We therefore apply a two-stage approach to estimation of the *antimicrobial use* regression by replacing the actual value of g with the predicted values of g from a regression of grazing on a set of explanatory variables. In two-stage instrumental variable estimation, an adjustment must be made to attain consistent covariance estimates (Greene 2011),

which we perform.⁶ Evidence of over-dispersion was found in the data, which could be due to heterogeneity in household preferences or the nature of the process generating the excess zeros (Mullahey 1986). The Vuong test (Vuong 1989) suggests that the excess zeros are generated by a separate process, justifying a zero-inflated Poisson regression.

A final regression estimates the relationship between current livestock illness, antimicrobial use, and grazing rates. *Current illness* is also a count variable (see figure 2.2) and a Vuong test suggests that a zero-inflated Poisson regression is justified. The standard errors are again adjusted for instrumental variable use as they were in the antimicrobial regression.

Results

We present results for the grazing regression, the antimicrobial use regression, and the illness regression in turn. In the grazing regression (table 2.3), the coefficient for *rainfall* is negative, large and statistically significant ($P < 0.001$), consistent with grazing intensity being higher in arid environments whereas feed and fodder is brought to livestock in the high rain fed areas and grazing is only used as an extensive margin. The coefficients for ethnicity indicators, *Arusha* and *Chagga*, are also negative relative to the Maasai; this is consistent with the grazing behaviors of these ethnicities.

These ethnic dummy variables are excluded instruments for the second stage antimicrobial regression, where ethnic grazing practices are hypothesized to be more long-term, historical phenomena shaped by environment, culture and land tenure issues, while antimicrobial use is a

⁶ The maximum likelihood covariance matrix is $\hat{\sigma}^2(\mathbf{Z}'\mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{Z})^{-1}$, where \mathbf{Z} are potentially endogenous variables and \mathbf{X} are exogenous. This estimate is biased because the standard second stage estimated variance $\hat{\sigma}^2 = \mathbf{n}^{-1}(\mathbf{y} - \hat{\mathbf{Z}}\boldsymbol{\beta})'(\mathbf{y} - \hat{\mathbf{Z}}\boldsymbol{\beta})$ are calculated using the predicted values from the first stage regressions. A consistent estimate of the σ^2 is calculated as $\hat{\sigma}_{ub}^2 = \mathbf{n}^{-1}(\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})'(\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})'$, based on the original values of instrumented variables in \mathbf{Z} , and the unbiased covariance matrix is calculated using $\hat{\sigma}_{ub}^2$, the unbiased estimate of σ^2 .

modern risk management phenomenon that is more fluid and not subject to these factors. Therefore, controlling for ecological factors and livestock and human densities, ethnic background is taken to affect antimicrobial use through livestock management practices like communal grazing.

Distance to Urban and *Distance to Market* are proxies for human and livestock densities and market access. Urban areas tend to be located at higher rainfall regions within our sample, and distances to markets tend to be short. Their associated coefficients are consistent with higher communal grazing rates in steppe environments that receive lower rainfall and support lower human and livestock densities.

For the antimicrobial use regression, the results show a positive relationship between *communal grazing* and *antimicrobial use*, corroborating *hypothesis 1* (table 2.4). The null hypothesis that *communal grazing* does not affect *antimicrobial use* is rejected at 1 per cent level of significance ($P < 0.001$) in the logit regression, while we fail to reject the null hypothesis in the case of Poisson regression. These results suggest that, conditional on controls, *communal grazing* is associated with higher antimicrobial use, but does not (statistically speaking) influence how many types of antimicrobials a household will use. This pattern might result if households tend to use a broad-spectrum antimicrobial (like oxytetracycline in our sample) for all disease challenges, or if they face just one or a few diseases for which one antimicrobial will suffice. Overall, a 10 per cent increase in the *communal grazing* rate is associated with about 7 per cent increase in *antimicrobial use* evaluated at sample means (i.e. $(\partial a / \partial g) / (\bar{g} / \bar{a})$). It is worth noting that *communal grazing* captures herd-contact imperfectly, and there could be other mechanisms of herd contact like watering holes and livestock transactions.

Ethnic dummy variables are used as excluded instruments for *communal grazing*. The

Durbin-Wu-Hausman test fails to reject the exogeneity of the instruments. However, there may be unobservable characteristics associated with certain ethnicities that may affect antimicrobial use directly and bias the instrumental variable estimates. *Income, distance to market, distance to urban* and use of *govt. vet* are controlled for in the second stage regression to minimize the bias caused by unobservable differences in ethnicities that affect *antimicrobial use*.

The analysis also shows a positive effect of *prior illness* on *antimicrobial use*, which is consistent with *hypothesis 2*. A unit increase in the *prior illness* number is associated with an increase in antimicrobial usage of 0.87 and the coefficient is significant at 5 per cent level for both the Logit and Poisson regression components. This result is consistent with how reference levels and loss aversion play a role in behavior (Kahneman et al. 1991; Tversky and Kahneman 1991). "Availability bias" can be another reason why farmers may use more antimicrobials after experiencing salient illness events in the recent past (Tversky and Kahneman 1973). To the extent that herd owners understand the disease risks associated with *communal grazing* and use *prior illness* as an indicator of underlying disease risk, they can affect subjective risk assessment and therefore the extent of *antimicrobial use*.

Higher household *income* is associated with higher antimicrobial adoption rates, but not the number of antimicrobial types used. If household production and consumption are separable activities, if livestock husbandry is a purely financial enterprise, and if antimicrobial use is solely providing benefits in terms of reduced livestock morbidity and mortality, we might expect household income to have no effect on antimicrobial use (Marsh et al. 2016). There are several reasons why income may have an effect. First, if liquidity constraints affect the ability of households to purchase antimicrobials, then income may affect antimicrobial purchases (Carter and Yao 2002). Second, antimicrobial use for livestock may provide human health benefits to the

extent that antimicrobial use in household livestock mitigates zoonotic disease incidence. Third, while livestock may be an important economic asset, household herds and their wellbeing may hold cultural significance beyond their market, income and consumption value (Quinlan et al. 2016).

Rainfall is also positively related to *antimicrobial use*, given grazing practices and other controls. Higher rainfall can support taller grass, which can lead to high tick intensity in herds and may lead to higher disease transmission risk and more frequent use of antibiotics, antiprotozoans and acaricides.

The method of consultation that households use can also influence antimicrobial use. Our results show that use of *govt. vet* is associated with an intercept shift of -0.3; a lower rate of antimicrobial holding and use. Although we cannot identify underlying drivers of this result and variation in use of veterinary services is closely tied to the three primary ethnic groups identified in this study, it is consistent with professional advice acting to reduce antimicrobial use (all else constant) relative to private use by herd owners. Note, however, that the use of veterinary services is an endogenous decision, likely affected by the cost of and access to professional services. Large herd owners may choose to make antimicrobial use decisions on their own depending on the fee structure of professional veterinary health care providers, and fees may be larger in rural areas relative to urban/peri-urban settings due to travel cost differences.

Distance to urban does not appear to be correlated with *antimicrobial use*. Nevertheless, *distance to market* is associated with a decrease in *antimicrobial use*, perhaps due to higher acquisition costs or, perhaps, less disease challenge through inter-herd contact.

Table 2.5 provides illness regression results with one regression that excludes *antimicrobial*

use as a regressor (Regression 1) and one that includes an instrument for *antimicrobial use*.⁷

Regression 1 shows that an increase in *communal grazing* is associated with a higher incidence of sick animals. This is consistent with *hypothesis 1*, suggesting that communal grazing may lead to higher rates of illness through higher transmission.

This first regression can be interpreted as a reduced form regression in which household demand for antimicrobials is implicit, and it is included primarily as a robustness check to compare with Regression 2.

Regression 2 (columns 3 and 4 of table 2.5) includes an instrumental variable for antimicrobial use (the predicted values from the regression in table 2.4). The associated negative parameter under “No Sick Animals” indicates that the probability of having no illness is negatively associated with antimicrobial use. The positive coefficient under “Number of Sick Animals” indicates that there is a positive association between *antimicrobial use* and the number of sick animals. To relate this result back to our theoretical model, recall that the marginal effect of antimicrobial use on illness is $\frac{\partial l^*}{\partial a^*} = v\gamma\alpha_a < 0$, suggesting we would expect to see a negative relationship between antimicrobial use and illness. Note, however, that our *current illness* measure is the number of current reported illnesses, and therefore better characterized as $v\gamma$ rather than $v\gamma\alpha$. As such, our available metric is an incomplete measure of illness because it does not measure the degree or duration of illness – the characteristics of illness that therapeutic antimicrobial use would most likely affect. Thus, the positive relationship between *antimicrobial use* and *current illness* in this regression is consistent with a scenario in which antimicrobial use

⁷ Figure 2.2 shows an outlier observation with reported current illness of nearly 400 animals. Both regressions in the table remained qualitatively unchanged in both parameter magnitude and statistical significance. We therefore report only the regressions based on the full sample.

is primarily therapeutic instead of preventive, which, based on out-of-sample anecdotal field evidence, appears to be the case in most households. Conditional on grazing practices, illness frequency increases when background risk increases ($\gamma_\rho > 0$), and *hypothesis 2* is that antimicrobial demand increases with background illness risk, and so the estimated positive relationship between *antimicrobial use* and *current illness* is likely picking up this signal and its influence on therapeutic antimicrobial use.

Conclusion

Infectious disease management and grazing decisions are important elements of agro-pastoral livestock husbandry. Our results show strong relationships between communal grazing, livestock illness, and antimicrobial use. We estimate the impact of grazing patterns and prior livestock illnesses on antimicrobial demand using a zero-inflated Poisson regression model. Identification within this framework is achieved by making use of the variation in ethnicity of households in our sample. We also examine the relationship between current illness rates, grazing and antimicrobial use. Our results show that disease risk perceptions and communal grazing play important roles in determining disease outcomes and the demand for antimicrobials.

The paper relies on communal grazing and prior illness as indicators of underlying risk over which herd owners make antimicrobial use decisions. Communal grazing is directly linked with exposure and disease transmission, while prior illness is informative about current risk and can also have a psychological framing effect on pastoralists' beliefs about disease outcomes. Both communal grazing and prior illness are positively related to an increased probability of having antimicrobials on hand for livestock use. Prior livestock illness in the last month also is positively related to having more antimicrobials on hand. In turn, we find that communal grazing

is positively related to the current number of sick animals, as is antimicrobial use. While we control for endogeneity using an instrumental variable approach, the positive relationship between antimicrobial use and current illness could reflect therapeutic antimicrobial use rather than a practice of using antimicrobials for prophylaxis (disease prevention).

There are externalities associated with both communal grazing and antimicrobial use. Although communal land tenure has important strengths as a property rights regime, especially in terms of risk management in volatile climate zones (Agrawal, 2001; Ostrom, 2015), it can incentivize overgrazing (Ciriacy-Wantrup and Bishop, 1975; Runge, 1981), and potentially be associated with disease transmission externalities to the extent that herds pass on disease to other herds sharing the communal grazing land. Antimicrobial use has two potentially offsetting effects that can be magnified by communal grazing. First, antimicrobial use that reduces the intensity and duration of pathogen shedding can reduce pathogen transmission to other herds, but it might also lead to a larger fraction of pathogen populations being antimicrobial resistant, leading to reduced effectiveness of future antimicrobial use. We show that through its potential to increase disease transmission rates, communal grazing may also exacerbate overuse of antimicrobials from an economic efficiency perspective.

Therefore, for optimal communal grazing and antimicrobial use in terms of economic efficiency, it is important to align the private benefits of communal grazing and antimicrobial use with the social benefits related to the two activities. Although our data do not allow examination of how antimicrobial use in this context influences development of antimicrobial resistance, understanding incentives for antimicrobial use in agropastoralist systems may help devise strategies to limit the emergence and persistence of antimicrobial resistance in these populations.

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Figures



Figure 2.1. Northern Tanzania from Mt Meru to the southern slopes of Kilimanjaro, West to Ngorongoro showing major highways and location of ethnic groups sampled

Source: Google maps

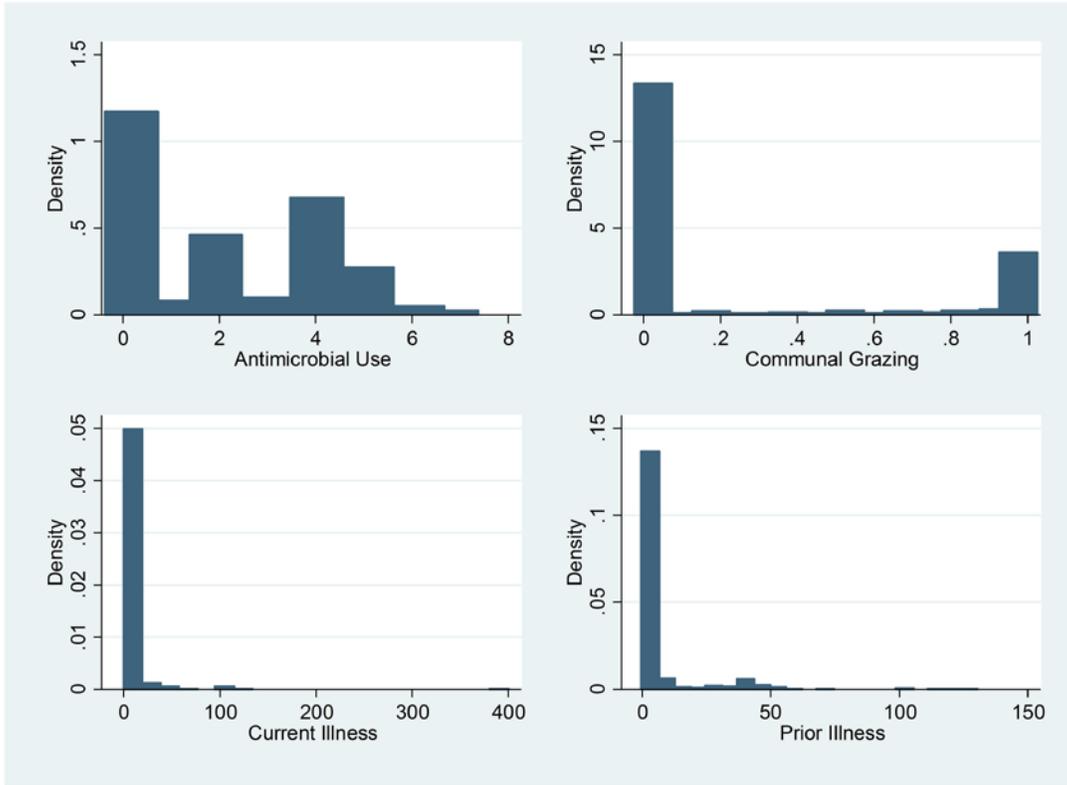


Figure 2.2. Histograms of communal grazing rates, antibiotic use, prior illness and current illness variables

Tables

Table 2.1 Data Description

Variable	Description
<i>Communal Grazing (g)</i>	Fraction of owned animals that graze outside the homestead or compound.
<i>Antimicrobial Use (a)</i>	Number of types of antimicrobials in farm inventory. Guttman scale from 0-7. The inventories included four types of antibiotics (oxytetracycline, penicillin, streptomycin and sulfonamide and Tylosin), acaricides, anti-protozoal drugs and syringes and needles that indicated self-use.
<i>Prior Illness (ρ)</i>	The number of animals reported sick in the year, prior to current illnesses.
<i>Current Illness (proxy for $v\gamma$)</i>	The number of animals reported sick currently.
<i>Sheep/Goats</i>	Number of sheep and goats owned by a farm.
<i>Cattle</i>	Number of cattle owned by a farm.
<i>Use Govt. Vet</i>	Indicator variable equal to 1 if the farm uses the government veterinary services, zero otherwise.
<i>Income</i>	Total household income in Tanzanian currency.
<i>Distance to Urban</i>	This variable maps the log of distance from a household to an urban center in kilometers.
<i>Distance to Market</i>	This variable maps the log of distance from a household to a market in kilometers.
<i>Household Size</i>	Total number of people living in a household.
<i>Rainfall</i>	Indicator variable if village average annual rainfall is greater than average rainfall of the total region of the sample. Estimate of average annual precipitation, in inches, was calculated from years 2008 - 2013 from the weather stations located in the area. The average was calculated at 39.2 inches.
<i>Arusha</i>	Indicator variable equal to 1 if household ethnicity is Arusha, 0 otherwise.
<i>Chagga</i>	Indicator variable equal to 1 if household ethnicity is Chagga, 0 otherwise.
<i>Other</i>	Indicator variable equal to 1 if household ethnicity is neither Maasai, Chagga, or Arusha, 0 otherwise.

Table 2.2. Summary statistics (N = 382)

	Mean	Standard Deviation	Min	Max
<i>Antimicrobial Use</i>	1.69	1.62	0	7
<i>Communal Grazing</i>	0.318	0.454	0	1
<i>Prior Illness</i>	15.04	28.66	0	130
<i>Current Illness</i>	11.02	33.99	0	400
<i>Sheep/ Goat</i>	76.97	200.16	0	2,415
<i>Cattle</i>	62.12	233.17	0	3,150
<i>Income</i>	960,821	1,520,000	0	3,800,000
<i>Household Size</i>	9.91	7.5	1	41
<i>Use Govt. Vet</i>	0.32	0.466	0	1
<i>Rainfall (inches)</i>	39.2	25.1	18.3	82.5
<i>Distance to Urban (km)</i>	46.26	41.22	3.58	174.91
<i>Distance to Market (km)</i>	3.08	6.15	0.1	60
<i>Arusha (percent)</i>	21.98	-	0	1
<i>Maasai (percent)</i>	50.72	-	0	1
<i>Chagga (percent)</i>	24.4	-	0	1
<i>Other</i>	2.9	-	0	1

Table 2.3. Communal grazing regression. Fractional Probit results

Dependent Variable: Communal Grazing	Coefficient	Marginal Effects
<i>Rainfall</i>	-1.64*** (0.204)	-0.266
<i>Chagga</i>	-1.96*** (0.49)	-0.296
<i>Arusha</i>	-4.18*** (0.35)	-0.333
<i>Other</i>	-0.57 (0.51)	-0.12
<i>Cattle</i>	0.0026 (0.002)	0.001
<i>Sheep/Goat</i>	0.002 (0.005)	0.001
<i>Govt. Vet.</i>	-0.065 (0.28)	-0.011
<i>Household Size</i>	0.007 (0.011)	0.002
<i>Income</i>	-0.097 (0.16)	-0.016
<i>Distance to Urban</i>	1.02*** (0.17)	0.166
<i>Distance to Market</i>	0.023 (0.084)	0.003
Pseudo R-Squared	0.52	

Number of observations = 382. *** indicates statistical significance at 1% level.

Table 2.4. Antimicrobial use regression. Zero-inflated Poisson

Dependent variable: Antimicrobial Use	Decision not to Use Antimicrobials^a	Number of Antimicrobials	Marginal Effects
<i>Communal Grazing^b</i>	-20.67*** (6.50)	0.0352 (0.17)	3.71
<i>Prior Illness</i>	-3.05** (1.51)	0.206** (0.082)	0.877
<i>Cattle</i>	-0.008 (0.069)	0.0003 (0.00014)	0.001
<i>Sheep/Goats</i>	-0.005 (0.006)	0.002 (0.001)	0.001
<i>Govt. Vet</i>	2.96*** (0.72)	0.065 (0.098)	-0.299
<i>Income</i>	-0.10*** (0.03)	-0.003 (0.01)	0.013
<i>Household Size</i>	-0.026 (0.062)	0.0009 (0.004)	0.006
<i>Rainfall</i>	-4.71*** (0.93)	-0.035 (0.033)	0.833
<i>Distance to Urban</i>	0.604 (0.49)	0.042 (0.056)	-0.001
<i>Distance to Market</i>	0.91* (0.53)	0.019 (0.039)	-0.093
Vuong Test: ZIP vs Poisson			9.97
Likelihood Ratio Test (p-value): Poisson vs NB			0.5
Likelihood Ratio Test (p-value): ZIP vs ZINB			0.23

^aThe model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of not choosing antibiotics.

^bThe predicted values from the regression summarized in table 1.3 are used as the instrument for communal grazing.

*, **, *** indicate statistical significance at 10, 5 and 1% respectively. N = 382.

Table 2.5. Current Illness, Zero-inflated Poisson regression

Dependent Variable	Regression 1		Regression 2	
	<i>No Sick Animals</i>	<i>Number of Sick Animals</i>	<i>No Sick Animals</i>	<i>Number of Sick Animals</i>
Current Illness				
<i>Communal grazing</i>	0.23 (0.34)	1.14*** (0.097)	0.36 (0.41)	1.02*** (0.102)
<i>Antimicrobial use^a</i>	-	-	-0.81*** (0.14)	0.17*** (0.034)
<i>Sheep/Goats</i>	-0.002 (0.008)	0.001** (0.0008)	-0.0013 (0.001)	0.009 (0.009)
<i>Cattle</i>	-0.0009 (0.0008)	-0.003 (0.005)	-0.0008 (0.0008)	-0.0075 (0.005)
<i>Rainfall</i>	0.287 (0.28)	-0.059 (0.058)	-0.34 (0.28)	0.127 (0.079)
<i>Distance to Urban</i>	-0.39** (0.16)	0.061 (0.05)	0.175 (0.16)	-0.087 (0.058)
<i>Distance to Market</i>	0.04 (0.13)	0.19*** (0.02)	0.06 (0.138)	0.20*** (0.021)
Vuong Test Statistic	5.15		6.35	

** , *** indicate statistical significance at 5 and 1% respectively.

^aThe predicted values from the regression summarized in table 1.4 is used as the instrument for antimicrobial use. N=382.

CHAPTER THREE: RISK MANAGEMENT, DISEASE LOSSES AND HERD
ACCUMULATION IN LIVESTOCK-DEPENDENT HOUSEHOLDS
OF NORTHERN TANZANIA

Abstract

Livestock-dependent households in East Africa face substantial livestock disease risk, and a number of livestock management strategies can affect disease incidence and household welfare. This article examines the relationships between disease-related livestock death and abortion, and vaccination and herd restocking decisions. We develop a theoretical model and derive testable hypotheses about the relationships between these outcomes and management practices, and test them using a system of econometric regressions. Controlling for endogeneity of management decisions, our main findings are: (i) herd owners restock in response to livestock death, but replacement is less than one-for-one, and herd owners tend to replace cattle lost to disease-related death with sheep and goats; (ii) restocking is a contributor to higher livestock disease death and abortions, presumably through inter-herd disease transmission; (iii) vaccinations reduce disease deaths, implying that vaccine availability and use may improve herd and household welfare.

Introduction

Livestock-dependent households in East Africa often live within precarious social, environmental, and economic settings (Little et al. 2001; Smith, Barrett and Box 2000; Bailey et al. 1999). In particular, livestock keepers face considerable risks in terms of climate variability, price volatility and livestock disease (ibid). Livestock keepers use a variety of risk management practices in the face of weather variability and disease risk. Migration, seasonal transhumant grazing practices, vaccinations and preventive antimicrobial use are important *ex ante* risk mitigating strategies. Therapeutic medicine and means of herd maintenance and accumulation after drought and disease losses, such as through loans, gifts and purchases are crucial *ex post* risk coping strategies for livestock keeping households in East Africa (Barrett, Smith and Box 2001; Dercon 2002). Disease and drought cycles and the costs of associated prevention, mitigation and coping strategies may lead these households into 'poverty traps' that may persist in the long-run (Lybbert et al. 2004; McPeak and Barrett 2001; Santos and Barrett 2016; Kraay and McKenzie 2014; Toth 2015).⁸

Livestock disease transmission and health outcomes depend on a suite of environmental factors and household herd management decisions. Management strategies like livestock quarantine and vaccination can limit individual animal exposure and susceptibility. Livestock vaccination, when available and cost effective, can be an important measure to prevent diseases that negatively affect households. Factors affecting the adoption and use of vaccines include local disease prevalence, access to veterinary services and vaccine availability in the region,

⁸ Poverty trap has been defined as a low income, low asset equilibrium from which escape is difficult if not impossible (McPeak 2006).

individual risk perceptions, and income available for vaccine investment (Ahmed et al. 2018; Marsh et al. 2016).

Apart from vaccinations, replacing livestock (restocking by introduction of new animals into the herd) after a death or an abortion through purchase, lending, or by gift is a common and important household strategy for herd maintenance (McPeak 2006). However, livestock introductions from outside the herd can also be a source of infectious disease (Fèvre et. al 2001; Gardener, Willeberg and Mousing 2007; Marshall, Carpender and Thunes 2009). This risk of pathogen transmission and consequent losses due to restocking may be more acute in pastoral areas where herds are grazed communally and access to veterinary services is limited (Inagolet et al. 2008; Selby et al. 2013).

The objective of this paper is to examine the relationships between livestock management practices and disease-related asset losses (livestock abortions and deaths) based on primary survey-based cross-sectional data collected in northern Tanzania.⁹ We focus specifically on livestock death due to disease and abortion incidence as illness outcomes, and management in the form of vaccination for illness prevention and animal replacement decisions for herd maintenance and accumulation. To examine these relationships, we develop a theoretical model of livestock management decisions in the context of herd disease challenge, and derive a set of testable hypotheses relating to the objectives above. A system of econometric regression equations is developed and used to test the hypotheses about livestock introduction and vaccination, and their impact on livestock abortions and disease-related deaths. Because livestock health management practices are theoretically responsive to disease and illness risk

⁹ Due to this paper's analytical focus, livestock deaths refer to non-abortion-related livestock losses, and livestock losses refers generally to livestock deaths and/or abortions. The focus of the paper is on disease-related losses, but we have and use data on our analysis on drought related losses as well.

through herd owner disease management incentives, management activities and disease outcomes are jointly determined. Therefore, a simultaneous system of regression equations is applied, with careful treatment of the endogeneity of management decisions.

Using our econometric regression strategy, we test whether: (i) animal introductions lead to increased abortion incidence and disease-related deaths in a herd; (ii) whether disease prevention in the form of vaccinations curtails livestock death due to disease; (iii) whether the demand for animal introductions responds to abortion incidence and livestock deaths due to disease in herds. We find that restocking is both a response and contributor to livestock death. Herd owners restock in response to disease and drought-related deaths, but replacement is less than one-for-one. The magnitude of introductions is smaller than the size of negative asset shocks in northern Tanzania, which may indicate households' limited ability to insure against catastrophic events. Herd owners tend to replace cattle losses with sheep as much or more than with cattle, which is consistent with a trend toward smaller stock in the region (McCabe 2003; Bollig 2006; Goldman and Riosmena 2013). Further, we find that restocking is not just costly in terms of replacement costs but is also a contributor to higher livestock disease deaths and abortions, presumably as an inter-herd disease transmission mechanism. Finally, we find that vaccinations reduce disease death rates, suggesting that vaccination availability and use may improve herd and household welfare; however, no sampled household vaccinated against more than three livestock diseases, possibly due to lack of vaccine availability or veterinary services.

This article contributes to the literature in several ways. First, we conceptualize herd restocking, vaccination decisions and disease-related death and abortion outcomes in an equilibrium framework and econometrically address the feedback mechanisms between these management decisions and economic outcomes by using a set of simultaneous regression

equations. This simultaneous interaction between disease risk, restocking and vaccination decisions and outcomes has not been explored in the literature. Second, the paper not only analyzes the demand for livestock introductions as a response to livestock death, as in previous studies (Lybbert et al. 2004; Speranza 2010), but also examines herd restocking in response to livestock abortions, a loss that could directly impede herd growth. Third, the paper contributes to the understanding of risk factors for disease associated with herd restocking. Limitations of restocking as a risk-sharing or insurance strategy are discussed in light of the risk of disease transmission.

The article is organized as follows. Section 2 consists of the theoretical model. Data and econometric methods are described in Section 3 and 4 respectively. Section 5 presents results and discussion, and section 6 concludes the paper.

A Model of Vaccination Use and Livestock Introductions

A theoretical model of the relationship between livestock introductions, drought and disease outcomes and vaccination practices is developed next as a foundation for deriving hypotheses and to guide estimation strategy. We assume that households act as if to maximize net herd value by utilizing quasi-fixed inputs such as available labor and accessible land, livestock vaccination investments and herd introductions, where herd introductions can be both a response to disease losses and a source of disease introduction into the herd. To reduce notational clutter in the analytical model, we assume one livestock type and combine disease-related deaths and/or abortions into a general concept of livestock loss; but we later distinguish these for estimation. The household's decision problem is characterized as

$$\max_{L,v,n} \pi = p(y(L; k) + n)(1 - \delta(v, n; g, \rho)) - wn - cv - w_1 L - r, \quad (1)$$

where p is the marginal value of an animal in terms of its productivity in the herd, y is pre-loss herd size, which might be thought of as a target or preferred herd size in the absence of disease. It is a function of labor, L , and quasi-fixed land and capital resources available to the household, denoted by k . The disease loss rate, $\delta(\cdot) \in [0,1]$, is the fraction of animal units lost by disease through abortions and/or death, and is assumed to be negatively related with livestock vaccinations v , and positively related with introductions n , i.e., $\delta_v < 0$ and $\delta_n > 0$, where subscripts indicate partial derivatives. The loss rate is also assumed to be positively associated with a background disease burden ρ , ($\delta_\rho > 0$) and grazing movements, g , ($\delta_g > 0$). Livestock grazing practices, g and introductions, n , capture inter-herd contact which is related to disease prevalence in the region (Bronsvort et al., 2004; Rufael et al., 2008; Schoonman and Swai, 2010). The marginal cost of an introduction is w (e.g. the market price of an animal), c is the marginal cost of vaccination, w_1 is the cost of labor and r represent any fixed costs such as land or capital rent applicable to the livestock enterprise.

The first-order necessary conditions for maximizing with respect to v , n and L are,

$$\frac{\partial \pi}{\partial v} = -p\delta_v(y + n) - c = 0. \quad (2)$$

$$\frac{\partial \pi}{\partial n} = p(1 - \delta) - p\delta_n(y + n) - w = 0. \quad (3)$$

$$\frac{\partial \pi}{\partial L} = py_L(1 - \delta) - w_1 = 0. \quad (4)$$

Equation 2 implies that households choose to vaccinate to the point that the marginal benefit of vaccinations in terms of loss mitigation, $-p\delta_v(y + n)$, is equal to the marginal cost of

vaccinations, c . Equation 3 implies that households will supplement after-loss herd size with introductions as long as the purchase cost is no greater than the in-herd value net of disease losses to introductions ($p(1 - \delta)$) plus the marginal cost of disease transmission due to herd introduction, $-p\delta_n(y + n)$. Equation 4 implies that households choose to allocate labor for livestock management to the point that marginal revenue product, $py_L(1 - \delta)$, is equal to the marginal cost of labor, w_1 . Background disease prevalence, ρ , and associated loss rate, δ , affect the optimal herd size, y^* , through its impact on marginal revenue product.

Define the vector of exogenous factors $\theta = (p, w, c, w_1, g, \rho, k)$. The first-order conditions (Equations 2 and 3) implicitly define the optimal demand functions for vaccinations, $v^* = v(\theta)$, and introductions, $n^* = n(\theta)$, which in-turn implies endogenous damage rate $\delta^* = \delta(v^*, n^*; g, \rho) \equiv \delta(\theta)$. Livestock loss from illness in physical terms is $l^* = \delta^*(y^* + n^*)$, and depends on endogenous introductions and vaccination use. The value of disease losses would be $pl^* = p\delta^*(y^* + n^*)$. Equation 4 implicitly defines the optimal demand function for labor, $L^* = L(\theta)$.

Several hypotheses and implications for empirical strategies follow. Vaccinations reduce disease losses by $\frac{\partial l^*}{\partial v^*} = \delta_v(y^* + n^*) < 0$, suggesting the following hypothesis:

Hypothesis 1: Disease losses are negatively related to vaccinations.

The marginal effect of herd introductions n^* on losses l^* evaluated at v^*, L^* and n^* is represented by $\frac{\partial l^*}{\partial n^*} = \delta_n(y^* + n^*) + \delta > 0$, suggesting:

Hypothesis 2: Disease losses are positively related to herd introductions.

Further, after a catastrophic event, households may introduce animals in the herd to maintain or grow the pre-loss herd size. Assuming no substantive liquidity constraints and approximately efficient markets, equilibrium introductions in the herd will equal the disease losses if pre-loss herd size is to be maintained, i.e., $n^* = \delta^*(y^* + n^*)$, $\Rightarrow n^* = \frac{\delta^*}{1-\delta^*}y$. This equation can help us derive the relationship between introductions and fraction of losses, evaluated at v^* , L^* and n^* , as $\frac{\partial n^*}{\partial \delta^*} = \frac{1}{(1-\delta^*)^2} > 0$, which implies our third hypothesis:

Hypothesis 3: Increase in disease losses will increase the demand for animal introductions.

While the three hypotheses derived from the model are intuitive, this model also highlights that vaccinations $v^* = v(\theta)$ and introductions $n^* = n(\theta)$ are endogenous choices, driven by exogenous biophysical and economic factors. Disease losses $l^* = l(v^*, n^*, L^*; g, \rho, k)$ are directly affected by management decisions and a set of exogenous household characteristics and disease conditions, and indirectly affected through management decisions by a broader set of exogenous variables. The endogeneity of vaccinations and introductions as components of the set of factors affecting disease losses has important implications for econometric estimation strategy, but because the specifics of the available data also inform estimation strategy, a description of the data is provided next.

Data

Data were collected as part of the “Social, Economic and Environmental Drivers of Zoonotic Disease in Tanzania” (SEEDZ) project. This was a cross-sectional survey conducted across six districts in Arusha region (Arusha, Karatu, Longido, Meru, Monduli, and Ngorongoro districts) and four districts in Manyara region (Babati Rural, Babati Urban, Mbulu, and Simanjiro districts)

between January and December, 2016. A multistage sampling design was used. Villages were selected from a spatially referenced list of all villages in the study area (from the Tanzanian National Bureau of Statistics (NBS)) using a generalised random tessellation stratified sampling (GRTS) approach (Stevens and Olsen 2004). Within each village, two to three sub-villages were randomly selected, and up to 10 households were included in each sub-village based on willingness to participate. In total, data were collected from 404 households in 49 sub-villages, and the dataset is made up of one record (observation) per household collected from a questionnaire survey conducted with the household head.¹⁰

Table 3.1 describes the variables used in the analysis, and Table 3.2 provides summary statistics. *Vaccinations* (v in our theoretical model) is the count of vaccinations used for different diseases within a household (variable names are presented in italics throughout). The diseases covered by these vaccinations include anthrax, foot and mouth disease, lumpy skin disease, black quarter, East Coast fever, contagious bovine pleuro-pneumonia, peste de petis ruminants (Ovine rinderpest), and Rift Valley fever.¹¹ *Vaccinations* range from zero to three, with zero being no types of vaccines used within a herd and each additional unit referring to an additional type of vaccine. This implies that although vaccinations are being used, they do not cover the wide range of livestock diseases faced by households. Of the households in our sample, 81.5 percent have not vaccinated their cattle for any type of disease in the last 12 months, 16 percent have used one type of vaccine, 2.5 percent have used 2, and 1 percent have used three (Figure 3.1, upper left

¹⁰ All participants conducting questionnaires provided written informed consent. The protocols, questionnaire and consent procedures were approved by the ethical review committees of the Kilimanjaro Christian Medical Centre (KCMC/832) and National Institute of Medical Research (NIMR/2028) in Tanzania, and in the UK by the ethics review committee of the College of Medical, Veterinary and Life Sciences, University of Glasgow.

¹¹ No Rift Valley fever vaccine was licensed in Tanzania at the time of the study. However, the vaccine may have been acquired across the border from Kenya. There can be potential recall bias in vaccination reporting as households may not know which diseases have animals been vaccinated against or may forget.

panel). The most frequently used vaccines are for contagious bovine pleuro-pneumonia and anthrax, followed by vaccines for lumpy skin disease and foot-and-mouth disease.

Our analytical model focuses on general disease losses $l^* = l(v^*, n^*, L^*; g, \rho, k)$. Our data distinguish between livestock abortions and other livestock deaths. Average *Disease Deaths* in the past 12 months in the sample is 11.15 animals (including cattle, sheep, and goats). Mean deaths due to drought are about 9 animals in the preceding year. Average *Livestock Abortions* reported in the past 12 months by the household is 0.69. The distributions of all the variables related to disease outcomes, disease prevention and introductions are presented in Figure 3.1.

Only one livestock type is distinguished in the analytical model, but our data distinguish between cattle, sheep and goats. [*Cattle, Sheep, Goats*] *Introductions* (represented by n) are count variables representing the number of livestock of each type introduced into the herd from any source in the past 12 months. *Cattle, Sheep* and *Goat Introductions* means are 1.61, 0.78 and 1.50, respectively (Figure 3.1). The mean herd size net of introductions (y in our model) are 53, 61 and 64 for cattle, sheep and goats, respectively, and represented by the variables *Cattle, Sheep*, and *Goats*.

Land Owned is the amount of cropland and grazing land owned by the household, and averages about 9 acres per household in our sample. We use this variable as a proxy for resources available for supporting a herd, and hypothesize that it might contribute to herd size decisions. We utilize a set of variables relating to grazing and watering practices, which we hypothesize may affect disease transmission risk through inter-herd contact. On average in our sample, households cover about 10 kilometers of *Transhumance Distance* seasonally to find suitable grazing areas, and they travel for about an hour daily for grazing and watering purposes (*Grazing Time* and *Watering Time*, respectively). To capture the village-level environment

within which each household resides, we create *Sub-Village Vaccination*, *Sub-Village Disease Deaths* and *Sub-Village Abortion* rates. Table 3.1 provides information on how these sub-village averages for vaccinations, disease deaths and abortions are created. These variables help as exogenous instruments in the identification of our endogenous variables. As noted in Table 3.1, the natural logarithms are of several of the exogenous variables in part because it eases parameter interpretation.

Estimation

To test our hypotheses and estimate the relationships between management and disease outcomes, we estimate (i) the effect of disease prevention (vaccinations) on abortions and disease deaths, (ii) the demand for animal introductions in response to abortions and disease-related deaths in a herd and (iii) the effect of herd accumulation on abortions and disease-related deaths. The theoretical model provides guidance for an estimable system of regressions that accounts for the interdependences among management decisions and outcomes. It suggests a system of equations and a strategy for identifying the drivers of management decisions. Our data distinguish between abortion and death losses, so let $l = (d, a)$, where d is *Disease Deaths* and a is *Abortions*. Introductions in our data are specific to livestock type, so redefine n as the vector \mathbf{n} includes *Cattle Introductions*, *Sheep Introductions*, and *Goat Introductions*. Together, the analytical model and data suggest four sets of equations that provide a basis for testing our hypotheses and estimating relationships (bold variables indicate a vector of variables):

$$v = f_v(\mathbf{n}^*, d^*, \mathbf{Z}_1, Z_2, \mathbf{Z}_3; \varepsilon_v) \quad (4a)$$

$$\mathbf{n} = f_n(d^*, a^*, \mathbf{Z}_1, \mathbf{Z}_4; \varepsilon_n) \quad (4b)$$

$$d = f_d(v^*, \mathbf{n}^*, \mathbf{Z}_1, \mathbf{Z}_3, Z_5; \varepsilon_d) \quad (4c)$$

$$a = f_a(\mathbf{n}^*, \mathbf{Z}_1, \mathbf{Z}_3, Z_6; \varepsilon_a). \quad (4d)$$

Vaccinations (v) and *Cattle, Sheep, and Goat Introductions* (\mathbf{n}) are management decisions, whereas *Disease Deaths* (d) and *Livestock Abortions* (a) are outcomes. As in the analytical model, the asterisks associated with each of them on the right-hand-side of the equations are intended to highlight that these four variables are endogenously determined within the system as a function of several sets of exogenous variables \mathbf{Z}_i , representing factors affecting management choices, where:

- \mathbf{Z}_1 = number of Sheep, Goats & Cattle, respectively
- Z_2 = leave-out Sub-Village Vaccination averages
- \mathbf{Z}_3 = *Grazing Time, Watering Time, and Transhumance Distance*
- \mathbf{Z}_4 = *Cattle, Sheep & Goat Drought Deaths; Land Owned & Household Size*
- Z_5 = *Sub-Village Disease Death*
- Z_6 = *Sub-Village Abortion*

Unobserved, random elements ε_i in Equations 4a-4d are included to recognize random elements of the associated regression estimated below. Figure 3.2 illustrates the relationships embodied in these equations.

Vaccination demand v (Equation 4a) depends on introductions (\mathbf{n}) of sheep, goats and cattle, respectively, *Disease Deaths* (d) and a set of exogenous variables that directly impact incentives to vaccinate, including pre-existing herd size (\mathbf{Z}_1), grazing practices (\mathbf{Z}_3), which we hypothesize to be correlated with disease transmission risk. The leave-out *Sub-Village Vaccination* average (Z_2) is exogenous to the household's vaccination decisions and included in the equation to account for sub-village level exogenous factors affecting local supply of vaccinations and factors affecting general vaccination demand in the sub-village (e.g. general information and acceptance

of vaccinations in the area).¹² Introductions may drive vaccination use if introduced livestock are regularly vaccinated; and introductions may introduce disease in the herd, indirectly increasing demand for vaccination. Because of the cross-sectional nature of our data, we hypothesize that *Disease Deaths* and *Vaccinations* simultaneously affect each other in that deaths provide information feedback on disease risk and therefore affect vaccination demand, and vaccinations may directly affect disease losses through the inoculation effect within the survey recall time frame.

Introductions n (Equation 4b) depend on endogenous variables *Disease Death* (d) and *Livestock Abortions* (a), herd sizes (Z_1), and livestock drought deaths, owned land and the number of household members (Z_4). Livestock losses (d and a) are included as direct determinants of *Introductions* because owners may replace lost animals by acquiring replacements from outside the herd in the event of a livestock death or the abortion, which represents the loss of an expected introduction from within the herd.

Disease Death (d) in Equation 4c depends on *Vaccinations* (v), *Introductions* (n), herd sizes (Z_1), grazing and watering practices (Z_3), and *Sub-Village Disease Death* (Z_5). Lastly, in Equation 4d, *Livestock Abortions* (a) depend on livestock introductions (n), herd sizes (Z_1), grazing and watering distances (Z_3), and the leave-out sub-village abortion average, *Sub-Village Abortion* (Z_6). *Introductions* are included in Equations 4c and 4d because the introduction of livestock from outside the herd may also lead to disease introduction into the herd, and therefore higher disease-related livestock death and abortion rates. Livestock introductions are unique in

¹² In addition to vaccinations, quarantine practices like separating the newly introduced animal from herd to identify disease symptoms or treatment with acaricide or anthelmintics prior to introduction can also be important disease prevention strategies, but our data do not allow us to quantitatively capture the entire gambit of quarantine practices with any accuracy (however qualitative data does support this). Vaccination rates also depend on vaccination supply factors such as ease of access and cost. However, our data are limited in this regard.

our modeling framework because they have a clear bi-directional relationship with disease outcomes: introductions may be a response to loss, and may also increase loss rates.

Endogeneity of regressors may lead to biased and statistically inconsistent parameter estimates, and false inference. For example, while vaccinations are expected to reduce livestock disease losses, they are likely to be used more where the prevalence of the related disease is highest, potentially leading to a positive correlation between vaccination and livestock losses in the data even if vaccinations are largely effective at reducing losses.

A standard two-stage instrumental variable approach is used in order to avoid bias and statistical inconsistency that might result from the inclusion of endogenous regressors. The two-stage process is as follows (Green 2011). In stage 1, “Reduced form” equations for v , \mathbf{n} , d , and a are estimated first based only on exogenous variables in the system, omitting the left-hand-side endogenous variables, and including additional exogenous variables in the system. In stage 2, the predicted values from these first-stage regressions, (basically the empirical counterparts to v^* , \mathbf{n}^* , d^* , and a^* but purged of the regression residuals) are included in the outcome regressions as instruments in place of the original endogenous variables. This process in principle purges correlation between endogenous regressors and the regression disturbance that is the source of bias.

Parameter identification in each second-stage equation is dependent on the availability of excluded exogenous variables in the system available for inclusion in the first stage reduced form regressions. The variables in the vectors \mathbf{Z}_1 through \mathbf{Z}_6 are designed to represent sufficient exclusion restrictions to assure identification. In general for parameter identification in any equation, there must at least one excluded exogenous variable for each included endogenous variable on the right-hand side of a given equation. For example, the *Vaccination* equation v

includes four endogenous variables, \mathbf{n} and d . The variables Z_4 and Z_5 are not included in v but are included in \mathbf{n} and d respectively, and act to identify their associated parameters in the *Vaccination* equation through their effects on the first stage estimates. Similarly, there are by construction in equations 4a-4d enough excluded exogenous variables to account for the included endogenous variables in each regression, thereby satisfying the necessary conditions for parameter identification in each equation.

Finally, the functional form of the regression equations depend in part on the nature of the data as well. The dependent variable in each of the equation is a count variable (as illustrated in Figure 3.1). A Poisson regression is used for the vaccination equation, while zero-inflated Poisson regression is used for introductions, disease death and abortion equations due to high numbers of zero values in the data. Evidence of over-dispersion was found in all regressions except the vaccination equation. Over-dispersion could be due to heterogeneity in household preferences or the nature of the process generating the excess zeros (Mullahey, 1986, Yoder et al. 2014). The Vuong test (Vuong 1989) suggests that the excess zeros may have caused over-dispersion, justifying a zero-inflated Poisson regression in three of the four estimation equations. Stata[®] version 14 was used for regression analysis using the *poisson* and *zip* routines for the Poisson and Zero Inflated Poisson regressions, respectively. Because predicted values from first-stage regressions are included in the second-stage regressions, the covariance matrix for each second-stage equation is adjusted to obtain unbiased standard errors.¹³

¹³ In two-stage instrumental variable estimation, an adjustment must be made to attain consistent covariance estimates (Greene, 2011). The Maximum Likelihood covariance matrix is $\hat{\sigma}^2(\mathbf{Z}'\mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{Z})^{-1}$, where \mathbf{Z} are potentially endogenous variables and \mathbf{X} are exogenous. This estimate is biased because the standard second stage estimated variance $\hat{\sigma}^2 = n^{-1}(\mathbf{y} - \hat{\mathbf{Z}}\boldsymbol{\beta})'(\mathbf{y} - \hat{\mathbf{Z}}\boldsymbol{\beta})$ are calculated using the predicted values from the first stage regressions. A consistent estimate of the σ^2 is calculated as, $\hat{\sigma}_{ub}^2 = n^{-1}(\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})'(\mathbf{y} - \mathbf{Z}\boldsymbol{\beta})$, based on the original values of instrumented variables in \mathbf{Z} , and the unbiased covariance matrix is calculated using $\hat{\sigma}_{ub}^2$, the unbiased estimate of σ^2 .

Results

The results for *Vaccination* equation are provided in Table 3.3. The *Sub-Village Vaccination* averages are positively related to *Vaccination* rates. This may indicate the presence of peer effects, learning, or correlations in vaccination access within villages. Informal qualitative data from interaction with respondents during data collection indicates that some communities in the sample have better access to and relationships with veterinary services and hence vaccination adoption could be community-wide phenomenon.¹⁴ In some cases, livestock vaccination in the study area is centrally coordinated through the Ministry of Agriculture, Livestock and Fisheries, typically with mass vaccination of a large of proportion of animals in the same village or sub-village at the same time.¹⁵ However, some vaccinations like ECF are dependent even more so on household's own initiative and are not actively distributed by government programs.

Table 3.4 provides the results for *Cattle*, *Sheep* and *Goat Introductions* in the household. For each livestock type in Table 3.4, the first column models the probability of no introductions in the herd, while the second column models the probability of increase in the number of livestock introduced, given that households introduced at least one animal. For example, *Goat Drought Death* reduces the likelihood of no sheep introduction as indicated by a negative coefficient of -1.34, although this coefficient is not statistically significant at conventional test sizes. However, *Goat Drought Death* positively and significantly ($p < 0.001$) relates to an increased number of sheep introductions. The overall effect of drought-related goat deaths is positive on sheep introductions.¹⁶

¹⁴ The first-stage reduced form results for the endogenous variables in our system, *Vaccinations*, *Introductions*, *Disease Mortality* and *Livestock Abortions* are shown in the Appendix (Table A2.1-A2.4)

¹⁵ To account for the unobservable village-level effects, a specification with village fixed-effects was also tested for all regressions. Our results are robust to the inclusion of village-level fixed effects.

¹⁶ Marginal effects were calculated using *margins* command in Stata® 14.

Sheep and goat introductions are positively related to drought and disease-related deaths, supporting hypothesis 3 of our theoretical model, while cattle appear to be replaced most often with small stock. It is worth noting that the relationship between death and introduction is not one-to-one. For example, in the *Goat Introduction* regression, about 5 goat deaths lead to introduction of 1 goat. Disease and drought may represent aggregate risk rather than idiosyncratic risk and may stress the farm-households of whole village or sub-village. This can subsequently lower the local supply of livestock, making purchasing or loaning more difficult and costly for households. Since replacement is costly and one death is not replaced by one introduction, transfers into the herd may not compensate for the entire magnitude of negative shocks, suggesting limited effectiveness of restocking as a risk-sharing strategy. Given that the magnitude of introductions and negative asset shocks differ significantly, subsistence farmers with small herd sizes may be at risk of losing all of their herd. In expectation of large mortality losses, some farmers may have larger ex ante herd size so that they can have a reasonable ex post herd size (Lybbert et al. 2004; McPeak 2006). Given that our data is a cross-section, it is difficult to distinguish between restocking done for precautionary saving versus ex post herd rehabilitation.

Results also suggest that goat deaths are replaced at a higher rate than sheep and cattle, and the focus seems to be on buying or introducing small stock in the herd. Since our data is only a snapshot in time, it does not allow us to examine herd composition dynamics. However, herd diversification and a gradual shift in herd composition towards small stock in pastoral and agro-pastoral households of Eastern Africa has been documented (Goldman and Riosmena 2013; McCabe 2003; Bollig 2006). Small stock have been used as a short-run risk coping measure and a means to later build larger cattle herd sizes as they are cheaper per animal, easier to manage

given ecological constraints and have a higher reproduction rate, making them a preferable choice for restocking (Oxby 1994; Toulmin 1994; Ahmed et al., 2002; Kamara, Swallow and Kirk 2004).

Table 3.4 regressions show that *Livestock Abortions* apparently do not induce households to acquire new animals. There could be a few reasons for this. First, perhaps the incidence of reproductive loss in the herd is not large enough to cause significant damage to expected herd growth and hence abortion does not cause a significant loss to the herd. Second, farmers may expect some percentage of reproductive failures every reproduction cycle and hence do not react to such events. And finally, milk may be a primary benefit and household motivation for pregnancies, and purchasing a replacement for the lost animal would not compensate for that, whether or not the milk production were negatively affected along with the cause of the abortion event.

Table 3.5 provides the results of *Disease Death* equation. As discussed in the methods section, livestock *Introductions* and *Vaccinations* are replaced with instruments produced as predictions from the equations presented in Tables A3.1 and A3.2.

Vaccinations are shown to increase the likelihood of no disease-related death, and decrease the number of disease-related deaths conditional on death occurring, corroborating hypothesis 1. *Vaccinations* use increases the likelihood of no reported deaths (as indicated by the positive coefficient of 0.119 although this coefficient is not statistically significant at conventional test sizes, and *Vaccinations* tends to reduce the number of deaths, as indicated by the negative coefficient of -1.84 (p-value < 0.01). The estimated marginal effect is -17.18, so vaccinating against one additional type of disease is related to a decrease of about 17 disease-related deaths

per year (-15.3 at sample medians) within a household.¹⁷ To put this in context, only 18.5 percent of households have used any type of vaccine in the last 12 months, and the average herd size (including goats, sheep and cattle) in our sample is about 177, so the addition of one vaccine type at sample means can save about 10% of the herd from disease-related deaths in representative household in the sample. Table A3.4 reports the species-specific regressions and shows that the marginal effect of *Vaccinations* on *Cattle*, *Sheep* and *Goat Disease Death* is -9.29, -5.5 and -8.5, respectively. The most frequently used vaccines are for contagious bovine pleuro-pneumonia and anthrax followed by vaccines for lumpy skin disease and foot-and-mouth disease, respectively.¹⁸ Contagious bovine pleuro-pneumonia is an important cause of mortality in cattle, and anthrax can be an important cause for mortality in all ruminants (Lembo et.al 2011; Onono, Wieland and Rushton 2014). The not surprising coincidence of active vaccination of these two sources of disease deaths seems likely to be the basis of the relatively large marginal effect of vaccination on disease death described above. Other studies corroborate these results as well, having shown human capital and productivity benefits of livestock vaccinations and antimicrobials in terms of higher nutritional intake, control of zoonotic diseases and food-borne illnesses, and higher rates of schooling (Marsh et. al 2016; Mosites et al. 2016).

Cattle, *Sheep* and *Goat Introductions* are positively related to *Disease Death*, which is consistent with our hypothesis 2 of the theoretical model. The marginal effects show that introduction of one head of cattle is related with a loss of 0.23 heads at sample means, and 0.33 and 0.38 for sheep and goats respectively. Again, the average herd size is 177 and herds range

¹⁷ This large marginal effect is robust to model specification, ranging from -11.13 based on OLS to -20.45 with a standard Poisson, The marginal impact on *Disease Death* of a one unit increase in *Vaccinations* is calculated to be -20.45 with a Poisson regression specification and -11.13 with an OLS regression specification.

¹⁸ Some of the vaccinations used in the sample are species-specific - e.g., East Coast fever vaccine may only directly affect cattle and may have no direct effect on sheep and goats.

into the thousands, so one infected introduced animal may have wide-ranging consequences. In percentage terms, a 10% increase in *Cattle, Sheep and Goat Introductions* is associated with a 2.4%, 0.7% and 0.6% increase in *Disease Death*, respectively. The role of livestock introductions and inter-herd transfers through various pathways for herd maintenance, precautionary saving and ex post risk-sharing has been widely recognized in the literature (McPeak 2006; Lybbert et al. 2004; Carter and Barrett 2006). However, our results suggest that disease exposure risk associated with livestock restocking may be among the costs of doing so. If animal introductions are correlated with disease spread and disease losses, then these restocking strategies are costly beyond the purchase cost of animals, and suggests an important risk associated with inter-household trading, lending, and gifting of animals.

Bidirectional causality between *Disease Death* and *Introductions* is particularly difficult to statistically differentiate given our data limitations. Herd owners may replace livestock to replenish their herd after a death, but livestock *Introductions* may also introduce disease into the herd and affect the incidence of disease-related death and abortions. The identification strategy and the strength of the instruments used in our analysis become critical. Recall that the predicted values of *Introductions* from first-stage regressions are used as instruments in the second stage *Death* and *Abortions* regressions (Table A3.1). F-statistics in the first stage regressions can be used to assess instrument strength (Staiger and Stock 1997, Greene 2011). The first-stage F-statistics of the joint test of instruments (*Cattle, Sheep, and Goat Drought Death, Land Owned and Household Size*) are 18.4, 140.88 and 43.25 for *Goat, Sheep and Cattle Introduction* equations, respectively. All F-statistics are greater than 10, which suggests that our instruments are relatively strong, instrumental variable bias is less than 10%, and consequently the positive and significant coefficients on *Introductions* are likely not overly influenced by replacement

behavior. Nonetheless, given the nature of our cross-sectional recall data, if our results are biased due to partial conflation of replacement and disease introduction effects, our estimates are likely biased upward, in the sense that the true impact of livestock introductions on livestock mortality through disease introduction would be lower than our estimated effects.

Sheep, *Goat* and *Cattle* herd sizes are positively related to *Disease Death* (significantly so at conventional levels, with p-value < 0.001). This could follow simply from the fact that there are more animals available to become ill; but it could also be driven in part by a lower labor per animal ratio and less care per animal, by differences in management that influence pathogen transmission, or because disease control may be costly for larger herds. Herd size has been identified as a risk factor for infection prevalence for several diseases (Makita et al., 2011; Rizzo et al., 2016). Transhumance and daily grazing activities are not statistically significant at conventional levels in this regression; however, other studies have shown that these activities lead to higher disease transmission (Ahmed et al. 2017; Bronsvort et al., 2004; Rufael et al., 2008; Schoonman and Swai., 2010). *Sub-Village Disease Death* is positively and significantly related to household-level disease-related deaths and controls for the spatial and aggregate level of disease mortality risk faced by other households in the area, which is intended here to represent a baseline risk.

Table 3.6 provides the results of the *Livestock Abortions* equation. First, notice that *Vaccinations* is not included as a regressor in this model. Since, the pathogens against which animals are vaccinated against in the sample are not major causes of abortion, we do not make abortion a function of vaccinations: vaccinations play a limited role in preventing abortive diseases in our sample. Nonetheless, a regression with predicted values of vaccinations was also performed, and the results with and without *Vaccinations* do not differ significantly. Vaccination

use was related to an increase of about 3 abortions in the sample, and the coefficient was positive and statistically significant (p-value < 0.001). This may be an indication of unaccounted-for reverse causality between *Livestock Abortions* and *Vaccinations* in the regression.

Introductions show a complex relationship to abortions in our regression results. *Cattle Introductions* are associated with a decreased likelihood of at least one abortion (p-value < 0.05), but an increase in the number of abortions given at least one. In contrast, *Goat Introductions* are associated with an increase in the likelihood of at least one abortion, and also higher abortions given at least one, but again. The net (marginal) effect of introductions is negative for sheep, while goats and cattle appear to be positively associated with abortion. Similar regressions for each species is reported in Appendix Table A3.5, which suggest that goat introductions are potentially the most important risk factor for abortion incidence as compared with other types of introductions. These results might suggest that goats maybe important reservoirs of abortigenic pathogens for other species. For example, goats and sheep are known to be important reservoirs of of *Brucella* infection in northern Tanzania (Viana et al. 2016), with these pathogens causing abortions in all ruminant species.

Watering and *Grazing Time* is positively related to *Livestock Abortions* incidence suggesting that animals may be becoming infected with pathogens that cause reproductive losses at or during travel to communal water points. It could also be that animals walking further to grazing/water are more energetically compromised or in poorer condition – resulting in more abortions due to metabolic causes (i.e. not directly infectious disease-related). Table 3.6 shows evidence only of a statistically significant positive effect of *Grazing Time* on abortion count. The net effect of *Sub-Village Abortion* rates on household abortion incidence is positive (though the coefficients are insignificant at conventional levels of hypothesis testing), suggesting that

proximity to other local herds with these pathogens may be contributing to disease transmission and abortion outcomes.

Conclusion

Livestock husbandry generally includes a broad array of activities, including herd maintenance, feeding and watering practices, and disease avoidance and treatment. Based on data from northern Tanzania, we examine the relationships between animal introductions, disease-related deaths and livestock abortions and the effect of disease prevention strategies on livestock deaths. We develop a theoretical model of livestock management decisions in the context of herd disease challenge, and use this model to derive a set of hypotheses. Livestock management decisions and outcomes may be jointly (endogenously) determined, therefore, a system of econometric regression equations, with careful treatment of endogeneity, is developed to test hypotheses about livestock introduction, vaccination, and their impact on abortions and disease-related death.

Our results suggest that livestock mortality is an important driver of animal introductions into household herds, while abortions do not statistically affect introduction rates. The relationship between mortality and introduction may not be one-to-one, suggesting that households take time to rebuild herds after animal losses. The slow rate of herd restocking may be a matter of consumption smoothing over time. But it may also be a consequence of limited saving, credit, and insurance opportunities in low-income rural communities. While a great diversity of informal mechanisms for credit and insurance exist among pastoralists and agro-pastoralists (Besley 1995; Dercon 2005), liquidity and credit constraints may still persist and may hamper

the ability of the household to restock their herds as they would like, potentially leading to lower herd sizes and poverty traps.

We also find that cattle, sheep, and goat introductions are important drivers of disease-related deaths, while only goat introductions seem to affect herd-level abortion rates. New animals may bring pathogens with them that may lead to more illness, lower productivity and higher mortality within the herd, thus reducing the welfare and limiting the income and consumption smoothing associated with restocking. Our finding that goat introductions may lead to higher abortion rates in combination with trend toward a larger focus on small stock (McCabe 2003; Bollig 2006; Goldman and Riosmena 2013) suggests that this health effect from introduction could have important livestock health implications. Further, many of the important abortigenic pathogens are zoonotic, which has potentially important human health implications, because they may lead to disease incidence in humans as well (Cash-Goldwasser et al. 2017).

Furthermore, vaccinations appear to result in greatly reduced disease-related deaths, suggesting that vaccination adoption can improve herd and household welfare in a meaningful way. However, households in our sample only vaccinate against a limited number of the large number of potential pathogens in this setting. There is likely to be due to access and supply chain issues related to vaccination availability for rural communities, hampering their ability to effectively use vaccinations against livestock diseases.

Animal health outcomes and livestock management strategies are interdependent. Animal health outcomes like death and abortion can impact on the livestock management strategies because they provide useful information on risk and management effectiveness, while management decisions like vaccinations, grazing practices and herd restocking can impact animal health outcomes and the wellbeing of livestock-dependent households. Disease control

technologies like vaccinations can reduce disease-related livestock deaths and can result in improved herd health, which in turn can increase livestock productivity, food security, and household income, wealth, and indirectly even human health and education. Similarly, herd restocking is widely used as a means of maintaining herd sizes in the face of drought and disease losses, but can be a risk factor in terms of disease introduction and spread in the herd.

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Figures

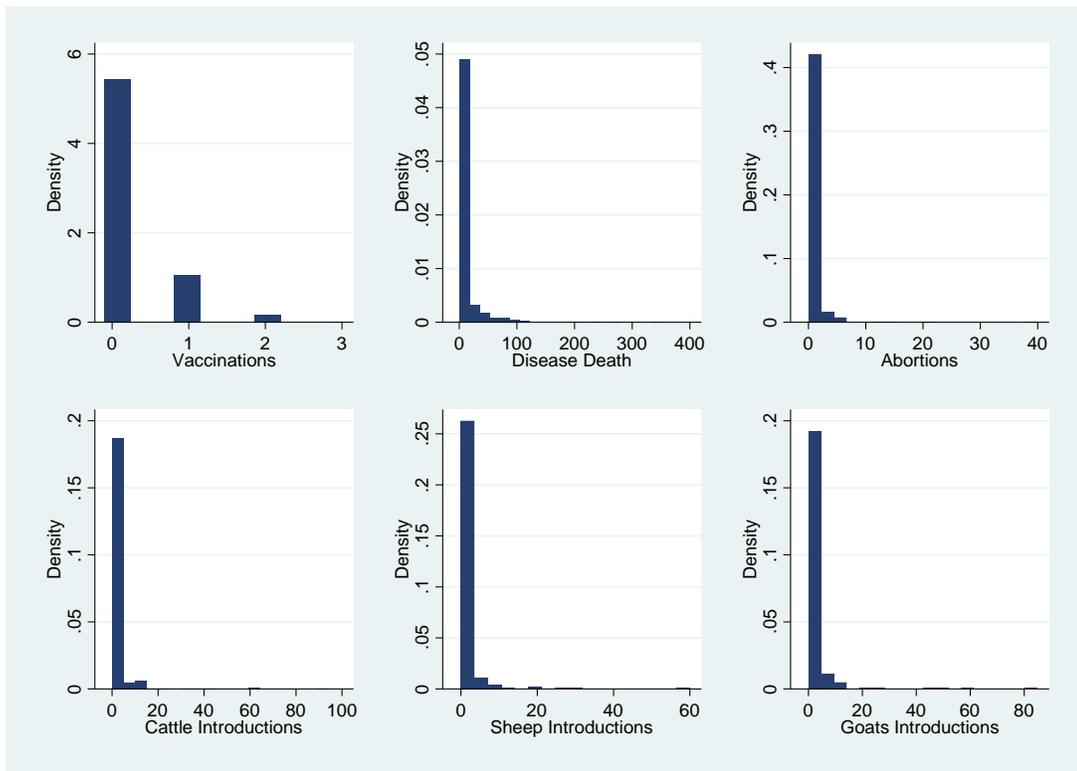


Figure 3.1: Histograms of *Vaccinations, Disease Death, Livestock Abortions, Cattle, Sheep and Goat Introductions*

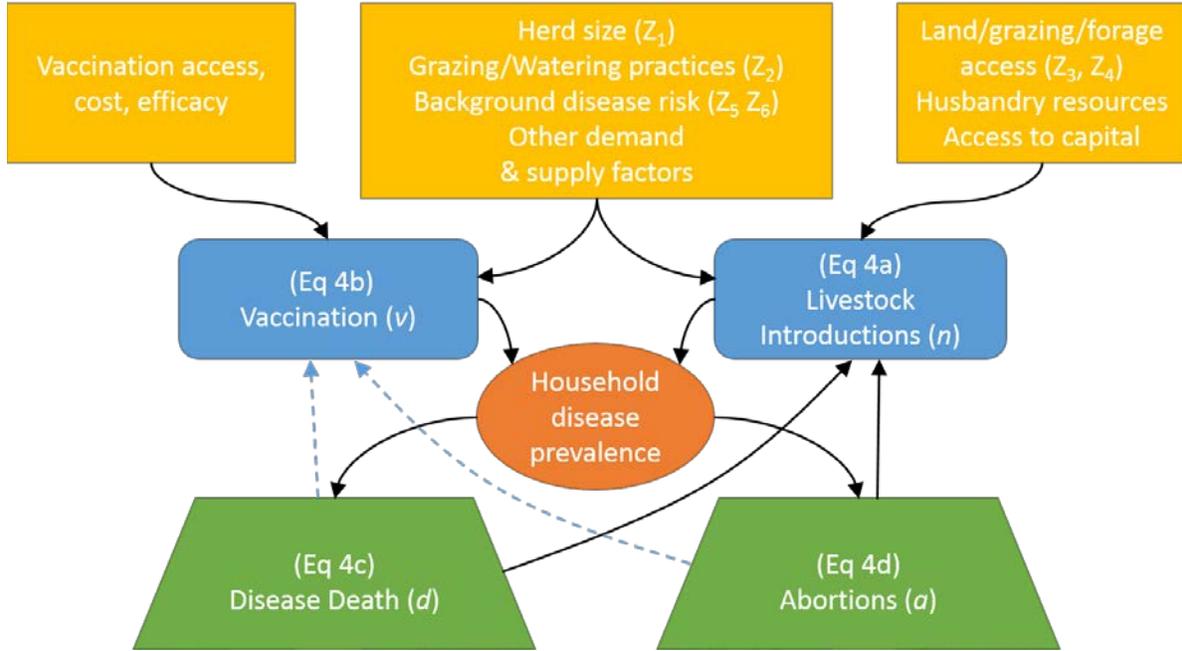


Figure 3.2: Feedback Mechanisms between Vaccinations, Disease Losses and Introductions

Tables

Table 3.1: Data Description

Variable	Definition
<i>Vaccinations</i>	Count of different types of vaccinations applied to the household herd in the past 12 months.
<i>Disease Deaths</i>	The number of cattle, sheep or goats reported dead due to disease in a household in the past 12 months.
<i>Livestock Abortions</i>	The number of cattle, sheep or goats that reported abortions in a household the past 12 months.
<i>Cattle Introductions</i>	Number of cattle introduced into a household through market or non-market transactions in the past 12 months
<i>Sheep Introductions</i>	Number of sheep introduced into a household through market or non-market transactions in the past 12 months.
<i>Goat Introductions</i>	Number of goats introduced into a household through market or non-market transactions in the past 12 months.
<i>Cattle</i>	Log of the total number of cattle present in the household net of introductions.
<i>Sheep</i>	Log of the total number of sheep present in the household net of introductions.
<i>Goats</i>	Log of the total number of goats present in the household net of introductions.
<i>Land Owned</i>	Number of acres owned by the household.
<i>Transhumance Distance</i>	Log of the Euclidean distance between household's home and seasonal grazing camp. Measured in Kilometers.
<i>Grazing Time</i>	Log of the time taken by livestock keepers and animals to walk to grazing points, measured in minutes.
<i>Watering Time</i>	Log of the time taken by livestock keepers and animals to walk to water points, measured in minutes.
<i>Sub-Village Vaccinations</i>	Sub-village level leave-out mean of vaccinations, calculated as $\bar{v}_i = \frac{\sum_{j \neq i} v_j}{N-1}$, where v_i is vaccination number of each household and N is the number of households in the sub-village.
<i>Sub-Village Disease Death</i>	This is the sub-village level leave-out mean of total livestock disease mortality calculated as $\bar{m}_i = \frac{\sum_{j \neq i} m_j}{N-1}$, where m_i is mortality number of household i and N is the number of households in the subvillage.
<i>Sub-Village Abortions</i>	This is the sub-village level leave-out mean of livestock abortions calculated as $\bar{q}_i = \frac{\sum_{j \neq i} q_j}{N-1}$, where q_i is livestock abortion number of household i and N is the number of households in the sub-village.
<i>Goat Drought Death</i>	Log of the number of goats died within a household during the last drought.
<i>Sheep Drought Death</i>	Log of the number of sheep died within a household during the last drought.
<i>Cattle Drought Death</i>	Log of the number of cattle died within a household during the last drought.
<i>Household Size</i>	Number of household members including children.

Table 3.2: Summary Statistics (N = 386)

	Mean	Standard Deviation	Min	Max
<i>Vaccinations</i>	0.218	0.483	0	3
<i>Disease Death</i>	11.15	31.73	0	350
<i>Livestock Abortions</i>	0.69	2.70	0	40
<i>Cattle Introductions</i>	1.61	7.25	0	94
<i>Sheep Introductions</i>	0.78	4.059	0	60
<i>Goats Introductions</i>	1.50	6.70	0	85
<i>Cattle</i>	53.57	122.7	0	1,200
<i>Goats</i>	61.19	120.11	1	1,000
<i>Sheep</i>	63.85	174.7	1	1,800
<i>Land Owned</i>	9.40	20.38	0	320
<i>Transhumance Distance</i>	10.34	25.36	0	281.58
<i>Watering Time</i>	3.36	1.19	0	6.39
<i>Grazing Time</i>	69.7	123.22	0	1,440
<i>Sub-Village Vaccinations</i>	0.215	0.254	0	1.33
<i>Sub-Village Abortions</i>	0.80	2.18	0	20
<i>Sub-Village Disease Death</i>	1.59	2.89	0	17.85
<i>Goat Drought Death</i>	2.61	14.15	0	200
<i>Sheep Drought Death</i>	2.38	16.21	0	260
<i>Cattle Drought Death</i>	2.78	15.2	0	200
<i>Household Size</i>	7.02	5.03	1	37

Table 3.3: Vaccination Equation Results - Poisson Regression

Dependent Variable	Coefficient	Standard Errors
Vaccinations		
<i>Sub-Village Vaccination</i>	1.14**	0.495
<i>Transhumance Distance</i>	0.121	0.095
<i>Cattle</i>	0.122	0.171
<i>Goats</i>	0.132	0.128
<i>Sheep</i>	0.222*	0.128
<i>Sheep Introductions</i> ^a	-0.0001	0.0002
<i>Cattle Introductions</i> ^a	0.122*	0.073
<i>Goats Introductions</i> ^a	0.0006*	0.0003
<i>Watering Time</i>	-0.196	0.133
<i>Grazing Time</i>	-0.055	0.161
<i>Disease Death</i> ^a	-0.026	0.016
	Vuong Test Statistic:	0.0023
	LR Test: NB vs Poisson (P-Value):	0.5

***, **, * indicate significance at 1, 5 and 10% levels respectively.

^a Predicted values from a first stage regression.

Table 3.4: Cattle, Sheep and Goats Introduction Regressions (Zero-Inflated Poisson)

	Zero Cattle Introduced^a	# Cattle introduced	Marginal Effects	Zero Sheep Introduced	# Sheep introduced	Marginal Effects	Zero Goats Introduced	# Goats introduced	Marginal Effects
<i>Disease Death^b</i>	-0.012 (0.016)	-0.02*** (0.007)	-0.02	0.043 (0.034)	0.151*** (0.032)	0.16**	-0.023 (0.056)	0.101 (0.24)	0.09
<i>Livestock Abortions^b</i>	-0.148 (0.097)	0.008 (0.023)	0.015	0.239 (0.578)	0.08 (0.36)	-0.036	-0.324 (0.645)	0.375 (0.266)	0.21
<i>Cattle</i>	-0.096 (0.293)	0.846*** (0.149)	2.84***	-0.66*** (0.30)	0.097 (0.139)	1.23**	0.348 (0.272)	-0.745*** (0.096)	-1.61***
<i>Sheep</i>	-0.483** (0.23)	-0.195** (0.095)	0.273**	-0.64** (0.27)	0.594*** (0.204)	3.83***	-0.255 (0.233)	-0.121*** (0.07)	0.72**
<i>Goats</i>	0.516* (0.306)	0.539*** (0.124)	0.309**	-0.15 (0.337)	-0.116 (0.144)	-0.06	-0.247 (0.24)	0.401*** (0.078)	4.73***
<i>Goat Drought Death</i>	-0.154 (0.419)	-0.119 (0.095)	-0.015	-1.34 (0.92)	0.24*** (0.061)	0.23**	0.043 (0.38)	0.419*** (0.122)	0.22**
<i>Cattle Drought Death</i>	-0.01 (0.293)	-0.189** (0.084)	-0.047	0.092 (0.411)	-0.112 (0.31)	-0.052	0.143 (0.306)	0.202* (0.105)	0.013
<i>Sheep Drought Death</i>	0.216 (0.521)	-0.439** (0.20)	-0.133**	1.55 (1.03)	0.46 (0.47)	-0.061	0.034 (0.38)	-0.554*** (0.147)	-0.16**
<i>Household Size</i>	0.176 (0.18)	-0.051 (0.057)	-0.18	-0.04 (0.165)	-0.079 (0.167)	-0.09	0.491* (0.27)	0.371*** (0.077)	0.14**
<i>Land Owned</i>	0.041* (0.02)	0.011 (0.012)	0.033	-0.009 (0.008)	0.003 (0.002)	0.007	0.028 (0.023)	0.012 (0.008)	-0.14
<i>Vuong Test (p-value)</i>	3.92 (0.000)			3.96 (0.000)			4.29 (0.000)		

^aThe model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no introduction in the herd.

^bPredicted values from first stage regressions.

***, **, * indicate significance at 1, 5 and 10% levels respectively.

Table 3.5: The Effect of Vaccinations and Introductions on Livestock Disease Death - Zero-Inflated Poisson Regression

	Zero Disease Mortality ^a	Disease Mortality #	Marginal Effects
<i>Vaccinations</i> ^b	0.119 (1.37)	-1.84*** (0.186)	-17.18***
<i>Cattle Introductions</i> ^c	-0.15 (0.239)	0.021*** (0.007)	0.23**
<i>Sheep Introductions</i> ^c	-0.43 (0.29)	0.043*** (0.011)	0.33**
<i>Goats Introductions</i> ^c	-0.235 (0.19)	0.071*** (0.011)	0.38**
<i>Cattle</i>	0.09 (0.26)	0.288*** (0.028)	1.08**
<i>Sheep</i>	-0.386*** (0.144)	0.231*** (0.026)	2.18***
<i>Goats</i>	-0.215 (0.145)	0.277*** (0.026)	0.289**
<i>Transhumance Distance</i>	0.130 (0.113)	-0.022 (0.013)	-0.008
<i>Grazing Time</i>	0.043 (0.147)	0.025 (0.026)	0.009
<i>Watering Time</i>	-0.246 (0.19)	-0.196*** (0.016)	-0.09*
<i>Sub-Village Disease Death</i>	-0.212** (0.104)	0.033*** (0.005)	0.54***
Vuong Test (P-Value)	4.54 (0.000)		

^aThe model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no mortality in the herd.

^bPredicted values from a first-stage regression of *Vaccinations* on all exogenous variables in the system.

^cThe predicted values from the first-stage regressions of *Cattle*, *Sheep* and *Goat Introductions* on all exogenous variables in the system.

*, **, *** indicate statistical significance at 10, 5 and 1% respectively.

Table 3.6: The Effect of Introductions on Livestock Abortions - Zero-Inflated Poisson Regression

Dependent Variable: <i>Livestock Abortions</i>	Zero Livestock Abortions^a	# Livestock Abortions	Marginal Effects
<i>Cattle Introductions</i> ^b	0.306** (0.138)	0.092*** (0.025)	0.084
<i>Sheep Introductions</i> ^b	-0.073 (0.148)	-0.034*** (0.007)	-0.055
<i>Goats Introductions</i> ^b	-0.433 (0.307)	0.109*** (0.013)	0.29***
<i>Cattle</i>	-0.343 (0.266)	0.058 (0.0712)	0.102
<i>Sheep</i>	0.024 (0.180)	0.212*** (0.053)	0.143**
<i>Goats</i>	-0.174 (0.233)	0.0017 (0.052)	0.084
<i>Transhumance Distance</i>	-0.035 (0.128)	0.010 (0.035)	0.012
<i>Grazing Time</i>	-0.204 (0.184)	0.128** (0.048)	0.35
<i>Watering Time</i>	-0.442** (0.189)	0.066 (0.053)	0.147**
<i>Sub-Village Abortions</i>	-0.587 (0.364)	-0.008 (0.02)	0.242
Vuong Test (P-Value)	2.94 (0.0017)		

^a The model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no abortions in the herd.

^b The predicted values from the first-stage regressions of *Cattle*, *Sheep* and *Goat Introductions* on excluded and included exogenous variables.

*, **, *** indicate statistical significance at 10, 5 and 1% respectively.

Appendix

Table A3.1: Cattle, Sheep and Goats Introduction First-Stage Reduced Form Regressions (Zero-Inflated Poisson)

	Zero Cattle Introduced^a	# Cattle introduced	Zero Sheep Introduced	# Sheep introduced	Zero Goats Introduced	# Goats introduced
<i>Cattle</i>	-0.269 (0.168)	0.706*** (0.074)	-0.387* (0.212)	-0.006 (0.106)	0.117 (0.165)	-0.29*** (0.053)
<i>Sheep</i>	-0.219 (0.145)	-0.205** (0.081)	-0.263 (0.218)	0.90** (0.144)	-0.17 (0.14)	0.014 (0.059)
<i>Goats</i>	0.115 (0.161)	0.13 (0.088)	0.294 (0.186)	-0.10 (0.08)	-0.47** (0.18)	0.14*** (0.01)
<i>Cattle Drought Death</i>	0.198 (0.225)	-0.107 (0.068)	0.45 (0.388)	-0.033 (0.159)	0.28 (0.24)	0.213*** (0.071)
<i>Sheep Drought Death</i>	0.128 (0.208)	-0.071 (0.075)	0.134 (0.267)	0.178** (0.091)	0.134 (0.203)	-0.095 (0.066)
<i>Goat Drought Death</i>	0.001 (0.232)	-0.046 (0.07)	-0.216 (0.288)	0.029* (0.010)	-0.23 (0.21)	0.087 (0.057)
<i>Household Size</i>	0.033 (0.083)	0.065*** (0.015)	0.11 (0.093)	0.072*** (0.02)	0.062 (0.087)	0.153*** (0.158)
<i>Land Owned</i>	0.024* (0.014)	0.011** (0.005)	-0.006 (0.006)	0.005*** (0.002)	0.014 (0.012)	0.01** (0.004)
<i>F-Statistics (regression)</i>	43.25 (0.000)		140.88 (0.000)		18.4 (0.000)	

^aThe model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no introduction in the herd.

***, **, * indicate significance at 1, 5 and 10% levels respectively.

Table A3.2: First-Stage Reduced Form Vaccination Regression - Poisson Regression

Dependent Variable: <i>Vaccinations</i>	Coefficient	Standard Errors
<i>Sub-Village Vaccination</i>	1.39***	0.363
<i>Transhumance Distance</i>	0.106	0.091
<i>Cattle</i>	0.208*	0.123
<i>Goats</i>	0.091	0.087
<i>Sheep</i>	0.105*	0.071
<i>Watering Time</i>	-0.157*	0.089
<i>Grazing Time</i>	0.113	0.116
F-Statistic	25.06	

***, **, * indicate significance at 1, 5 and 10% levels respectively.

Table A3.3: First-Stage Reduced Form Livestock Disease Death and Livestock Abortions Regressions - Zero-Inflated Poisson

	Zero Disease Mortality^a	Disease Mortality #	Zero Livestock Abortions	# Livestock Abortions
<i>Cattle</i>	-0.13 (0.147)	0.288*** (0.028)	-0.008 (0.184)	0.076 (0.05)
<i>Sheep</i>	-0.39*** (0.108)	0.231*** (0.026)	0.058 (0.115)	0.38*** (0.037)
<i>Goats</i>	-0.05 (0.116)	0.277*** (0.026)	-0.38** (0.161)	0.23*** (0.047)
<i>Transhumance Distance</i>	0.087 (0.096)	-0.022 (0.013)	-0.092 (0.118)	-0.07*** (0.025)
<i>Grazing Time</i>	0.021 (0.12)	0.025 (0.026)	-0.156 (0.165)	-0.045 (0.037)
<i>Watering Time</i>	-0.17 (0.125)	-0.196*** (0.016)	-0.29* (0.17)	0.094** (0.038)
<i>Sub-Village Disease Death</i>	-0.141** (0.07)	0.033*** (0.005)	-	-
<i>Sub-Village Abortions</i>	-	-	-0.47 (0.30)	-0.023* (0.012)
<i>F-Statistic for excluded instruments</i>	338.75 (0.000)		17.50 (0.002)	

^aThe model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no mortality in the herd.

*, **, *** indicate statistical significance at 10, 5 and 1% respectively.

Table A3.4: Effect of Livestock Introductions on Disease Death; Species-Specific Regressions

	Zero Cattle Mortality^a	Cattle Mortality Count	Marginal Effects	Zero Goat Mortality	Goat Mortality Count	Marginal Effects	Zero Sheep Mortality	Sheep Mortality Count	Marginal Effects
<i>Vaccinations^b</i>	-1.609 (3.85)	-6.08*** (0.82)	-9.29***	1.35 (1.37)	-1.24*** (0.299)	-8.52***	-0.29 (1.52)	-1.53*** (0.266)	-5.51***
<i>Cattle Introductions^b</i>	-0.624* (0.341)	-0.125*** (0.028)	0.161***	0.028 (0.14)	0.005 (0.012)	-0.034	-0.246 (0.174)	-0.10*** (0.015)	-0.065*
<i>Sheep Introductions^b</i>	0.300 (0.34)	0.40*** (0.054)	0.21**	-0.035 (0.178)	0.19*** (0.025)	0.44**	0.38* (0.20)	0.19*** (0.025)	0.22*
<i>Goat Introductions^b</i>	-0.159 (0.162)	-0.031 (0.043)	0.045	0.019 (0.132)	-0.008 (0.02)	-0.069	0.19 (0.126)	0.049** (0.02)	0.165
<i>Cattle</i>	-0.194 (0.32)	0.64*** (0.079)	0.151***	0.180 (0.253)	-0.073 (0.045)	-0.036	0.115 (0.267)	0.56*** (0.068)	0.13*
<i>Sheep</i>	-0.582** (0.236)	-0.45*** (0.075)	-0.002	-0.21 (0.15)	0.08* (0.045)	0.17*	-1.23*** (0.22)	0.071 (0.59)	0.27**
<i>Goats</i>	0.70*** (0.229)	0.385*** (0.076)	0.022	-0.64*** (0.220)	0.50*** (0.072)	0.35***	0.361* (0.218)	0.22*** (0.065)	0.013
<i>Transhumance Distance</i>	0.282* (0.144)	0.29*** (0.049)	0.031	0.074 (0.115)	-0.07*** (0.025)	-0.014**	0.10 (0.125)	-0.21*** (0.028)	-0.094*
<i>Grazing Time</i>	-0.157 (0.178)	0.031 (0.07)	0.014	0.071 (0.15)	-0.006 (0.038)	-0.011	-0.127 (0.175)	0.112** (0.044)	0.064**
<i>Watering Time</i>	-0.156 (0.216)	-0.25*** (0.086)	-0.033*	-0.155 (0.16)	-0.008 (0.04)	0.013	0.036 (0.178)	-0.132** (0.088)	-0.051
<i>Sub-Village Disease Death</i>	-0.195* (0.104)	0.019 (0.016)	0.151*	-0.206** (0.094)	0.072*** (0.011)	0.65***	-0.125 (0.089)	-0.02 (0.013)	0.086
Vuong Test (P-Value)	3.19 (0.000)			4.03 (0.000)			3.93 (0.000)		

^aThe model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no mortality in the herd. ^bThe predicted values from the first-stage regressions of *Cattle*, *Sheep* and *Goat Introductions* and *Vaccinations* on excluded and included exogenous variables. *, **, *** indicate statistical significance at 10, 5 and 1% respectively.

Table A3.5: Effect of Livestock Introductions on Abortions; Species-Specific Regressions

	Zero Cattle Abortions^a	Cattle Abortions Count	Marginal Effects	Zero Goat Abortions	Goat Abortions Count	Marginal Effects	Zero Sheep Abortions	Sheep Abortion Count	Marginal Effects
<i>Cattle</i>	-0.481*	-0.28***	-0.045	0.253**	0.142***	0.095	-0.221	-0.048	0.073
<i>Introductions^b</i>	(0.275)	(0.056)		(0.12)	(0.032)		(0.178)	(0.073)	
<i>Goat</i>	-0.32	0.041*	0.031	-0.115	0.099***	0.24***	-0.318	0.101***	0.31***
<i>Introductions^b</i>	(0.202)	(0.088)		(0.184)	(0.017)		(0.25)	(0.035)	
<i>Sheep</i>	0.089	0.078	0.022	-0.149	-0.095***	-0.075	0.649**	0.278***	-0.047
<i>Introductions^b</i>	(0.074)	(0.142)		(0.128)	(0.024)		(0.266)	(0.095)	
<i>Cattle</i>	0.510	0.674***	0.249*	-0.105	-0.001	0.062	-0.443	-0.26	-0.048
	(0.439)	(0.20)		(0.241)	(0.083)		(0.386)	(0.203)	
<i>Sheep</i>	-0.287	-0.398**	-0.153	0.364*	0.139*	0.022	-0.796**	0.442*	0.82**
	(0.273)	(0.165)		(0.21)	(0.075)		(0.374)	(0.25)	
<i>Goats</i>	0.572	0.719***	0.259	-0.75***	0.114	0.165**	0.759*	0.066	-0.37
	(0.368)	(0.181)		(0.255)	(0.085)		(0.384)	(0.144)	
<i>Transhumance</i>	-0.278	-0.119	-0.004	-0.142	0.052	0.176	0.336*	-0.007	-0.21
<i>Distance</i>	(0.176)	(0.088)		(0.128)	(0.046)		(0.196)	(0.096)	
<i>Grazing Time</i>	-0.102	0.067	0.057	-0.290	0.05	0.263	-0.1304	0.062	0.055
	(0.279)	(0.169)		(0.182)	(0.063)		(0.26)	(0.144)	
<i>Watering Time</i>	-0.188	0.130	0.109	-0.234	0.038	0.209	-0.417	0.124	0.140
	(0.265)	(0.163)		(0.185)	(0.067)		(0.255)	(0.121)	
<i>Sub-Village</i>	-1.006***	0.044	0.236**	-0.016	0.034	0.05	0.108	0.327	0.338
<i>Abortions</i>	(0.316)	(0.036)		(0.16)	(0.032)		(0.193)	(0.177)	
<i>Vuong Test (P- Value)</i>	2.60			2.93			4.38		
	(0.004)			(0.002)			(0.000)		

^aThe model predicts the outcomes of zero observations and therefore reported signs for the estimates here are for the probability of no abortions in the herd.

^bThe predicted values from the first-stage regressions of *Cattle*, *Sheep* and *Goat Introductions* on excluded and included exogenous variables.

*, **, *** indicate statistical significance at 10, 5 and 1% respectively.

CHAPTER FOUR: MOBILE MONEY AND HEALTHCARE USAGE: EVIDENCE FROM EAST AFRICA

Abstract

This paper uses a difference-in-difference framework to estimate and explore the effects of mobile money transfer technology (MMT) on healthcare usage in the face of negative health shocks. We use survey data from 2013-16 with quarterly observations on about 1,600 households of 10 villages in the Kisumu region of Western Kenya. We find evidence that MMT, through informal borrowing and lending mechanism, helps households increase utilization of formal healthcare services in terms of visits to a clinic, and consultation and medication expenditures, in comparison with the non-users of this technology. This better utilization of formal healthcare services may result in better health and poverty reduction. We infer that effects follow from lower transaction costs of borrowing and lending and easier risk sharing due to the use of MMT.

Introduction

Lack of access to financial services restricts the ability of poor households to save and invest and engage in formal insurance mechanisms (Johnson and Nino-Zarazua 2011; Dupas and Robinson 2009). Therefore, poor households often rely on informal risk sharing mechanisms during periods of distress. This informal risk sharing and insurance is generally incomplete due to information asymmetries and transaction costs (Gertler and Gruber 2002; Townsend 1995; Kochar 1995; Gertler, Levine and Moretti 2006, 2009). Mobile money transfer technology (MMT) has the potential of increasing this risk sharing in presence of income shocks as it allows its owners to store monetary value on a mobile phone and this value can be sent or received simply by text messages, thus reducing the transaction costs associated with borrowing and lending (Jack and Suri 2014; Suri and Jack 2016; Munyegera and Matsumoto 2016; Blumenstock, Eagle and Fafchamps 2011).¹⁹

The objective of this paper is to test the impact of MMT on risk-sharing in the face of negative health shocks. Jack and Suri (2014) use a difference-in-difference specification to examine the changes in the response of consumption to negative unexpected income and health shocks across MMT users and non-users. Our paper builds on this work by using the Socio-Economic Survey (SES) conducted by Kenya Medical Research Institute (KEMRI) and Centers for Disease Control (CDC) and by focusing on the impact of MMT adoption on health expenditures and healthcare use under negative health shocks. Additionally, our focus is on rural households, whereas Jack and Suri (2014) lump urban and rural households together and use rural-urban fixed effects to control for unobserved differences between rural and urban areas.

¹⁹ To illustrate the reduction in transaction costs, Jack and Suri (2014) document that the average distance of person-to-person remittance in Kenya is 200 km, which costs about \$5 to travel. With the help of MMT, funds can be transferred by a simple SMS, saving time and money.

MMT adoption may be especially important for insurance purposes in rural areas which often have higher poverty rates and less access to formal financial services. However, inadequate MMT agent services in rural areas can discourage households from adopting this technology (Morawczynski and Pickens 2009).

Effective and accessible healthcare has been recognized as pivotal in improving living standards and reducing poverty. Credit constraints and high cost of health services keep more than a billion people in low and middle income countries from using optimal levels of healthcare (Harris et al. 2011). Given that borrowing within informal networks is the predominant insurance mechanism, MMT can help households overcome these credit constraints by making it easier to borrow money from far off relatives and friends. Healthcare use is particularly important in our setting as communicable diseases like malaria, diarrhea and respiratory disorders are endemic in the region (Thumbi et al. 2015).

Jack and Suri (2014) show that users of MMT are able to smooth consumption for total, food and other non-health expenditure categories under these negative shocks and find a positive and significant effect of MMT on risk sharing in these categories. In contrast, our results indicate that the risk sharing effects are concentrated on health expenditures and healthcare use in the presence of a negative health shock, but other categories of expenditures (such as those examined by Jack and Suri (2014)) are not affected. By using a different dataset and focusing specifically on healthcare use, this paper contributes to the literature by showing that users of MMT, through increased informal borrowing, are able to use more healthcare services compared to non-users in the presence of health shocks. This suggests that MMT can be an effective tool for overcoming very short-run credit constraints and financing of unplanned and sudden expenditures imposed by illness. This access to credit in the time of need, usually through

informal networks (Fafchamps and Lund 2003; Fafchamps and Gubert 2007; Jack and Suri 2014), may lead to timely diagnosis, prevention and treatment of disease, and thus have important repercussions for household health.

Furthermore, unlike Jack and Suri (2014), we find that households' quarterly non-health consumption is insured against negative health shocks while the health budget increases with the shock. This may imply that households need money for healthcare use in the very short-run in the face of illness and are able to adjust other expenditures over the quarter. Households in our sample may not require credit through MMT for food consumption under income shocks as they may smooth food consumption through storage, gifts (via network of kin), and substitution between on-farm food production and buying from the market (Asfaw and Braun 2004; De Weerdt and Dercon 2006). Similarly, the insurance effect of MMT adoption on education expenditure may be limited as households may easily forecast ahead for education expenses as they tend to incur regularly at the beginning of each term, while health expenses may come as emergencies (Marsh et al. 2016).

MMT adoption is endogenous, and the validity of our identification strategy rests on the assumption that health shocks are exogenous. We find that health shocks are uncorrelated with observables, suggesting that these shocks are exogenous and equally affect users and non-users of MMT, rendering our panel difference-in-difference a valid identification design. Like Jack and Suri (2014), we allow for all observable household characteristics to affect risk sharing by interacting them with health shocks. This allows us to control for other changes in household's environment and also for how these changes may affect household's consumption smoothing ability.

MMT can allow for consumption smoothing through liquidation of savings or through increased remittances and loans. Jack and Suri (2014) and Munyegera and Matsumoto (2016) find that remittances are the main mechanism through which households are able to smooth consumption. We test the impact of MMT adoption on likelihood of acquiring a loan (formally or informally) with our difference-in-difference strategy. We find that MMT users are 5 percentage points more likely to acquire loans than non-users during a negative health shock, indicating that borrowing may be the main mechanism.

In other studies, MMT has been associated with an increase in the privacy of transactions, thereby providing more freedom to women in choosing where to spend their money and also improving the gender parity situation within households (Aker et al. 2011; Jackiela and Ozier 2015). Users of mobile money spent cash on more diverse items, sold fewer non-durable assets and cultivated more diverse crops in the randomized control trial conducted by Aker et al. (2011). In smallholder setting, financial inclusion and MMT adoption has been linked with higher farm input use, higher farm profits and off-farm employment (Suri and Jack 2016; Kikulwe et al. 2014).

The article is organized as follows. Section 2 consists of the data and background. The econometric framework is described in Section 3. A discussion of results is in section 4, and section 5 concludes.

Background and Data

Mobile money was started in 2007 and its adoption grew steadily over time. The owners of MMT, which is provided by Safaricom, Airtel, Orange and Essar, can exchange cash for e-money at any “mobile money agent” locations which are easily accessible even in rural areas.

Further, they can send this money to anyone in the country with a text message, even if recipient is not a registered mobile money holder and even if the phone operates on another network. Depositing funds for e-money is free, while an SMS costs about 30 Kenyan Shillings (40 cents). Withdrawals are charged at about 1-2 percent and the price is higher if the recipient is not a registered owner of the facility or uses a different cellular network.²⁰

Our data have been drawn from the longitudinal Socio-Economic Survey (SES)²¹, conducted in the Kisumu Region, near Lake Victoria, of Kenya. The SES is compiled from quarterly visits to about 1600 households in 10 villages. The survey period was roughly from February 2013 to December 2016.

Table 4.1 provides descriptions of the variables. Table 4.2 provides the means and standard deviations of the variables of interest. Average *Total Expenditure* during a quarter is about 10,127.8 Kshs. (~\$101) with education and other expenditures constituting the largest expenditure categories. *Other* expenditures may include expenditures related to livestock and crop farming, or recreation. The average *healthcare expenditure* for household during a quarter is 516.46 (~\$5).

We define healthcare use through three variables; *Visits Made* to a clinic, whether or not medication expenditure was incurred (*Medication*) and whether or not a consultation fee was paid during the last quarter (*Consultation*). *Visits Made* to a clinic indicates the number of visits to a formal healthcare facility, but does not indicate if such a facility was used to just buy

²⁰ Registration only requires a National ID card or Passport. Detailed information regarding pricing for one of the cellular service is available at <https://www.safaricom.co.ke/personal/m-pesa/getting-started/m-pesa-rates>

²¹ This survey was launched by Paul G. Allen School for Global Animal Health at Washington State University in collaboration with the Kenya Medical Research Institute and U.S. Centers for Disease Control and Prevention (known as the KEMRI/CDC Research and Public Health Collaboration) and the University of Washington with a goal to reduce poverty and hunger and improve health and education.

medicines or for doctor consultation. In the region, one of the hospitals charges no consultation fee and the *Visits Made* variable in such a case may only capture opportunity cost of time and transportation costs. We also want to examine if users of *MMT* are more likely to use this technology for medication expenditures or consultation expenditures or both and *Medication* and *Consultation* variables help us determine that.

The user rates of *MMT* remain around 60 percent at the household level in our sample during all time periods while the overall cell phone ownership remains around 70 percent. Average adoption rates of *MMT* over the survey period are shown in Figure 4.1. In our region and sample, the rate of penetration of this technology hasn't been increasing over time, whereas other studies of mobile money report an increasing trend in the adoption of this technology (Munyegera and Matsumoto 2016; Jack and Suri 2011, 2014). Barriers to use this technology include failed transactions, dissatisfaction over mobile carriers' customer service and cash float shortages especially in rural areas (Morawczynski and Pickens 2009).

Shock is an indicator variable equal to 1 if any household member has been sick (could not go to work or go to school) in the past 3 months, 0 otherwise. In the sample, health shocks are the most dominant shocks compared to livestock health shocks and crop loss. On average, 42% of the households report illness incidence within the household in the preceding quarter. In some of the time periods, as high as 52% households report illness, suggesting that risk due to disease is a dominant feature in these households. Figure 4.2 illustrates the proportion of households that experience the *shock* during each survey period.

Table 4.2 also reports the level of cash savings and the percentage of households that take a loan (formally or informally) during the survey period. 10% of the households report that they took a loan during the survey period. Only 44% of the population reported that they had positive

cash savings, and mostly the savings were less than 5,000 Kshs. (~\$50), while 56% reported that they had no cash savings. There were significant difference in the wealth of households. The wealth variable is constructed from farm and off-farm incomes, value of livestock and value of crop inventory. This component of wealth can also be thought of as savings, since livestock are often used as precautionary savings assets (McPeak 2006). Other assets that could help in risk sharing like acres of land owned and ownership of a phone enter as independent variables in the analysis.

Empirical Framework

Our focus is to determine the impact of *MMT* on consumption and healthcare use in the face of health shocks. Following Jack and Suri (2014), we employ the following difference-in-difference specification to test whether consumption and healthcare usage of users and non-users of *MMT* differs under health shocks:

$$Expend_{ivt} = \alpha_i + \gamma shock_{ivt} + \beta shock_{ivt} * MMT_{ivt} + \lambda MMT_{ivt} + \mu X_{ivt} + \delta_{vt} + \epsilon_{ivt} \quad (1)$$

where $Expend_{ivt}$ is (a) expenditures for different consumption categories, and (b) healthcare usage captured by visits to a clinic and expenditures on medication and consultation, in household i , village v , and time t . $shock_{ivt}$ is a dummy variable equal to 1 if the household reported illness in the preceding quarter, 0 otherwise. MMT_{ivt} is a dummy variable equal to 1 if any member of the household is a user of mobile money technology, 0 otherwise. α_i are the household fixed effects and δ_{vt} are village by time dummy variables that control for time invariant household heterogeneity and aggregate level shocks, respectively. X_{ivt} contains occupational dummy variables, whether or not a household owns a mobile phone or not, travel time to the hospital/clinic, highest educational attainment of the household, total adult household

members and children, total household wealth, household's savings level, owned acres and whether or not a household took a loan. This empirical strategy also closely emulates Gertler and Gruber (2002) and Gertler, Levine and Moretti (2006, 2009).

There are two main concerns that may cause problems in the interpretation of β in the above specification. First is the endogeneity of MMT adoption. The validity of our identification strategy rests on the assumption that health shocks are exogenous and are equally likely to affect users and non-users of MMT. If health shock is not exogenous and is correlated with observables or MMT adoption, then β may not capture the causal effect of MMT use on risk sharing. Following Jack and Suri (2014), we test the exogeneity of health shocks by examining if they are correlated to adoption of MMT or a number of household-level variables.

$$shock_{ivt} = \alpha_i + \eta MMT_{ivt} + \rho X_{ivt} + \delta_{vt} + e_{ivt} \quad (2)$$

The results for this regression have been reported in Table 4.3. A correlation between MMT_{ivt} adoption and $shock_{ivt}$ would be indicative of selection bias in our difference-in-difference estimates. We find that our $shock_{ivt}$ variable is not correlated with the MMT_{ivt} variable (i.e., $\eta = 0$), alleviating the concern that adoption of MMT may be correlated with the bad health state. Furthermore, we do not find evidence of strong correlations between $shock_{ivt}$ and X_{ivt} , which may suggest that $shock_{ivt}$ is also uncorrelated with the unobserved error term.

The second main concern is that exogeneity of $shock_{ivt}$ may not be enough for a consistent interpretation of β in equation (1). Since MMT is correlated with observables like education, owning a cell phone and wealth, and these variables may also be used for risk sharing and consumption smoothing, which implies that β may not necessarily be capturing the effect of MMT on risk sharing. We follow Jack and Suri's (2014) strategy of interacting X_{ivt} with the $shock_{ivt}$ to control for these other mechanisms through which risk sharing can happen and

alleviate concerns around the interpretation of β . Therefore, the following regression is our preferred specification:

$$\begin{aligned} Expend_{ivt} = & \alpha_i + \gamma shock_{ivt} + \beta shock_{ivt} * MMT_{ivt} + \lambda MMT_{ivt} + \mu X_{ivt} \\ & + \theta shock_{ivt} * X_{ivt} + \delta_{vt} + \epsilon_{ivt} \end{aligned} \quad (3)$$

where all of the variables are the same as equation (1), while the term $shock_{ivt} * X_{ivt}$ is included to control for risk-sharing effects through mechanisms other than MMT .

Since the dependent variable is in natural logarithms in many regressions and our variables of interest are dummy variables, the transformation of multiplying estimators with 100 and interpreting them as percentage changes is erroneous (Halvorsen and Palmquist 1980; Garderen and Shah 2002). To interpret β, γ and λ as percentage change, we use Kennedy's (1981) transformation of these estimators and use delta method for standard errors to obtain unbiased estimators of percentage change in all semi-logarithmic regressions.²²

The differences in the extent of consumption smoothing between users and non-users of MMT may arise from their borrowing behavior. The ability to obtain a loan, especially from an informal channel, should respond more to shocks for MMT users as compared to non-users. To test for this mechanism of risk sharing, we examine the impact of MMT on loans with the following linear probability model.

$$\begin{aligned} loan_{ivt} = & \alpha_i + \gamma shock_{ivt} + \beta shock_{ivt} * MMT_{ivt} + \lambda MMT_{ivt} + \mu X_{ivt} \\ & + \theta shock_{ivt} * X_{ivt} + \delta_{vt} + \epsilon_{ivt} \end{aligned} \quad (4)$$

where $loan_{ivt}$ is a dummy variable equal to 1 if household acquired a loan (formally or informally) in the past quarter and 0 otherwise, while right-hand side variables are the same

²² Kennedy's Transformation: % change = $100 \left(\exp \left\{ \beta - \frac{1}{2} Var(\beta) \right\} - 1 \right)$

except $loan_{ivt}$ is not a control variable anymore. Linear probability models are used for *Medication*, *Consultation* and *Loan* regressions as probit models with fixed effects can give biased estimates (Neyman and Scott 1948).

For the regressions that do not include log-dependent variables, standard errors are clustered at the household level to account for the serial and intra-household correlation in errors for all regression specifications.

Results

Effect on Expenditures

The results of the difference-in-difference regressions for per capita expenditures in different categories under a health shock are reported in Table 4.4. Jack and Suri (2014) find that health shocks decrease the consumption of non-users of *MMT*; in contrast, we find that health shocks do not significantly affect the non-health expenditures. This result suggests that households are able to smooth their consumption against illness shocks. This may imply that health shocks may be transitory, short-run in nature and are not large enough to affect consumption significantly. It may also be that the health shocks are predominantly focused on children (and other non-earning members of the household) and therefore may not affect earnings and expenditure.²³ Since we are unable to distinguish between the severities of shocks, we may be missing important information on households' ability to insure.

Robustness checks for per capita expenditure regressions are provided in the Table A4.1 and A4.2 of the Appendix. These results are in line with the results presented by Genoni (2012),

²³ Our data does not provide information on the gender and age of the individual affected by disease. Therefore, we are unable to look at disaggregated effects.

Islam and Maitra (2012), Townsend (1995), and Kochar (1995) who suggest that households may be well insured against illness. On the other hand, Dercon and Krishnan (2000), Gertler and Gruber (2002) and Cochrane (1991) find that illness events significantly affect consumption and income.

We find that all households experience a large jump in health expenditures during a *shock*. However, users of MMT spend about 57% more per capita on health than the non-users, suggesting that they are acquiring more healthcare services than non-users during a *shock*. This risk sharing in health consumption predominantly occurs through transfers between informal networks of kin (Fafchamps and Lund 2003; Fafchamps and Gubert 2007; De Weerd and Dercon 2006). *MMT* increases the borrowing and lending within these informal networks by reducing the transaction costs associated with these transfers (Jack and Suri 2014; Munyegera and Matsumoto 2016). Since the non-health expenditures are not affected by the negative health shock and risk sharing is only concentrated in healthcare expenditures, this could mean that households may need payments for the very short-term to go to a doctor and later, they are able to adjust their budget over the course of the quarter. This also indicates that even though all households spend more on healthcare during a health shock; however, they may still want to spend even more to be able to use optimal or best healthcare facilities, but are not able to because of budget constraints.

We find that food and education expenditures are insured against health shocks and adoption of *MMT* does not affect risk sharing in these consumption categories (Table 4.4, Column 1 and 3). Perhaps there exist other mechanisms of insurance that play a role in insurance of food consumption. Consumption smoothing in food may occur through storage, in-kind gifts within informal networks, and substitution between on-farm production and market purchases rather

than borrowing cash (Asfaw and Braun 2004; De Weerd and Dercon 2006). Similarly, education expenditure can be easily forecasted as the expenses usually occur at the beginning of the school term, whereas health expenditures may be incurred as a surprise due to an exogenous *shock* (Marsh et al. 2016). *MMT* plays an important role in helping households finance these unexpected, short-run expenditures through ease of borrowing and lending among households.

The *MMT* dummy variable is positively and significantly related to per capita expenditures in most of the regression specifications, indicating that selective adoption of *MMT* is perhaps correlated with and captures the effect of wealth and other variables that affect expenditures. However, since *shock* is exogenous and users and non-users are equally likely to experience it, this does not pose a threat to the validity of our identification strategy.

Effect on Healthcare Use

Table 4.5 provides the estimates of the impact of *MMT* on *Visits Made* to a clinic/hospital in the presence of health shock. Column 1, Table 4.5 reports results for baseline OLS regression with only time by village fixed effects included to control for aggregate village-level shocks.

According to this specification, users of *MMT* visit a formal healthcare facility 0.63 times more than non-users in presence of a *shock*. In Column 2 through 4, we add household fixed effects, covariates, and covariates and interaction of covariates with the *shock*, respectively. By adding household fixed effects, the time invariant endogeneity due to unobserved household characteristics is controlled for and the coefficient on *MMT*Shock* is 0.56. Adding the covariates (Column 3) do not change this estimate, while adding covariates and their interaction with the *shock* results in coefficient of 0.49 on *MMT*Shock*. The changes across column 2 to 4 are fairly small and the results are robust across these specifications. Since the correlation between *MMT*

and other covariates can obscure the interpretation of the coefficient on *MMT*Shock*, as discussed in the empirical framework section, therefore, the paper allows for risk sharing through other mechanisms via interaction of *shock* with covariates, making column 4 the preferred specification. Coefficients on *MMT*Shock* are statistically significant at 1% level of significance (p-value < 0.001) for all specifications.

One concern could be that the use of *MMT* may change the financial environment of the households in terms of use of savings, loans and other financial instruments. Therefore, controlling for them may cause ambiguities in the effect of *MMT*. However, the results in column 2 and 4 differ by only 0.06 times for the coefficient of *MMT*Shock*, indicating that the impact is robust across specifications, alleviating this concern.

Table 4.6 presents the role of *MMT* in medication use. The paper finds evidence that users of *MMT* are 0.16 percentage points more likely to spend on medication during illness periods than the non-users. Kisumu region is associated with high malarial incidence, respiratory problems and febrile illness (Thumbi et al. 2015) and timely medication like anti-malarials can significantly improve regional health. The results are robust across the specifications.

Table 4.7 presents the role of *MMT* in covering consultation costs. Results suggest that users are 0.15 times more likely to incur a consultation cost during illness period as compared to the non-users and the coefficient is statistically significant at 1% level of significance, suggesting an improvement in healthcare use for the *MMT* users. Tables 4.5, 4.6 and 4.7 provide evidence on the role of *MMT* in improving healthcare utilization during illness periods. This is an important result as households in developing countries are either not able to use formal healthcare or because of credit constraints are unable to buy optimal amount of healthcare, which results in prolonged illness, higher morbidity and mortality rates and loss of income (Jutting 2004; Schultz

and Tansel 1997). Even though formal healthcare facilities are inadequate in developing countries (Das, Hammer, and Leonard 2008), pursuing formal healthcare can still significantly improve health outcomes through timely receipt of treatment and important medication like anti-malarials and oral rehydrate salts (Adhvaryu and Nyshadham 2015).

There could be two potential mechanisms through which *MMT* can help in risk sharing. One, this technology could be connected to a bank account and can help in liquidation of savings. Two, remittances and loans from relatives that live in far off regions or transactions within tribal and family circles could help in risk sharing. Since families in Kenya are dispersed over large distances due to internal migration and employment opportunities, lowering of transaction cost can have crucial effects on frequency and timeliness of needed remittances. Users of *MMT* receive remittances from longer distance and more diverse networks than non-users (Jack and Suri 2014; Munyegera and Matsumoto 2016). The importance of remittances and transaction costs in consumption smoothing in informal networks has also been documented by Yang and Choi (2007).

To account for the first mechanism of risk sharing, we control for the savings level and interact savings level with shocks to ensure that the savings mechanism is controlled for. Furthermore, about 90% of our sample reports that they have savings of less than \$50, suggesting that risk sharing might be happening through transactions and informal borrowing rather than savings. Table 4.8 imperfectly examines the second mechanism and illustrates the role of *MMT* in the likelihood of acquiring a loan. Users of *MMT* are 13 percentage points more likely acquire a loan in general and about 2 to 5 percentage points more likely to acquire a loan in the face of health shocks, compared to non-users, depending on different specifications. This may suggest that borrowing is the main mechanism for risk sharing in presence of an adverse

health shock. The *Took Loan* variable documents loans from formal as well as informal sources. Our estimates of borrowing will be underestimated to the extent that remittances from kin are based on relationships of reciprocity and are not accounted as loans by households.

Conclusion

This paper examines the role of MMT on risk sharing in consumption and builds on the work of Jack and Suri (2014) by using a different dataset and focusing on healthcare expenditures and use, which has not been the focus of their study or any other study related to MMT. Furthermore, our sample consists of rural households. To the extent that financial services are unavailable in rural areas of developing countries, MMT can bridge this gap between formal financial sectors and the unbanked rural poor. On the other hand, weak or unsatisfactory network services in rural areas may dissuade households from adopting this technology.

We find that during times of illness, users of MMT spend 57% more per capita, are 16 percentage points more likely to buy medication, 15 percentage points more likely to pay consultation fees, and utilize more formal healthcare facilities than non-users of the technology. Previous studies related to MMT adoption illustrate that risk sharing effects are financed by increased borrowing and remittances. We also show that users of MMT take more formal and informal loans during health shocks. Given that remittances from kin may not be entirely accounted as loans, our estimates of borrowing may be underestimated. These results imply that the technology can be used to overcome credit constraints which hamper the ability of the households to use necessary healthcare and this may have far-reaching consequences for household health outcomes, especially in poor households.

In contrast to Jack and Suri's (2014) findings, this paper shows that the risk sharing effects of MMT are concentrated on healthcare expenditures and use, instead of non-health expenditures, in presence of negative health shocks. Since all households in our sample are able to smooth consumption in presence of a health shock, and the expenditure on healthcare increases for all households (for MMT users more than non-users), this could imply that the technology is especially beneficial in getting very short-term loans/remittances for going to a doctor and then households are able to adjust their budget during the course of the quarter. While food intake can be smoothed via storage and in-kind transfers, and education expenditure can be forecasted ahead of time, health expenditure can be incurred as an emergency, requiring immediate credit for utilization of healthcare facilities. This immediate need for health insurance can be provided by MMT through reduction in transaction costs and increased transfers within informal networks. While this increase in healthcare consumption during illness for MMT users is important in the short-run, it may have longer-run impacts if timely utilization of healthcare services decrease mortality and long term illness. Also, the long run impacts could be substantial if household welfare and poverty is a function of random shocks in health status. However, the article does not concern itself with estimating the consequences of increased healthcare use.

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Figures

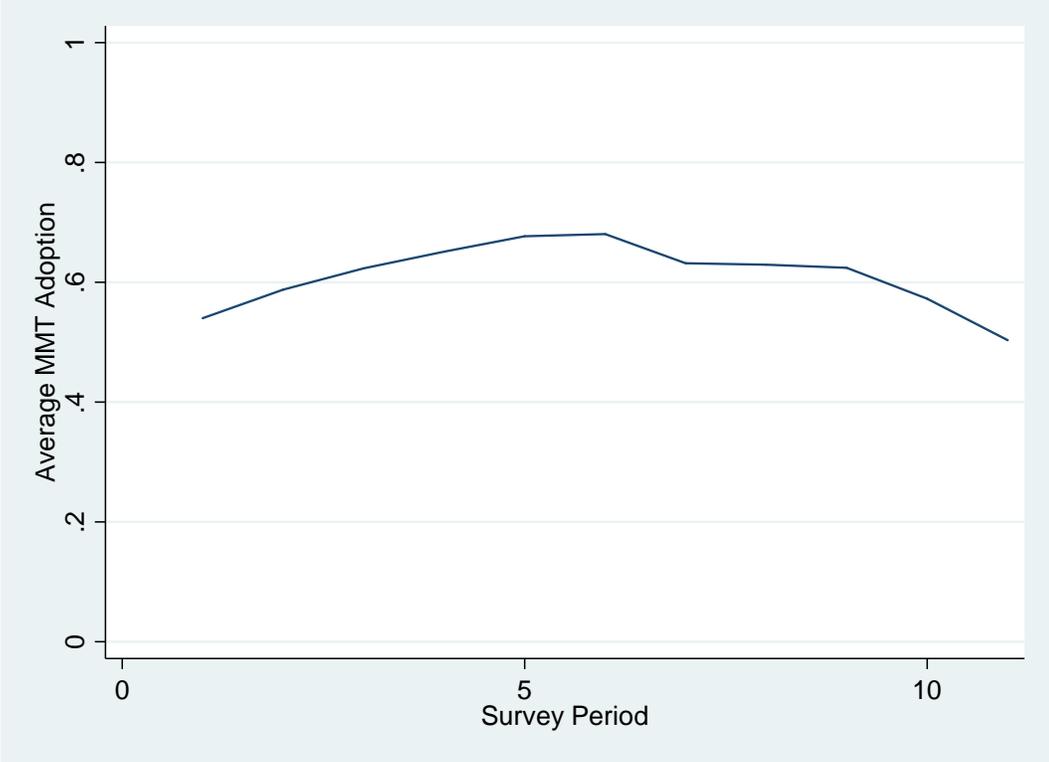


Figure 4.1: Average MMT adoption over time

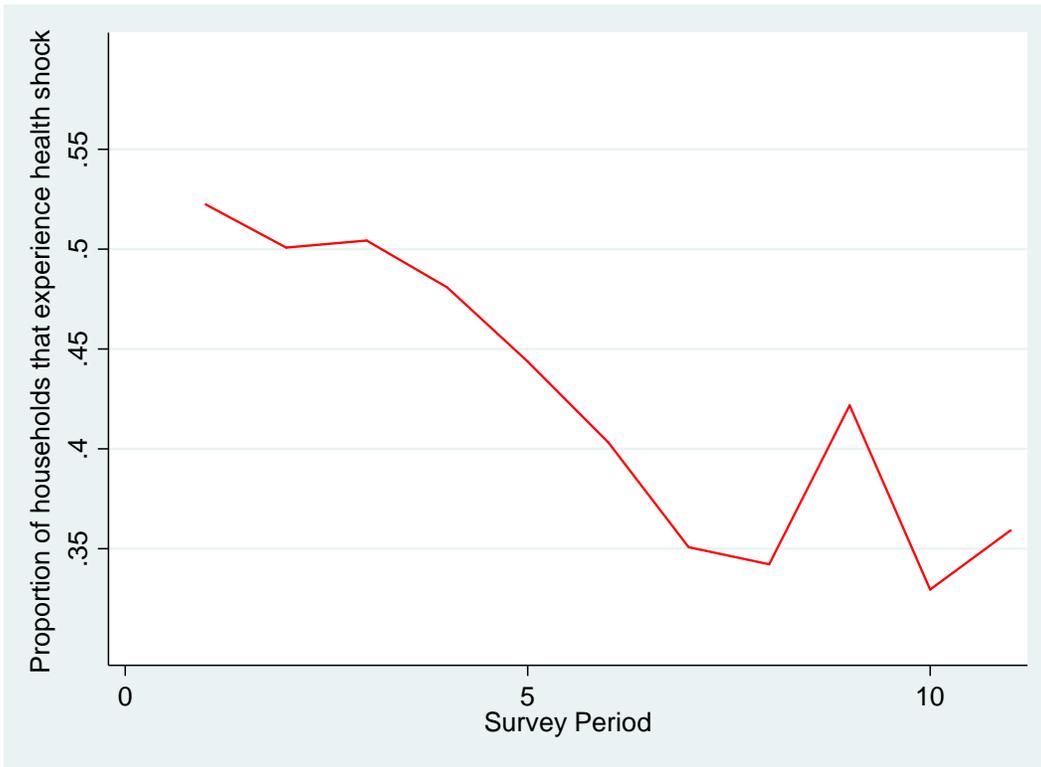


Figure 4.2: Proportion of households that experience a health shock in each time period

Tables

Table 4.1: Data Description

Variable	Description
<i>MMT</i>	Indicator variable = 1 if any member of the household owns a mobile money savings and transfer (MMT) account, 0 otherwise.
<i>Shock</i>	Indicator variable = 1 if any household member has been sick (could not go to work or go to school) in the past 3 months, 0 otherwise.
<i>Visits Made</i>	Number of visits made to a hospital/clinic in the past 3 months.
<i>Medication</i>	Indicator variable = 1 if the household spent on medicines in the past 3 months, 0 otherwise.
<i>Consultation</i>	Indicator variable = 1 if the household spent on consultation (doctor or traditional healer) in the past 3 months, 0 otherwise.
<i>Education Expenditure</i>	The natural log of the total per capita expenditure on education by the household in the last 3 months.
<i>Healthcare Expenditure</i>	The natural log of the total per capita expenditure on health care by the household in the last 3 months.
<i>Clothing Expenditure</i>	The natural log of the total per capita expenditure on clothing by the household in the last 3 months.
<i>Food Expenditure</i>	The natural log of the total per capita expenditure on food by the household in the last 3 months.
<i>Other Expenditure</i>	The natural log of total per capita expenditure on ‘other’ things – not captured by categories above by the household in the last 3 months.
<i>Total Expenditure</i>	The natural log of the total per capita expenditure by the household in the last 3 months.
<i>Children</i>	Household members of age less than or equal to 10.
<i>Adult HH members</i>	Household members of age greater than 10.
<i>College Education</i>	Indicator variable = 1 if highest education attainment of the household is college education, 0 otherwise.
<i>Secondary Education</i>	Indicator variable = 1 if highest education attainment of the household is secondary education, 0 otherwise.
<i>Primary Education</i>	Indicator variable = 1 if highest education attainment of the household is primary education, 0 otherwise.
<i>Savings < \$70</i>	Indicator variable = 1 if households cash savings are < \$70, 0 otherwise.
<i>\$70 < Savings < \$175</i>	Indicator variable = 1 if households cash savings are between \$70 and \$175, 0 otherwise.
<i>Savings > \$175</i>	Indicator variable = 1, if household cash savings are greater than \$175, 0 otherwise.
<i>Took Loan</i>	Indicator variable = 1 if household received a loan in the past 3 months, 0 otherwise.

<i>Cell Phone Ownership</i>	Indicator variable = 1, if household owns a mobile phone, 0 otherwise.
<i>Owned Acres</i>	Acres of land owned by the household
<i>Wealth</i>	Income from crops, livestock and off-farm activities plus the market value of the livestock and crop inventories.
<i>Farmer</i>	Indicator variable = 1 if household head's primary occupation is farming, 0 otherwise.
<i>Self Employed</i>	Indicator variable = 1 if household head's primary occupation is off-farm self-employed, 0 otherwise
<i>Household Help</i>	Indicator variable = 1 if household head's primary occupation is household help, 0 otherwise

Table 4.2: Summary Statistics

	Mean	SD
<i>Food Expenditure (Kshs)</i>	778.9	583.7
<i>Healthcare Expenditure (Kshs)</i>	516.46	3,515.8
<i>Education Expenditure (Kshs)</i>	3,907.01	11,563.31
<i>Clothing Expenditure (Kshs)</i>	464.64	1,174.9
<i>Other Expenditure (Kshs)</i>	3,726.87	5,252.12
<i>Total Expenditure</i>	10,127.8	74,223.34
<i>Visits Made</i>	1.06	1.70
<i>Consultation (percent)</i>	0.087	0.28
<i>Medication (percent)</i>	0.30	0.45
<i>MMT (percent)</i>	0.61	0.48
<i>College Education (percent)</i>	0.05	0.23
<i>Primary Education (percent)</i>	0.45	0.49
<i>Secondary Education (percent)</i>	0.29	0.45
<i>Shock (percent)</i>	0.42	0.49
<i>Wealth (Kshs.)</i>	84,921	77,183
<i>Adult HH Members</i>	4.45	2.36
<i>Children < Age 10</i>	1.62	1.81
<i>Cell Phone Ownership (percent)</i>	0.72	0.47
<i>Owned Acres</i>	0.70	5.92
Household Head Occupation		
<i>Dummies (percent)</i>		
<i>Farmer</i>	0.43	0.49
<i>Self Employed</i>	0.14	0.34
<i>Salaried</i>	0.03	0.19
<i>Other</i>	0.08	0.27
<i>Household Help</i>	0.32	0.43
Financial Instruments		
<i>No Savings (percent)</i>	0.56	0.48
<i>Savings < \$70 (percent)</i>	0.43	0.49
<i>\$70 < Savings < \$175</i>	0.005	0.07
<i>Savings > \$175</i>	0.003	0.05
<i>Took Loan (percent)</i>	0.106	0.31

Table 4.3: Correlates of Health Shock – Linear Probability Model

	<i>Health Shock</i>
<i>MMT</i>	0.09 (0.08)
<i>Wealth</i>	0.0004 (0.0003)
<i>Savings</i>	-0.092 (0.063)
<i>College Education</i>	0.065 (0.047)
<i>Primary Education</i>	0.036 (0.035)
<i>Secondary Education</i>	0.045 (0.042)
<i>Children</i>	0.011** (0.005)
<i>Total Household Members</i>	0.02** (0.006)
<i>Occupation - House help</i>	0.061 (0.081)
<i>Occupation - Self Employed</i>	-0.021 (0.033)
<i>Occupation - Salaried</i>	-0.102 (0.083)
<i>Cell Phone Ownership</i>	-0.037 (0.029)
<i>Took Loan</i>	0.063** (0.025)
<i>Owned Acres</i>	-0.0003 (0.0002)
R-Squared	0.04
No. of Observations	12,149

Table 4.4: The Effect of Mobile Money on Expenditure (in Logs) during a Health Shock

	<i>Education Expenditure</i>	<i>Health Expenditure</i>	<i>Food Expenditure</i>	<i>Clothing Expenditure</i>	<i>Other Expenditure</i>	<i>Total Expenditure</i>	<i>Non-Health Expenditure</i>
<i>Shock</i>	0.061 (0.13)	2.01*** (0.22)	-0.036 (0.11)	0.042 (0.107)	0.082 (0.10)	0.34 (0.31)	0.014 (0.118)
<i>MMT</i>	1.42*** (0.26)	0.22** (0.10)	0.127 (0.35)	1.66*** (0.215)	0.093 (0.067)	0.55*** (0.055)	0.56*** (0.055)
<i>Shock*MMT</i>	0.024 (0.17)	0.568*** (0.146)	-0.056 (0.077)	0.33* (0.174)	0.011 (0.103)	0.086 (0.079)	0.046 (0.078)
No. of Observations	14,603	14,604	14,608	14,607	14,601	14,599	14,602
Time by Village Effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Household Fixed Effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Controls	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Controls*Shock	Yes	Yes	Yes	Yes	Yes	Yes	Yes

***, **, * indicate significance at 1, 5 and 10%.

Standard Errors are clustered at the household level

Table 4.5: The Effect of Mobile Money on Visits to a Clinic

Dependent Variable	(1)	(2)	(3)	(4)
<i>Visits Made to Clinic</i>				
<i>Shock</i>	1.19*** (0.073)	1.10*** (0.084)	0.964*** (0.023)	0.791*** (0.146)
<i>MMT</i>	0.271*** (0.036)	0.294*** (0.045)	0.13 (0.08)	0.18 (0.16)
<i>Shock*MMT</i>	0.633*** (0.084)	0.556*** (0.097)	0.588*** (0.059)	0.486*** (0.088)
No. of Observations	15,392	15,392	14,613	14,613
Time by Village Effects	Yes	Yes	Yes	Yes
Household Fixed Effects	No	Yes	Yes	Yes
Controls	No	No	Yes	Yes
Controls*Shocks	No	No	No	Yes

***, **, * indicate significance at 1, 5 and 10% respectively.
Standard errors are clustered at the household level.

Table 4.6: The Effect of Mobile Money on Medication – Linear Probability Model

Dependent Variable	(1)	(2)	(3)	(4)
<i>Medication (Yes/No)</i>				
<i>Shock</i>	0.214*** (0.011)	0.192*** (0.012)	0.186*** (0.012)	0.317*** (0.036)
<i>MMT</i>	0.103*** (0.008)	0.12*** (0.009)	0.089*** (0.017)	0.10*** (0.02)
<i>Shock*MMT</i>	0.144*** (0.015)	0.129*** (0.016)	0.141*** (0.016)	0.161*** (0.031)
No. of Observations	15,385	15,385	14,607	14,607
Time by Village Effects	Yes	Yes	Yes	Yes
Household Fixed Effects	No	Yes	Yes	Yes
Controls	No	No	Yes	Yes
Controls*Shock	No	No	No	Yes

***, **, * indicate significance at 1, 5 and 10% respectively.
Standard errors are clustered at the household level.

Table 4.7: The Effect of Mobile Money on Consultation – Linear Probability Model

Dependent Variable	(1)	(2)	(3)	(4)
<i>Consultation (Yes/No)</i>				
<i>Shock</i>	0.082*** (0.007)	0.07*** (0.007)	0.07*** (0.008)	0.08*** (0.02)
<i>MMT</i>	0.014*** (0.003)	0.016*** (0.01)	0.033*** (0.001)	0.0032 (0.011)
<i>Shock*MMT</i>	0.084*** (0.01)	0.016*** (0.005)	0.076*** (0.01)	0.15*** (0.02)
No. of Observations	15,385	15,385	14,607	14,607
Time by Village Effects	Yes	Yes	Yes	Yes
Household Fixed Effects	No	Yes	Yes	Yes
Controls	No	No	Yes	Yes
Controls*Shock	No	No	No	Yes

***, **, * indicate significance at 1, 5 and 10%.

Standard Errors are clustered at the household level

Table 4.8: The Effect of Mobile Money on Acquisition of Loans – Linear Probability Model

Dependent Variable	(1)	(2)	(3)	(4)
<i>Took Loan (Yes/No)</i>				
<i>Shock</i>	0.014*** (0.003)	0.0079* (0.004)	0.0082* (0.004)	0.0069 (0.011)
<i>MMT</i>	0.145*** (0.006)	0.116*** (0.006)	0.137*** (0.013)	0.175*** (0.017)
<i>Shock*MMT</i>	0.016* (0.008)	0.018** (0.008)	0.022** (0.008)	0.056** (0.022)
No. of Observations	15,392	15,392	14,609	14,609
Time by Village Effects	Yes	Yes	Yes	Yes
Household Fixed Effects	No	Yes	Yes	Yes
Controls	No	No	Yes	Yes
Controls*Shocks	No	No	No	Yes

***, **, * indicate significance at 1, 5 and 10% respectively.

Standard errors are clustered at the household level.

Appendix

Table A4.1: The Effect of Mobile Money on Education, Health and Food Expenditures (in Logs) during a Human Illness Shock – Robustness Checks

	<i>Education Expenditure</i>	<i>Education Expenditure</i>	<i>Health Expenditure</i>	<i>Health Expenditure</i>	<i>Food Expenditure</i>	<i>Food Expenditure</i>
<i>Shock</i>	0.12* (0.069)	0.075 (0.068)	1.25*** (0.066)	1.25*** (0.067)	0.005 (0.027)	0.038 (0.027)
<i>MMT</i>	1.04*** (0.063)	0.894*** (0.096)	0.301*** (0.047)	0.239*** (0.081)	0.177*** (0.02)	0.135*** (0.029)
<i>Shock*MMT</i>	0.063 (0.085)	0.068 (0.086)	0.479*** (0.082)	0.519*** (0.084)	0.01 (0.031)	0.009 (0.03)
No. of Observations	15,375	14,603	15,377	14,604	15,381	14,608
Time By Village Effects	Yes	Yes	Yes	Yes	Yes	Yes
Household Fixed Effects	Yes	Yes	Yes	Yes	Yes	Yes
Controls	No	Yes	No	Yes	No	Yes
Controls*Shock	No	No	No	No	No	No

***, **, * indicate significance at 1, 5 and 10%.

Standard Errors are clustered at the household level

Table A4.2: The Effect of Mobile Money on Clothing, Other, Total and Total Non-Health Expenditures (in Logs) during a Human Illness Shock – Robustness Checks

	<i>Clothing Expenditure</i>	<i>Clothing Expenditure</i>	<i>Other Expenditure</i>	<i>Other Expenditure</i>	<i>Total Expenditure</i>	<i>Total Expenditure</i>	<i>Non-Health Expenditure</i>	<i>Non-Health Expenditure</i>
<i>Shock</i>	0.024 (0.05)	0.031 (0.05)	0.091 (0.11)	0.088 (0.10)	0.17*** (0.035)	0.189*** (0.048)	0.017 (0.035)	0.036 (0.035)
<i>MMT</i>	1.10*** (0.053)	1.07*** (0.09)	0.151* (0.067)	0.101 (0.07)	0.567*** (0.029)	0.784*** (0.052)	0.576*** (0.029)	0.497*** (0.044)
<i>Shock*MMT</i>	0.032 (0.073)	0.032 (0.074)	0.019 (0.11)	0.012 (0.107)	0.11 (0.41)	0.16 (0.47)	0.029 (0.049)	0.038 (0.041)
No. of Observations	15,380	14,607	15,338	14,601	15,374	14,594	15,374	14,602
Time by Village Effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Household Fixed Effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Controls	No	Yes	No	Yes	No	Yes	No	Yes
Controls*Shock	No	No	No	No	No	No	No	No

***, **, * indicate significance at 1, 5 and 10%.

Standard Errors are clustered at the household level