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Simulating transmission and control of *Taenia solium* infections using a Reed-Frost stochastic model

Niels C. Kyvsgaard [a,c,*], Maria Vang Johansen [b,c], Hélène Carabin [d]

[a] *Department of Veterinary Pathobiology, Faculty of Life Sciences, University of Copenhagen, Stigbøjlen 4, DK-1870 Frederiksberg C, Denmark*
[b] *DBL-Institute for Health Research and Development, Charlottenlund, Denmark*
[c] *WHO/FAO Collaborating Centre for Emerging and Other Parasitic Zoonoses, Danish Centre for Experimental Parasitology, Department of Veterinary Pathobiology, Faculty of Life Sciences, University of Copenhagen, Frederiksberg C, Denmark*
[d] *Department of Biostatistics and Epidemiology, College of Public Health, University of Oklahoma Health Sciences Center, OK, USA*

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Abstract

The transmission dynamics of the human-pig zoonotic cestode *Taenia solium* are explored with both deterministic and stochastic versions of a modified Reed-Frost model. This model, originally developed for microparasitic infections (i.e. bacteria, viruses and protozoa), assumes that random contacts occur between hosts and that hosts can be either susceptible, infected or 'recovered and presumed immune'. Transmission between humans and pigs is modelled as susceptible roaming pigs scavenging on human faeces infected with *T. solium* eggs. Transmission from pigs to humans is modelled as susceptible humans eating under-cooked pork meat harbouring *T. solium* metacestodes. Deterministic models of each scenario were first run, followed by stochastic versions of the models to assess the likelihood of infection elimination in the small population modelled. The effects of three groups of interventions were investigated using the model: (i) interventions affecting the transmission parameters such as use of latrines, meat inspection, and cooking habits; (ii) routine interventions including rapid detection and treatment of human carriers or pig vaccination; and (iii) treatment interventions of either humans or pigs. It is concluded that mass-treatment can result in a short term dramatic reduction in prevalence, whereas interventions targeting interruption of the life cycle lead to long-term reduction in prevalence.

Keywords: *Taenia solium*; Deterministic and stochastic models; Transmission dynamics; Control

1. Introduction

The tapeworm *Taenia solium* is endemic in most pig-raising developing countries of Africa (Phiri et al., 2003), the Americas (Flisser et al., 2003) and Asia (Rajshekhar et al., 2003). The adult stage of the parasite is only found in humans, and the infection is spread from humans to the intermediate host – the pig – through eggs shed in faeces. The ingested eggs develop to metacestodes in pigs, migrate mainly to the muscular tissues and lodge as cysticerci. Humans in turn acquire taeniasis by eating raw or undercooked pork meat infected with *T. solium* metacestodes. The human health impact of the parasite is mainly due to the ability of the eggs to infect humans. In this case, humans act as an accidental intermediate host where ingested eggs can develop into cysticerci in muscle tissue or in the brain. In the later case, the disease is called neurocysticercosis (NCC) and may cause seizures and/or epilepsy and other neurological disorders (Bern et al., 1999; Singh and Prabhakar, 2002; Garcia et al., 2003a). The agricultural and human health impact of the infection can lead to an important monetary burden in some areas where the infection is endemic (Carabin et al., 2006).

The infection has been considered as 'potentially eradicable' by the International Task Force for Disease Eradication (WHO, 2003. Control of neurocysticercosis. Report by the Secretariat. World Health Organization. Fifty-sixth

* Corresponding author. Tel.: +45 3528 3752; fax: +45 3528 2757.
E-mail address: nck@life.ku.dk (N.C. Kyvsgaard).

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World Health Assembly. 6 March 2003 (available February 2006 at www.who.int/gb/ebwha/pdf_files/WHA56/ea5610.pdf)) as transmission, theoretically, is easy to interrupt due to the absence of known wildlife reservoirs and the fact that pigs are the only, but essential, intermediate hosts. Theoretically, the life cycle can be interrupted at several stages by different approaches such as anthelmintic treatment of the human host and/or pigs, health education, sanitation, restrictions of roaming pigs, vaccination of pigs (which is under development), meat inspection and proper cooking of pig meat. However, WHO recognised that there is 'no evidence yet that eradication is feasible within a reasonable time frame' (WHO, 2003. Control of neurocysticercosis. Report by the Secretariat. World Health Organization. Fifty-sixth World Health Assembly. 6 March 2003 (available February 2006 at www.who.int/gb/ebwha/pdf_files/WHA56/ea5610.pdf)).

In practice, a combination of interventions may be needed to eliminate the infection from an area. However, which control strategies are actually effective in a specific area may depend on the specific transmission conditions of that area. There are relatively few field studies documenting the impact of interventions on pigs and/or human infection. Small scale studies in a limited number of villages suggest that mass treatment of humans, or health education combined with restrictions on roaming pigs, can reduce human and pig infection prevalence (Sarti et al., 1997, 2000; Allan et al., 1997; Garcia et al., 2006). In Tanzania, a study conducted in 42 villages measured the impact of a health education intervention on the incidence of infection in pigs after 12 months, but did not measure the impact on human infection (Ngowi, 2005). These results need to be confirmed on a larger scale and in the longer term or explored with models such as the one presented here. To our knowledge, there is no model available for the quantitative transmission dynamics of the infection. In fact, the need for such a model was emphasized more than 15 years ago but was never addressed (Gemmell and Lawson, 1989; Lawson and Gemmell, 1989).

The object of this work is to develop a simple mathematical model of the transmission dynamics of *T. solium* infections. This first step in model building gives basic insight into the transmission dynamics of *T. solium* as well as the theoretical effects of different interventions.

2. Materials and methods

2.1. The choice of model

The model described in this paper is a modification of the Reed-Frost model (Halloran, 2001), a chain binomial model, which was developed in both a deterministic and a stochastic version. The first step in the development of new mathematical transmission models consists of the understanding of the basic transmission pattern of the infection (Koopman, 2004). The simplest form of model is the SIR model, where individuals can be classified as susceptible (S), infected (I) or 'recovered and presumed immune' (R) at any point in time. This form of model differs from more typical models of macroparasites, where the number of parasites within each host is modeled (Anderson and May, 1992). The SIR model assumes that all individuals come in contact with one another randomly and that there is a fixed population size.

In the Reed-Frost model, transmission between the infected and susceptible categories depends upon a probability of transmission from each contact made during a prespecified model-based time increment. The time increment of the model is typically equal to the latent period of the infectious agent (Martin et al., 1987; Halloran, 2001). One important assumption behind the Reed-Frost model is that exposure to two or more infected people (or infected pigs) at the same time is considered as two independent binomial events.

The general formula for the Reed-Frost model is:

$$I_{t+T} = S_t \times (1 - q^{I_t}) \quad (1)$$

where I_{t+T} is the number of new infected individuals occurring during the time interval (T), S_t is the number of susceptible individuals at time t, q is the probability of a susceptible escaping infection due to a contact with one infected individual ($q = 1 - p$, where p is the probability of contact), T represents the time increment of the model, t is the current time (Martin et al., 1987). When there is more than one infected individual, then the probability of escaping infection from contact with I_t infected individuals at time t is q^{I_t}. The probability of each susceptible individual becoming infected during the time interval T is thus $1 - q^{I_t}$. The number of newly infected individuals is obtained when $1 - q^{I_t}$ is multiplied by the number of susceptible individuals in the population.

2.2. Modified Reed-Frost model

The proposed human taeniasis–pig cysticercosis model adapts this simple Reed-Frost model to include both definitive and intermediate hosts. It also includes a dynamic population of the intermediate host by including birth and slaughter of pigs. The human population is assumed to remain stable for the duration of the simulation of 120 months (10 years). The time increment T is set at 3 months which roughly corresponds to the prepatent period in humans (about 2 months) and the time from infection to the development of fully mature metacestodes in pigs (10–12 weeks) (Pawlowski, 2002).

In the model, humans can belong to two categories: HS (susceptible humans) or HI (infected with taeniasis). It is assumed that humans return to full susceptibility to re-infection after expelling the worm spontaneously or following treatment. We have omitted a category of recovered humans being resistant to re-infection. This is done for simplicity and is not likely to affect the outcome of the model significantly as the prevalence of infection is very low (Table 1).

Table 1
Prevalence of adult *Taenia solium* in humans and cysticercosis in pigs as reported in selected epidemiological studies

Country	Adult *T. solium* in human		Cysticercosis in pigs		Reference
	Eggs (%)	Copro-antigen (%)	Tongue palpation (%)	Antibody detection (%)	
Bolivia (Chaco)	1.3			37	Carrique-Mas et al. (2001)
Peru	0–6.7			42–75	Garcia et al. (2003b)
Mexico (Morales)	0.3		4		Sarti et al. (1992)
Mexico	0.2–2.4		1–24	4–35	Flisser et al., 2003
Guatemala	1 and 2.8		4 and 14		Garcia-Noval et al. (1996)
Guatemala		5.1 and 1.9		40 and 64	Allan et al. (1997)

Only studies with data on both human taeniasis and porcine cysticercosis from the same communities have been included.

Pigs can belong to three categories: PS (susceptible pigs), PI (infected pigs) or PR ('recovered and presumed immune' pigs). The pigs move from the susceptible state (PS) to the infected state (PI) upon contact with infected human faeces according to a time-varying probability (see Eq. (2) below), and subsequently move to the 'recovered and presumed immune' state (PR) by recovery and development of immunity. The SIR compartmental model is illustrated in Fig. 1.

The transmission from human to pig is modelled as follows: every 3 months, the probability of infection from one infected human to one susceptible pig is β (human-to-pig probability). The probability of avoiding infection, for each pig when exposed to one human, is thus $1-\beta$. The probability of each pig being infected by any infected human is time-dependent in that it varies according to the number of infected humans at time t (HI_t). Hence, $1-(1-\beta)^{HI_t}$ is the probability of each pig becoming infected when exposed to all infected humans present in the community at time t. This leads to the following number of new pig infections during time increment T:

$$\text{newPI}_{t+T} = \text{PS}_t \times (1-(1-\beta)^{\text{HI}_t}) \quad (2)$$

where newPI_{t+T} is the number of newly infected pigs during time period T starting at time t. PS_t is the number of susceptible pigs at time t.

It is assumed that the infected pigs recover and develop immunity according to Eq. (3):

$$\text{newPR}_{t+T} = \text{PI}_t \times \varepsilon \quad (3)$$

where the probability of each infected pig to recover and develop immunity over 3 months is (ε). Immunity is assumed to be life-long in a situation where most pigs have short life expectancies, usually being slaughtered at about 1 year of age in developing countries. Hence, very few pigs are expected to live long enough to revert to susceptibility.

New pigs are born into the susceptible group according to the pig birth rate (λ) multiplied by the total number of pigs in the population at that time:

$$\text{newPS}_{t+T} = (\text{PS}_t + \text{PI}_t + \text{PR}_t) \times \lambda \quad (4)$$

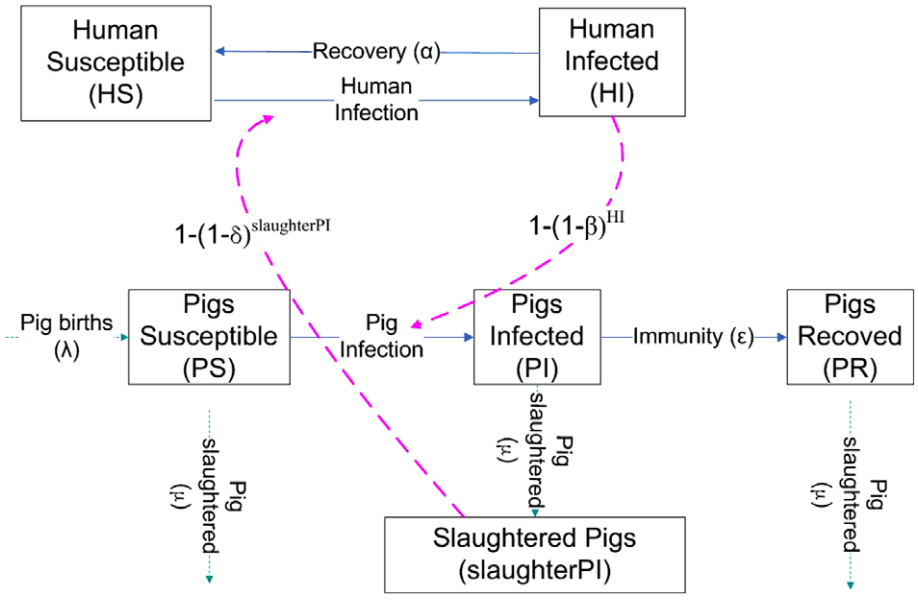

Fig. 1. Flow diagram of the model. The figure shows the categories of humans (susceptible HS and infected HI) and pigs (susceptible PS, infected PI, and 'recovered and presumed immune' PR) and the movement of individuals between these categories from the present to the next time-step shown as unbroken arrows. The interaction between the two host species is shown in dotted arrows.

Pigs are slaughtered from all categories with the rate μ. For example, the number of slaughtered pigs from the infected group becomes (the other two groups are not shown):

$$\text{slaughtPI}_{t+T} = \text{PI}_t \times \mu \quad (5)$$

Humans are infected as a function of the number of infected slaughtered pigs at time t and the pig-to-human transmission probability (δ). Similarly to the probability of infection in pigs, the probability of any human to become infected varies with time according to the number of infected slaughtered pigs present in the community at time t:

$$\text{newHI}_{t+T} = \text{HS}_t \times (1 - (1 - \delta)^{\text{slaughtPI}_t}) \quad (6)$$

where newHI_{t+T} is the number of newly infected humans during time increment T. HS_t is the number of susceptible humans at the time t. The number of infected pigs slaughtered during the period T is slaughtPI_t. δ is the probability of infection for each susceptible human exposed to the meat from one infected pig.

The infection in humans is not permanent but can be terminated by either spontaneous elimination of the parasite or by treatment as determined by the human-recovery probability (α):

$$\text{newHS}_{t+T} = \text{HI}_t \times \alpha \quad (7)$$

The transmission parameters (human-to-pig transmission probability β and pig-to-human transmission probability δ) are composite parameters. The human-to-pig probability of infection (β) can vary according to latrine use, survival of eggs in the environment and pig management practices (roaming). The pig-to-human transmission probability (δ) is influenced by governmental and non-formal meat inspection and condemnation and by cooking practices.

With a given set of transmission parameters, R_0, the basic reproductive number, was estimated by seeding a single infected human into an otherwise *T. solium*-free population and observing the number of new cases arising from this case over the duration of adult and larval infectivity. To calculate only the number of new infections arising from this initial infection, a modified version of the model was created where the initial formula $\text{HI}_{t+T} = \text{HI}_t + \text{newHI}_{t+T} - \text{newHS}_{t+T}$ was changed to $\text{HI}_{t+T} = \text{HI}_t - \text{newHS}_{t+T}$, whereby no second generation of infected humans was allowed. R_0 was in turn estimated as the summation of newHI over the period of infection in the population:

$$R_0 = \sum_t \text{newHI}_t, \quad (8)$$

where $\text{HI}_{t=0} = 1$ and where newHI only refers to the offspring of the first generation. Identical results were obtained with the introduction of one initial infected pig into a totally susceptible population.

2.3. Choice of start parameters for the model

The population is set to a community of 1000 persons and 200 pigs, which could reflect the situation where the community consists of 200 families with one pig per family. In smallholder farming communities of the developing world, it is common that each household will only raise one or two pigs (Sarti et al., 1992; Phiri et al., 2003; Ngowi, 2005). The pigs in the model population are assumed to roam around and hence scavenge on human faeces under conditions where latrines are not present, are not being used or are easily accessible to pigs. We will assume that all pigs are slaughtered and their meat consumed in this community.

The model starts with a human taeniasis prevalence of 2% and a pig infection prevalence of 20% (Fig. 1). These prevalences are the equilibrium values of the model using the transmission parameters listed in Table 2. These prevalence values have been chosen based on a selection of well-designed epidemiological studies conducted in several areas of the developing world as detailed in Table 1. However, a straight comparison of the results from these studies is difficult as the samples have been analysed with diagnostic tests that have variable sensitivities and specificities. For example, in pigs, sensitivity values with confidence intervals (CI) for infection have been estimated as 0.21 (CI 0.14–0.26), 0.22 (CI 0.15–0.27), 0.36 (CI 0.26–0.41) and 0.87 (CI 0.62–0.98) for tongue inspection, meat inspection, antibody ELISA and antigen ELISA, respectively (Dorny et al., 2004). In addition, prevalence data usually reflect the situation in one village or region of the country.

The parameter values used in our model are listed in Table 2. Human recovery rate (α) was set to 0.25 per 3 months corresponding to a mean life time of the adult worm of 1 year. Literature on this topic is scarce. Whilst a case of autoinfection with three metacestodes had a

Table 2
Parameter values used in the model

Parameter	Meaning	Value	Unit	Rationale
T	Time step interval	3	Months	Based on prepatent period of *Taenia solium*
β	Probability of transmission from human to pig at contact	0.01		Based on the ratio of pig to human infection
δ	Probability of transmission from pig to human at contact	0.0005		Based on the ratio of pig to human infection
ε	Development of immunity in pigs	0.25	Per 3 months	Assumption
μ	Rate of pig slaughter	0.25	Per 3 months	Slaughtered pigs are replaced
λ	Birth rate of pigs	0.25	Per 3 months	Pig life expectancy of 1 year
α	Rate of human recovery	0.25	Per 3 months	Adult *T. solium* life expectancy of 1 year

duration of 2 years and 3 months (Pawlowski, 2002), it is believed that the average life expectancy of the adult parasite is closer to 1 year (Ana Flisser, UNAM, Mexico, personal communication, 2005).

The true human-to-pig transmission probability (β) has, to our knowledge, never been reported. However, we have found that a value of 0.01 can be justified as it corresponds to each infected human infecting one pig every 3 months with a probability (β) of 1%. In other words, each infected human can give rise to two infected pigs in a population of 200 susceptible pigs over a period of 3 months. This number is more dependent on existing sanitation and restrictions on pig movements in each community than on the biotic potential of the parasite.

The pig recovery rate (ε) was set at 0.25 per 3 months, which is equivalent to a mean life time of the metacestode of 1 year.

The three groups of pigs (PS, PI, PR) are slaughtered according to the pig-slaughter-rate (μ). It is 0.25 per 3 months in this example, meaning that pigs have a life expectancy of 1 year, which is reasonable in the context of indigenous pigs in a developing country (Marlon Hernández, UNA, Nicaragua, personal communication, 2005). New pigs enter the susceptible group at the same rate that they die, since people tend to replace a pig that was just slaughtered. Hence, the birth rate in pigs (λ) is also 0.25 per 3 months. The transmission parameters of the SIR models are sensitive to changes in population size (de Jong, 1995) which was consequently fixed by setting the birth and slaughter rates to the same value.

The pig-to-human transmission probability (δ) is assumed to be equal to 0.0005 meaning that one infected pig when slaughtered will give rise to 0.5 infected persons in the present population of 1000 susceptibles. This probability is supported by the prevalence data in Table 1, where the prevalence in pigs is much higher (often 10-fold) than that of the adult worm in humans.

2.4. The stochastic version of the model

The initial deterministic model was developed in a spreadsheet (Excel®) and has been used for teaching parasite dynamics. A stochastic version of the model uses individuals as units and will not allow non-integers in any compartments. Infection and recovery events (Eqs. (2), (3), (6) and (7)) were modelled stochastically, assuming a binomial distribution and using the transmission probabilities mentioned above. For example, when calculating the number of new human infections for each time increment T, each susceptible human has a probability, $p = 1 - (1 - \delta)^{\text{slaughtPI}_t}$, of becoming infected [Eq. (6)]. Hence, each individual may or may not be moved to compartment HI according to probability p. The number of newly infected humans in the stochastic model corresponds to the random draw of the binomial distribution with parameters p and sample size $N = \text{HS}_t$. Pig birth and pig slaughter rates were kept deterministic. The same initial values were used as for the deterministic version. For each set of transmission parameters, the outcome of 5000 simulations was analyzed for 2.5% and 97.5% percentiles of prevalence among humans and pigs at all time points. This model was written in "R" (R Development Core Team, 2004. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. http://www.R-project.org). Both versions are available from the authors on request.

2.5. Modelling the effect of control strategies affecting the basic transmission parameters

Better use of latrines or restrictions on pig movements are both modelled by reducing the human-to-pig probability (β) compared with the initial setting. We simulated the use of latrines by reducing the human-to-pig rate (β) from 0.01 in the start parameters given in Table 2 to 0.005 from month 48 onwards.

Improvements in meat inspection or the better cooking of meat were modelled by reducing the pig-to-human probability (δ) from 0.0005 in the initial settings to 0.00025 from month 48 onwards. This would correspond to the detection and condemnation of half of the infected carcasses, to having half of the infected pigs being slaughtered, inspected and condemned or of having half of the population cooking pork meat sufficiently.

2.6. Modelling of repeated interventions: rapid identification of human carriers and pig vaccination

Identification of human tapeworm carriers followed by treatment was modelled by increasing the human-recovery-rate (α) from 0.25 to 0.40 starting from month 48 until the end of the simulation. This would be the equivalent of reducing the life expectancy of the adult worm by approximately 40% among those infected or having a screening programme where 40% of the infected humans would seek medical attention, be diagnosed and treated for their infection from month 48 onwards.

Vaccination with recombinant oncosphere antigens have shown promising results with up to 100% protection in experimental studies (Flisser et al., 2004). Vaccination of pigs was modelled by transferring susceptible pigs (PS_t) to the 'recovered and presumed immune' state (PR_t). The vaccination programme simulated included mass vaccination every 12 months from the 48 month time point with 100% efficacy and 90% coverage.

2.7. Modelling of anthelmintic mass treatments

Mass treatments of either humans or pigs were also modelled. Human mass treatment (with 100% efficacy and 90% coverage) was modelled by setting the human-recovery rate (α) to 0.9 at the 48 month time point. Treatment of pigs was modelled as having an immediate effect by moving 90% of infected pigs (PI_t) into the 'recovered

and presumed immune' compartment (PR_t), assuming a coverage of 90% and an efficacy of oxfendazole of 100% (Gonzalez et al., 1998) at the 48 month time point.

Finally, we modelled a combined strategy with repeated pig vaccination every 12 months with a one-time mass treatment of humans.

3. Results

3.1. Behaviour of the model

The initial parameters (Table 2) are set to simulate an endemic situation. R_0 for this scenario was estimated to 1.75. The prevalence in humans stabilizes just below 2%, whereas the prevalence in pigs stabilizes around 20%. The prevalence among humans and pigs from the single replication of the stochastic model shows that considerable variation can be expected over time. The 2.5% and 97.5% percentiles of the 5000 simulations of the stochastic version of the model indicate that a high degree of variation is expected even between communities with the same transmission parameters (Fig. 2a and b).

3.2. Modelling the effect of control strategies affecting the basic transmission parameters

The results of improving the use of latrines are shown in Fig. 2c and d. R_0 for this scenario was estimated to 1.75

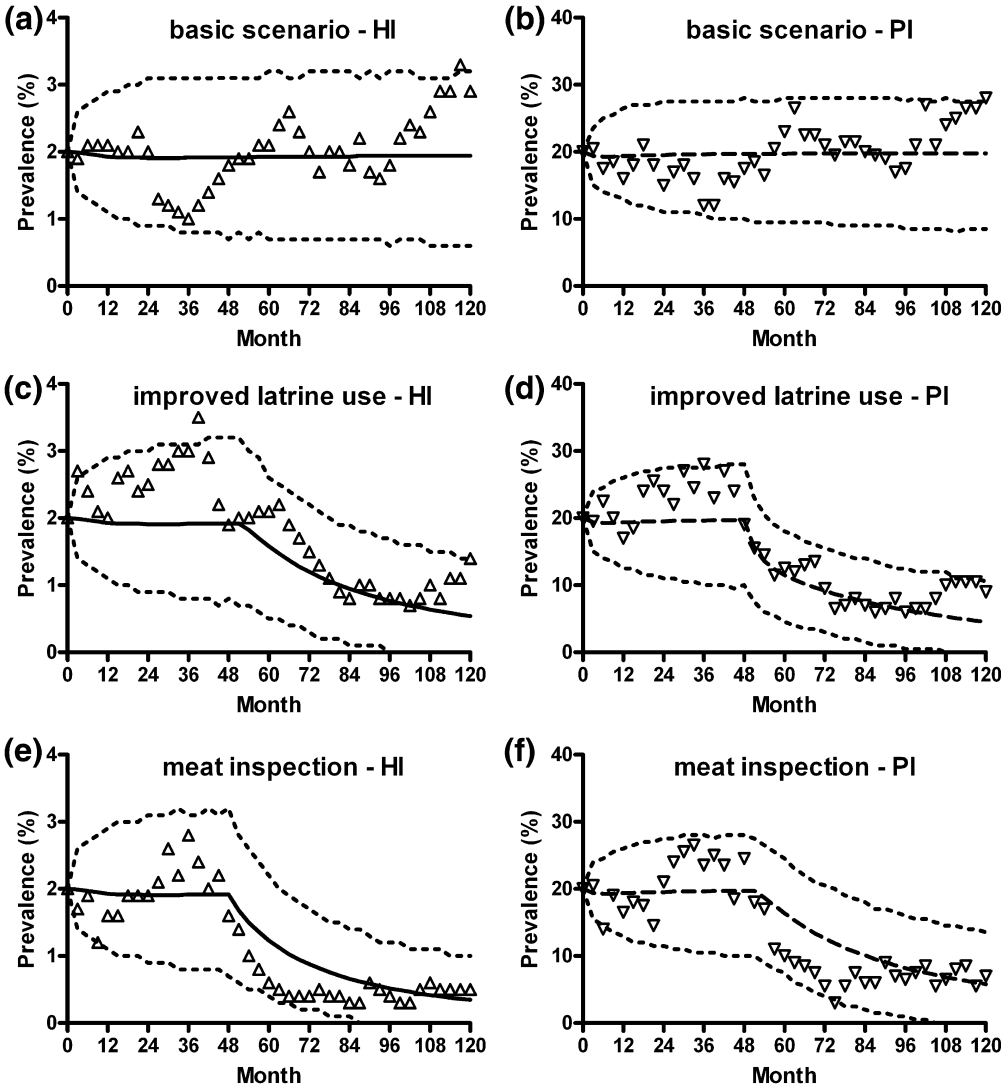

Fig. 2. Simulations of the development over time in the number of infected humans in a population of 1000 and infected pigs among a population of 200. The three graphics differ with respect to transmissions parameters. The solid line (—) represents the prevalence in humans whereas the dashed line (- - - -) represents the prevalence in pigs, as estimated by the deterministic version of the model. The dotted lines (····) indicate the 2.5% and 97.5% percentiles of 5000 simulations of the stochastic version of the model. The triangles represent a randomly selected replication of the model for the prevalence in humans (△) and pigs (▽). (a and b) Prevalence in humans and pigs, respectively, of the reference scenario with the settings indicated in Table 2. The human-to-pig probability is 0.01 and the pig-to-human probability is 0.0005. (c and d) Lower transmission from human to pig by more extensive use of latrine or by fencing of pigs. The human-to-pig probability is changed to 0.005 from month 48. (e and f) Lower transmission from pig-to-human by meat inspection or better cooking practices. The pig-to-human probability is changed to 0.00025 from month 48.

before intervention and 0.85 after implementing the intervention. Both pig and human prevalences were reduced when compared with the initial prevalences prior to 48 months. In the stochastic simulations, 12% of the repetitions showed a prevalence of 0 in the human population 72 months after the start of the intervention and 7% of the repetitions reached a prevalence of 0 in the pig population.

Meat inspection and condemnation of infected carcasses led to a rapid reduction in the human prevalence (Fig. 2e and f) whereas the reduction in the pig prevalence was relatively slower. R_0 for this scenario was estimated as 1.75 before intervention and 0.85 after implementing the intervention. The stochastic simulations showed a prevalence of 0 at the end of the simulation period in 19% and 8% of replications for the human and pig populations, respectively.

Both control strategies led to the same estimate of R_0 post-intervention since they both cut transmission probability by half.

3.3. Modelling of repeated interventions: rapid identification of human carriers and pig vaccination

Screening for human taeniasis followed by treatment of the carriers led to a rapid decline in prevalences among both humans and pigs. R_0 for this scenario was estimated at 1.75 before intervention and 1.1 after intervention. In the stochastic model, a prevalence of 0 after 120 months was reached in 13% and 4% of the repetitions for the human and pig population, respectively (Fig. 3a and b).

Repeated vaccination of pigs with 90% coverage every 12 months gave a sustained reduction in the prevalences of porcine cysticercosis and human taeniasis (Fig. 3c and d). The stochastic simulation showed prevalences of 0 in 8% of the replications for human taeniasis and in 4% of the replications for porcine cysticercosis.

3.4. Modelling of anthelmintic mass treatments

Fig. 4a and b illustrates the results from the human mass treatment scenario. This control approach led to a temporary decline in human taeniasis and pig cysticercosis prevalence, after which the prevalences reverted back to their initial values. The 5000 repetitions of the stochastic simulation resulted in a prevalence of human taeniasis of 0 in 3% of the replications and a prevalence of porcine cysticersosis in 2% of the replications at the end of the simulation period.

The mass treatment of pigs led to a temporary decline in pig prevalence and a small reduction in human taeniasis (Fig. 4c and d). There were less than 1% of stochastic replications which resulted in a final prevalence of 0 among both the human and pig populations.

A single mass treatment of humans in combination with a pig vaccination programme led to a rapid decline in prevalence among both humans and pigs (Fig. 4e and f). Unlike the results obtained with mass treatment alone, the

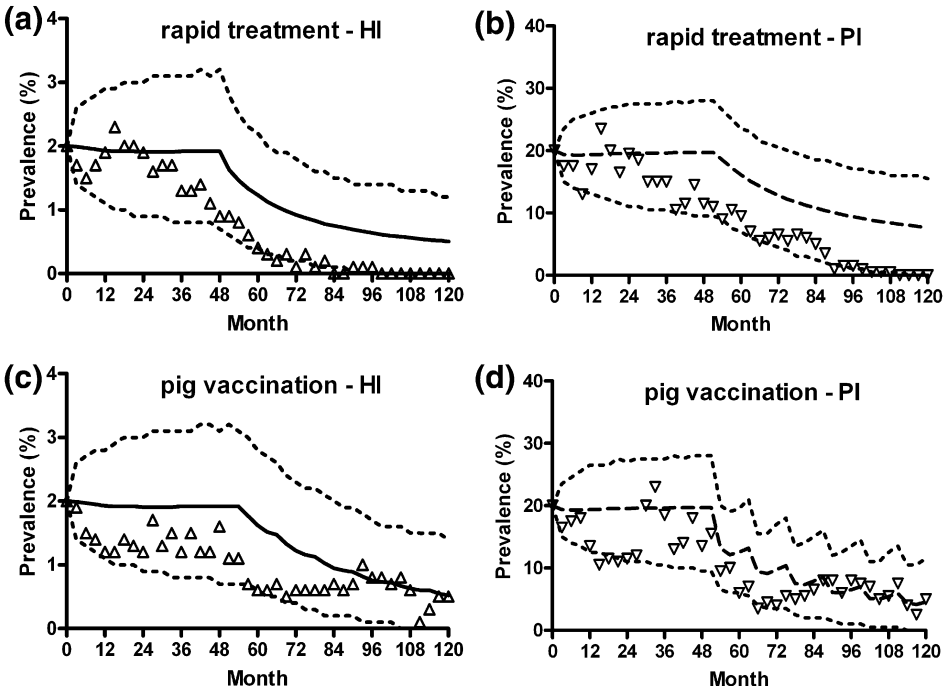

Fig. 3. Simulation of repeated interventions. (a and b) Targeted treatment of human taeniasis cases through rapid identification and treatment from month 48. (c and d) Repeated vaccination of pigs every 12 months from month 48. The solid line (—) represents the prevalence in humans whereas the dashed line (- - - -) represents the prevalence in pigs, as estimated by the deterministic version of the model. The dotted lines (····) indicate the 2.5% and 97.5% percentiles of 5000 simulations of the stochastic version of the model. The triangles represent a randomly selected replication of the model for the prevalence in humans (△) and pigs (▽).

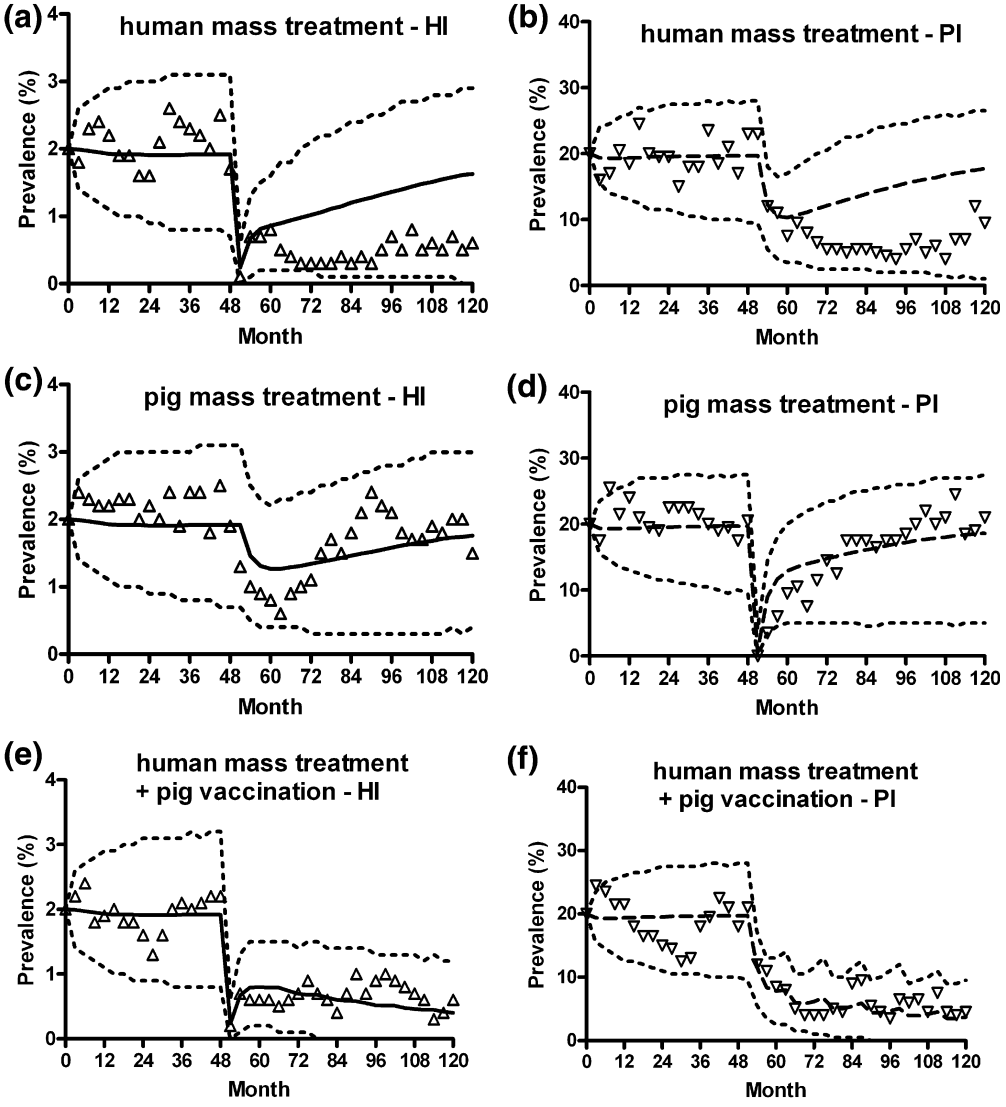

Fig. 4. Simulation of mass treatment of either humans or pigs can be simulated by changing the transmission parameters at a given time point. (a and b) Human mass treatment at month 48. (c and d) Pig mass treatment at month 48. (e and f) Human mass treatment at month 48 followed by pig vaccination every 12 months. The solid line (—) represents the prevalence in humans whereas the dashed line (- - - -) represents the prevalence in pigs, as estimated by the deterministic version of the model. The dotted lines (····) indicate the 2.5% and 97.5% percentiles of 5000 simulations of the stochastic version of the model. The triangles represent a randomly selected replication of the model for the prevalence in humans (△) and pigs (▽).

prevalences were maintained at a low level with the combined interventions. At the end of the simulation period, 24% of the replications of the stochastic model showed a prevalence of 0 among humans and 15% of the replications showed a prevalence of 0 in the pig population.

4. Discussion

The main goal of the present work has been to create a model suitable to explore the impact of alternative control approaches on the transmission dynamics of *T. solium*. It suggests that mass-treatment can result in a short term dramatic reduction in prevalence, whereas intervention targeting interruption of the life cycle leads to long-term reduction in prevalence. We believe that the model illustrates principles well, but it should not be used as a tool to predict exact proportions (e.g. of latrine use or of population to treat) or timing (e.g. of vaccination). We hope that the present work will serve as an inspiration for future field studies, for the construction of more precise models and to predict the number of neurocysticercosis cases that could be prevented by these interventions.

Transmission dynamics models are very useful tools with which to assess the impact of interventions in a population. When combined with cost data, these models can be used to guide policy makers in deciding which control measures are likely to be the most cost-effective and/or cost-beneficial. We believe we have developed the first transmission dynamics model for *T. solium* infections in humans and pigs. Human cysticercosis has not been included in the model at this point as the purpose of the model is to evaluate the impact of different control measures on

transmission of the parasite. Even though this model has some limitations (see later), both the deterministic and stochastic versions of the model reproduce reasonably well the expected ratio of human taeniasis to pig cysticercosis (Table 1).

The stochastic simulations indicate that high variations in prevalences are to be expected in field studies of taeniasis/cysticercosis even among communities having the same transmission conditions. This high variation is probably due largely to the small size of the simulated communities. In real life, human contacts and trading of pigs between villages may lead to less variation between villages and may also affect the impact of interventions within a single village. The variation is nonetheless important to note as it has been recommended to include several study units (e.g. communities) in epidemiological studies of parasitic infections, given the high level of heterogeneity between communities (Basáñez et al., 2004).

The model points to three main groups of interventions: (i) actions leading to permanent reductions in transmission through sanitation and pig management; (ii) repeated interventions through pig vaccination or the early identification and treatment of human tapeworm carriers and; (iii) point interventions such as mass treatment of humans or pigs.

Human sanitation and pig management include actions that would lead to a reduction in transmission through better use of latrines, restriction of pig movement in the villages, inspection and condemnation of infected meat and proper cooking of pork meat. We have chosen relatively moderate levels of interventions, which changed R_0 from 1.75 of the initial scenario to 0.85 after intervention. Our simulations show that the impact of these interventions may not be very dramatic in the short term but can lead to substantial reductions in prevalence in the long term. In an intervention study, Sarti et al. (1997) found that health education together with a reduction in the access of pigs to sources of infection and roaming restriction were very efficient, leading to a reduction in prevalence of cysticercosis in pigs from 2.6% to 0% by lingual examination 1 year after the intervention. The limitation of that study was that only one village was studied pre- and post-intervention, thus the generalizability of the results is limited. A recent randomized field trial conducted in 42 villages in rural Tanzania showed that health and pig management education led to a reduction of 42.5% (95% CI: −3.4%, 70.3%) in the incidence of pig infection measured by antigen ELISA 1 year after intervention (Ngowi, 2005).

In the modelling of pig vaccination, we have assumed 100% protection and 90% coverage. Such high levels of protection have been achieved in experimental studies (Flisser et al., 2004), but need to be confirmed in the field. A coverage of 90% is optimistic and we believe that these results probably represent a best case scenario for the effectiveness of pig vaccination. We have modelled a scenario with repeated mass vaccination every 12 months, which can reduce the prevalence considerably. This may be achievable if cysticercosis vaccines could be added to national immunization campaigns against classical swine fever or other preventable porcine infections. The ideal situation would, however, be to vaccinate each piglet just after the disappearance of maternal immunity (Lightowlers, 2003) which is not feasible in rural areas of the developing world.

Rapid identification of human carriers followed by anthelmintic treatment seems to be an attractive alternative to mass treatment with a good and sustained impact on prevalence. This approach has previously been recommended by Sarti and Rajshekhar (2003), but they also stressed that a strong, sustainable primary health system is needed for the approach to be successful. The other limitations of this approach are that patients need to recognise they are infected, seek medical attention (i.e. have the resources to do so) and also be diagnosed as positive. Also, the poor sensitivity of a simple coprological examination of faeces would lead to several false-negative results. The two alternatives above would obviously be resource-demanding and may not be available nor cost-effective in developing countries.

Point interventions include human mass treatment and pig mass treatment. The impact of large scale mass treatment programmes with praziquantel against schistosomiasis in *T. solium* endemic areas on taeniasis/human cysticercosis should be monitored. Our model predicts that these interventions can give dramatic results in the short term, but rarely result in the total elimination of transmission, thus leading to a return to the original endemic situation. The short-term reduction has been observed in a study from Guatemala, where Allan et al. (1997) found a reduced prevalence in both humans (prevalence reduced from 3.5% to 1%) and pigs (seroprevalence reduced from 55% to 7%) 10 months after human mass treatment with niclosamide. Our model predicts that the prevalence would return to pre-intervention levels unless accompanied by actions which reduce the basic transmission parameters. In a study where mass treatment was combined with changes in transmission conditions, Sarti et al. (2000) found a sustained reduction in prevalence of taeniasis in humans and cysticercosis in pigs 42 months after praziquantel treatment. The authors point to the fact that, during the observation period, the community also experienced improvements in sanitary conditions, maintaining pig in pens and a reduction in the proportion of pigs having access to human faeces. However, as mentioned above, only one community was included, which considerably limits generalizability. The recently published findings of Garcia et al. (2006), demonstrating a reduction in infection pressure but no elimination of the parasite after combined human and porcine mass chemotherapy, are also in line with the findings of our model.

The model results of a human mass treatment followed up by regular pig vaccination suggest that mass treatment could have a role in control programmes if it is followed by more sustained actions (e.g. pig vaccination, latrines

or meat inspection). The advantage is that a substantial reduction in prevalence can be achieved right from the outset of the control programme.

We have assumed that we could use a chain binomial model with only the host categories Susceptible, Infected and Recovered and presumed immune (SIR). There are three reasons why using a microparasite model for cysticercosis is appropriate, even though it is evidently a simplification. Firstly, the transmission from pig to human through the consumption of undercooked pork can be seen as parallel to the 'sufficient contact' assumed in the SIR models. We must assume though that each pig is infected, on average, with the same number of larvae and that each human eats, on average, the same amount of meat over a period of three months. Second, the human carrier is usually infected with only one tapeworm (Pawlowski, 2002; Ana Flisser, UNAM, Mexico, personal communication, 2005). Third, transmission from human to pig can be considered as a contact event since free-roaming pigs typically scavenge on human faeces. We assume here that the daily shedding of eggs from one tapeworm is constant, leading to a constant probability of infection from any infected human to any susceptible pig. This is in contrast to the situation where this route is limited and transmission mostly takes place indirectly by mechanical vectors or by dispersal in water. In the latter case, models which have been used for transmission of other *Taenia* species, which include egg dispersal and different worm-burdens in the hosts, may be more appropriate (Gemmell and Lawson, 1989; Lawson and Gemmell, 1989).

The SIR models for transmission of microparasites assume random contact between infected humans and pigs. This is certainly the case in communities where pigs are allowed to roam freely and have access to scavenge on human faeces. Restrictions on pig movements may not result in a uniform reduction of the human-to-pig transmission probability, but rather introduce a situation where individual pigs will have different probabilities of being infected depending upon their proximity to the household with a *T. solium* carrier. Such a clustering of human taeniasis and porcine cysticercosis has been observed in some field studies (Sarti et al., 1992; Garcia et al., 2003b). It will thus be important to explore the inclusion of a spatial dimension in future models.

Another limitation of the SIR approach is that there is no modelling of different infection intensities in the pig. In the present model, all pigs are assumed to an harbour identical number of metacestodes, whereas field studies have found high variations in cyst burdens. Boa et al. (2002) found between 76 and 80,340 cysts in 24 naturally infected pigs in Tanzania. However, the relation between metacestode numbers and infection probability is far from simple. Although animals with a higher number of metacestodes have a higher probability of being detected at meat inspection (Kyvsgaard et al., 1990), many pigs from at-risk communities are slaughtered and marketed through informal channels where there is no meat inspection (Cysticercosis Working Group in Peru, 1993). Due to the absence of a clear density-dependent association between metacestode numbers and risk of infection in humans, the assumptions of the present model are still likely to be valid. Indeed, our model reproduces reasonably well the expected prevalences of human taeniasis and porcine cysticercosis and their ratio. An improvement in future models could be to include two or three infection categories (cyst burdens in the pig). This has been done in a model for *Schistosoma japonicum* infection (Riley et al., 2005).

It has not been possible to find sufficient field data on all the parameters used in the model. This was also observed by Craig et al. (1996) who stated that 'the transmission dynamics of *T. solium* have not been described' and point to adult worm longevity, re-infection rates and biotic potential as particularly important. A good estimate of the variability of the longevity of the adult worm may help in explaining differences in prevalence between age groups which have been observed in some studies (Garcia et al., 2003b) and would also give a better estimate of the benefit of human treatment in the control of the infection. If the duration of infection is found to be long, this may make treatment of humans a more cost-effective option, whereas a rapid turn-over of the infection in humans will increase the number of treatments which are required to reach the same impact.

The long-term fate of metacestodes in pigs remains to be elucidated. In the present model, it is assumed that infected pigs develop immunity to re-infection, but there is relatively little data to show whether pigs are actually able to eliminate an already established infection. Serological field studies have indicated that more pigs reacted with antibody ELISA than circulating antigen ELISA tests (Pouedet et al., 2002), which could indicate that some pigs had eliminated the infection. However, Nguekam et al. (2003) found viable metacestodes without any decline in circulating antigen 6 months after infection of piglets, indicating that piglets infected at a young age may not necessarily be able to eliminate the infection.

Future studies and models should aim at getting a better picture of the dynamic aspects of this infection. Data on infection rates and the life span of the parasites in humans and pigs, together with information about human movements and pig trading, will give a better understanding of observed prevalence data. Such data will also be of assistance in the creation of more complex models, and in turn better control.

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