Journal of Human Evolution 108 (2017) 92–109

Contents lists available at ScienceDirect

Journal of Human Evolution

journal homepage: www.elsevier.com/locate/jhevol

Selection to outsmart the germs: The evolution of disease recognition and social cognition

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ARTICLE INFO

Article history:
Received 24 November 2015
Accepted 26 February 2017
Available online 17 May 2017

Keywords:
Agent-based model
Disease transmission
Cooperation
Hominin evolution
Social complexity
Kin selection

ABSTRACT

The emergence of providing care to diseased conspecifics must have been a turning point during the evolution of hominin sociality. On a population level, care may have minimized the costs of socially transmitted diseases at a time of increasing social complexity, although individual care-givers probably incurred increased transmission risks. We propose that care-giving likely originated within kin networks, where the costs may have been balanced by fitness increases obtained through caring for ill kin. We test a novel hypothesis of hominin cognitive evolution in which disease may have selected for the cognitive ability to recognize when a conspecific is infected. Because diseases may produce symptoms that are likely detectable via the perceptual-cognitive pathways integral to social cognition, we suggest that disease recognition and social cognition may have evolved together. Using agent-based modeling, we test 1) under what conditions disease can select for increasing disease recognition and care-giving among kin, 2) whether providing care produces greater selection for cognition than an avoidance strategy, and 3) whether care-giving alters the progression of the disease through the population. The greatest selection was produced by diseases with lower risks to the care-giver and prevalences low enough not to disrupt the kin networks. When care-giving and avoidance strategies were compared, only care-giving reduced the severity of the disease outbreaks and subsequent population crashes. The greatest selection for increased cognitive abilities occurred early in the model runs when the outbreaks and population crashes were most severe. Therefore, over the course of human evolution, repeated introductions of novel diseases into naïve populations could have produced sustained selection for increased disease recognition and care-giving behavior, leading to the evolution of increased cognition, social complexity, and, eventually, medical care in humans. Finally, we lay out predictions derived from our disease recognition hypothesis that we encourage paleoanthropologists, bioarchaeologists, primatologists, and paleogeneticists to test.

1. Introduction

Exposure to disease is a major cost of sociality (Nunn and Altizer, 2006; Rifkin et al., 2012; McCabe et al., 2015). Despite this, hominins have evolved extraordinary social complexity (Tomasello, 2014), including a strikingly social way of mitigating the effects of socially transmitted diseases—we provide care to diseased individuals. Such care hinges on the ability to recognize disease in others. Currently, the cognitive basis of this ability is not well understood. In this paper, we present the novel hypothesis that the ability to recognize disease may have evolved together with social cognition in hominins.

A synthesis of paleoanthropological, ethnographic, and host-parasite research suggests that increasing social complexity during the origin of *Homo* dramatically increased disease risk (Sugiyama, 2004; Rifkin et al., 2012; Harper and Armelagos, 2013; McCabe et al., 2015). Thus, part of the selection for increasing cognitive abilities in *Homo* may have been selection to accurately assess the disease risk presented by interaction partners. In this paper, we integrate findings from the literature on hominin social structure, hominin disease ecology, disease recognition in

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http://dx.doi.org/10.1016/j.jhevol.2017.02.009
0047-2484/

nonhuman animals, and human social cognition. Based on these data, we create an agent-based model to examine under what conditions increased cognition and care-giving could have evolved in the hominin lineage. Using our results, we create predictions deriving from our novel disease recognition hypothesis of hominin cognitive evolution that can be tested by paleoanthropologists, paleogeneticists, bioarchaeologists, and primatologists.

1.1. Broadening social networks between hominin subgroups

Across birds and mammals, larger communities show greater levels of contagious parasites, environmentally transmitted parasites, and vector-borne parasites (Rifkin et al., 2012). Though network modularity (sub-grouping) may reduce the transmission risks in large communities where many dyads do not interact (Griffin and Nunn, 2012), hominin networks appear to have connected spatially distant subgroups, facilitating transmission within a fission–fusion, multi-level society (Hill et al., 2011; Grove et al., 2012).

Hominin community sizes have been reconstructed as having expanded over time, from ~50 individuals in apes and small-brained australopiths to 100–120 in late *Homo erectus* and *Homo heidelbergensis*, and 120–150 in *Homo neanderthalensis* and *Homo sapiens* (Aiello and Dunbar, 1993; Dunbar, 1998; Gamble et al., 2011; Grove et al., 2012; Layton et al., 2012). This is believed to have produced an increase in social network size and complexity (Grove et al., 2012). As hominins dispersed towards northern latitudes and community sizes increased, the home-range requirements for sustaining them would have also increased (Grove et al., 2012). This produced communities whose daily nutritional needs were too large to be fulfilled in the amount of space a cohesive group could cover each day (Grove et al., 2012). The result is thought to have been the evolution of a multi-level fission–fusion system in which larger communities subdivide, rather than foraging cohesively (Grove et al., 2012). This would have enabled large communities of hominins to forage across greater areas and expand into new habitats, yet still obtain the benefits of a large social network, such as information transfer, social learning, and cooperation (Grove et al., 2012; Layton et al., 2012). Thus, even though mean population density decreased over time as hominins dispersed northward, overall community size and social network size likely increased (Grove et al., 2012; Layton et al., 2012).

Community size estimates for modern hunter-gatherers range from 125 to a few thousand people (Layton et al., 2012). The extensiveness of human social networks was documented in a study showing that while chimpanzee males typically only interact with about 20 other males, a modern male hunter-gather may watch over 300 other men make tools (Hill et al., 2014). The evolution of such long-distance social networks linking different subgroups (Hill et al., 2014) may have prevented the reduction in disease risk that might otherwise be expected to have occurred as hominin density decreased (Armelagos et al., 2005). The extensive, community-wide social networks of hominins would have facilitated widespread pathogen transmission, including any novel pathogens acquired as hominins spread into new habitats (McCabe et al., 2015).

1.2. Increasing connectedness within groups

Simultaneously with the expansion of networks connecting subgroups, the complexity of networks within the subgroups also likely increased with the evolution of cooperative breeding during the origin of *Homo*. *Homo habilis* and *H. erectus* fossil assemblages show an increased number of immature relative to mature individuals compared to *Australopithecus africanus* assemblages, suggesting high mortality among immatures (Tobias, 2006), shortened interbirth intervals, increasing energetic demands on reproducing females, and a shift towards cooperative breeding (Aiello and Key, 2002). Ethnographic work supports this view of humans as cooperative breeders, revealing greatly expanded social networks that include multiple providers (hunting males, post-reproductive females) for females and young (Hawkes, 2003; Hill et al., 2009; Hrdy, 2009). This contrasts with chimpanzees, in which the young are solely dependent upon their mothers (Burkart et al., 2009). Collectively, these studies suggest that as community size increased during the origin of *Homo*, so did the complexity of the social networks linking both greater numbers of individuals and different demographics (e.g., young dependents, post-reproductive females, hunting males). The close cooperation, interdependence, and density of social networks within cooperatively breeding hominin groups would have facilitated the spread of diseases within these groups (McCabe et al., 2015).

1.3. Hominin disease ecology

The shift to larger networks linking subgroups within a larger community and greater connectedness within cooperatively breeding groups is believed to have selected for enhanced social cognition (e.g., prosociality, shared-intentionality, theory of mind) that facilitated prolonged, close interactions among individuals and promoted social learning, cooperation, technological advances, and cumulative culture (Whiten, 2000; Tomasello et al., 2005; Byrne and Bates, 2007; Herrmann et al., 2007; van Schaik et al., 2012; Burkart et al., 2014). However, such intense, close proximity interactions would have also facilitated disease transmission (McCabe et al., 2015). Recent work in genetics and evolutionary medicine indicates that hominins harbored numerous pathogens before the advent of agriculture and animal domestication (Harper and Armelagos, 2013). This includes endoparasitic worms (Hoberg et al., 2001; Hurtado et al., 2008), lice (Harper and Armelagos, 2013), tuberculosis (Stone et al., 2009), typhoid fever (Harper and Armelagos, 2013), whooping cough (Harper and Armelagos, 2013), herpes viruses (Harper and Armelagos, 2013), and Epstein Barr virus (Harper and Armelagos, 2013). Thus, hominins were likely under strong selection to assess the disease status of others.

1.4. Disease recognition in animals and humans

Comparative evidence suggests that disease recognition may have been present in early hominins (citations below). Several species with relatively low social complexity have been documented to recognize disease, often either avoiding diseased conspecifics or taking advantage of sick and weakened competitors, e.g., social lobsters (Behringer et al., 2006), pipefish (Rosenqvist and Johansson, 1995), bullfrog tadpoles (Kiesecker et al., 1999), rodents (Kavaliers et al., 1997), house finches (Bouwman and Hawley, 2010; Zylberberg et al., 2012), but see (Nunn, 2003) for a study which found that primates did not use genital inspections to avoid mating with partners infected with sexually transmitted diseases. While the underlying cognitive processes are not well understood, these studies suggest that recognition is based on diverse symptoms including olfactory/chemical cues (Kavaliers et al., 1997; Kiesecker et al., 1999), visual detection of spots (Rosenqvist and Johansson, 1995), and behavioral changes including lethargy and feather fluffing (Bouwman and Hawley, 2010; Zylberberg et al., 2012). Though the amount of cognitive processing required to detect disease may differ by symptom type, the wide array of cues and recognition in multiple species suggests that some simple form of disease recognition could have been basal in hominins.

Infectious pathogens can cause noticeable symptoms that could potentially be detected via the perceptual-cognitive pathways that

are integral to social cognition in primates. Subtle differences perceived in conspecific faces (Leopold and Rhodes, 2010; Sartori et al., 2011), voices (Belin et al., 2004; Belin, 2006), and movement/gait (Loula et al., 2005; Sartori et al., 2011; Peterman et al., 2014) may enable not only the decoding of conspecifics' identities, emotions, and intentions, but also facilitate the detection of disease. This could include changes in facial coloration and texture due to fever, rashes, or nasal discharge, changes in vocalizations due to coughing, nasal discharge, or reduced lung capacity, and changes in movement/gait due to weakness, lethargy, or signs of pain (Hart, 1988; Chapman et al., 2005; Fink and Matts, 2008). Thus, if the detection of social information and disease involve the same perceptual-cognitive pathways, then disease circulating within hominin populations may have selected for increased cognitive capacities and care-giving.

Importantly, such disease recognition would not require individuals to have an abstract concept of disease. Following the well-accepted definition of cognition as information processing (Neisser, 1967; Deaner et al., 2006; Byrne and Bates, 2007; Herrmann et al., 2007; Lee, 2007; Reader et al., 2011; Fernandes et al., 2014; Woodley et al., 2015), the cognitive aspect would be processing the proximate cues that distinguish healthy individuals from diseased individuals (such as changes in appearance or behavior). Selection for such disease recognition would operate at the ultimate level of causation (Tinbergen, 1963; Sherman, 1988), favoring individuals who were able to discriminate who was healthy and who was not. Those who avoided infectious individuals or provided care to ill kin would increase their reproductive fitness. Similarly to how kin recognition can operate without individuals having an abstract concept of kin (Rendall, 2004), disease recognition could operate without a concept of disease.

1.5. Care-giving among animals and humans

The literature contains numerous reports of striking cases of social care given by animals, including dolphins that cooperatively supported a dying conspecific who could no longer swim (Park et al., 2013), an elephant that attempted to lift a collapsed and dying conspecific to her feet (Douglas-Hamilton et al., 2006), primates that groom, stand watch over, and/or chase others away from dying group members (Nakamichi et al., 1996; Anderson et al., 2010; Bezerra et al., 2014), and an otter group that provisioned an elderly female (Davenport, 2010). Though very interesting, these reports do not provide evidence of widespread long-term care that would be expected to have a more significant selective influence on the evolution of a species.

Some of the best opportunities for systematically investigating care-giving in animals have come from studies of populations with high prevalences of severe injuries (Byrne and Stokes, 2002; Stokes and Byrne, 2006; Beamish and O'Riain, 2014) or congenital disabilities (Turner et al., 2014). These studies generally suggest that, instead of relying on social care, severely injured or disabled individuals survive by adapting and making adjustments themselves, rather than receiving accommodation or assistance (Byrne and Stokes, 2002; Stokes and Byrne, 2006; Beamish and O'Riain, 2014; Turner et al., 2014). The exception to this is social grooming (Dittus and Ratnayeke, 1989). Wound cleaning has been shown to be an important mechanism for avoiding infections and it is widespread in animals (Dittus and Ratnayeke, 1989; Hart, 2011). Thus, wound cleaning may have been a basal form of social care in hominins.

In addition, evidence from modern foraging, hunting, and horticultural peoples suggests that provisioning people who are ill or injured is important in reducing the mortality rate (Sugiyama, 2004). For example, Sugiyama (2004) found that over 50% of individuals reported at least one time in their lives when they were incapacitated and could not forage for at least a month. During such times, provisioning was critical to their survival (Sugiyama, 2004). Based on this evidence, we expect that hominins could have significantly reduced the mortality arising from disease and infection-related injuries through provisioning (Sugiyama, 2004) and wound cleaning (Dittus and Ratnayeke, 1989). Additionally, food sharing networks of hunting males also served as provisioning networks during times of illness (Gurven et al., 2000; Sugiyama and Chacon, 2000; Sugiyama, 2004), suggesting that the evolution of social care may have co-evolved with cooperative breeding.

1.6. Care-giving in the fossil record

Fossil evidence of hominins surviving illness, injuries, and disabilities goes back nearly two million years to include fossils from *H. erectus, H. heidelbergensis, H. neanderthalensis*, and *H. sapiens*. While the following discussion is not exhaustive, it does illustrate the variety of conditions hominins survived, the time depth of the fossil record, and the taxa included. In *H. erectus,* examples of survival after illness include: premortem loss of all but one tooth in the 1.77 Ma cranium and mandible from Dmanisi (D3444 and D3900 [Lordkipanidze et al., 2005, 2006]), possible hypervitaminosis A in the 1.6 Ma KNM-ER 1808 (Walker et al., 1982), evidence of a herniated disc in the 1.5–1.6 Ma Nariokotome boy KNM-WT 15000 (Grove et al., 2012; Haeusler et al., 2013; Schiess et al., 2014), and a healed cranial lesion caused by trauma or burning in the 0.6 Ma Hulu 1 cranium, also called Nanjing 1 and Tangshan 1 (Shang and Trinkaus, 2008; Wu et al., 2011). Among *H. heidelbergensis*, the following have been observed: craniosynostosis and neurocranial deformities in the 0.53 Ma immature cranium 14 from Sima de los Huesos, Atapuerca, Spain, who survived for at least approximately five years (Gracia et al., 2009); a 0.53 Ma adult male pelvis and lumbar spine, SH Pelvis 1, showing lesions and degeneration possibly resulting from lumbar kyphotic deformity, spondylolisthesis, and Baastrup disease (Bonmati et al., 2010); and a squamous temporal lesion that shows healing on the 0.35 Ma Broken Hill cranium Kabwe 1 (Montgomery et al., 1994; McBrearty and Brooks, 2000; Grove et al., 2012). In Neandertals, examples include: Aubesier 11, dated to at least 0.17 Ma, which shows significant tooth loss and alveolar lesions (Lebel et al., 2001; Lebel and Trinkaus, 2002), and Shanidar 1, dated at 0.73–0.4 Ma, who lost much of his right arm, may have been blind on one side, and suffered from hyperostotic disease (Crubezy and Trinkaus, 1992; Hublin, 2009). *Homo sapiens* individuals who survived severe conditions include: a child, Qafzeh 12, dated to approximate 0.095 Ma, who showed signs of hydrocephaly and survived until about 3 years old (Tillier et al., 2001); an older child, Qafzeh 11, also dated to 0.95 Ma, that had a healed cranial fracture (Coqueugniot et al., 2014); and an adult female, Dolní Věstonice 3, dated to approximately 0.027 Ma, who sustained a severe injury to her face that might have interfered with eating (Trinkaus and Jelinek, 1997; Trinkaus et al., 2006).

While all of these individuals might have benefited from care, comparative evidence from nonhuman primates suggests that care is not necessary (Dettwyler, 1991; DeGusta, 2002, 2003). Studies of wild baboons and great apes show that primates frequently survive even when a hand or foot is maimed or severed, e.g., in snares (Byrne and Stokes, 2002; Munn, 2006; Stokes and Byrne, 2006; Beamish and O'Riain, 2014). Though these animals may show changes to their activity budgets (Beamish and O'Riain, 2014), altered locomotor patterns (Munn, 2006), and reduced feeding efficiency (Byrne and Stokes, 2002; Stokes and Byrne, 2006), survival appears to be high, with some groups having as many as ~20% of their members permanently disabled (Munn, 2006). Extensive tooth loss also appears to be survivable. Apes and other primates

have been observed to survive antemortem tooth loss comparable to that observed in the fossil record (DeGusta, 2002; Cuozzo and Sauther, 2004). DeGusta (2002) provides a review of cases in which chimpanzees were observed to survive with tooth loss similar to Aubersier 11, and Cuozzo and Sauther (2004) reported that tooth loss is common among ring-tailed lemurs, with one individual surviving with 80% tooth loss. Overall the evidence from the fossil record and animal studies indicates that while various fossils have clearly survived severe health conditions, it is very difficult to rule out the possibility that they may have survived without care (Dettwyler, 1991; DeGusta, 2002, 2003).

1.7. The modeling approach

It is currently not possible to determine when extensive social care evolved in the human lineage, but how it might have evolved and what conditions might have selected for it can be considered. We expect that, because kinship is a fundamental property of primate (including human) social networks (Silk, 2009), providing care to the diseased may have originated along kin networks. Hamilton's (1964) rule of inclusive fitness predicts that individuals will act altruistically when: benefit to the recipient * relatedness to recipient > costs to the altruist. Thus, individuals could increase their own reproductive fitness in two ways: 1) by avoiding ill individuals, particularly nonkin, and 2) by providing care to ill kin who, upon recovery, would reproduce. Whether the fitness benefits are greater when individuals avoid ill conspecifics or provide care (thus risking becoming infected) will depend upon the benefits, the degree of relatedness, and the costs.

Here, we use agent-based modeling to test a varying intensity of disease scenarios and quantify selection pressures for increased cognition and care-giving. Agent-based models provide powerful, quantitative insights into disease transmission, including predicting the impact of current/future outbreaks and planning intervention/prevention strategies, e.g., influenza (Guo et al., 2015), Ebola (Merler et al., 2015). We take the innovative approach of applying these techniques to reconstruct the potential impact of disease on hominin evolution.

A modeling approach is valuable because, while our knowledge is increasing, (i.e., Harper and Armelagos, 2013), we do not have sufficiently detailed data concerning how/when disease load changed during hominin evolution to be able to test whether the evolution of care-giving co-occurred with increasing cognitive abilities, social complexity, and disease risk. Therefore, we use agent-based modeling to examine under which conditions disease could select for increased cognition and care-giving. We hypothesize that 1) disease will produce care-giving among kin and an increase in average population intelligence, 2) that varying disease characteristics will produce variation in the strength of selection, and 3) that care-giving will produce greater selection for cognition than an avoidance strategy.

2. Material and methods

2.1. Study design

We created two models for comparison. The first (Model 1: Care-giving model) simulates disease transmission in a population of hominins who give care. (The description is in the Supplementary Online Material [SOM] Section A in ODD format [Overview, Design concepts, Detail]. The code is available in SOM Code File 1, and can be opened with standard text editing programs such as WordPad.) In order to more fully explore the model and how care-giving may alter the progression of disease through the population, we created a control model (Model 2: avoidance only) similar to the first except that agents avoid diseased kin and provide no care. (The ODD description is in SOM Section B. The code is available in SOM Code File 2.)

2.2. Model 1: care-giving model

2.2.1. Disease characteristics We programmed an SIS (susceptible-infected-susceptible) model in Netlogo 5.0.5 (Wilensky, 1999; Railsback and Grimm, 2011). We created four hypothetical diseases with case fatality rates modeled after Ebola (2014 outbreak: 70% [Aylward et al., 2014; WHO, 2014a]), Crimean-Congo hemorrhagic fever (40% [WHO, 2013]; CCHF, hereafter), measles (~10% [WHO, 2014b]), and a low risk comparison, such as scabies (fatality rate set at 1%, though scabies is generally not fatal [WHO, 2015]). We did not attempt to precisely simulate the natural history of these diseases. Rather, these diseases were chosen to represent a range of fatality rates occurring in socially transmitted diseases.

2.2.2. Optimizing the disease transmission rates Because transmission rates have complex relationships with virulence and host density (e.g., trade-off hypothesis [Alizon et al., 2009]), we screened possible transmission rates to determine what would be optimal for persistence of these diseases in this population. For the Ebola-like, CCHF-like, and measles-like diseases, we ran the model 1000 times in Netlogo's BehaviorSpace, varying the probability of transmission from 10% to 100% by increments of 10. For the scabies-like disease, we ran the model 1000 times varying the probability of transmission from 1% to 98.5% by increments of 2.5. The inclusion of lower transmission values for the scabies-like disease is based on literature showing that less virulent diseases tend to propagate slower (e.g., Ewald, 1993; Alizon et al., 2009). Then, for each disease, we selected the runs that had both healthy and diseased individuals after 100 time steps. We averaged the probability of transmission across those successful runs to obtain a transmission rate that is optimal for each respective disease: Ebola-like 78%, CCHF-like 33%, measles-like 10%, and scabies-like 2%. The higher transmission rates in the diseases with higher fatality rates are consistent with the relationship between virulence and transmission documented in the literature (Alizon et al., 2009).

2.2.3. Determining the probability of recovery after care We expect that the earliest forms of social care given by hominins would have been assistance with hygiene, including keeping wounds, sores, and topical infections clean as in nonhuman primates (Dittus and Ratnayeke, 1989), provisioning those who are too ill to forage with food and water (Sugiyama, 2004), and watching over individuals who may be too ill to themselves be vigilant against predators (Nakamichi et al., 1996; Anderson et al., 2010; Bezerra et al., 2014). None of these forms of care requires medical knowledge, yet evidence from nonhuman primates (Dittus and Ratnayeke, 1989) and human foraging groups (Sugiyama, 2004) suggests that they are effective at reducing mortality rates.

It is difficult to estimate how effective each of these care-giving techniques would be for each of our hypothetical diseases. In nature, the more incapacitated the individual is and the longer the recovery takes, the greater the chances that the individual would succumb to dehydration, starvation, or predation unless care is given. Because we did not wish to bias the effectiveness of the care towards the more severe diseases, we set the probability of recovery after care at 0.5 for all diseases. This reflects an equal chance of recovery and failure to recover.

2.2.4. The population The landscape is a 40 × 40 cell grid that wrapped horizontally and vertically. Each cell represents 5 km^2, making the landscape 200 km^2. This is within the confidence intervals of the space requirements calculated for a community of

H. erectus, H. heidelbergensis, H. neanderthalensis, and *H. sapiens* using the gas model in Grove et al. (2012). Table 1 summarizes the group sizes, densities, and space requirements, as presented in Grove et al. (2012).

The carrying capacity of the landscape is set at 200. Two hundred was chosen because it is large enough to encompass the group sizes predicted for hominins based on cranial capacities, brain volumes, and neocortex ratios of fossil hominins (Table 1, Aiello and Dunbar, 1993; Gamble et al., 2011; Grove et al., 2012), but is generally smaller than community sizes reported for modern humans (e.g., Layton et al., 2012; Hill et al., 2014). We set the carrying capacity above the calculated community sizes for hominins, e.g., ~150 or smaller (Aiello and Dunbar, 1993; Dunbar, 1998; Gamble et al., 2011; Grove et al., 2012), to allow for the event that the actual community sizes of the model populations would likely be lower than the carrying capacity.

2.2.5. Initialization The program is initialized with 10 agents randomly placed on the landscape. Each agent is randomly assigned an intelligence score (0–1). In the model, the intelligence score is the likelihood of an agent correctly identifying the disease status of another agent. We refer to it as intelligence because we expect that the ability to recognize disease is related to a more general ability for efficient information processing, including social information (e.g., Deaner et al., 2006; Byrne and Bates, 2007; Herrmann et al., 2007; Lee, 2007; Reader et al., 2011; Fernandes et al., 2014; Woodley et al., 2015). As the population grows, each offspring's intelligence is drawn from a normal distribution with the parent's intelligence as the mean and a standard deviation of 0.15.

2.2.6. Population growth and genetic structure The population grows at each time step of the model when healthy agents reproduce according to the formula: ([1 − [number of agents/carrying-capacity]] * number of healthy agents). Reproduction occurs asexually. Offspring are placed within a radius of three grid cells of the parent, producing spatial clustering of kin as is consistent with human and nonhuman primate groups (Chapais and Berman, 2004; Silk, 2009; Hatchwell, 2010; Hill et al., 2011).

Relatedness is tracked by links between agents with the links containing the relatedness value. Parent-offspring relationships receive relatedness values of 0.5 and offspring inherit the links of the parent but with 1/2 the relatedness value. Because offspring inherit the links of the parent, sibling relationships are included in the model with a relatedness value 0.25. To prevent the model from becoming too computationally intensive, patrilineal relationships, plus matrilineal relationships beyond a relatedness of 0.25, were not modeled. This decision is supported by findings showing that kin recognition occurs most reliably for close matrilineal kin identified via familiarity (e.g., Chapais et al., 1997; Chapais and Berman, 2004). The population represents a single, kin structured community with multiple matrilines. Space displays the contact structure between agents and random movement simulates mixing within the population.

2.2.7. Space With a carrying capacity of 200 individuals and a landscape of 200 km^2, our model has a maximum population density of 1 individual/km^2, which is within the confidence intervals calculated for *H. habilis* and *H. erectus* (Table 1; Grove et al., 2012). However, the purpose of our model is not to attempt to reconstruct a particular hominin species or population. We made this decision because the population densities and number of levels of fissioning have been reconstructed to vary dramatically even within species, depending upon the habitat quality and latitude (Atkinson et al., 2008; Powell et al., 2009; Grove et al., 2012). Instead, hominin societies are conceptualized as more generic fission–fusion communities in which subsets of individuals are out of contact with other subsets of individuals (Grove et al., 2012; Layton et al., 2012). This is represented in our model by the restrictions created by the movement, care-giving, and infection radii. The care-giving radius (5) and infection radius (5) are equal to reflect that agents who are close enough to give care are also close enough to become infected. Similarly, agents who avoid infectious kin by moving away will also be moving away from potential care-givers should they themselves become infected. These radii of five grid cells represent 25 km^2 and are in the upper range of the distance that modern hunter-gatherers travel from camp when they will return to camp later the same day (Grove et al., 2012; Layton et al., 2012).

2.2.8. Disease and care-giving After four time steps of the model, 25 agents are randomly infected with one of the diseases. This is approximately 16% of the population and reliably seeds the disease into the population without increasing to 100% prevalence.

Healthy agents evaluate the relatedness and disease status of other agents within a radius equivalent to five grid cells. The infection radius is also set at five grid cells, thus any healthy agent that can provide care is also close enough to be infected.

Kin are accurately recognized and the accuracy of disease recognition is a function of the agent's intelligence. A random number between 0 and 1 is drawn. If the number is below the agent's intelligence value, the disease status is correctly recognized. Otherwise, the agent's disease status is incorrectly recognized (healthy kin are classified as diseased or diseased kin are classified as healthy). These individuals make up the group the agent perceives to be its diseased kin (perceived diseased kin). Whether the error is a false positive (healthy kin classified as diseased) or a false negative (diseased kin classified as healthy) is determined by the disease status of the kin agent. Thus, the likelihoods of false positive and false negative errors are functions of disease prevalence. As the proportion of diseased agents increases, false positives decrease and false negatives increase.

Agents randomly select one of their perceived diseased kin and decide whether to provide care based on a modification of

Table 1
Summary data calculated from the hominin dataset presented in Appendix Table A1 of Grove et al. (2012).[a]

Genus	Taxon	Community size (Individuals)			Population density (I/km^2)			Area required (km^2)		
		Lower CI	Median	Upper CI	Lower CI	Median	Upper CI	Lower CI	Median	Upper CI
Homo	Early *Homo*	43.249	56.276	71.402	0.366	0.584	0.802	51.529	92.525	188.043
Homo	*habilis*	46.8415	60.476	76.2795	0.577	0.822	1.068	43.8705	73.56	132.306
Homo	*erectus*	66.43	83.158	102.406	0.545	0.785	1.025	70.289	113.994	200.766
Homo	*heidelbergensis*	70.9845	88.389	108.389	0.3	0.514	0.728	94.736	164.6655	339.368
Homo	*neanderthalensis*	72.622	90.266	110.5325	0.196	0.407	0.618	116.066	217.395	536.199
Homo	*sapiens*	78.763	97.292	118.541	0.196	0.407	0.618	127.537	240.876	613.916

[a] Values and confidence intervals (CI) are medians calculated from the published dataset. To keep our terminology consistent, we refer to community size (number of individuals) where Grove et al. (2012) refers to group size. Community sizes are not whole numbers because Grove et al. (2012) calculated them from cranial volumes. Population density = individuals (I)/km^2. We follow the taxonomic scheme given in Grove et al. (2012).

Hamilton's rule, which predicts altruism when: relatedness between the recipient and altruist * benefit to the recipient > cost to the altruist (Hamilton, 1964). We adapted this formula so that agents provide care when: relatedness between the care-giver and the recipient * probability of recovery after care > probability of transmission to care-giver * probability of infection being fatal. If the inequality is fulfilled (thus care is given) and the recipient was in fact diseased (not just perceived to be diseased), a random number between 0 and 1 is generated and if it is below the probability of recovery, the diseased individual recovers. If the random number was above the probability of recovery, the recipient remains diseased. A new random number is drawn for the care-giver and if it is below the probability of transmission to the care-giver, then the care-giver is infected. If the recipient was erroneously categorized as diseased, but is actually healthy (a false positive error), there is no change in the disease statuses of the recipient or the care-giver. It is worth noting that when a false negative error occurs (diseased kin are classified as healthy), the agent that made the error does not incur a cost that is explicitly coded into the model in the form of an immediate and definite infection risk. However, the agent does potentially incur emergent costs through the interactions between agents. This may occur in two ways: a) if that diseased kin agent dies (later in the model run), the kin network available to give care is reduced, simulating a loss of inclusive fitness to the agent that failed to recognize the disease in its kin, and b) the presence of diseased kin in the population increases the risk that others, including the agent that failed to recognize the disease in its kin, will become infected.

If healthy agents have no perceived diseased kin, they move to a grid cell with no other agents on it within a radius of eight grid cells. If no empty cells are available, the agent does nothing. A movement radius of eight cells represents 40 km^2. This is the median daily total travel distance used by Grove et al. (2012) to calculate hominin area requirements and it is based on data compiled from modern hunter-gathers (e.g., Layton et al., 2012).

2.2.9. Avoidance of infectious individuals If the randomly selected recipient (from the agent's perceived diseased kin) does not fulfill the inequality for receiving care, the agent moves to a grid cell with no other agents on it within a radius of eight grid cells. This can occur due to a low relatedness with the recipient of care, high costs of exposure to the disease, or a low likelihood of recipient recovery. Under these conditions, the agent avoids the diseased individual instead of providing care. Note that nonkin do not receive care, thus if no perceived diseased kin are within the care-giving radius, the agent moves.

Because the care-giving radius and the infection radius are set at five grid cells, and this is less than the movement radius (eight), agents that do not provide care can move out of the infection radius. The effectiveness of movement as a disease avoidance strategy is based on chance and the density of infected individuals. By chance, the healthy agent may move to a grid cell that is outside of the infection radius of the diseased agent. However, as the density of infected agents increases, so does the likelihood that the healthy agent will move to a grid cell that is within the infection radius of another diseased agent. This reflects the difficulties of avoiding exposure when there is a high density of infectious individuals in the population. If no empty cells are available, the agent does nothing.

2.2.10. Mortality and disease transmission The model generates a random number for each diseased agent. If the number is below the probability of fatality, that agent dies. All healthy agents have a probability of becoming infected from any infected agent within a radius of five grid cells based on the probability of transmission. Five grid cells represent the upper range of the daily travel radius for modern hunter-gatherers (25 km^2; Grove et al., 2012; Layton et al., 2012). A random number (0–1) is drawn for each healthy agent in danger of infection. If the number is below the probability of transmission, the agent is infected. If an agent is in danger of infection from more than one diseased agent, the process is repeated for each infectious agent in five grid cells.

2.2.11. Model analysis We ran the model 2000 times for 100 time steps for each disease. We considered runs to be successfully completed when both the disease and population had persisted (defined as $\geq$1 diseased agent and $\geq$1 healthy agent at 100 time steps). The first 1000 successfully completed runs were divided into 10 groups of 100. We calculated average population size, average disease prevalence, average percentage of diseased individuals who received care (percent care), and average population intelligence at each time step across the 100 runs. This created an n of 10 average runs for which we made curves depicting the changes in each of these output variables for the four diseases we considered. We used the 10 averages in the subsequent statistical tests instead of the original 1000 runs to avoid inflating our sample size, and thus the power of our tests (Railsback and Grimm, 2011).

2.2.12. Statistics We compared the endpoints of the curves by comparing the output variables (average population size, average disease prevalence, and average percent care) across the diseases at time step 100 using one-way analysis of variance (ANOVA; n = 10 average runs/disease). We calculated the change in average population intelligence between the first and 100th time step, tested whether the differences were different from zero using one-sample t-tests, and whether these differences varied across disease types using a one-way ANOVA. We calculated maximum slopes for the curves of the average percent care and the average population intelligence using grofit (Kahm et al., 2010) in R 2.13.1 (RCoreTeam, 2011) and RStudio 0.98.1062 (RStudio, 2014). We tested whether the slopes differed across disease types using a one-way ANOVA. Some violations of normality and equal variances existed (SOM Tables S1–S4). One-way t-tests were bootstrapped with 1000 samples for robusticity to non-normality and 95% bias corrected accelerated confidence intervals were calculated (Field, 2013). Though one-way ANOVAs are generally robust to such violations when groups have equal sample sizes, when variances were unequal, we used the Brown-Forsythe F-ratio. Alpha was set at 0.05 and multiple comparisons across disease types were Bonferroni corrected when variances were equal and Tamhane T2 corrected when they were unequal. Statistical tests were run in SPSS Statistics 22 or 23 unless otherwise stated.

2.3. Model 2: control model—avoidance only

Following the initial analysis of the care-giving model (Model 1), we programmed a control (Model 2: avoidance only) to further explore how care-giving may have altered the progression of disease through hominin populations. This model used the same population and diseases, but differed in two ways. First, agents who have perceived diseased kin avoid them instead of providing care. All agents with perceived diseased kin move randomly to an empty grid cell within a radius of eight. Second, if the agent has no perceived diseased kin or there are no empty grid cells within a radius of eight, the agent does not move. This differs from the care-giving model in which agents with no diseased kin also move to an empty grid cell within eight. (Because agents that give care do not move, this was necessary in the care-giving model to ensure movement within the population.) We made this second change to the avoidance model to be conservative with respect to our expectation that only care-giving will produce intelligence changes. This second change increased selection on avoidance behavior

because in Model 2 (avoidance only), the only opportunity agents have to move is when they are avoiding diseased kin.

2.3.1. Model analysis and statistics We used the same procedure as above to create 10 average runs for each output variable for each disease. We conducted one-sample *t*-tests to determine whether the difference in average population intelligence between the first and 100th time steps were significantly different from zero for the scabies-like, measles-like, CCHF-like, and Ebola-like diseases. We used two sample *t*-tests to determine whether the population size, prevalence, and intelligence at the 100th time steps differed between models 1 and 2. Some violations of normality and equal variances existed (SOM Tables S1–S4). *T*-tests were bootstrapped with 1000 samples for robusticity to non-normality and 95% bias corrected accelerated confidence intervals were calculated (Field, 2013). When Levene's test showed violations of the assumptions of equal variances, we report results calculated without assuming equal variances (Field, 2013). Alpha was set at 0.05.

2.4. Analysis of the intelligence curves produced by Model 1 (care-giving)

We analyzed the trajectories of the intelligence curves of the 10 average runs for each disease using linear mixed-models run in R 3.2.4 (RCoreTeam, 2015) using the nlme package. We used this approach to relate infection prevalence to changes in mean intelligence, while taking into account population size. We tested for an interaction between prevalence and population size on changes to mean intelligence by including an interaction term in the model: prevalence * population size. As the data are longitudinal (i.e., time series), we allowed for autocorrelated errors using an ARMA process, incorporated time as a fixed effect, and used the averaged simulation run as the random effect. We checked for issues of multicollinearity using variation inflation factor and checked the residuals of the models for non-normality, heteroscedasticity, and autocorrelation. (Model: change in mean intelligence ~ time + prevalence * population size + random intercept.) In order to keep the paper focused on the evolution of increasing average population intelligence, we did not conduct this analysis on the Model 2 curves, which showed either no increase or a decrease in average intelligence.

3. Results

3.1. Model 1: care-giving model

After 100 time steps, the four diseases produced significantly different population sizes, disease prevalence, percentages of the diseased who received care, and average population intelligences (Tables 2 and 3, Fig. 1). The Ebola-like disease, unlike the other three, produced no care-giving and no change in average population intelligence (Table 4, Fig. 1). Both the Crimean-Congo hemorrhagic fever-like (CCHF-like) and measles-like diseases show initial increases in both care-giving and intelligence followed by a plateau (Fig. 1). The CCHF-like disease produced a care-giving rate of 4.7%, a final intelligence level of 0.62, and a 12% net change in intelligence. Of the four diseases, the measles-like disease produced the highest rate of care-giving (6.7%) and the highest average population intelligence (0.71) at the final time step. This was generated by the greatest maximum slopes for care-giving and intelligence changes and the greatest net change in intelligence over time (21%). The scabies-like disease showed a strikingly different pattern. As prevalence steadily increased, because the fatality rate was low, care-giving decreased. Infected individuals did not provide care and rarely died, meaning that the number of healthy individuals able to provide care decreased. This produced a negative slope for care-giving, though low increases in average population intelligence were still observed (care-giving rate: 1.4%, final average population intelligence: 0.53, net intelligence change: 3%; Tables 2 and 3).

3.2. Model 2: control model—avoidance only

The model two results revealed two important findings. First, an avoidance strategy did not result in an increase in average population intelligence (Tables 5 and 6). The net change in intelligence over time was not significantly different from zero under the scabies-like and measles-like conditions (Table 5). Under the CCHF-like and Ebola-like conditions, the average population intelligence decreased significantly (Table 5).

Second, a visual inspection of Figures 2–4 shows that the progression of the diseases through the population differed under Model 1 (care-giving) and Model 2 (avoidance only). Descriptive statistics are provided in SOM Table S5. For the scabies-like and measles-like diseases, when agents gave care, the final population sizes were higher and the final prevalences were lower (Figs. 2 and 3, Table 6). A visual inspection of Figure 3B reveals that when agents give care, the "boom and bust" cycle of disease outbreaks in the population was reduced, with prevalence increasing and decreasing less dramatically. For the CCHF-like disease, the final population sizes differed, however prevalence did not differ (Table 6). An inspection of Figure 3C shows that the cycle of outbreaks was very similar in the care-giving and avoidance conditions. For the Ebola-like disease, final population size and final prevalence did not differ in the care-giving and avoidance conditions.

3.3. Analysis of the intelligence curves produced by Model 1 (care-giving)

For each of the scabies-like, measles-like, and CCHF-like diseases, time was negatively related to changes in intelligence (Table 7). Thus, the largest increases occurred early in the run with smaller increases occurring later. In the case of the Ebola-like disease, intelligence did not change, thus there was no relationship between time and changes in mean intelligence. For the scabies-

Table 2
Means and standard deviations (SD) for each disease for final population sizes (number of individuals), final disease prevalences (percent of the population that is infected), final percent care (percentage of diseased individuals who received care), final average population intelligence, the net intelligence change between time steps 1 and 100 (Intelligence change), the maximum slope for percent care (Slope care), and the maximum slope for average population intelligence (Slope intelligence) from Model 1 (Care-giving).

Disease	Population size (Individuals)		Prevalence (%)		Percent care (%)		Intelligence		Intelligence change		Slope care		Slope intelligence	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Scabies	184.07	0.77	84.78	0.42	1.37	0.11	0.53	0.01	0.03	<0.01	−0.00006	0.00003	0.0006	0.00007
Measles	133.64	2.02	70.15	0.76	6.74	0.43	0.71	0.01	0.21	0.01	0.00053	0.00006	0.0043	0.00032
CCHF	120.96	3.47	33.63	1.75	4.73	0.50	0.62	0.01	0.12	0.02	0.00022	0.00005	0.0025	0.00042
Ebola	157.24	3.25	10.32	0.51	–	–	0.50	0.01	0.00	0.01	–	–	0.0003	0.00020

Table 3
One-way ANOVAs showing significant differences across disease types for the final population size, final disease prevalence, final percent care, final average population intelligence, the net intelligence change between time steps 1 and 100, the maximum slope for percent care, and the maximum slope for average population intelligence for Model 1 (Care-giving)[a].

Test	F-statistic	Df	*p*	Smallest mean difference	*p*
Final population size	1131.78[BF]	3, 24.47	<0.001	≥12.68[T]	<0.001
Final prevalence	11,275.24[BF]	3, 15.24	<0.001	≥0.15[T]	<0.001
Final percent care	492.03[BF]	2, 18.61	<0.001	≥0.02[T]	<0.001
Final intelligence	579.51[UC]	3, 36	<0.001	≥0.03[B]	<0.001
Intelligence change	464.463[BF]	3, 23.13	<0.001	≥0.03[T]	<0.001
Maximum slope percent care	377.10[UC]	2, 27	<0.001	≥0.0003[B]	<0.001
Maximum slope intelligence	421.732[BF]	3, 21.61	<0.001	≥0.0002[T]	≤0.03

[a] All multiple comparisons between disease types were significant, thus only the smallest mean difference and corresponding *p*-value are shown per test. Df = degrees of freedom.
[UC] F-statistic, uncorrected; [BF] Brown-Forsythe F-statistic; [B] Bonferroni correction for multiple comparisons; [T]Tamhane's T2 test for multiple comparisons.

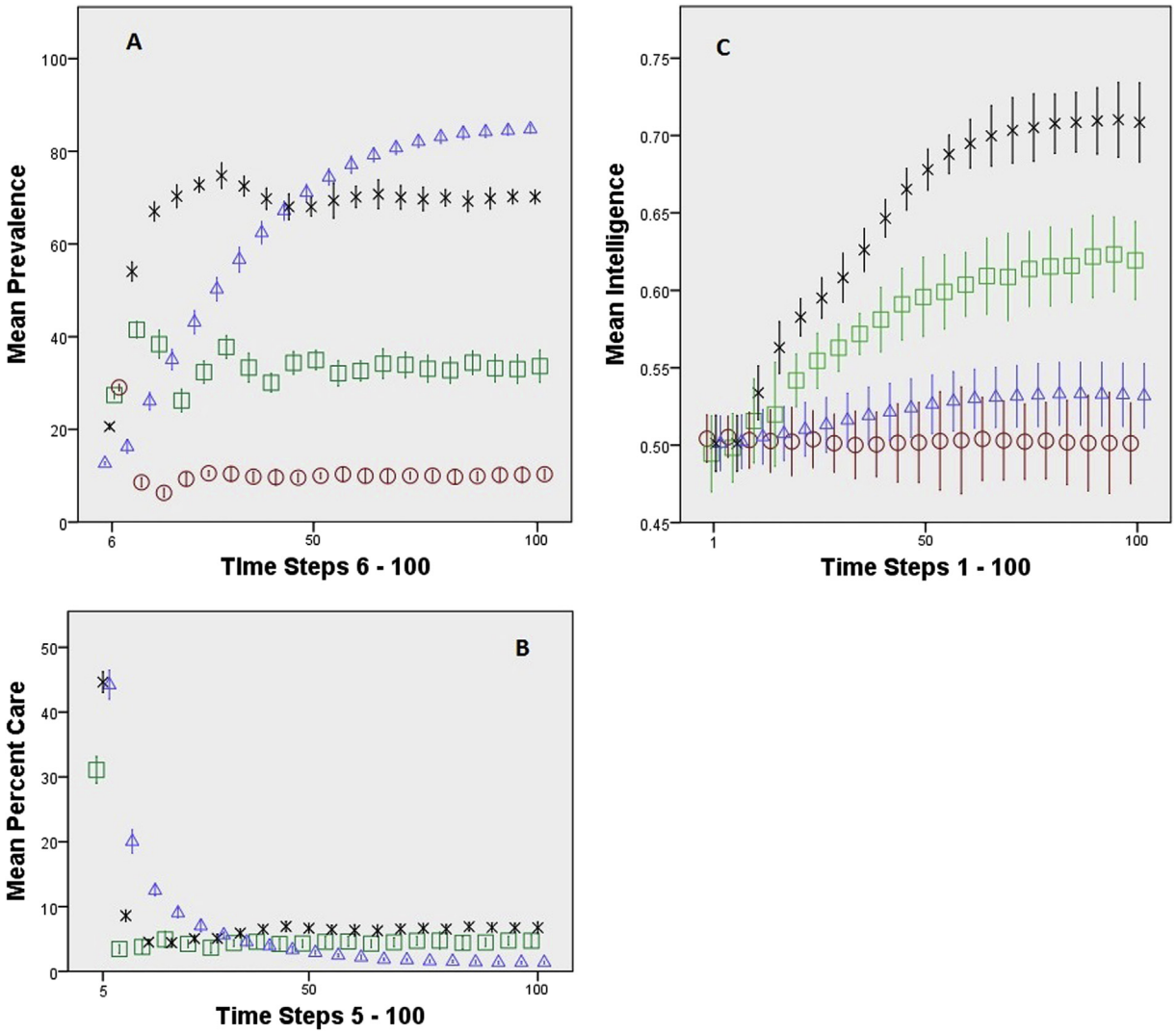

Figure 1. A) Changes over time in disease prevalence (percentage of the population that is infected), (B) percentage of diseased individuals who received care, and (C) average population intelligence. For each disease, the 10 average runs have been averaged within each time step. The Ebola-like, CCHF-like, measles-like, and scabies-like diseases are shown in red circles, green squares, black Xs, and blue triangles, respectively. Approximately every fourth time step is shown. Error bars are ± two standard deviations. Figure 1B does not show the Ebola-like disease because no care was given. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

like disease, variance inflation factor (VIF) scores indicated high collinearity between dependent variables (VIF scores >100). When we dropped population size from the analysis, VIF scores fell below seven. In this reduced analysis, changes in intelligence were positively related with prevalence (Table 7, Fig. 5).

For the measles-like disease, changes in intelligence were positively related with both prevalence and population size, with the greatest increases in intelligence occurring at larger population sizes and high prevalences (Fig. 6). For the CCHF-like disease, the proportion of the variation explained by the analysis (marginal

Table 4
One-sample *t*-tests on the Model 1 results showing that the difference in average population intelligence between the first and 100th time steps were significantly different from zero for the scabies-like, measles-like, and CCHF-like diseases, but not for the Ebola-like disease[a].

Test	*t*	Df	*p*	CI: Lower	CI: Upper
Scabies-like	22.18	9	**<0.001**	0.028	0.033
Measles-like	44.78	9	**<0.001**	0.196	0.216
CCHF-like	19.36	9	**<0.001**	0.111	0.137
Ebola-like	−0.824	9	0.431	−0.010	0.005

[a] Significant *p*-values are bolded. Df = degrees of freedom, CI = confidence interval.

Table 5
One-sample *t*-tests on the Model 2 results showing that the difference in average population intelligence between the first and 100th time steps were significantly different from zero for the CCHF-like and Ebola-like diseases, but not for the scabies-like and measles-like diseases.[a]

Test	*t*	Df	*p*	CI: Lower	CI: Upper
Scabies-like	−0.997	9	0.352	−0.005	0.001
Measles-like	−1.292	9	0.236	−0.025	0.005
CCHF-like	−24.000	9	**0.001**	−0.160	−0.138
Ebola-like	−58.939	9	**0.001**	−0.216	−0.200

[a] Significant *p*-values are bolded. Df = degrees of freedom, CI = confidence interval.

Table 6
Two-sample *t*-tests comparing population size, prevalence, and mean intelligence values at the 100th time step for each disease under Model 1 (care-giving) versus Model 2 (avoidance) conditions[a].

Disease	Variable	*T*	Df	*p*	CI: Lower	CI: Upper
Scabies-like	Pop. Size	43.178	11.011	**0.001**	28.833	31.344
	Prevalence	−49.675	18	**0.001**	−0.105	−0.096
	Intelligence	7.786	18	**0.001**	0.031	0.052
Measles-like	Pop. Size	9.669	18	**0.001**	9.621	14.569
	Prevalence	−3.000	18	**0.016**	−0.029	−0.007
	Intelligence	30.699	11.148	**0.001**	0.205	0.233
CCHF-like	Pop. Size	−3.165	18	**0.003**	−5.906	−1.296
	Prevalence	0.740	18	0.464	−0.007	0.015
	Intelligence	37.944	18	**0.001**	0.254	0.282
Ebola-like	Pop. Size	−0.024	14.171	0.982	−3.696	3.923
	Prevalence	0.305	18	0.748	−0.004	0.005
	Intelligence	46.049	18	**0.001**	0.200	0.218

[a] When Levene's test indicated that the variances are unequal, we report the *t*-values, degrees of freedom (df), *p*-values, and confidence intervals (CI) calculated without assuming equal variances (Field, 2013). Significant *p*-values are bolded.

$R^2 = 0.15$) was reduced compared to the measles-like (marginal $R^2 = 0.57$) and scabies-like (marginal $R^2 = 0.47$) diseases. However, similar to the measles-like disease, an interaction effect between prevalence and population size was present, indicating that at low prevalences changes in intelligence were negatively related to population size, but at higher prevalences they were positively related with population size (Fig. 7). Thus, the greatest changes in intelligence occurred at low prevalences and low population sizes or high prevalences and high population sizes. No relationships between time, prevalence, or population size were found for the Ebola-like disease because the Ebola-like disease produced no changes in intelligence (Tables 5 and 7, Fig. 8).

4. Discussion

Our findings suggest that the evolution of care-giving may have created a profound shift in how hominins evolved in the presence of their pathogens. The avoidance approach (Model 2) likely represents the basal condition, under which disease either does not select for or against increasing cognitive abilities (high prevalence, low fatality diseases) or selects against it (low prevalence, high fatality diseases). In contrast, under the care-giving condition (Model 1), care-giving not only selected for increasing cognitive abilities, but also altered and controlled the progression of some of the diseases throughout the population. We discuss both models and their implications in detail below.

4.1. Model 1

Our results from Model 1 suggest that disease circulating among kin can select for care-giving among kin and greater cognitive abilities. Furthermore, the diseases produced selection of varying strengths, with higher care-giving rates producing greater increases in average population intelligence. The findings are relevant to the evolution of care-giving in hominins as they suggest that not all diseases produce care-giving behavior. The high fatality and transmission rates of the Ebola-like disease, when applied to Hamilton's rule (Hamilton, 1964), generated costs that were greater than the benefits of care-giving, even to close relatives, thus, all agents avoided ill kin rather than providing care. Such diseases are not likely to have facilitated the evolution of care-giving or increased social cognition. The CCHF-like disease had intermediate probabilities of fatality and transmission, leading to care-giving only to close kin (parents and offspring: $r = 0.5$) and not to more distant relatives like grandparents, grandchildren, or siblings ($r = 0.25$), who were avoided when ill (note that the model only includes matrilineal relatedness, thus relatives are matrilineal grandparents, grandchildren, and half-siblings). This produced substantial care-giving behavior and selection for increasing intelligence, but the selection was weaker than for the measles-like disease, where care was given to both close and more distant relatives. The scabies-like disease, while it produced care-giving for both close and more distant relatives, produced only low rates of care-giving and correspondingly weak selection for increasing intelligence. These effects result from the very low fatality rate of the scabies-like disease; the population size appears to have been regulated largely by the carrying capacity set in the model (i.e., habitat supports 200 individuals) rather than by the disease. Therefore, as disease prevalence increased, there was a lack of healthy individuals who could provide care to their diseased kin, leading to a low rate of care-giving, lower population turnover, and lower increases in average population intelligence. Overall, these simulations suggest that diseases that are most likely to have led to the evolution of care-giving in the human lineage were those with low costs to care-givers that persisted at a prevalence low enough not to disrupt the kin networks along which care was provided. Although only healthy agents could give care and reproduce in our model, high rates of costly care-giving may not be expected if kin have sub-lethal diseases that do not reduce their reproductive success.

It is noteworthy that for all three diseases that produced care-giving, the final rate of care-giving was low, with a maximum of 6.7% of the diseased receiving care under measles-like conditions. Furthermore, a recovery rate of only 50% after care suggests that over the course of hominin evolution, even low rates of relatively ineffective care may have been sufficient to select for increasing intelligence and disease recognition.

4.2. Model 2

The Model 2 results demonstrate that avoidance alone does not select for greater cognitive abilities. Avoidance produced no net change in average population intelligence in the scabies-like and measles-like conditions and a decrease in average population intelligence for the CCHF-like and Ebola-like diseases. The scabies-like and measles-like diseases produced higher population sizes and disease prevalences above 50%, thus an agent who moves away from

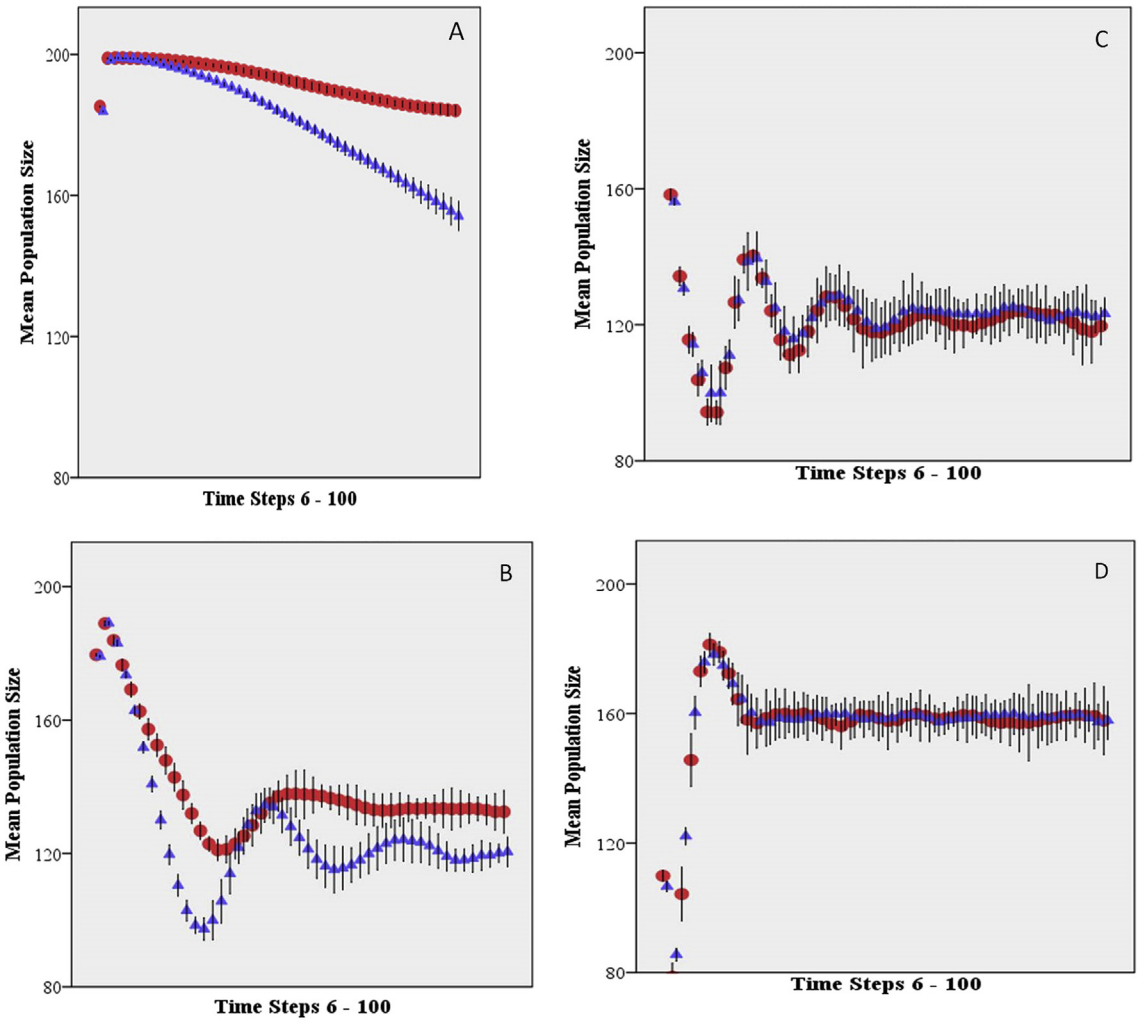

Figure 2. Changes in population size (number of individuals) over time produced by Model 1 (care-giving) and Model 2 (avoidance only) in the scabies-like (A), measles-like (B), CCHF-like (C), and Ebola-like (D) diseases. Models 1 and 2 are shown in red circles and blue triangles, respectively. Only even numbered time steps are shown. Error bars are ± two standard deviations. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

infected kin is likely to encounter other infected individuals. This results in a lack of selection for disease recognition and avoidance. In contrast, the CCHF-like and Ebola-like diseases produced lower population sizes and prevalences below 50%, thus an agent who avoids infected kin is less likely to encounter other infected agents. This results in selection to isolate oneself. The most efficient way for agents to isolate themselves in a population with a prevalence under 50% is to miscategorize healthy individuals as ill, thus triggering avoidance. Because lower intelligence agents have less accurate disease recognition, this produces selection to decrease intelligence.

These findings are relevant for species that do not give care. It suggests that avoidance of high prevalence, low fatality diseases is likely to be an ineffective strategy. As a result, these diseases do not exert selection for or against cognitive abilities under an avoidance-only paradigm. In contrast, avoidance is an effective strategy against low prevalence, high fatality diseases, producing selection for avoidance behavior and selection against sociality.

4.3. Implications of care-giving

A comparison of the results from Model 1 (care-giving model) with Model 2 (avoidance model) indicates that care-giving alters the progression of the disease through the population. For the scabies-like and measles-like diseases, care-giving resulted in significantly higher population sizes and lower prevalences than an avoidance-only strategy. Thus for these diseases, which are the two diseases for which care was given to both close and distant kin ($r = 0.5$ and $r = 0.25$, respectively), care-giving served to control the disease in the population.

Two of the diseases, the measles-like and the CCHF-like diseases, show distinct pulses of disease outbreaks and population crashes ("boom and bust" dynamic, Figs. 2 and 3). These dynamics are consistent with work documenting similar pulsed outbreaks in measles (Keeling and Grenfell, 1997). Interestingly, the lack of congruence between the relatively constant slope of the intelligence curves (Fig. 4) and the boom-bust oscillations of population size and prevalence reflects the fact that selection on intelligence is occurring throughout the boom-bust cycle and not intermittently only when specific conditions are met (e.g., a particular population size or prevalence). This dynamic is quantified through the interaction term of the mixed model analysis in which intelligence increases are the result of complex interactions between prevalence and population size. Because the two diseases progress differently through the population, they also exert selection on intelligence in slightly different ways. The measles-like disease produces one oscillation of the boom-bust outbreak cycle of population and

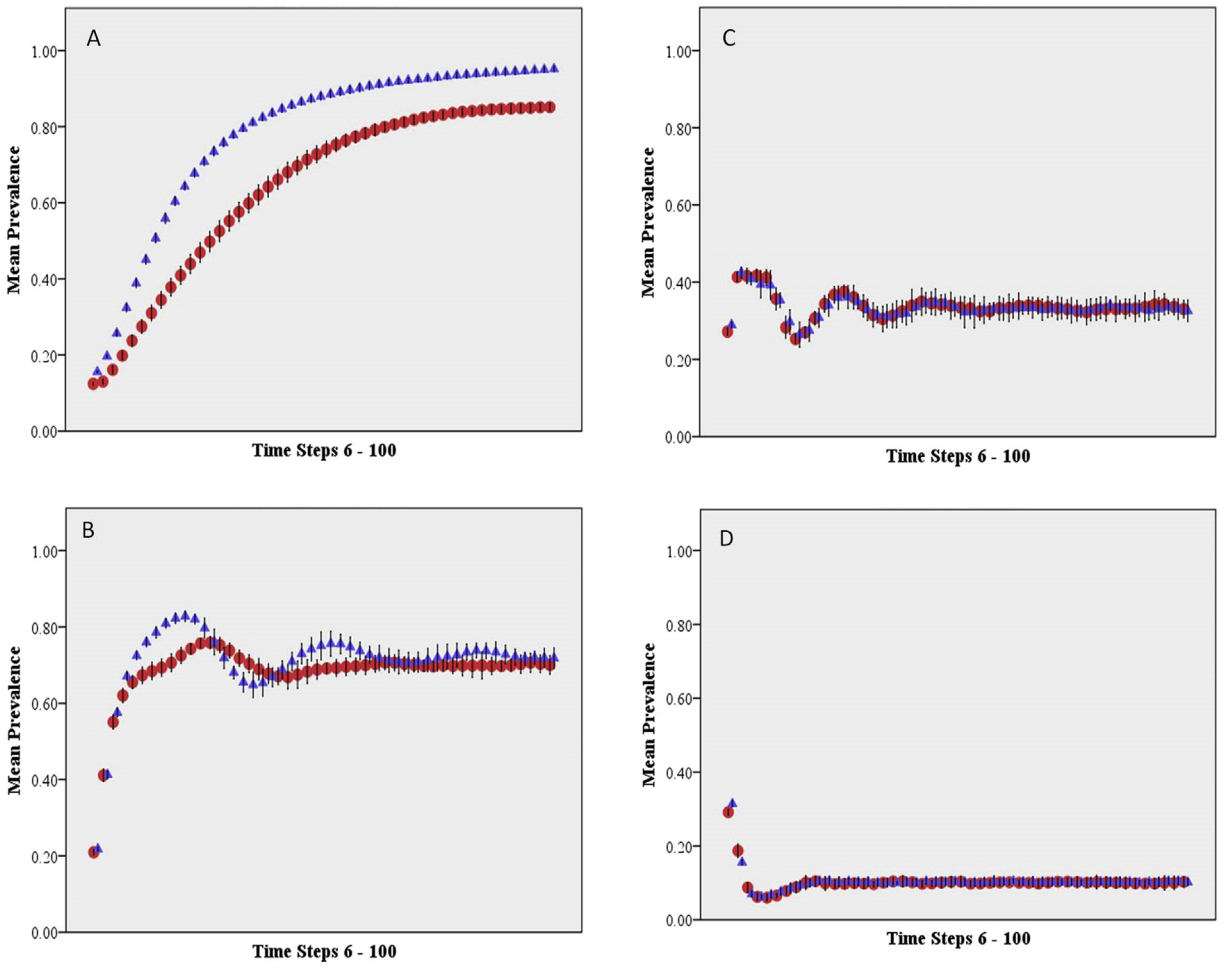

Figure 3. Changes in prevalence over time (percentage of the population that is infected) produced by Model 1 (care-giving) and Model 2 (avoidance only) in the scabies-like (A), measles-like (B), CCHF-like (C), and Ebola-like (D) diseases. Models 1 and 2 are shown in red circles and blue triangles, respectively. Only even numbered time steps are shown. Error bars are ± two standard deviations. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

prevalence peaks and crashes; the CCHF-like disease produces multiple, more rapid oscillations.

The measles-like disease shows a very pronounced "bust" phase early in the run. Population size is high when the disease is first introduced (Fig. 2B, Model 1 curve). This produces a high rate of care-giving and strong selection for intelligence (Fig. 6B, left panel). As the prevalence increases (Fig. 3B, Model 1 curve), low intelligence matrilines recognize diseased kin less accurately and provide less successful care, causing them to succumb to the disease. This produces a decrease in population size and an increase in average population intelligence (Fig. 4B, Model 1 curve). At high prevalences, selection for intelligence is maintained regardless of the population size (Fig. 6B, right panel). Intelligence plateaus about half way through the run, when the population size rebounds slightly but remains low and prevalence decreases slightly from its earlier peak and remains moderate. With a low population size, intermediate prevalence, and a decreased rate of care-giving (Fig. 1B, measles-like curve), the population maintains the higher intelligence, but does not continue to increase it (Fig. 6B, change in intelligence approaches 0 on left side of middle panel). Intelligence plateaus as the boom-bust outbreak oscillations cease.

The CCHF-like disease produces a very pronounced boom-bust cycle with several peaks and crashes in population size and prevalence. Selection for increasing intelligence occurs both during low population sizes and low prevalences (Fig. 7B, left panel) and during high population sizes and high prevalences (Fig. 7B, right panel). When the boom-bust dynamic stops about halfway through the run and the population stabilizes at intermediate population sizes and prevalences, intelligence plateaus (Figs. 2C, 3C, and 4C, Model 1 curves; Fig. 7B, middle panel).

Interestingly, when the population infected with the measles-like disease engages in care-giving, it experiences less pronounced oscillations of the "boom and bust" outbreak cycle (Fig. 3), indicating that care-giving serves to control the spread of the disease through the population. Because of the higher risks of providing care under the CCHF-like conditions, only close kin ($r = 0.5$) receive care. This lower level of care is less effective at controlling the spread of the disease, perhaps suggesting that a certain threshold must be achieved in order to disrupt the boom-bust outbreak cycle. Alternatively, the higher fatality rate and more rapid transmission of the CCHF-like diseases produces faster outbreak cycles, which may make it more difficult for care-giving to disrupt the boom-bust outbreak cycle even though it still selects for increasing cognitive abilities.

For both the measles-like and CCHF-like diseases, the most pronounced outbreaks occur early in the model run, which is also when the greatest increases in intelligence are occurring (Figs. 6A and 7A). In the second half of the run, when the boom-bust dynamic is less pronounced, intelligence plateaus. This suggests that over the course of human evolution, sustained increases in

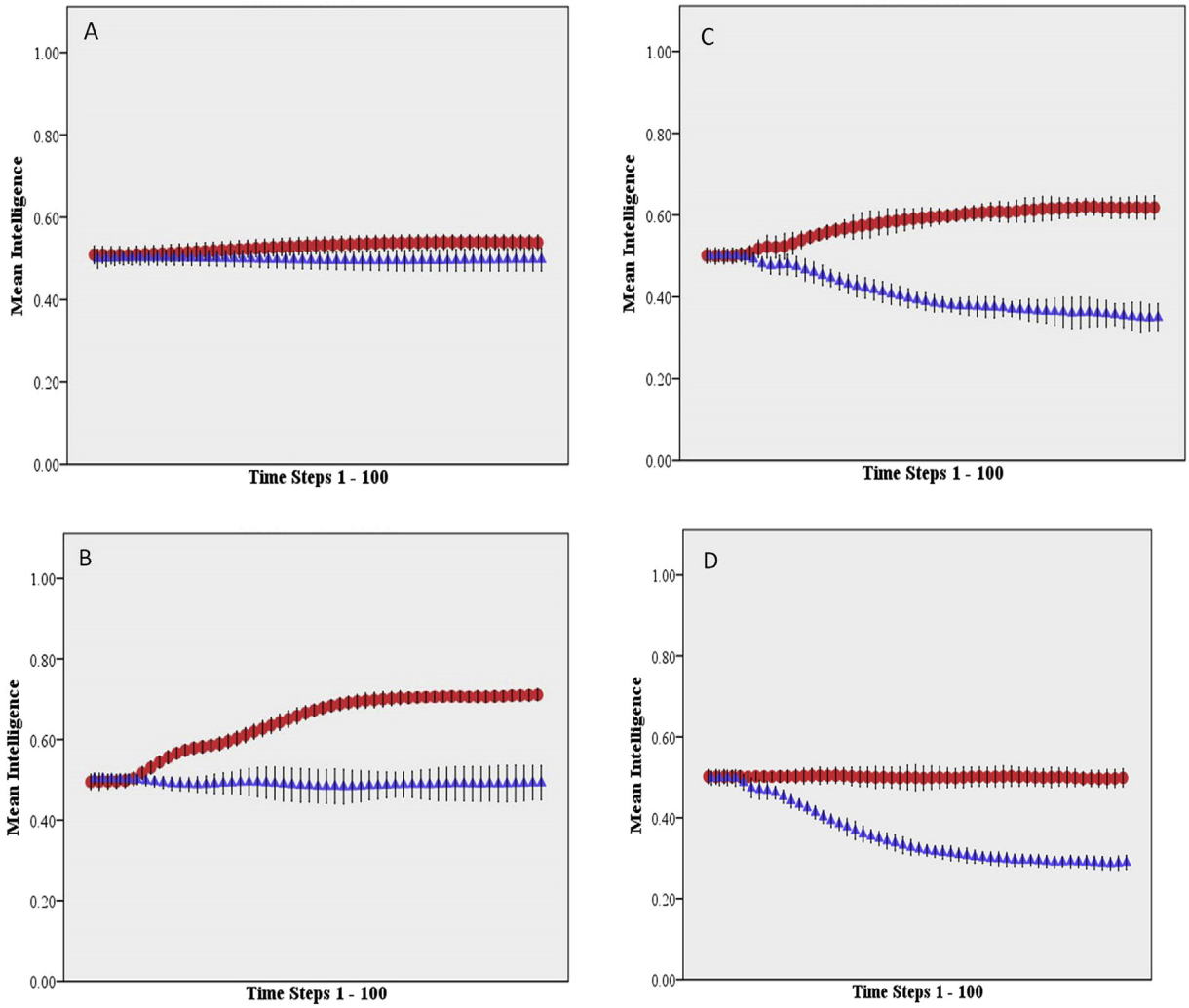

Figure 4. Changes in average population intelligence over time produced by Model 1 (care-giving) and Model 2 (avoidance only) in the scabies-like (A), measles-like (B), CCHF-like (C), and Ebola-like (D) diseases. Models 1 and 2 are shown in red circles and blue triangles, respectively. Only even numbered time steps are shown. Error bars are ± two standard deviations. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Table 7
Mixed-model analyses run on the Model 1 (care-giving) results examining the effects of prevalence, population size, and the interaction between the two on intelligence changes for each disease[a].

Disease	Analysis	r^2m[b]	Variable	B	SE	df	*t*	*p*
Scabies-like[b]	Prevalence	0.468	Intercept	−0.002	0.034	888	−0.055	0.956
			Time	−1.084	0.086	888	−12.641	<0.001
			Prevalence	0.460	0.085	888	5.411	<0.001
Measles-like	Prevalence	0.565	Intercept	−0.065	0.075	946	−0.871	0.384
			Time	−0.585	0.076	946	−7.650	<0.001
			Population size	0.291	0.063	946	4.590	<0.001
			Prevalence	0.431	0.046	946	9.276	<0.001
			Population size * Prevalence	−0.143	0.021	946	−6.713	<0.001
CCHF-like	Prevalence	0.146	Intercept	0.039	0.050	946	0.785	0.433
			Time	−0.400	0.051	946	−7.848	<0.001
			Population size	0.052	0.051	946	1.014	0.311
			Prevalence	−0.104	0.052	946	−2.023	0.043
			Population size * Prevalence	0.060	0.020	946	3.023	0.003
Ebola-like	Prevalence	0.001	Intercept	0.008	0.039	946	0.218	0.827
			Time	−0.010	0.039	946	−0.247	0.805
			Population Size	−0.043	0.049	946	−0.873	0.383
			Prevalence	0.002	0.073	946	0.031	0.976
			Population size * Prevalence	0.013	0.022	946	0.571	0.568

[a] r^2m measures how much variation in mean intelligence can be explained by the fixed effects (time + prevalence * population size). β values are standardized regression coefficients. SE is the standard error and df is the degrees of freedom.

[b] r^2c values were the same as r^2m. r^2c measures how much variation is explained by the whole model (including the random effect of simulation run). That the two measures were the same indicates that there were no systematic differences between runs of a given disease.

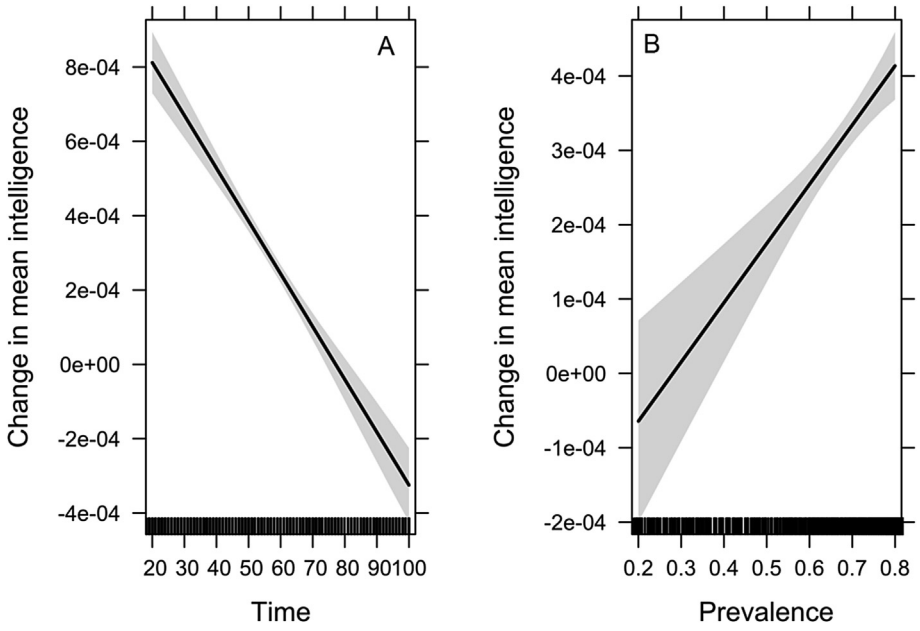

Figure 5. Graphs showing the results of the analyses exploring the effects of prevalence on the change in intelligence for the scabies-like disease. Change in intelligence was calculated as the mean intelligence in a given time step minus the mean intelligence in the previous time step. The gray areas are the 95% confidence intervals. The closely spaced, black, vertical lines at the bottom indicate where on the X-axis the data points occur. (A) Change in intelligence is negatively correlated with time and (B) positively correlated with prevalence (Table 7).

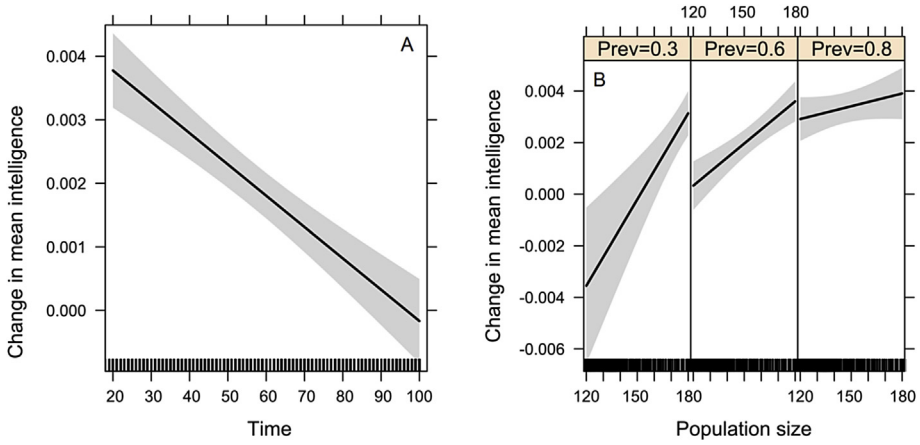

Figure 6. Graphs showing the results of the analyses exploring the effects of prevalence, population size, and their interactions on the change in intelligence for the measles-like disease. Change in intelligence was calculated as the mean intelligence in a given time step, minus the mean intelligence in the previous time step. The gray areas are the 95% confidence intervals. The closely spaced, black, vertical lines at the bottom indicate where on the X-axis the data points occur. (A) Change in intelligence is negatively correlated with time (Table 7). (B) Interaction effects between population size and prevalence ("Prev"). Population size is on the X-axis. The X-axis scale of the middle panel is shown at the top of the panel. The difference in intelligence is shown on the Y-axis. The prevalences shown represent the range of prevalences experienced by the population (see Fig. 1A). The greatest positive selection on intelligence occurred when prevalence and population size are high. Population size has a large effect when prevalence is low (B, left panel) and a small effect when prevalence is high (B, right panel).

intelligence may have occurred through repeated introductions of novel diseases into naïve populations. The greatest selection would have occurred shortly after their introduction, when the disease was spreading and care-giving behavior had not yet managed to reduce the size of the outbreaks and subsequent population crashes.

4.4. Significance for human evolution

Our model was parameterized based upon group sizes, spatial scales, and population densities derived from the fossil record and modern foraging peoples (Grove et al., 2012; Layton et al., 2012). Our goal was not to recreate a particular hominin population, but to explore the effects of different disease characteristics on the evolution of care-giving and increased cognition in a population with hominin characteristics.

In our SIS model, recovered individuals are just as susceptible as those who were never infected. However, for many diseases, recovered individuals are temporarily or permanently immune to re-infection, potentially increasing their ability to provide care. We expect that immunity would increase the rate of care-giving. Diseases likely to select for care-giving among kin may be those that frequently infect children and then convey lifetime immunity. Under this scenario, adults who survived to reproduce would have

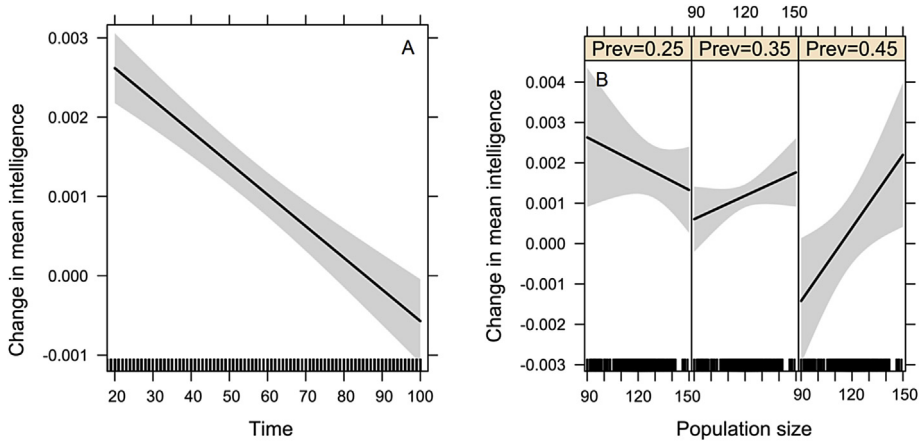

Figure 7. Graphs showing the results of the analyses exploring the effects of prevalence, population size, and their interactions on the change in intelligence for the CCHF-like disease. Change in intelligence was calculated as the mean intelligence in a given time step, minus the mean intelligence in the previous time step. The gray areas are the 95% confidence intervals. The closely spaced, black, vertical lines at the bottom indicate where on the X-axis the data points occur. (A) Change in intelligence is negatively correlated with time (Table 7). (B) Interaction effects between population size and prevalence. Population size is on the X-axis. The X-axis scale of the middle panel is shown at the top of the panel. The difference in intelligence is shown on the Y-axis. The prevalences shown represent the range of prevalences experienced by the population (see Fig. 1A). The greatest increases in average population intelligence occurred at low population sizes and low prevalences (B, left panel) and at high population sizes and high prevalences (B, right panel).

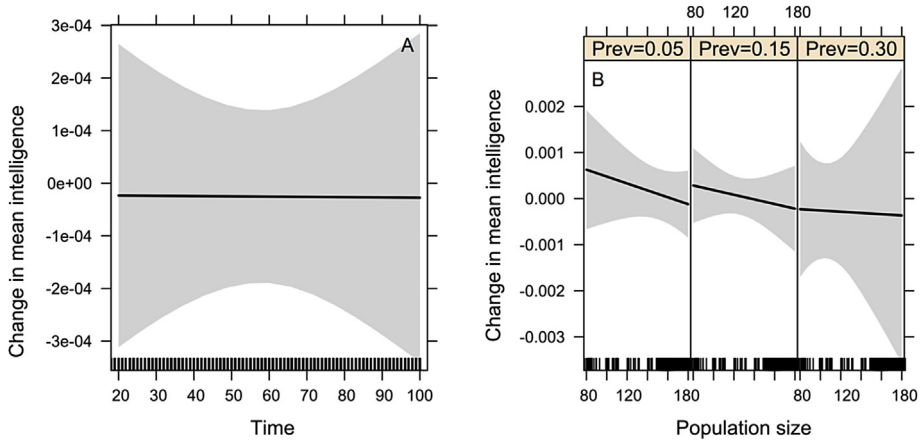

Figure 8. Graphs showing the results of the analyses exploring the effects of prevalence, population size, and their interactions on change in intelligence for the Ebola-like disease. Change in intelligence was calculated as the mean intelligence in a given time step, minus the mean intelligence in the previous time step. The gray areas are the 95% confidence intervals. The closely spaced, black, vertical lines at the bottom indicate where on the X-axis the data points occur. (A) No significant change in intelligence over time. (B) Potential interaction effects between population size and prevalence. Population size is on the X-axis. The X-axis scale of the middle panel is shown at the top of the panel. The difference in intelligence is shown on the Y-axis. The prevalences shown represent the range of prevalences experienced by the population (see Fig. 1A). Because intelligence does not change over time, there are no significant correlations with prevalence, population size, or the interaction of the two (Table 7).

extensive knowledge of the disease's symptoms, making recognition likely, and the immunity to enable them to provide effective care. Several well-known childhood diseases that follow this pattern (e.g., measles, smallpox) have been dated to the origins of agriculture, animal domestication, and subsequent population increases (Harper and Armelagos, 2013). However, as more genetic studies are conducted, increasing numbers of pathogens are showing pre-agricultural origins, including some that were previously believed to be post-agricultural. Tapeworms and TB (once thought to be post-agricultural), plus typhoid fever, whooping cough, and Epstein Barr virus, among others, have been shown to predate agriculture (Hoberg et al., 2001; Hurtado et al., 2008; Stone et al., 2009; Harper and Armelagos, 2013), suggesting that ancestral hominins harbored significant numbers of infectious diseases. Based on our models, diseases with low risks to care-givers, high inclusive fitness pay-offs for care-givers, and prevalences low enough not to disrupt the kin networks along which care could be given would have exerted the strongest selection for increased cognition. Through repeated introductions of novel diseases over millions of years, such diseases could have selected for accurate disease recognition, increased care-giving among kin, and produced the social and cognitive origins of human medical care.

4.5. A novel hypothesis of human cognitive evolution and future directions

Our novel hypothesis of primate, including human, cognitive evolution is not mutually exclusive with the social brain hypothesis (Dunbar, 1998). As social species evolved the cognitive capacities for social cognition, such as processing information gleaned from faces (Leopold and Rhodes, 2010; Sartori et al., 2011), voices (Belin et al., 2004; Belin, 2006), and movement patterns (Loula et al., 2005; Sartori et al., 2011; Peterman et al., 2014), they may have also obtained the ability to use this information to recognize disease symptoms.

Additionally, while our hypothesis links disease recognition and social cognition, it is important to realize that the hypothesis is not dependent on a modular model of primate cognitive evolution (Tooby and Cosmides, 1992; Herrmann et al., 2007). Correlated evolution between disease recognition and social cognition is possible regardless of whether social cognition has evolved independently of other cognitive functions (Tooby and Cosmides, 1992; Herrmann et al., 2007) or as part of a generalized intelligence or "g factor" (Deaner et al., 2006; Lee, 2007; Reader et al., 2011; Fernandes et al., 2014; Woodley et al., 2015). Finally, we make several predictions that enable paleoanthropologists, archaeologists, primatologists, human ecologists, geneticists, and immunologists to test our novel hypothesis of human cognitive evolution.

Humans and nonhuman primates have very similar disease profiles in that we share many of the same diseases, with viral, bacterial, and gastrointestinal parasitic zoonoses transmitted from nonhuman primates to humans and vice versa (Chapman et al., 2005; Wolfe et al., 2007; Jones et al., 2008; Lloyd-Smith et al., 2009). However, what has received very little attention is how humans and nonhuman primates may differ in the expression of disease symptoms. Humans, relative to nonhuman primates, have much less body hair. Though our nakedness may reduce ectoparasite load (Pagel and Bodmer, 2003; Weiss, 2007), it also provides a visually unobstructed surface for displaying rashes, lesions, swelling, inflammation, and bruising. Humans, relative to nonhuman primates, also have white scleras around their eyes, a signal that has been argued to draw attention to gaze direction (Kobayashi and Kohshima, 2001; Tomasello et al., 2007), but also turns a dramatic "bloodshot" red when we are under emotional stress or ill (Provine et al., 2011). Thus, we predict that if humans have been selected to solicit care from others, they should display exaggerated signals of ill health relative to nonhuman primates experiencing the same disease and degree of morbidity/mortality.

Additionally, it is becoming increasingly possible to date the origins of many diseases afflicting humans (Stone et al., 2009; Harper and Armelagos, 2013). As more accurate dates are obtained for more diseases, it will be possible to examine whether hominin populations carried an increased disease load as they increased in social complexity. Social complexity could be operationalized in the fossil record through the brain size-group size relationship (Aiello and Dunbar, 1993; Dunbar, 1998; Gamble et al., 2011; Grove et al., 2012; Layton et al., 2012), through evidence of increased behavioral and technological complexity in the archaeological record (Gowlett et al., 2012; Shultz et al., 2012), or through fossil evidence for the shift to cooperative breeding (Aiello and Key, 2002; Shultz et al., 2012). Therefore, we predict that if larger hominin communities sustained greater disease loads, then periods of rapidly increasing community sizes (operationalized with expanding brain sizes [Aiello and Dunbar, 1993; Dunbar, 1998; Gamble et al., 2011; Grove et al., 2012]) should coincide with the evolution of diseases new to hominins. Similarly, if social learning/cooperation lead to increased disease transmission (McCabe et al., 2015), then increasing behavioral/technological complexity in the archaeological record (Gamble et al., 2011; Gowlett et al., 2012; Shultz et al., 2012) should coincide with the evolution of diseases new to hominins. Additionally, if cooperatively breeding increased disease transmission, then evidence for cooperative breeding in the fossil record (Aiello and Key, 2002; Shultz et al., 2012) should coincide with the evolution of diseases new to hominins, particularly those that afflict children. These predictions are not mutually exclusive. According to the results of our model, we would expect a high proportion of these diseases to present low costs and high fitness payoffs to care-givers and persist at prevalences that are low enough not to disrupt the kin networks along which care is provided. Possibilities include infections that leave survivors immune.

An additional avenue for examining the role of disease during the evolution of human social complexity would be through cross-species comparisons of immune investment. If hominins have experienced an unusually high rate of disease exposure, either through their extensive social networks or through providing care to diseased kin, they may have invested heavily in immune defenses. Recent work on introgression between anatomically modern humans (AMH) and Neandertals has proposed that one of the major advantages may have been the acquisition of novel immune genes from Neandertals as AMH expanded northward into new environments and encountered novel pathogens (Houldcroft and Underdown, 2016). Prior studies indicate that there are cross-species differences in immune investment according to mating system (but not group size or density in primates; Nunn et al., 2000), the risk of environmentally transmitted parasites and injuries due to predator attacks in anthropoids (Semple et al., 2002), coloniality in birds (Moller et al., 2001), and cooperative breeding in birds (Spottiswoode, 2008). This leads us to make a further set of predictions. We expect that if the increased social complexity of hominins required them to invest heavily in immune defenses, the human immune system should show similar adaptations to other species that have extremely large social networks and high interaction rates. Similarly, if the evolution of cooperative breeding required hominins to invest heavily in immune defenses, then the human immune system should show similar adaptations to other cooperatively breeding species. Finally, if the evolution of providing care to diseased conspecifics required hominins to invest heavily in immune defenses, the human immune system should show adaptations that are either extreme or unusual. (Again, these predictions are not mutually exclusive.) While many of the earlier studies were done with white blood cell counts (Nunn et al., 2000), the field of ecological immunology is growing rapidly with new techniques being continually developed (Downs et al., 2014; Larsen et al., 2014). This should make it increasingly possible to parse out how different selective forces may have acted on different elements of a species' immune system.

5. Conclusions

Our model indicates that disease circulating amongst kin groups can select for care-giving among kin and greater cognitive abilities. Moreover, the characteristics of the diseases can generate different strengths of selection. Diseases with lower costs and higher pay offs produced stronger selection, yielding higher care-giving rates and greater increases in average population intelligence. When a care-giving strategy was compared with an avoidance-only strategy, the care-giving strategy controlled the transmission of the disease through the population by reducing the severity of disease outbreaks and population crashes. Because this cycle of outbreaks and population crashes was associated with the most rapid increases in intelligence, we propose that the repeated introduction of novel diseases into naïve populations may have led to sustained selection for increasing disease recognition and cognitive abilities throughout human evolution. Moreover, the unique ability of hominins to control the spread of disease through care-giving behaviors may have facilitated increased social complexity and ultimately lead to the evolution of medical care in humans. Our modeling has resulted in a set of predictions derived from our disease recognition hypothesis of hominin cognitive evolution that can be tested by paleoanthropologists, archaeologists, geneticists, and primatologists.

Acknowledgments

This work was funded by the Fonds de Recherche du Québec—Nature et Technologies and the Québec Center for

Biodiversity Science. The funders were not involved in the study design, the collection, analysis and interpretation of data, writing of the report, or decision to submit it.

Supplementary Online Material

Supplementary online material related to this article can be found at http://dx.doi.org/10.1016/j.jhevol.2017.02.009.

Author contributions

SEK designed the study, programmed the model, analyzed the data, and wrote the manuscript. TRB and CAC contributed to all stages. RWB contributed to the development of the ideas and manuscript preparation.

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