# Intercontinental Networks Between Africa and Asia Across the Indian Ocean: What Do Village Chickens Reveal?

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## INTRODUCTION

The prehistory of the Indian Ocean world can be likened to a complex historical jigsaw puzzle, and has attracted deep interest from various disciplines (Chaudhuri 1985; Pearson 2011). The objective has been to find and fit together the various pieces to complete and demystify the puzzle. At present, the assembled pieces reveal a multiplex pattern of cultural contacts, trade, and biological translocations, including intercontinental linkages and interactions that shifted according to region and over time.

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The Indian Ocean, 73.56 million km<sup>2</sup> in area, and characterized by significant ecological and cultural diversity, witnessed some of the world's earliest seafaring and maritime activities. Evidence from archaeo-botany and archaeo-zoology reveals wild and domestic plants and animals, weeds, and spices were translocated east and westward across the Indian Ocean between diverse geographic regions (see Boivin and Fuller 2009; Boivin et al. 2009; Fuller and Boivin 2009; Fuller et al. 2011). These contacts and translocations led to major socioeconomic transformations that contributed to the evolution of languages, ideas, and technologies, including the alteration of the genetic constitution of humans, plants, and animals (Arnold 1995; Pearson 2011). These are reflected in the complexity of the different cultures, languages, and genetic traits on the present-day coastal communities of eastern Africa and Madagascar. They reflect rich and ancient long-distance linkages with the Middle East, and Asia, although mystery still surrounds the long-term evolution of such connections.

The advent of seafaring was a critical catalyst for intercontinental linkages that placed water masses at the heart of international trade routes and interactions. Through seafaring activities, many domesticates were dispersed along maritime corridors and these influenced substantially the development of agriculture. Domestic chicken were an intrinsic part of these translocations in historic times, possibly much earlier. The debate over the origin and movement of domestic village chickens is therefore an important one in understanding and reconstructing the trajectories of prehistoric human activities and relationships.

In this chapter, the current state of molecular genetic evidence based on the analysis of mtDNA datasets of village chickens is reviewed, attention being drawn to emerging scenarios for the dispersal of the species and therefore of early interaction and contacts which led to the emergence of complex trade networks that have been described in classical texts such as the *Periplus Maris Erythraei* (Casson 1980, 1989; Chami 1999a; Cappers 2006).

# Domestic Chicken as a Biological Marker to Track Human Migration and Interactions

Domesticated animal and plant species are attractive options for unraveling patterns of human migrations. They offer a means to circumvent the sampling and analysis of rare and often scarce ancient human and animal remains. Some selected examples of wild and domestic animals that have been used to trace human movements and migrations are shown in Table 11.1. Chickens are a mostly sedentary species (Johnsgard 1999), have a restricted home range, and are incapable or poorly adapted to self-disperse by any means (Collias and Collias 1996; Kelly 2006). These factors together with their sociocultural and economic significance for humans imply that their current extensive dispersal and global distribution (Simoons 1994) is the result of anthropogenic dispersals. Nevertheless, a full account of their past translocations via maritime and terrestrial corridors still remains uncertain.

Animal species	Possible origin and distribution
Zebu cattle (Bos indicus)	South Asia; Widespread across eastern and southern Africa (Hanotte et al. 2002)
Sheep (Ovis aries)	The Fertile crescent; Widespread worldwide (Chessa et al. 2009)
Goats (Capra hircus)	The Fertile crescent; Widespread worldwide (Liukart et al. 2001; Fernandez et al. 2006)
Asian house shrew ( <i>Suncus murinus</i> )	South/Southeast Asia; Currently widespread in Indian Ocean (Fuller and Boivin 2009)
Asian tiger mosquito (Aedes albopictus)	Southeast Asia; Widespread in Madagascar, Indian ocean islands, across Africa, Europe, and the Americas (Vazeille et al. 2001; Benedict et al. 2007)
Black/ship rat ( <i>Rattus rattus</i> )	South/Southeast Asia; Widespread in Indian Ocean (Fuller and Boivin 2009)
House gecko	Natural distribution across mainland Eurasia; Translocated to
(Hemidactylus)	Indian Ocean islands via natural and anthropogenic means
House mouse (Mus musculus)	Asia (northern India to Southwest Asia); Transferred along terrestrial and maritime routes (Fuller and Boivin 2009)
Pygmy shrew (Suncus etruscus)	South/Southeast Asia; Transferred by direct maritime route to Madagascar (Omar et al. 2011)
Feral domestic pig (Sus scrofa)	Eurasia multiple times; Widespread in Indian Ocean (Walsh 2007)
Javan Moongose (Herpestes javanicus)	South/Southeast Asia (Walsh 2007)
Indian civet (Viverricula indica)	South/Southeast Asia; Widespread in Indian Ocean (Walsh 2007; Larson et al. 2010)

 Table 11.1
 Some selected domestic and wild animal species dispersed across the Indian Ocean

Adapted and modified from Fuller and Boivin (2009).

## DOMESTIC VILLAGE CHICKENS IN AFRICA

#### Theories on Chicken Domestication, and Occurrence in Africa

The main wild ancestor of domestic chicken, the red junglefowl Gallus gallus, occurs in sub-Himalayan northern India, southern China, and Southeast Asia (Delacour 1957; Johnsgard 1999). Whether or not the species was domesticated in a single geographic center in Southeast Asia (Niu et al. 2002; Fumihito et al. 1994, 1996) or across the geographic range of the wild species in South, East, and South-East Asia (Liu et al. 2006; Kanginakudru et al. 2008; Miao et al. 2013) remains a subject under intense debate among scholars. The issue of chicken domestication seems more complex than it appears with emerging molecular genetic evidence revealing possibilities of hybridization between all the species of the genus Gallus except Gallus varius (Nishibori et al. 2005), and the contribution of the yellow skin gene to domestic chicken by the grey junglefowl, Gallus sonneratii, which is endemic to southern India (Eriksson et al. 2008). Indeed, hybridization between wild and domestic fowls has been observed in Yunnan, China (Chang 2009), and has also been inferred in northern Vietnam (Berthouly et al. 2009).

The first skeletal remains of domestic chicken came from Chinese archaeological sites of Chishan in Hebei Province, and Peiligan in Henan Province dating to around 8000 years ago (Chow 1984; Rodwell 1984–1985). However, the validity of these bones has recently been questioned because their reanalysis has shown them to be of pheasants (Peters 1998; Deng et al. 2014). In the Indian subcontinent, evidence of the wild Gallus in Damdana, in the Ganges region, dates to between the fourth and second millennium BCE (Thomas et al. 1995 cited in Fuller 2006), while, several finds point to the presence of chicken by the mid-third millennium BCE in the western regions of Gujarat and in the Indus Valley, areas where the wild progenitor is absent today (Fuller 2006). Other finds from North India, within the home range of the wild progenitor, also date to the second half of the third millennium BCE (Fuller 2006). Very little archaeological evidence for early agriculture in mainland Southeast Asia exists (Glover and Bellwood 2004). It is not clear therefore whether chicken domestication occurred independently in this region. Thailand has been proposed as a center of chicken domestication (Fumihito et al. 1994, 1996). The earliest G. gallus remains identified in Thailand archaeological sites date to approximately 4000 years ago (Higham 1989). The cultural importance of chickens in Thailand is demonstrated by the interment of chickens alongside humans in the archaeological sites of Non Nok Tha and Ban Na Di (Higham 1989). Preserved chicken remains from archaeological sites in Island Southeast Asia are scarce and their utilization by ancient humans is often inferred based on their depiction on pottery or in paintings than by the occurrence of their remains in archaeological sites (Bellwood 2007).

The significance of domestic chicken in the sociocultural life and subsistence economy of most African societies (MacDonald 1992, 1995a) has been interpreted to suggest one of three possibilities: a long-term presence on the continent; a late arrival and quick integration into local customs and traditions (MacDonald 1995a,b), or multiple introductions at different time periods to fulfill multiple functions. However, no archaeological data has so far been found to support any of these suggestions (Williamson 2000).

Linguistic evidence, on the other hand, supports an early introduction and complex history of arrival and dispersal across Africa. Working on the basis of the distribution pattern of the root word for fowl across three African language groups, Williamson (2000) suggested at least two separate introductions and three routes of dispersal into West Africa—two across Central Africa and the Sudano-Sahelian zone from the east coast of Africa and one from North Africa across the Sahara. Further, noting that the terminologies relating to domestic animals in Madagascar appear to have been derived from the Swahili language, Blench (2008) suggested that the domestic chicken found in the island could have been introduced from the Comoros islands or East Africa.

Archeological evidence for the arrival of the chicken in, and its dispersal across, Africa remains scant and, in some cases, disputed. The picture is further complicated by the challenging task of identifying domestic chicken bones from those of indigenous African galliform's (MacDonald 1992). The few remains that have been identified show that, at the earliest, the domestic chicken was present in Egypt around the second millennium BCE (Houlihan and Goodman 1986). Until recently, the oldest, securely identified chicken remains in West Africa were from Jenne-Jeno, in modern-day Mali, dated to 500–850 CE (MacDonald 1995b)— although this is contested as it has been suggested that these finds most likely date to the eighth or ninth century CE (Dueppen 2011). New evidence from Kirikongo, in Burkina Faso, indicates that the chicken was common in West Africa by the sixth century CE, where it was probably

present as early as the first century CE (Dueppen 2011). Research in East Africa shows that the chicken was common in several sites by the eighth to ninth centuries CE (Horton and Mudida 1996; Wilson and Omar 1997; Boivin et al. 2013). The earliest undisputed findings are from Unguja Ukuu, in Zanzibar Island dating to the sixth to mid-eighth century CE (Juma 2004). In southern Africa, evidence points to the occurrence of the chicken around the eighth to ninth century CE (see review by Mwacharo et al. 2013).

On the basis of the geographic distribution and dating of the purportedly most ancient undisputed zoo-archeological (c. 1567-1320 BCE) findings, as well as artistic (c. 1425-1123 BCE) and literary (1504-1450 BCE) evidence, it is currently considered that the chicken may have initially entered Africa through Egypt, dispersed southwards along the Nile Valley to Nubia, where archeological evidence dates the presence of chicken to the late fifth century CE (Houlihan and Goodman 1986), and subsequently reached West Africa through the Sudano-Sahelian corridor (MacDonald and Edwards 1993; Fuller et al. 2011). MacDonald and Edwards (1993) further suggested an independent diffusion into West Africa through the Sudano-Sahelian belt from the east African coast. This was perhaps related to the Indian Ocean trading networks. Boivin et al. (2013) point to the common simultaneous occurrence of remains of the common rat, Rattus rattus (a ship borne introduction), and the chicken in several sites on the coast and islands of eastern Africa, as well as in southern Africa, dating from the mid to late first millennium CE. This suggests an influx of the two species due to intensifying Indian Ocean trade.

### Genetic Evidence Based on the Analysis of mtDNA Sequences

In the past two or so decades, researchers have analyzed mitochondrial DNA (mtDNA) as a standard way of reconstructing dispersal routes and dispersal chronology of domestic animals in different geographic regions (Bruford et al. 2003). Such reconstructions have been achieved by assessing phylogenetic relationships of haplotypes and Clades for various wild and domestic species. Some of these species include rats (Matisoo-Smith and Robins 2004), sheep (Chessa et al. 2009), goats (Fernandez et al. 2006), cattle (Edwards et al. 2007), pigs (Larson et al. 2010), and the chicken (Storey et al. 2012). Three factors render mtDNA attractive in this respect. First, its occurrence in high copy number in the mitochondria of most eukaryotic cells makes it appropriate for studying modern and

ancient samples (Clayton 1991). Second, its almost complete maternal inheritance and rare recombination (Ho and Gilbert 2010; Pakendorf and Stoneking 2005), makes it appropriate to trace the maternal lineage of species. Third, its high mutation rate and polymorphism, especially of the control (D-loop) region, (Pakendorf and Stoneking 2005), makes it the fragment of choice for within-species comparisons.

Nine mtDNA clades (A, B, C, D, E, F, G, H, I) have been defined from an analysis of the first 539 base pairs of the control region of domestic chickens from Europe and Asia as well as wild red jungle fowl (Liu et al. 2006; Miao et al. 2013). Seven clades (A–G) had sequences from both domestic and wild chickens. In this chapter, the nomenclature of the mtDNA clades observed in domestic chicken follows that of Liu et al. (2006). A few studies have analyzed a similar fragment in village chickens from countries around the Indian Ocean (Fig. 11.1; Tables 11.2 and 11.3). These include from Africa (Razafindraibe et al. 2008; Adebambo et al. 2010; Muchadeyi et al. 2008; Mtileni et al. 2011; Mwacharo et al. 2011; Lyimo et al. 2013; Wani et al. 2014; Elkhaiat et al. 2014; Al-Qamashoui 2014), the Middle East (Liu et al. 2006), the Arabian Peninsula



Fig. 11.1 Pie charts showing the proportion of the different mtDNA clades observed in domestic village chickens from countries/regions bordering the Indian Ocean.

Liu et al. (2006) study	' nomencla	ture												
Clades in Reference study	Equivalent cl	ades observ	ed in African o	und Asia s	tudies									
Liu et al. 2006; Miao et al. 2013	Muchadeyi et al. 2008	Silva et al. 2008	Razafindraibe et al. 2008	Sulandari et al. 2008	Adebambo et al. <b>2010</b>	Dana 1 et al. e	Mwacharo et al. <b>2011</b>	Mtileni et al. 2011	Zein and Sulandari 2012	Lyimo ] et al. <b>2013</b>	Bhuiyan et al. 2013	Wani et al. 2014	Elkhaiat et al. 2014	Al- Qamashoui 2014
<ul> <li>Clade A (observed in South China and Japan)</li> <li>Geographic center of origin: Yunnan province China and/or surrounding areas)</li> </ul>	B1	SLvtHap 36 & 35		IIId		A	a	A	pIII		A			A
<ul> <li>Clade B (observed in Yunnan China)</li> <li>Geographic center of origin: Yunnan China and/</li> </ul>	B2	SLvtHap 33 & 32				В	U	B						
or surrounding areas – Clade C (observed in Guangxi and Guangdong	А		I	II		D/C	Α	D	Π	D	D			C
China and Japan) – Clade D (observed in Indonesia and India, and in														
Chinese and Japanese gamecocks) – Geographic center of														
origin: South and Southwest China and/or surrounding areas (i.e., Vietnam, Burma, Thailand, India)														

Nomenclature of mtDNA control region clades across different studies, their possible origin and equivalent clades following

Table 11.2

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Ilades in Reference study	Equivalen	it clades observed	in African	and Asia str	ıdies									
– Clade E (observed in Surope, Middle East and	C	SLvtHap 1 & 13	II	IV	IV	н	D	щ	N	щ	н	IV	Щ	Е
ndia)														
- Geographic center of														
origin: Indian subcontinent														
- Clade F (observed in							Е	ц			Ц	IIIa		
(unnan China)														
<ul> <li>Geographic center of</li> </ul>														
nigin: Yunnan China and∕o														
djacent areas														

Region/country/study	Countries	Sample	Freque	ncy of	<sup>c</sup> clades	a (%)	
		size	C/D	Α	В	Ε	F
Madagascar							
Razafindraibe et al. (2008) South Africa	Madagascar	77	84			16	
Mtileni et al. (2011) South-East Africa	South Africa	111	19	20	2	57	2
Muchadeyi et al. (2008)	Zimbabwe	99	55			45	
	Malawi	19	100				
East Africa							
Mwacharo et al. (2011)	Kenya	211	45	<1		54	
	Uganda	123				100	
Lyimo et al. (2013)	Tanzania	101	36			64	
Ethiopia and Sudan							
Muchadeyi et al. (2008)	Sudan	20				100	
Mwacharo et al. (2011)	Sudan	135				98	2
	Ethiopia	42			2	96	2
Wani et al. (2014)	Sudan	81				99	1
West Africa							
Adebambo et al. (2010)	Nigeria	232				100	
North-East Africa							
Elkhaiat et al. (2014)	Egypt	36				100	
Al-Qamashoui (2014)	Somaliland	15	7	6		87	
The Middle East and Arabian	Peninsula						
Al-Qamashoui (2014)	Oman	100	2	4		94	
	Saudi Arabia	61			2	98	
	Yemen	31	4		3	93	
Liu et al. (2006)	Middle East <sup>b</sup>	16		12	13	75	
Indian subcontinent							
Bhuiyan et al. (2013)	Bangladesh	85	29	11		45	15
Liu et al. (2006)	India	27	41		3	56	
Silva et al. (2008)	Sri Lanka	132		12	16	15	
Southeast Asia							
Liu et al. (2006)	Indonesia	12	42		25	33	
Zein and Sulandari (2012)	Indonesia	210	84	4	2	8	
Sulandari et al. (2008)	Indonesia	483	75	11	1	11	2
Across Eurasia							
Liu et al. $(2006)^{c}$	Europe and Asia	836	10/5	27	23	19	8

**Table 11.3**Clades observed from the analysis of mtDNA D-loop sequences ofvillage chickens from countries around the Indian Ocean

<sup>a</sup>Nomenclature follows that of Liu et al. (2006) study.

<sup>b</sup>Iran, Turkmenistan, Azerbaijan

<sup>c</sup>Liu et al. also observed clades G and I which are not present in domestic chicken from Africa, the Indian Subcontinent, Island Southeast Asia, the Middle East, and Arabian Peninsula

(Al-Qamashoui 2014), Sri Lanka (Silva et al. 2008), India (Liu et al. 2006), Bangladesh (Bhuiyan et al. 2013), and Indonesia (Liu et al. 2006; Zein and Sulandari 2012; Sulandari et al. 2008) (see Tables 11.2 and 11.3). Of the seven mtDNA clades observed in domestic and wild chickens (Liu et al. 2006), at least two are found in countries bordering the Indian Ocean (see Fig. 11.1; Table 11.3). The most common are clades C/D and E, while A, B, and F are rare (Fig. 11.1; Table 11.3). This suggests the presence of significant genetic diversity and possibilities of multiple origins and introductions.

Clade E is the most diverse and is widely distributed across the countries studied so far bordering the Indian Ocean (Fig. 11.1; Table 11.3). The next most common is clade C/D. In Africa, it occurs in countries adjacent to the Indian Ocean. It has so far not been observed in the continents hinterland (Fig. 11.1; Table 11.3). Outside Africa, the clade is predominant in Indonesia and occurs, albeit at low frequencies compared to clade E, in Bangladesh, India and in the Arabian Peninsula. It has not so far been observed in the Middle East and in Sri Lanka (Table 11.3). Clades A, B, and F occur in only four countries in Africa and at very low frequencies (Table 11.3). Clade A has been observed in Kenya, South Africa, and Somaliland; clade B in Ethiopia and South Africa and clade F in Ethiopia, Sudan, and South Africa (Table 11.3). Outside the African continent, clade A is present in Bangladesh and Sri Lanka, in Indonesia, in the Arabian Peninsula (Oman) and in the Middle East (Table 11.3). Clade B is present in India, Sri Lanka, Indonesia, the Arabian Peninsula and in the Middle East while clade F occurs in Bangladesh and Indonesia (Table 11.3).

#### Origin and Dispersal of the Five Clades

It has been suggested that clade C/D originates from Southeast Asia (Muchadeyi et al. 2008; Mwacharo et al. 2011; Miao et al. 2013). Liu et al. (2006) on the other hand, suggested an origin in South and Southwest China and/or surrounding areas, that is, Vietnam, Thailand, and Burma. The clade has a very large presence in the Indonesian islands (Fig. 11.1; Table 11.3). From its geographic distribution pattern, it has been argued that this clade reached East Africa (Mwacharo et al. 2011) including Madagascar (Razafindraibe et al. 2008) via a maritime corridor (Mwacharo et al. 2011). Based on the known history of human colonization of Madagascar (Razafindrazaka et al. 2010 and references therein;

Blench 2010), Razafindraibe et al. (2008) have suggested the origin of the clade to be the Indonesian islands; and that it is likely the legacy of Austronesian expansion to eastern Africa and Madagascar (Razafindraibe et al. 2008). Based on the decrease in diversity and frequency of this clade northwards from Madagascar along the Indian Ocean, Al-Qamashoui (2014) suggested it could have been introduced to East Africa and the Arabian Peninsula from Madagascar following its direct arrival in the island from either China or Indonesia. Another possibility is an introduction to the Arabian Peninsula, then to the Horn of Africa and East and southern Africa from India where the clade is also observed (Fig. 11.1; Table 11.3) across the Arabian Sea.

Given the available data, it is difficult to determine if this clade (C/D) arrived first in East Africa or Madagascar, or simultaneously along the eastern and southern Africa coastline including Madagascar. Several hypotheses offer themselves. One is that the clade traveled directly to East Africa, from where it was then introduced to Madagascar, and down the east African coast to southern Africa. A second is that it traveled first to Madagascar, and subsequently to East and southern Africa. The third possibility is that it was introduced simultaneously to Madagascar, eastern and southern Africa. Within Asia, the clade may have been introduced to Bangladesh and India from Indonesia across the Bay of Bengal. However, if it is assumed that the clade originates from South and Southwest China and adjacent regions as suggested by Liu et al. (2006), then an overland introduction will be the most likely. More data will be required before any of these hypotheses can be confirmed.

Liu et al. (2006) and Miao et al. (2013) proposed the geographic center of origin of clade E to be the Indian subcontinent (Table 11.2). This proposition gained the support of Muchadeyi et al. (2008) and Mwacharo et al. (2011). It is further backed by the commonly observed yellow skin phenotype among African (Daikwo et al. 2011; Melesse and Negesse 2011; El-Safty 2012) and Saudi Arabian (personal observation by the author) village chickens; a marker of introgression of the yellow skin gene (*BCO2*) into domestic fowls from the grey junglefowl of southern India (Eriksson et al. 2008). Whether or not this clade followed a maritime and/or terrestrial corridor to reach Africa and the Arabian Peninsula remains debatable. What may be certain however is that it was introduced to the Middle East, the Arabian Peninsula, Northeast,

West, eastern and southern Africa (Fig. 11.1; Table 11.3), three possible routes of dispersal are envisaged. One is an overland dispersal from the Indian subcontinent via the Middle East to the Arabian Peninsula and Northeast Africa (Egypt). It then traveled south, along the Nile Valley, then westwards across the Sudano-Sahelian zone into West Africa. A direct maritime introduction via the Arabian Sea into the Arabian Peninsula and the Horn of Africa (Somaliland, Diibouti, etc.) is also possible and is favored by Al-Qamashoui (2014). Another possibility is that the clade reached East Africa and Madagascar directly overseas from the Indian subcontinent, or from Egypt traveling along the Red Sea and east African coasts. This suggestion has also been proposed by Al-Qamashoui (2014) based on the observation of a southward decline in the frequency and diversity of the clade from the Arabian Peninsula to southern Africa (see Fig. 11.1). A terrestrial dispersal accompanying the expansion of Bantu-speakers into southern Africa from the Great Lakes region cannot be discounted. It is the only clade observed in West Africa (Adebambo et al. 2010), the original homeland of the Bantu-speakers, and in the interlacustrine region of East Africa (Mwacharo et al. 2011), where the first Bantu-speaking migrants arrived around 1000 BCE (Russell et al. 2014 and references therein). In Asia, the clade may have been introduced to Sri Lanka and Indonesia by traveling across the Bay of Bengal.

Liu et al. (2006) proposed the center(s) of origin of clade(s) A and B (Tables 11.2 and 11.3) as Yunnan Province in China and/or surrounding areas. The presence of identical or closely related haplotypes of these two clades in European local chickens and fancy breeds and commercial breeds of chicken (Muchadevi et al. 2008; Dana et al. 2010; Miao et al. 2013), led Mwacharo et al. (2011) to propose that they were introduced to Africa following the introduction of exotic and/or commercial breeds (broilers and layers) for crossbreeding purposes with local flocks to increase egg and meat production. The same can be used to explain the occurrence of these two clades in the Arabian Peninsula, the Middle East, the Indian subcontinent, and Indonesia (Fig. 11.1; Table 11.3). However, an earlier introduction to Africa from China via Sri Lanka, is also likely, as is, the possibility of overland introductions from Yunnan province to the Indian subcontinent and subsequently, to the Middle East and Arabian Peninsula. More data are required to further clarify and/or confirm the origin(s) and mode of dispersal of these two clades.

Clade F (Tables 11.2 and 11.3) has not been observed in commercial broilers and layers (Muchadeyi et al. 2008; Dana et al. 2010) and in European local chickens (Liu et al. 2006; Miao et al. 2013). Liu et al. (2006) have proposed the center of origin of the clade as South China (Yunnan province) and/or adjacent geographic regions such as Myanmar. The route(s) of introduction of the clade to Africa, Bangladesh, and Indonesia remains unknown. Its modern-day worldwide geographic distribution (Liu et al. 2006) hints to the possibility that it was most likely the consequence of either direct or indirect maritime introduction via Sri Lanka from Yunnan province. Its arrival in East Africa might have been facilitated by either the fifteenth century Chinese maritime trading or exploration activities across the Indian Ocean (Duyvendak 1939; Beaujard 2005; Mwacharo et al. 2011), and/or it traveled as a companion haplotype to other clades such as clade A. While its dispersal to Indonesia could have been through the Bay of Bengal, its dispersal to Bangladesh was most likely via a terrestrial route.

## CONCLUSIONS AND FUTURE DIRECTIONS

The Indian Ocean was a major arena for the exchange of flora and fauna from early times (Boivin et al. 2013; Fuller et al. 2011). Chickens were among the fauna that were transported from Asia to Africa, but there is still considerable debate as to their origins and dispersal patterns. The five mtDNA clades found in village chickens around the Indian Ocean rim, and the dating of zoo-archeological remains, highlight the important role in this exchange played by Africa's eastern and southern coastlines including Madagascar, the Indian subcontinent, and Southeast Asia. In this chapter, I attempt to outline what the discipline of molecular genetics, through an analysis of chicken mtDNA, further reveals about the issue. It is important to emphasize that the emerging picture from the analysis of such data is far from complete. Too few sites on the littorals of Africa and Asia bordering the Indian Ocean have been sampled and studied in detail, and the proposed tentative hypotheses offered here concerning the routes of dispersal need to be tested. Studies to date nonetheless offer some interesting preliminary observations, notably multiple origins and introductions for village chickens, and genetic contributions from South Asia, East Asia, and Southeast Asia. This highlights the complexity of the trans-Indian Ocean world interaction from early times.

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