



Short communication

United Arab Emirates: Phylogenetic relationships and ancestral populations

Ralph Garcia-Bertrand ^{a,*}, Tanya M. Simms ^{b,1}, Alicia M. Cadenas ^{c,1}, Rene J. Herrera ^d^a Biology Department, Colorado College, Colorado Springs, CO 8090, USA^b Department of Physics and Astronomy, University of Kansas, Lawrence, KS 66045, USA^c State of Virginia Forensic Laboratory, Richmond, VA 23219, USA^d Department of Molecular and Human Genetics, College of Medicine, Florida International University, Miami, FL 33199, USA

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ABSTRACT

In the current report, 109 unrelated individuals from the United Arab Emirates (UAE) were typed across 15 autosomal short tandem repeat (STR) loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D14S5433, vWA, TPOX, D18S51, D5S818 and FGA) routinely employed in population genetics analyses and compared across a set of ethnically and geographically targeted reference collections. UAE, located at the southeastern most portion of the Arabian Peninsula, in the tri-continental crossroads connecting Africa, Europe and Asia, has been influenced by a number of human dispersal waves from a plethora of sources including the Paleolithic “Out of Africa” migrations, the exodus of Neolithic pastoral agriculturalists from the Fertile Crescent and Northern Africa, as well as more recent migrations from Asia and the Middle East. We found that despite the high levels of consanguinity that characterize UAE, this population is genetically highly heterogeneous. When compared to various world-wide biogeographical regions, the Arabian Peninsula exhibits the highest intra-population variance. Admixture analyses indicate that UAE and Bahrain uniquely in Arabia share 23.7% and 22.9%, respectively, of their DNA with Southwest Asian populations. Similar and complex *Structure* profiles are seen among Arabian Peninsula populations underscoring the high genetic diversity of the region. Although UAE shares a number of genetic characteristics in common with the rest of the populations in the Arabian Peninsula, it is unique in terms of its relative high Asian genetic component, likely the result of geographical proximity to Southwest Asia, west-bound waves of migration and socio-political ties with territories to the east.

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1. Introduction

The territory presently occupied by the United Arab Emirates (UAE), located at the extreme southeastern corner of the Arabian Peninsula, represents an important nexus connecting the European, African and Asian continents and is theorized to have played a significant role as a conduit for the dispersal of modern humans. Besides UAE, the Arabian Peninsula is compartmentalized into Bahrain, Kuwait, Oman, Qatar, Saudi Arabia and Yemen, all Arabic speaking and predominantly Muslim countries.

Abbreviation: UAE, United Arab Emirates; STR, short tandem repeats; YBP, years before present; HLA, human leukocyte antigen; G6PD, glucose-6-phosphate dehydrogenase; PAI, polymorphic *Alu* insertion; HWE, Hardy–Weinberg equilibrium; GDI, gene diversity index; MP, Matching Probability; PD, Power of Discrimination; PIC, Polymorphic Information Content; PE, Power of Exclusion; TPI, Typical Paternity Index; MDS, multi dimensional scaling; SPSS, Statistical Package for the Social Sciences; NJ, neighbor-joining; WLS, weighted least square; MCMC, Markov Chain Monte Carlo.

* Corresponding author at: Biology Department, Colorado College, 14 East Cache La Poudre Street, Colorado Springs, CO 80903-3294, USA. Tel.: +1 719 389 6402; fax: +1 719 389 6940.

E-mail address: RBertrand@coloradocollege.edu (R. Garcia-Bertrand).

¹ These three authors contributed equally to the manuscript.

Small groups of hunter gatherers are speculated to have ventured into the Arabian peninsula as early as the Pleistocene era, approximately 54,000 years before present (YBP) (Petraglia and Alsharekh, 2003) but permanent settlements are only detected starting in Neolithic times (8000 YBP) when the newly developed agricultural lifestyle allowed for continuous habitation of a given region without the constant need for new hunting grounds (Hassan, 2002; Militarev, 2002; Shepard and Herrera, 2006a). The Levantine Corridor and the Horn of Africa have been posed as the two primary routes taken by early settlers into the peninsula from Africa, and several studies have pinpointed the Levant as the preferred of the two passageways (Luis et al., 2004; Regueiro et al., 2006; Rowold et al., 2007). More recently, pastoral agriculturalists (native to northeast Africa) are postulated to have traversed the Sinai Peninsula for entry into the Levant and from there, to Arabia (Beyin, 2006).

Luis et al. (2004) comprehensively examined frequency distribution and coalescence time patterns for Y-haplogroup E-M35 (E1b1b1) and its derivatives E-M78 (E1b1b1a) and E-M123 (E1b1b1c). Both subhaplogroups (E-M78 and E-M123) were detected in northeast Africa (Egypt) and the Arabian Peninsula (Oman), however time estimates for the two regions yielded noticeably older ages in Egypt when compared to Oman, supporting previous and subsequent reports

Table 1
Populations analyzed.

Region	Population	Abbreviation	Total # of alleles	N	Avg. heterozygosity	Reference
Arabian Peninsula	United Arab Emirates	UAE	136	109	0.77003	Present study
	Bahrain	BAH	127	50	0.79333	Shepard and Herrera (2006a,b)
	Kuwait	KUW	146	502	0.77080	Alenzia et al. (2008)
	Oman	OMN	142	141	0.77164	Shepard and Herrera (2006a,b)
	Qatar	QAT	135	133	0.70914	Pérez-Miranda et al. (2006)
Levant	Yemen	YEM	125	59	0.75820	Shepard and Herrera (2006a,b)
	Iraq	IRQ	130	103	0.78907	Barni et al. (2007)
Southwest Asia	Jordan	JOR	120	46	0.78551	Shepard and Herrera (2006a,b)
	Afghanistan	AFG	118	130	0.74951	Berti et al. (2005)
North Africa	Iran	IRN	141	150	0.77288	Shepard and Herrera (2006b)
	Pakistan	PAK	136	94	0.74965	Shepard and Herrera (2006a,b)
	Punjab (India)	PUN	134	86	0.77753	Shepard and Herrera (2006a,b)
	Egypt	EGY	140	119	0.78543	Shepard and Herrera (2006a,b)
Anatolia/Caucasus	Morocco (Arab)	MRA	137	387	0.77987	El Ossmani et al. (2007)
	Morocco (Berber)	MRB	125	104	0.75007	Coudray et al. (2007)
	Sudan	SUD	132	65	0.78647	Shepard and Herrera, (2006a,b)
	Georgia	GEO	125	65	0.78974	Shepard and Herrera (2006a,b)
Mediterranean	Turkey	TUR	137	500	0.78347	Yavuz and Sarikaya (2005)
	Greece	GRE	154	300	0.79637	Sánchez-Diz et al. (2008)
Balkan Peninsula	Sardinia	SAR	129	125	0.77620	Verzeletti et al. (2009)
	Albania	ALB	132	136	0.80833	Kubat et al. (2004)
	Croatia	CRO	138	195	0.78529	Projić et al. (2007)
	Macedonia	MAC	127	100	0.79667	Havas et al. (2007)
	Romania	ROM	176	1910	0.78195	Stanciu et al. (2009)
	Serbia	SER	129	100	0.78067	Veselinović et al. (2004)

which denote E-M35 as northeast African in origin (Cruciani et al., 2004, 2007; Di Gaetano et al., 2009; Ehret et al., 2004; El-Sibai et al., 2009).

Although the Levantine Corridor appears to have been favored by early migrants, several studies (Forster, 2004; Kivisild et al., 2004; Luis et al., 2004; Perez-Miranda et al., 2006) have provided data supporting the use of the Horn of Africa (Bab el Mandab Strait) as a gateway from and to Africa. This crossing has been historically utilized as the primary trading route between continental Africa and the Near East for the transport of myrrh, cattle, and later on, of East African slaves (Harris, 1971; Kivisild et al., 2004) during the period of the Arab slave trade. Examining mtDNA from Ethiopian and Yemeni samples, on opposite sites of the strait, Kivisild et al. (2004) observed comparable levels of

haplogroup L3, specifically L3f, L3h, L3i and L3x, in both populations (33% and 37%, respectively), alluding to gene flow between the Horn of Africa and Arabia and implying a genetic connection between Africa and the Near East via the Bab el Mandab Strait. Specifically, the authors argue that the detection of additional L subclades, namely L3e and L0k, in the Yemeni collection is likely the result of the transport of southeast Africans to the peninsula during the Arab slave trade (Kivisild et al., 2004; Rowold et al., 2007).

In addition to the aforementioned Out of Africa migrations, Peninsular Arabs have received substantial genetic contributions (albeit more recent) from various sources including other parts of the Middle East and Asia. Sub-haplogroup J-M267, of Middle Eastern descent (Semino

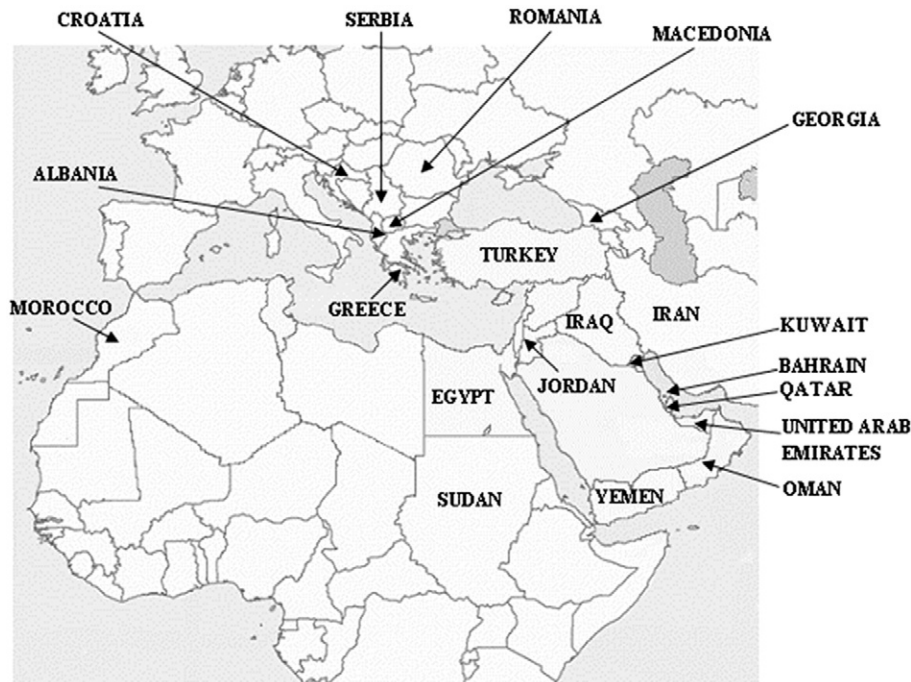


Fig. 1. Geographic locations of UAE and the reference collections.

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