

## Y Chromosomal Haplotypes and Common Surnames in the Population of Benghazi

Samir Elmrghni<sup>1\*</sup>, Yvette M. Coulson-Thomas<sup>2</sup>, Ron A. Dixon<sup>2</sup>, D. Ross Williams<sup>2</sup>, Mahmud Kaddura<sup>1</sup>

<sup>1</sup> Department of Forensic Medicine and Toxicology Faculty of Medicine University of Benghazi Libya

<sup>2</sup> School of Natural and Applied Sciences, University of Lincoln, Brayford Pool, Lincoln, LN6 7TS, UK

**\*Corresponding Author:** Samir Elmrghni, Department of Forensic Medicine and Toxicology Faculty of Medicine University of Benghazi Libya, **Email:** samir3272@yahoo.ie

**Abstract:** The fact that many societies employ patrilineal surnames has stimulated interest in the relationship between surname and Y haplotype. In a perfect world, a detailed Y haplotype would automatically provide the surname of the bearer. However, in reality, there are a several perturbing influences: In the current study informed consent was taken from 238 different Libyan male individuals (Benghazi region) and their DNA were typed and analysed, we concluded that 7 different haplotypes were shared by a total of 24 men out of 238 and most of them from individuals bearing the same surname (Aguri & Obidi) which supported the relationship between surname and Y haplotype.

**Keywords:** Haplotypes, Surname, Benghazi

### 1. INTRODUCTION

In individuals the Y chromosome is approximately 60 Mb long (million base pairs) long and contains only 78 genes. The SRY gene (sex-determining region Y) fixed on the Y chromosome encodes a protein that triggers the development of the testes and through an extended hormonal pathway causes a developing foetus to become male

With the exception of two regions, PAR 1 and 2 (PAR = pseudoautosomal region), located at the tips of the chromosome, no recombination occurs through meiosis. 95% of the Y chromosome is non-recombining, male specific, and is passed from father to son unaffected, unless mutations occur. The lack of recombination may be the reason why there are relatively few genes on the Y chromosome. If there is no chromosome crossing over, mutations within genes have little chance to be repaired or rectified and hence will be passed onto the next generation. [1].

Humans have always been curious about their history, often being deeply interested in issues such as ancestry and the origins of mankind, the basis and dynamics of morphological diversity and the geographic and chronological aspects of ethnic differentiation. These questions have

been addressed using expertise from various fields and biologists have played a notable and decisive role in deciphering our population histories.

Hereditary surnames contain information about relatedness within populations. They have been used as crude indicators of population structure and migration events, and to subdivide samples for epidemiological purposes. In societies that use patrilineal surnames, a surname should correlate with a type of Y chromosome, provided certain assumptions are met. Recent studies involving Y-chromosomal haplotyping and surname analysis are promising and indicate that genealogists of the future could be turning to records written in DNA, as well as in paper archives, to solve their problems surnames, considered key cultural markers, are being used to further investigate and enhance the genetic signals of population structure when analysing genetic data. Surnames are transmitted through the male line and they are inherited as alleles of a gene. Thus, their transmission should closely match that of DNA of the non-recombining region of the Y-chromosome (NRY). This co-inheritance, together with the low cost and ease of collecting and analyzing surname samples,

has made surname studies to deal with a great variety of questions and to achieve a wide space within the fields of Anthropology, Population Genetics, Forensic Genetics, Genealogical Genetics, Epidemiology among others [2]. Nevertheless, other surname characteristics make its use, as a proxy of Y chromosome (Y-C) lineages, be a “crude way to study human inbreeding and migration” [3].

Surnames are interesting because they have been patrilineally inherited since the 13th century and commonly used in the 1500s in several Western European regions [4].

The patrilineal inheritance of both surnames and Y chromosomes suggests that different strata of surnames should correspond to different strata of Y chromosomes. Since this relationship is likely to have become obscured not only by mutation but also by illegitimate births and the change of surnames, quantifying the residual correlation between the two characteristics would be of both theoretical and practical relevance. On the one hand, information about the history of patrilines is useful for the precise estimation of mutation rates and for the assessment of migration behaviours. On the other hand, surnames potentially provide a simple means of stratifying populations prior to Y-chromosomal analyses that target prehistoric events, thereby increasing their efficiency through a reduction in genotyping load. The aim of the present study was thus to assess the extent to which Y-STR haplotypes of Libyan males, born and living in the region of Benghazi, are indicative of a Libyan descent of their surnames.

**2. MATERIAL AND METHODS**

Permission was taken from 238 different Libyan male individuals (Benghazi region).

**Table1.** The 7 different most common haplotypes shared by 24 out of 238 unrelated males from the Benghazi Population

Number of shared haplotypes	DYS 19	DYS 389 I	DYS 389 II	DYS3 90	DYS 391	DYS 392	DYS3 93	DYS3 85 a&b	DYS4 38	DYS4 39	DYS4 37	DYS4 48	DYS4 56	DYS4 58	DYS6 35	YGA TA H4
7	14	13	29	23	11	11	12	13,19	10	11	14	20	14	18	21	11
4	14	13	29	23	11	11	12	13,19	9	11	14	20	14	18	21	11
4	14	13	29	23	11	11	12	13,19	9	11	14	20	14	19	21	11
3	13	14	29	24	9	11	13	13,14	10	10	14	20	16	18	21	12
2	14	13	29	23	11	11	12	13,19	9	12	14	20	14	19	20	11
2	14	13	29	23	11	11	12	13,19	10	12	14	20	14	18	21	11
2	14	14	29	23	11	14	13	13,13	10	10	14	18	16	16	24	11

**Table2.** Surname statistics for selected countries and populations

Country or population (% of total surveyed)	Mean no. of carriers /surname	Most frequent surname	% carrying Most frequent surname	% carrying 10 most frequent surnames	Hereditary surname time-depth (years)	Ref.
---	-------------------------------	-----------------------	----------------------------------	--------------------------------------	---------------------------------------	------

**2.1. DNA extraction**

DNA Extraction was following the laboratory protocol

**2.2. PCR amplification**

Was used regarding protocol instructions.

**2.3. Typing**

Through the ABI Prism 310xl Genetic Analyzer.

**2.4. Quality control**

Accession number: YA003680.

**2.5. Analysis of data**

Analysis included in the YHRD software package.

**3. RESULTS AND DISCUSSION**

In the present study, we noticed 7 different haplotypes which did not match were shared by a total of 24 men (Table 1) the Aguri (16 haplotypes) and Abidi (8 haplotypes) (both being common surnames in Benghazi) with some similarity in their shared haplotypes (some Aguri haplotypes shared Abidi haplotypes). For example, the first haplotype, shared by 7 individuals, includes 5 individuals bearing the surname Aguri and 2 individuals bearing the surname Obidi (Table 1). Table 2-describes Surname statistics for selected countries and populations for example in Great Britain the most common surname regarding to that study was Smith and in France was Martin and both studies regarding to hereditary depth time by years as shown in the table below.

Further studies are necessary regarding these types of shared haplotypes to know thcommon patrilineal surname in all parts of Libya.

Great Britain (75)	28	Smith	1.22	5.9	~700(England); ~300 (Wales)	[5] & [6]
Ireland (69)	63	Murphy	1.71	10.5	~900	[6] & [7]
Netherlands (28)	9	De Jong	0.54	3.7	~200	[8] & [6]
Germany (35)	23	Müller	0.89	3.9	~700	[6]& [9]
Norway (74)	29	Hansen	1.41	9.3	~100 (most of rural population)	[6] & [10]
France (32)	17	Martin	0.33	1.6	~500	[5] & [11]
Spain (21)	37	Garcia	3.66	19.8	~500	[6] & [8]
Italy (27)	12	Rossi	0.33	1.5	~600	[6] & [8]
India (0.3)	19	Sharma	2.44	12.8	Complex history	[6]
Japan (35)	904	Sato	1.44	10.4	~800 (governing classes); ~150 (majority)	[6]& [12]
China (22)	72195	Li	7.4	>30	~5000	[13]
Australia (37)	630	Smith	1.23	5.4	Most names Imported from elsewhere	[6]
USA (23)	43	Smith	0.9	4.8	Most names imported from elsewhere	[6]
Canada (13)	17	Smith	0.31	2.0	Most names Imported from elsewhere	[6]
Benghazi –Libya	24/238	Aguri & Abidi	7% & 3%		525	Present study

#### 4. CONCLUSION

Our analysis of 238 Libyan male (Benghazi region) observed that 24 different haplotype sharing similar surnames, demonstrates a remarkably strong relationship between these patrilineally inherited cultural markers and Y-chromosomal haplotypes.

#### REFERENCES

- [1] Sinclair, A.H., *et al.* (1990) A gene from the human sex-determining region encodes a protein with homology to a conserved DNA-binding motif. *Nature* 346, 240–244.
- [2] King TE, Ballereau SJ, Schürer KE, Jobling MA (2006) Genetic signatures of coancestry within surnames. *Curr Biol* 16: 384–388.
- [3] Crow JF (1983) Surnames as markers of inbreeding and migration. Discussion. *Hum Biol* 55: 383–397.
- [4] King TE, Jobling MA. (2009a). Founders, drift, and infidelity: The relationship between Y chromosome diversity and patrilineal surnames. *Mol Biol Evol* 26: 1093–1102.
- [5] McKinley R.A, (1990). A history of British surnames. *Longman*
- [6] Longley, Petal., (2009). PublicProfiler/worldnames <http://www.publicprofiler.org/worldnames/>
- [7] MacLysaght E, (1969). The surnames of Ireland. *Irish University Press*
- [8] Manni, F *et al.*, (2005). New method for surname studies of ancient patrilineal population structures and possible application to improvement of Y chromosome sampling. *American Journal of Physical Anthropology*.126:214-228
- [9] Curren-Briggs N, (1982). Worldwide family history. *Routledge and Kegan Paul*
- [10] Morgan F.E, (1981). The significance of Norwegian farm names. *Norwegian American Museum*
- [11] Morlet M.T, (1997). Dictionnaire étymologique des noms de famille. *Perrin*
- [12] Yasuda N, (1983). Studies of isonymy and inbreeding in Japan. *Hum Biology*.55: 263-276
- [13] Yuan Y, (2007). Science and culture of surnames. *Chinese National Geographic*.2:38-3

**Citation:** Samir Elmrgghni, Yvette M. Coulson-Thomas, Ron A. Dixon, D. Ross Williams, Mahmud Kaddura, Y Chromosomal Haplotypes and Common Surnames in the Population of Benghazi. *ARC Journal of Forensic Science*. 2017 2(1):9-11. <http://dx.doi.org/10.20431/2456-0049.0201003>

**Copyright:** © 2017 Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.