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Review Report

Research problems in Biological Anthropology: Flaws in sampling and in methods of results analysis

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Abstract - Anthropology has as ambition the study of the whole of humanity. It includes several specialties and sub-specialties that, despite their differences, offer an overall perspective that requires a holistic research approach. In Biological Anthropology, one of its specialties, anthropologists study biological variations in contemporary human populations in order to reveal their characteristics and their genetic relationships and to try, on the basis of analysis of these variations and those revealed in human fossils, to trace the evolution of human lineage through time. In this report, I provide an overview of some research major problems met in biological anthropology. I evoke especially the problems of the use of uncertain results analysis methods and those of incorrect samplings. In addition to the presentation of these problems and their consequences I present alternatives and suitable solutions. I also explain how some classic considerations resulting from some of these problems could hinder scientific progress in the topic in question. Hence, I believe it is time to avoid these problems, to eradicate the resulting considerations and to follow the most realistic research tracks.

Key words: Biological anthropology. Human fossils scarcity. Sampling flaws.
Analysis methods weakness. Classic questionable considerations.
Realistic research tracks.

Introduction

For better understanding research problems met in Biological Anthropology, it is important to begin by presenting the situation of this specialty within its large parent discipline ‘Anthropology’.

Since the beginning of the 19th century, particularly during the colonial encounter between Western people and colonized peoples, the term Anthropology was used to designate a discipline concerned by the study of human populations. However, several centuries before, important basic knowledge relating to different aspects of man, humanity and human populations was presented in many ancient texts of some Islamic Renaissance scholars in the wider Middle East such as Abu Rayhan al-Biruni, a Persian scholar (973-1048) and Ibn Khaldoun, a Tunisian scholar (1332-1406) (for more details see Chaabani 2012). But the majorities of Western anthropologists turn a blind eye to this historical fact and often do not mention it. This does not serve to highlight the scientific-historical truth that acknowledges that this science appeared in the Greater Middle East at a distinct scientific level prior to its time, several centuries before its designation ‘Anthropology’. Moreover, this historical fact raises the status of this science and removes the racist view often associated to its designation ‘Anthropology’ during the late colonial era (Chaabani 2012).

The study of man or anthropology has as ambition the study of the whole of humanity. It includes many specialties and sub-specialties that despite their differences, offer an overall perspective revolved around two main axes. The first axis represents the link between the present to the past; while the second represents the interrelationship between biology and culture. Hence two major branches, or specialties, have been developed: Biological Anthropology and Cultural Anthropology. In each one of them, anthropologists study the past and / or the present of humanity within numerous subspecialties (see **Fig. 1**). But whatever the specialty or sub-specialty in which their studies are made, they should follow a holistic approach by confronting, discussing and / or completing their research results with those, on the same subject, obtained in studies of other specialties and sub-specialties. In other words anthropologists need to couple their specific analytical methods with a global synthetic approach.

However, we must not forget to present the third branch, designated "Applied Anthropology", which is mainly focused on practical tracks aiming to solve human current problems such as those related to health, education or the environment, and therefore it would contribute to ensure the safety of the future of humanity (**Fig. 1**).

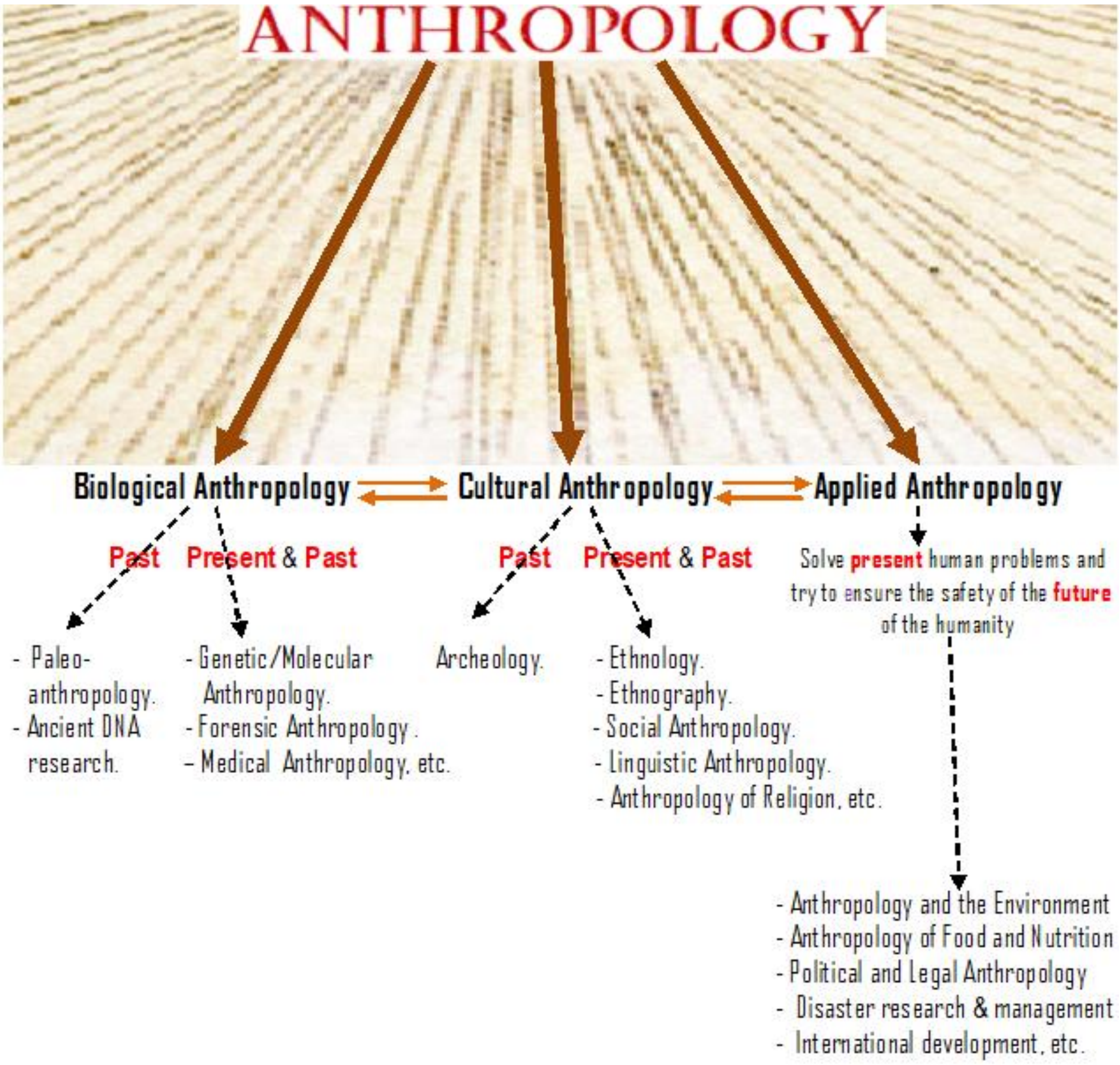

Fig. 1 Schematic presentation of major scientific and humanistic specialties and subspecialties of Anthropology and their interrelations.
(Anthropology, although currently enough wide, is in incessant development and extension to oversee other scientific and humanistic sub-specialties).

In Biological Anthropology, anthropologists study biological variations in contemporary human populations in order to reveal their characteristics and their genetic relationships and to try, on the basis of analysis of these variations and those revealed in human fossils, to trace the evolution of human lineage through time. In the present report I provide an overview of major research problems met in the two sub-specialties of biological anthropology (Paleoanthropology and Genetic/Molecular Anthropology). I evoke especially the problems of the use of uncertain results analysis methods and those of incorrect samplings. In addition to the presentation of these problems and their consequences I present alternatives and suitable solutions. I also explain how classic considerations resulting from some of these problems could hinder scientific progress in the topic in question.

Research problems in paleoanthropology and how to solve them

The science of paleoanthropology is mainly focused on trying to trace the evolution of our lineage through time using the fossil record (bones and teeth) and related archeological remains. Although this science is generally interesting, some research problems have led several paleoanthropologists to set some unacceptable and / or contradictory considerations, which would contribute to hindering the progress of this science and permit to consider it as a contentious science.

Although the human fossil research had been started from the 19th century the number of discovered fossils is yet insufficient to permit the application of rigorous statistical analyses. In addition to their remarkable scarcity, human fossils were often found in incomplete states and discovered at sparsely periods. Thus, each of these incomplete fossils had been analyzed in a separated study subject to mistake and imagination leading to questionable considerations and conclusions. As examples of the consequences of such problems, I can present the two most significant ones. The first example (**1**) concerns the consideration of the species *habilis* as belonging to our genus even after the publication of more rigorous studies that denied this consideration. The second example (**2**) concerns the unacceptable belief that the study of anatomical futures, particularly the discrete cranial traits, of human fossils alone is sufficient to identify and determine species within our genus *Homo.*

1) Problem of whether or not the species '*habilis*' belongs to our genus.

The discovery of *Homo habilis* began in 1959 from the finding of two teeth and officially designated in 1964 (Leakey *et al.*1964) but its placement into the human genus *Homo* was controversial: Although this species was initially considered to be a direct ancestor of modern humans, fossil discoveries in 1986 showed that *Homo habilis* had rather ape-like limb proportions. Additional fossils from other individuals were found and other names are attributed to *Homo habilis* and the debate continues.

However since 1999 two evidently more rigorous studies have been published showing that *habilis* cannot belong to our genus. In the first study a meticulous general revision of anatomical features of all available hominid fossils has been carried out and concluded that the two fossils called *Homo habilis* and *Homo rudolfensis* do not belong to the genus *Homo*, but they belong to a non-human ape species (Wood and Collard 1999). Therefore *Homo erectus*, emerged in sub-Saharan Africa at about 1.8 million years ago, is the early individual belonging to the genus *Homo*. This conclusion is strongly supported otherwise in a second rigorous study, which shows that *Homo erectus* is the first who have the anatomical features responsible for the possession of the endurance running ability and that of the real upright body form. This anatomical features (about 26 features), absent in all predecessors of *Homo erectus*, differentiate *Homo* peoples (Bramble and Lieberman 2004). Consequently, the bipedal gait restricted to walking, classically considered as a humanization criterion, would not be supported any more: It could be an ancient adaptation, which probably existed even before the divergence between apes and humans at about 5 million years ago. In fact fossils of Orrorin tugenensi fossil, 6 million year old, and Sahelanthropus tchadensis (Toumai), 7 million year old, are already adapted to the bipedal gait (Chaabani 2014).

Moreover, other more recent studies come to support and / or to complete these conclusions such as that of Tattersall and Schwartz (2008) in which they showed that the post cranial morphology of *Homo erectus*, although more robust, falls within the range of that of *Homo sapiens sapiens*. On the basis of all these notable conclusions, I have defined our genus as follows: "The first peoples belonged to the genus *Homo* are those designated *Homo erectus*: they possess the post cranial anatomical features of contemporary humans responsible for the real upright body form associated to the endurance running ability" (Chaabani 2014).

But unfortunately, until nowadays, several paleontologists continue to speak about *habilis* or other parallel designations as belonged to our genus. This odd comportment could be explained by the fact that if questionable information is presented in innumerable books and articles during one or a few decades, it would become almost a reality difficult to discard it particularly if some editors and authors are well positioned to support it.

2. The problem of defining the way that allows us to identify species in our genus

Numerous paleoanthropologists accept that analyses of anatomical features of human fossils, particularly the discrete cranial traits (DCT), could alone distinguish between species belonged to our genus: they tried to define modern man *Homo sapiens* as having modern DCT in contrast with *Homo erectus* having primitive DCT, and archaic *Homo sapiens* as having a mixture of modern and primitive DCT. But several arguments show that this consideration is questionable:

- The variation of DCT during the long existence period of *Homo* peoples shows a complex continuation and it is inconceivable to set limits within this variation for classing species, especially that it is not possible to know if it is within-species or among-species (Chaabani 2014).
- There is some degree of overlap in the ranges of DCT variation between species of our genus. For example, the complete *Homo erectus* fossil "Turkana Boy" found in Africa shows, in addition to the prevailing primitive DCT, some advanced features (Gish 1995). On the other hand human fossils considered anatomically modern, dated about 160,000 or 120,000 years ago, keep some primitive DCT (White *et al.* 2003; Klein 1992). This degree of overlap becomes important among the possible closely related subspecies such as the so called archaic *Homo sapiens*, and *Homo sapiens sapiens* to such an extent that paleoanthropologists avoid speaking about subspecies and they just use *Homo sapiens* for the designation of modern man (for more details see Chaabani 2014).
- The so-called modern DCT are not especially similar from place to place and therefore its identification presents a problem (Caspari and Wolpoff 2013). Even in the same geographic area, living populations show substantial morphological differences from populations of *Homo sapiens sapiens* living >5,000 years ago (Lahr 1996).

- Another argument concerns the evident incompatibility between the state of these DCT and the ancient mtDNA sequences analysis (Adcock *et al.* 2001; Relethford 2001).
– It is not reasonable to accept that discovered fossils of a single individual could represent the large population to which he belonged during the same existence period that, moreover, is often dated with wide probability for errors (for more details see Chaabani 2014).

In the light of all these critics, it seems that analyses of anatomical criterion such as discrete cranial traits (DCT) on only one fossil or a very small number of fossils is evidently of limited utility in distinguishing between species belonged to our genus. But unfortunately the resulting emergence date of our species 'sapiens', valued of 100 000 to 120 000 years ago based on analyses of these anatomical futures, persist and often considered until nowadays.

To resolve this complex problem, we must look for a more suitable criterion that permits a more accurate definition of modern man and therefore a more valid identification of modern human fossils. As I have noted previously (Chaabani 2008, 2014) such criterion do not need research: it is evidently present in our believe that modern humans differ from all being, including other *Homo* peoples, essentially by the superior potential cognitive abilities that for our ancestries could be determined indirectly from the vestige of their cultural products through analyses of archaeological material and other related data such as the emergence periods of the mother language and social complexity (for more detail see Chaabani 2008, 2014).

In fact these superior cognitive abilities reflect the high degree of the complexity of the brain structure and its functional neural organization that could be due essentially to a higher number of neurons and synaptic connections and perfection at the level of functional molecular factors. I have considered that this high degree of the brain complexity has been appeared in its complete high degree even in earliest modern humans and consequently it has not been evolved in the course of time. It is the rate of know-how and knowledge that has been grown conducting, from time to time, to some improvement of the manner and the intensity of the use of the brain potential aptitude. Thus, I have seen that the principal constant criterion that marks strongly the definition of modern man is the high degree of his brain complexity responsible for the superior cognitive abilities (Chaabani 2008, 2014).

The progression of the research technology in neuroimaging can contribute to solving the problem of classic anatomical features that, as I have just explained, are unable on their own to identify species of our genus *Homo*. In fact, this technology will allow us to better define the relationship between brain and endocast. Hence the study of the latter could help paleontologists to know some particularities of the brain in question (Balzeau and Mangin 2021). In other words, if this technology will permit to determine particularities reflecting the degree of complexity of the brain, through its endocast, it could reinforce and complete my proposition to analyze basic historical cultural results and vestiges of cultural products in order to differentiate fossils of modern man *Homo sapiens sapiens* with those of our precedent species '*erectus'*.

Research problems in Genetic/Molecular Anthropology and how to repair them

The ABO blood group antigens are the first protein markers used to provide genetic characterization of human populations. After the discovery and the use of several more polymorphic protein markers (classic markers), innumerable studies were done on different world populations. In these studies, for a best interpretation of results, researchers are often obliged to confront and / or to complement them with related historic and cultural data such as spoken languages (e.g. Cavalli-Sforza *et al.* 1988; Chaabani *et al.* 2000). Hence, they consider such studies as belonged rather to a new sub-specialty of the anthropological science 'Genetic Anthropology'. After the emergence of molecular biology technology and the determination and use of DNA markers in the human population studies, researchers often prefer to speak about 'Genetic/Molecular Anthropology'.

However, I must notice that before the discovery of genetic markers (in the early beginning of the 20th century), the biological diversity of human populations has been already started by measurements of observable physical characters particularly the skin color and the size and shape of the skull and the nose. In this way, some classical anthropologists had classified humans into races by setting imaginary limits in the continuous variations of physical characters. This was severely criticized particularly after the discovery and the use of genetic and molecular markers, which showed a surprisingly small amount of genetic variation noted throughout all present-day human populations and therefore it is not possible to set races in human populations (e.g. Jones 1981; Denaro *et al.* 1981, Langaney 1984, Barbujani *et al.* 1997). Although this problem of human races was disappeared over time, scarce researchers continue to use stupidly the term 'race' on the assumption that they aim to say 'ethnic group'!

Moreover, in more recent works, Relethford and Harpending (1994), going back to the measurement of observable physical characters, showed that the analysis of craniometric variation provides results on human genetic diversity within and among populations, similar to those obtained from genetic markers and DNA polymorphisms, while the analysis of skin color variation gives fairly different results. In fact, the worldwide distribution of human skin color seems correlated with the global distribution of ultraviolet radiation, suggesting past selection for dark skin near the equator and for light skin at greater latitudes. Thus, variations in skin color are adaptive, and their general analysis tells little about global population history and relationships (Jablonski and Chaplin 2000; Relethford 2002). However, under particular circumstances, skin color can be used with molecular markers, to enlighten ancient population movements (El Moncer *et al.* 2011). In a more recent study Betti *et al.* (2010) performed a similar set of analyses using a larger craniometric dataset and found a higher correlation of craniometric distance with geography than with temperature, suggesting that natural selection has had less impact on global craniometric variation than population history; while only traits of breadths and nasal measures showed a relatively greatest impact of climate.

Here, I present two major types of problems met in genetic/molecular anthropology: the first concerns the use of questionable results analysis methods and involvement in confusion, and the second concerns flaws in sampling processes.

1. Use of questionable results analysis methods

Although the majority of methods, particularly the statistical ones, used in analyses of genetic/molecular results are correct and acceptable, some complicated sophistical ones, used particularly in analyses of basic results intending for retracing the evolutionary history of human populations, are often questionable. I can take as example the study of Cann *et al.* (1987) that, in addition to using an unconvincing method, represented a starting point for the development of a conjectural confusion.

Weakness of the method used in Cann's study

In 1987 Cann *et al.* estimated the date of modern man emergence from analyzing mtDNA to about 200,000 years ago with a surprising large interval ranges from simple to double!!! In addition they considered that this emergence was occurred in sub-Saharan Africa. The method of basic results analysis used in this study was largely and severely criticized by several authors (e.g., Excoffier and Langaney 1989; Vigilant *et al.* 1991, Maddison 1991; Klyosov 2014; Chaabani 2014): In fact this method, as other similar ones, is complicated, theoretical and not sufficiently stable, and includes uncertain assumptions such as that of the mutation rate of the human mtDNA evolution. Later, different dates of modern man emergence have been estimated such as that of 137,000 ± 15,000 years ago from autosomal marker analysis (Stoneking *et al.* 1997). In any case, whatever the degree of validity of these methods, their application could give era estimations, which are not necessary those of the modern man emergence but they could extend back to any point in the *Homo* evolutionary history.

Emergence of a conjectural confusion starting from the Cann's study

The way of presenting things in the study of Cann *et al.* (1987) given rise to an annoying confusion, which transmitted and persisted in several posterior studies related to the same subject. This confusion concerns the model of the single origin of all current human populations that I can present as follows:

Two most known models were proposed to illustrate our origin: the model of the single origin and the multiregional model. As presented in **Fig. 2**, both models would agree with the fact that our evolution was started in sub-Saharan Africa by the emergence of *Homo erectus* (representing the first species, *erectus*, belonged to our genus *Homo*). According to the first model during the spread of this *Homo erectus* in the rest of the world, he evolved in only one place into modern man (representing our species and subspecies, *sapiens sapiens), Homo sapiens sapiens,* who, in turn spread throughout the earth, had completely replaced the preceding archaic populations without interbreeding; while the model of the multiregional origin argues that the early *Homo* peoples, *Homo erectus,* during their spread in the rest of the world they evolved into modern man (*Homo sapiens sapiens*) independently in different world regions.

The surprisingly small amount of genetic variation throughout all present-day human populations (Barbujani *et al.* 1997) and linguistic data (Shevoshkin 1989; Chaabani 2014) have supported strongly the model of single origin and showed that our origin is not only unique but also recent and consequently this model become a general theory: 'the theory of unique and recent origin of modern humans'.

The confusion consist of the fact that this well-accepted general theory of our single recent origin is confused with the 'Out of Africa' thesis in which, although the principle of the general theory has been adopted, the date and the single place of modern man emergence, that still represent a controversy, have been proposed. Hence the 'Out of Africa' thesis represents one of possible other versions of the general theory and not the general theory itself (Chaabani 2014). It seems that everyone who turn a blind eye to this confusion and go on with it, refuse indirectly other versions and / or try to influence young researchers to follow blindly the 'Out of Africa' version. The problem is that the alignment towards this version often occurs without presenting new convincing arguments. This has indirectly contributed to hindering scientific research progress on this theme since 1987.

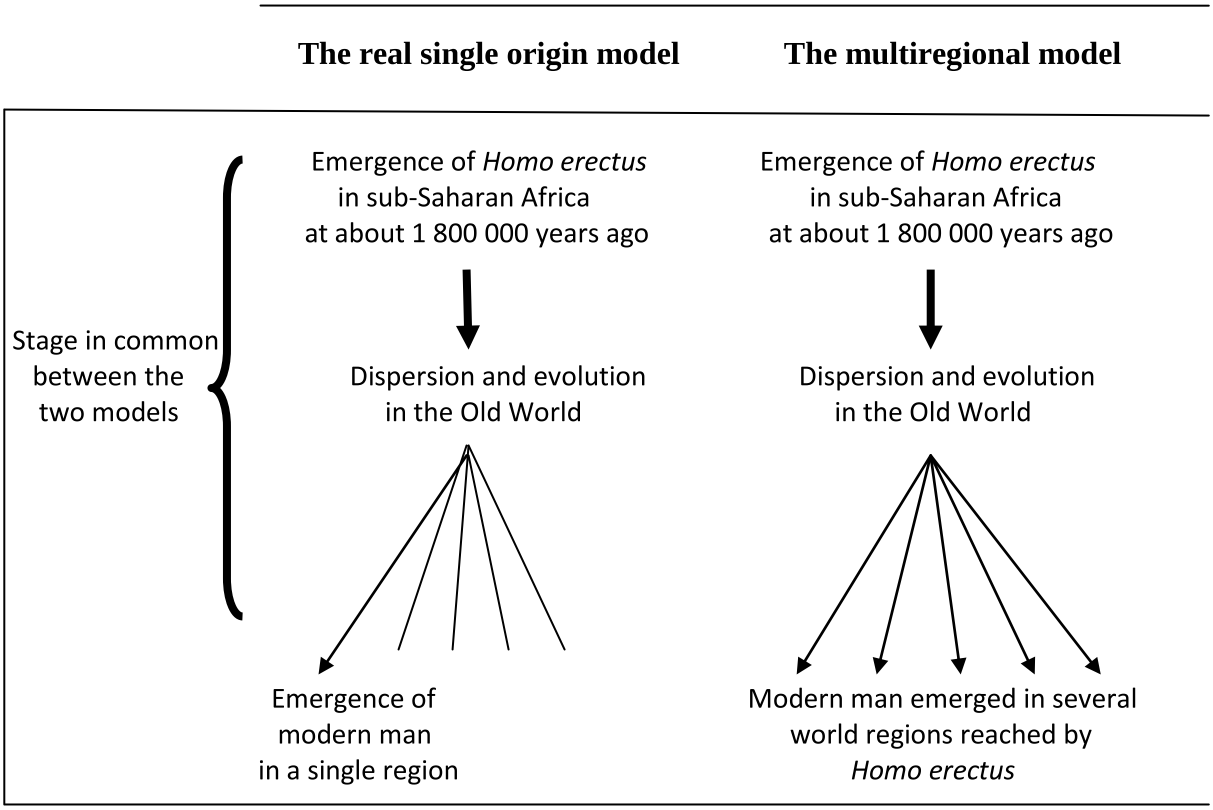

Fig. 2

A thesis free from all aforesaid problems as an example of a wise solution

One can say that such research problems would be mainly due to some constraints, difficulties and absence of other alternatives, which in some ways obliged researchers to apply even questionable methods and to adopt even uncertain considerations. As an answer to these questions and as an exemplary solution to such problems, I call back to my thesis (Chaabani 2014) on the same subject and in which I have followed clear and realistic approaches that distance it from all the above mentioned problems that I reassemble as follows:

* In paleoanthropology: - The problem of the scarcity of human fossils and therefore the use of only one fossil or a very small fossil sample. This led to two anxious affairs: - that of considering the species *habilis* as the first belonging to our genus even after the publication of evidently more rigorous studies that denied this consideration; and – the problem of the questionable consideration of the study of anatomical features, particularly the discrete cranial traits, as been able alone to determine species within the genus *Homo.*

* In genetic/molecular anthropology: The problem of the use of weak methods for analyzing basic results, and the possible involvement in confusions such as that between the general theory of our single and recent origin and possible different versions of this theory.

In fact, in my thesis (Chaabani 2014) I have resolved the two paleoanthropological problems by proposing an evident more rigorous definition of the first species of our genus '*Homo erectus*' and a more clear and reasonable definition of our species and subspecies '*Homo sapiens sapiens*' (already presented above). Accordingly I have resolved the genetic/molecular anthropological problems by implementing clear realistic approaches without using any complicated sophisticated questionable method for analyzing genetic/molecular basic results, and I have revealed the confusion between the general theory of our unique and recent origin and its possible different versions such as the thesis of 'Out of Africa' and my thesis 'Recent Out of Yemen'.

My version is a complete well-founded and well-argued thesis. Presented in a refined grand synthesis, it provided a reliable picture of our evolutionary history. First, from analyses of basic genetic results I have shown that the southern Arabian Peninsula would be the most probable place of a so recent emergence of modern man. Second, from an objective definition of modern man based on analyses of the vestige of cultural products and several rigorous basic results such as those related to the emergence of the mother language and complex societies (see details in Chaabani 2014) I have proposed dates, of about 45,000 years ago for the emergence of our species and 20,000 years ago for that of our subspecies.

Flaws in sampling processes in human populations studies

A sample refers to a smaller, convenient version of a larger group used in statistical testing. In the case of a genetic/molecular anthropological study of an entire population, we should select a large sample of asymptomatic unrelated person's representative to the entire population. However, the sampling strategy should be adapted to the particularity of each population such as for a large population that seems enough heterogeneous the sampling scheme could be stratified on the basis of geography and ethnicity.

The sampling process has been subject to flaws and vagueness, which unfortunately are rarely revealed and / or discussed. In fact, reviewers of manuscripts of genetic/molecular anthropological studies generally give more importance in checking methods and techniques used for revealing genetic or molecular markers than in checking the validity of the process of sampling. In addition reviewers generally do not belong to the studied population and therefore they do not know enough ethnic and geographic details on this population. Hence several flaws of sampling go unnoticed.

I can present the two most common problems of deficiencies and vagueness in sampling process as follows:

The use of small samples:

As stated above for an anthropological study of an entire population, statistically speaking, the population sample should be infinitely large: we should obtain samples of a few hundred to several hundred persons, or even more. However, due to practical constraints, samples studied are often relatively small or even very small reduced to 50 or 30 persons[1]. I believe that results obtained from these very small samples would be informative and preliminary admissible only if we take into account this problem during discussion and results analyses. For example in such very small samples it is difficult to find genetic or molecular markers, which could be present in weak frequencies in the entire population in question. Therefore, it is incorrect if on the basis of the study of such very small samples we conclude the absence of such rare markers in the entire population and/or to compare obtained results with those obtained from large correct samples.

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[1] However, a sample as small as 50 or 30 could be quite useful in studies having particular objectives different to that of an anthropological study of an entire population.

Lack of representativeness:

For an anthropological study of an entire population of a determined country, the sample should represent the population as a whole and not reflect any bias toward a specific anthropological feature. In other words, it should include persons originating from all regions of the country with sufficient balanced distribution.

Lack of representativeness, often due to practical constraints and difficulties or to the ignorance of the importance of the representativeness, is generally concealed by the fact that authors do not give clear accurate information about the sampling process. For example they note 'we collected a population sample from a determined country (or a sample from the north of this country), but in reality they collected this sample from only one of several villages located in the North of this country. Therefore, in contrary to what one can understand from their note, the sample cannot be considered as representative neither to the entire population of the country in question nor to its North, but it is a sample that concerns only people living in a limited small area 'village located in the North of the country in question'.

Problems met in some Tunisian population studies

In addition to these two most general problems met in sampling process, meticulous problems peculiar to this or that population could be revealed only by someone who knows sufficiently the history and the general ethnic and geographic structure of the population in question. Thus, as Tunisian, I prefer take as concrete examples those met in anthropological studies of the Tunisian population. For a better understanding of these problems, I must begin by presenting briefly the history, the culture and the genetic characteristics of the Tunisian population[2].

** Structure of the Tunisian population from a cultural-historical point of view*

The analysis of historical and cultural data on the Tunisian population leads us to conclude that the current Tunisian population is composed of a mixture between:

- An indigenous Berber majority, - A relatively large Arab contribution (mainly due to the expansion of Arabs, during the seventh century AD), - A less important Mediterranean contribution (such as Phoenicians and Romans), and - A very low relatively recent enters of sub-Saharan Africans (until now perceptible through the limited presence of dark skin families).

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[2] This subject is briefly evoked in my presentation in the first workshop of the Genome Tunisia Project, the 18 February 2022 (here, I present more examples and more explanations).

After several centuries this ethnic mixing was resulted in a homogeneous population having a rich and unique culture (Chaabani 2017, pages 20-22): indeed all Tunisians speak the Arabic language and keep a remarkable richness in traditions. Although they are mostly Muslims, we must avoid talking about religious belief because it is very complicated and, especially in a real republican regime, is individual rather than social.

* ***Composition and genetic/molecular characterization of the Tunisian population***

Results of genetic and molecular studies show that the ancestors of current Berbers had already received an ancient sub-Saharan African component (e. g. Chaabani *et al.* 1986; Chaabani and Cox 1988; Bahri *et al.* 2008; Chaabani *et al.* 2000. Ben Halima *et al.* 2015). This component present in the entire Tunisian population (as well as other populations of North Africa) could reach 39% and return to the first stage of the Neolithic age (about 9000 years ago) characterized by an ethnic contribution from Sudan (El Moncer *et al.* 2010). In fact, this ancient sub-Saharan component differentiates the Berbers and all North Africans from the populations of the other side of the Mediterranean where this component is generally very weak or undetectable.

However, this sub-Saharan African component is quite present in Middle East Arab populations, which show an obvious genetic proximity to populations of North Africa (e.g. Chaabani *et al.* 2000; Chaabani 2002; Bahri *et al.* 2012, 2013, 2014; Badro *et al.* 2013; Triki-Fendri *et al.* 2016). These results support the movements of ancient peoples from Arabia to ancient Mesopotamia and North Africa proposed by historians such as Barrou (1982) and Goodspeed (2007) and well elucidated within a theoretical proposal encompassing the evolutionary history of human populations (Chaabani 2014).

* ***Presentation of the problems***

After this overview on the cultural and genetic/molecular characteristics of the general Tunisian population, it is possible now to present some problems related to the sampling process detected in some Tunisian population studies as follows:

1. In some studies authors speak about a sample from the Tunisian population without noticing if it is representative to the entire population or not, or they indicate that the sample is from a relatively vast region; while it was collected from a very small district belonged to this region. Moreover, they take the liberty of comparing results obtained from such samples collected in very small different Tunisian districts between themselves and / or with those obtained from large representative correct samples of the

Tunisian population. Such incorrect comparative analyses could generally lead to suggest that the Tunisian population represents an adequate genetic heterogeneity; while comparative analyses of results obtained in studies carried out on samples from Tunisian, Algerian and Moroccan populations show that if we consider correct representative samples of large regions we often find a non-significant difference between the three populations as well as an adequate genetic homogeneity within the Tunisian population (Coudray *et al.* 2006; Bahri *et al.* 2008; El Moncer *et al.* 2010; Ben Halima *et al.* 2015). These findings reflect the genetic proximity between the two main ethnic groups (Berber and Arab) that made up the North African populations. They also allow us to conclude that the Tunisian population has, in addition to a rich and unique culture, a rich and adequate homogeneous gene pool. This reflects the extent to which culture fits with biology.

2. In fact, in describing the entire Tunisian population, we should not forget to mention the existence of some very small groups (about 3000 to 5000 individuals each) which, were more or less isolated, appear relatively less mixed with the rest of the Tunisian population while having the same culture. These are - some groups reputed Berber - a Jewish group in the Djerba Island, and –two or three dark-skin groups settled in southern Tunisia (El Moncer *et al.* 2011). Genetic studies have been carried out on some of these groups but unfortunately in some studies the results obtained are often misinterpreted, because unfortunately authors ignore the particularity of these groups and therefore they do not take it into account during the comparative analyses. In fact my personal investigations show that these groups were developed from a very small number of individuals who have a tendency to practice consanguineous marriage. Thus the founder effect combined with an exceptional high level of consanguinity can offer these groups a genetic profile relatively different from that of the ethnic of origin.

In any case, the study of these groups remains interesting if it is focused on a particular objective especially at the fundamental and medical level such as the possible detection of accidents or genetic peculiarities in the homozygous state (Lefranc *et al.* 1983, Chaabani *et al.* 1985).

3. Some astonishing, vague and inacceptable considerations could be seen in some studies. For example the expression: ‘samples selected from Arab speaking populations of the Tunisian region ……., known to belong to an Arab genealogical lineage’

- First all Tunisians, without any exception, speak Arabic, and the use of the expression Arab speaking populations would indicate or suggest, for non-Tunisian readers, that within the entire Tunisian population there are Arab speaking groups and no Arab speaking ones!!!

- Second, the expression ‘known to belong to an Arab genealogical lineage’ it is a vague inexact popular narration. In fact some dozens of years ago, I have done a meticulous investigation in such regions leading to the conclusion that these regions cannot be considered as reputed Arab. It is true that some persons of a these few regions think that they are rather Arabs, but if you ask each of them why he think so, he often answers because the surname of his father is very likely an Arabic one, but if you ask him if the surname of his mother is also an Arabic one, the answer is often negative (she is either not Arab taking account of one of her parents or of her two parents). You obtain similar answers if you ask him about the name and the origin of the mother of his father and go far in the genealogical lineage.

Thus it is wrong to collect a population sample from these regions considered them as Arabs. In fact a real honest scientific researcher must not believe to such popular questionable narration, which could be the result of the fact that in the majority of world human populations each person receives the surname of his father, and therefore he has tendency to assign his ethnic origin to that of his father.

However in such regions, we can collect particular sample from only men having surely Arab surname in order to investigate the genetic/molecular variability only on the Y-chromosome. Such strategy based on either self-declared ancestry or a number of selective criteria based on surnames are routinely adopted in human evolutionary genetics (for review see Risso *et al.* 2015).

Conflicts of Interest: The author declares no conflict of interest.

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