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## Ethnic Identifiers are Not Necessarily Excellent Population Identifiers: A Commentary from the Turkana in North-Western Kenya

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### **Abstract:**

*Ethnic identifiers have mostly been used as population references in human research. The ability of humans to learn or ape such ethnic identifiers (i.e. language, culture and subsistence activities) makes their status as true identifiers debatable. Equally, the heterogeneity (genetic, cultural, linguistic and even economically) of most human populations implies the likely erroneous conclusions that can be made whenever ethnic identifiers are taken as population identifiers. We hypothesise that the sampling location, GPS position might be better identifiers leaving room for accounting for the occurrence of possible differences especially when samples are obtained from similar population(s) but from different site(s) given the varied nurturing ability from the possibly disparate environmental conditions.*

**Keywords:** Ethnic identify, population identify, common descent

### **1. Does Common Ethnicity Imply Common Descent?**

Individuals having either a real or putative common ancestry with memories of a shared past and cultural focus on symbolic elements defining their identity like kinship, religion, language, shared territory, nationality or even physical appearance can be taken to constitute an ethnic group (Yancey *et al.*, 1976; Weber, 1978; Bulmer, 1986; Smith, 2002). The language, culture and subsistence activities associated with a given population can possibly denote its ancestry and thus act as its identity with the main assumption being that as part of the social inheritance, they are passed down from one generation to another (Geertz, 1993; Salt, 1996). In some instances, phenotypic features like height among the pygmy population for example and skin colour among the coloureds in south Africa have as well been treated as population identifiers with the assumption being that these ethnic labels i.e. language, culture, phenotype and subsistence activities are mainly transferred vertically along generations within populations (Yancey *et al.*, 1976; Salt, 1996; Smith, 2002).

However, some instances where these ethnic identifiers do not fit the strict vertical transmission have been demonstrated with possible exchanges between populations shown while the environmental effect on their heritability varying significantly (Roberts *et al.*, 1978; Li *et al.*, 2004; Gamazon and Perera, 2012; Stulp and Barrett, 2014). The probable language shift, for example, by the Chadic speakers with very minimal subsequent gene flow (Ehret, 1998, 2006; Černý *et al.*, 2009; Tishkoff and Kidd, 2004; Bryc *et al.*, 2010) as well as the possible loss of native languages by several populations like the pygmy, El Molo etc. (Serge, 2006, 2012; Wamalwa and Oluoch, 2013; Mberia, 2014), all depict how unstable linguistic classification can be as population identifiers. Through acculturation, some populations have acquired new cultural traditions never associated with them before like the Maasai and Kalenjin who are thought to have adopted some of their most distinguishing cultural traits like circumcision after encountering the Southern Cushites, Southern Nilotes and the Bantu all in their various phases of expansion and retreat (Newman, 1995). The Sandawe too have reportedly transformed almost fully into an agricultural economy following their interaction with the neighbouring farming groups (Newman, 1970, 1975; Petersen *et al.*, 2013; Yatsuka, 2015). Such cases of acculturation might have resulted from demic and or cultural diffusion; if it is *via* demic diffusion then genetic admixture between the populations involved is probable with cases of sex-biased genetic transmission happening where the dominant group mostly gets women from the dominated group (Barbieriet *et al.*, 2013; Petersen *et al.*, 2013; Verdu *et al.*, 2013). But if the acculturation process happened mainly through cultural transmission, then very minimal gene flow, if any, is expected between the populations involved (Fort, 2012; Jerardino *et al.*, 2014).

Globally, several migration events have taken place resulting in gene flow and eventual genetic admixture between many populations. The African continent has experienced the 'back to Africa' gene flow resulting into the Eurasian admixture as well as the Nilo-Saharan, Afro-Asiatic and Bantu populations migrating within the continent and assimilating most of the autochthonous hunter gatherer populations (Maxon, 1994; Newman, 1995; Nurse and Philipson,

2003; Berniell-Lee *et al.*, 2009; Veeramah *et al.*, 2010; Barbieri *et al.*, 2014; Liet *et al.*, 2014; González-Santos *et al.*, 2015). The Eastern African region has shown an increased Eurasian genetic influence with the Fulani nomadic pastoralists from the Central-Western Africa carrying the lactase persistence allele on the same haplotype as that in Eurasian populations thus showing a high possibility of gene flow between them (Enattah *et al.*, 2008; Lokki *et al.*, 2011; Henn *et al.*, 2012; Hodgson *et al.*, 2014; Pickrell *et al.*, 2014; Ranciaro *et al.*, 2014; Llorente *et al.*, 2015). The likely impetus for the Eurasian admixture within most African populations is thought to be the acquisition of the Neolithic culture from the Near East and its eventual transmission across the African continent (Pickrell *et al.*, 2014; Llorente *et al.*, 2015). The possibility that the livestock keeping tradition among southern African populations was acquired from an Eastern African population ahead of the Bantu entrance is likely. This has been shown courtesy of the Eastern African lactase persistence allele's presence within the Khoikhoi people (Breton *et al.*, 2014; Macholdt *et al.*, 2014; Ranciaro *et al.*, 2014). The presence of Khoesan lineages, with some thought to have already gone extinct, within the southern African Bantu populations and *vice versa* has as well been shown (Barbieri *et al.*, 2014). Within the central African region, possible genetic admixture between the Bantu and especially the Western pygmy populations has been shown (Patin *et al.*, 2009; Batini *et al.*, 2011). The coloured population in Southern Africa has been shown to not only have the Eurasian genotypes but African lineages too, especially the matrilineal alleles (Quintana-Murci *et al.*, 2010; Petersen *et al.*, 2013). Although the massive genetic legacy within most Northern African populations plausibly emanates from the Middle East and southern Europe, some genetic influence from sub Saharan too is present especially towards the Sahara (Černý *et al.*, 2009; Harich *et al.*, 2010; Fadhlaoui-Zid *et al.*, 2015). Within some northern African populations like the Berber, their genotypes are thought to represent the autochthonous dwellers of this region before the Eurasian and sub Saharan genetic influx (Henn *et al.*, 2012; Sánchez-Quinto *et al.*, 2012). With this revelation, it is generally clear that the African genetic landscape is mosaic in nature and thus no single region and or population can possibly claim genetic homogeneity. The apparent genetic heterogeneity notwithstanding, many of these populations are mainly identified and classified by virtue of their linguistic affiliation while others like the Western pygmies and the southern African coloured groups being identified mainly on the basis of their phenotypes i.e. the stature and skin colour whereas many others are categorised based on their main subsistence activity with labels like hunter gatherers, farmers etc.

## 2. The Turkana Situation

Taking the Turkana population as a case study, we note both the high phenotypic and matrilineal diversity resident within it. We as well note the use of a common language –Turkana, which likely is their 'unifying and identification' factor with a variety of subsistence activities like farming, fishing in addition to nomadic pastoralism which encompasses the majority. Two sub populations i.e. the Ngibotook and the Ngibocheros had initially been singled out as not having blended well with the other Turkana communities in terms of lifestyle and economy (Gulliver, 1951; Lamphear, 1992, 1993). The Ngibotook, it is understood, do not keep animals at all for they view them as the main cause of constant conflicts and deaths given the frequent raids. Interestingly, for the Ngibotook even when one of their girls marries into the Turkana sub populations practising pastoral nomadism and many herds of animals are paid as bride price, they (Ngibotook) opt to sell all the animals arguing that keeping them eventually attracts raiders. The Ngibotook themselves pay bride price in form of watermelons and a beehive. Based on these we propose that the Ngibotook possibly were an alien group which after assimilation by the present-day Turkana, only aped some aspects of the Turkana culture like language while shunning other unappealing traits like livestock keeping and crucially maintaining some of their unique cultural traits, a typical example of the segmented assimilation model (Portes and Zhou, 1993; Zhou, 1997; Xie and Greenman, 2005). It is as well possible that other populations might have been totally assimilated into the Turkana way of life *via* the straight-line assimilation model for they not only learned the language but also fully adopted all the other Turkana cultural aspects (Alba and Nee, 1997; Kinloch, 2001). The Ngisiger, for example, are thought to have been a remnant of the present-day Kalenjin, the Ngimaesorokho are supposedly constituted by an entire clan assimilated from the Laikipiak Maasai cluster while the Ngimeturana likely have their patrilineal ancestry from the Kuliak speaking hunter gatherers are all possible culprits of the straight-line assimilation model (Gulliver, 1951; Lamphear, 1992, 1993). On the basis of the economic activities of their probable source populations, we note that with the exception of the Kuliak speakers the other two i.e. Maasai and Kalenjin had a history of livestock keeping and hence might have found it easier to fully integrate with the other Turkana herders.

Another key phenotypic incompatibility amongst the Turkana is to do with the use of donkey milk. While in most Turkana subtribes donkey milk is not used as food apart from its medicinal value in treating whooping cough (Ohta, 1987; Twerda *et al.*, 1997), only the Ngilukumong reported drinking it. Given the high lactose content in the donkey milk, we hypothesise that most of the Turkana subtribes might possibly be lactase non-persistent. In Turkana, the word Ngilukumong loosely means *those who keep long horned cattle* and the fact that they use donkey milk despite its high lactose content might imply their lactase persistent phenotype given their dairying and possibly milk use history. While analysing the lactose tolerance phenotype among the Turkana, close to half of the study samples presented as being lactose intolerant. Even though we used the hydrogen breath test which has been associated with lower type I and II errors coupled with increased sensitivity (Peuhkuriet *et al.*, 1998; Shaw and Davies, 1999; Pohl *et al.*, 2010), we are nonetheless aware that possible cases of false positive and negatives might still abound shifting the frequency either way. Since the lactase phlorozin hydrolase also acts on the phlorizin present among most trees belonging to the *Rosaceae* family, it is then implicit that the phenotype data might not be due to dairying and milk use history *per se* (Wacker *et al.*, 1992; Ehrenkranz *et al.*, 2005; Troelsen, 2005; Mishra and Tiwari, 2011). It is therefore vital to note that the lactose tolerance phenotype results are possibly suggestive and thus the samples need to be subjected to genetic analyses to

establish the presence or otherwise of the selection footprints and potential candidate alleles identified before functional *in vitro* assays can be designed and carried out. According to the culture-historical hypothesis of lactase persistence, it is possible that some Turkana sub tribes derive from populations that had no history of dairying and milk use thus being lactase non-persistent (Simoons, 1970; McCracken, 1971; Holden and Mace, 2002). If this supposition holds then as a tribe, the Turkana might only have a putative common ancestry.

While using only six samples obtained from a refugee camp in Yemen, Triska *et al.*, (2015) reported high admixture levels within the Turkana with the major non-Nilo-Saharan components contributed by the Oromo, Bantu, Kordofanian and the Middle East populations. We acknowledge the absence of both the Khoesan and pygmy populations from the comparison data and hence we cannot necessarily rule out their genetic contribution to the present-day Turkana genotype.

The political instability in Rwanda, Uganda and Sudan has for a long time created refugees in these countries leading to setting up of the Kakuma Refugee Camp within Turkana County (<http://www.unhcr.org/pages/49e483a16.html>). This possibly led to the introduction of 'foreign' genotypes into the Turkana populace since some refugees escape from the refugee camp joining the locals mostly through marriage. The political stability that Kenya as a country has enjoyed leading to better infrastructural development relative to most of the neighbouring countries especially with the beginning of the free primary education, made people cross over from these neighbouring countries into Kenya especially along the border regions. Turkana region being one of these border regions might have received such 'foreigners' too. Once these people cross over into Kenya they'll try as much as possible to ape the Kenyan lifestyle which in this case is by being 'as much Turkana' as possible with the most obvious attempt being to learn the local language and culture. With the increase in the non-governmental organisations within Turkana region providing humanitarian aid to the locals, many other people who are not necessarily Turkana have come into this region as human labour while others come in as business people. The end result is that most centres like Lodwar, Lokichokio and recently Lokichar have become cosmopolitan in terms of the population composition. This is even complicated more by the recent revelation of oil deposits in this region which has led to an influx of people from all over the world and this might make the future Turkana populations to be more admixed than the extant one.

Throughout the entire Turkana populace, there are several persons who consciously recall their grandparents not being Turkana by birth but were instead captured during raids from the neighbouring communities like Samburu, Marille etc. yet they still refer to themselves as Turkana. Since most of these communities are patrilocal does it mean being Turkana is advantageous? What makes them 'think' they are Turkana and not Samburu or Marille, for example? And what is it that makes them 'feel' that they are indeed Turkana? Is it because they can speak the Turkana language and practice the Turkana culture?

The process of seeking identity in such cases often makes the dominant populations to ascribe the identity of the minority populations especially if they are deemed to be of an inferior social standing. Many such examples abound especially when most populations refer to the various hunter gatherer populations around them using derogatory terms such as Dorobo, Boni, Sanye etc. all implying how low the level of standing for such populations within the society was (Hobley, 1906; Bernsten, 1976; Kenny, 1981; Cronk, 1989, 2002; Stiles, 1993; Walsh, 1993). This in a way makes some of these minority populations to start copying the lifestyle and culture of the dominant population for example when the Sandawe in Tanzania, the Okiek and some Dorobo in Kenya have almost abandoned hunting for the farming as well as pastoralism associated with their neighbours (Bernsten, 1976; Cronk, 1989, 2002). However, in some cases the relationship between these two groups can be fluid with people moving into either lifestyle depending on the situation at hand. For example it is thought that when the Maasai lost their animals courtesy of droughts and or raids, majority of them joined the Dorobo in hunting and gathering but later on after rehabilitating their herds they would again get back to their 'Maasai lifestyles' by herding. This led many researchers to questioning as to whether the Dorobo were not just poor Maasai and *vice versa* (Bernsten, 1976; Kratz, 1980; Kenny, 1981; Cronk, 1989, 2002; Stiles, 1993; Walsh, 1993). The same thing supposedly happened to the Turkana after their herds were decimated by droughts and or raids; most of them are thought to have joined the fishing folk along Lake Turkana and the farming groups along the Turkwell and Kerio rivers.

### 3. Is This Situation Only Unique to the Turkana?

The complexity of the Maasai as a population can best be accounted for by the following excerpts from Spear and Waller (1993) .....The history of early Maasai migration into the Rift would appear to be one of accommodation and adaptation, with successive groups establishing themselves beside, and intermixing with, existing populations to produce the palimpsest of pluralist communities many of which were probably economically diversified, mixing herding with grain cultivation and, perhaps, hunting and gathering... .....Maasai are in fact among the recent arrivals on the East African scene; their adoption of a purely pastoral way of life is an even more recent innovation; and many people who speak Maa, the Maasai language, and call themselves Maasai are not pastoralists at all... This could as well imply that the various people currently being referred to as Maasai probably do only share a common language and culture but not descent! This can be best be seen in the admixture analyses where the Maasai present close to six possible ancestral populations in genome wide analysis studies and thus might have assimilated some of the hunter gatherer populations they encountered and derogatively referred to generally as the Dorobo denoting 'the poor people who do not have cattle' (Bernsten, 1976; Kratz, 1980; Spear and Waller, 1993; Cronk, 2002; Pagani *et al.*, 2012; Wagh *et al.*, 2012).

It is becoming evident that most extant ethnic groups are not genetically homogenous and thus the idea of ethnicity might possibly be a social construction with fairly porous borders rather than being *via* common ancestry (Barth, 1969; Hechtand Ribeau, 1991; Jenkins, 1994; Cooper *et al.*, 2003; Wimmer, 2008). Although individuals can quickly learn

new languages as well as acquire new cultural traits, their genetic legacy can persist for some time without being significantly altered. This therefore implies that some of these familiar ethnic labels cannot function as accurate guides to the genetic structure resident within extant populations as they might insufficiently define the ensuing biological relationships (Winkler and Sokal, 1987).

Since most medical and even evolutionary decisions are done on the basis of populations' ethnic labels, it is probable that the existing genetic diversity and structure are ignored (Risch *et al.*, 2002; Race, Ethnicity, and Genetics Working Group, 2005; Dries, 2009; Campbell and Tishkoff, 2010; Gamazon and Perera, 2012). With such omissions, it is plausible that most of the reference populations used in evolutionary studies might not be representative enough and by extension the conclusions too end up being inaccurate (Reich *et al.*, 2001; Risch *et al.*, 2002). From a medical perspective, it is likely that wrong therapeutic agents are administered onto populations following pharmacogenetic assumptions based on such 'faulty' ethnic identifiers which don't take the population's possible genetic diversity and structure into account. With the advent of personalised medicine, it is critical that populations are widely characterised using neutral genetic markers devoid of any ascertainment bias with respect to the populations studied and probably even the use of whole genome sequences might soon be feasible (Nebert and Menon, 2001; Foster and Sharp, 2004; Ma and Lu, 2011; Gamazon and Perera, 2012). This will possibly report on the true genetic heterogeneity and structure within populations before any further specific pharmacogenetic studies can be instituted (Daar and Singer, 2005). More importantly however, some populations which are subjected to a common selection pressure like infectious disease have portrayed similar selection footprints despite being of disparate ancestry (Dobon *et al.*, 2015).

Since it is always impossible to collect samples from each member of a given population, it is vital that while labelling samples, it should be done in a way so as to avoid making it appear like they were collected from all members of the population in question when in essence they might not be totally representative. This was the main concern for example after the HGDP was set up and the Yoruba sample was always treated as not only representative of the entire Yoruba tribe but also the African continent at large (Reich *et al.*, 2001).

With the concern by most linguists, for example that, the African linguistic groups are not representative, especially of the minority groups, there is need that before labels are preferred on some populations, the sample donors be consulted in order to get a proper description from the locals' point of view. This would go a long way to help avoid the 'false' bundling of communities into a single group just because they speak a certain language, practice certain cultural activities or thrive through some given subsistence activities. In most cases some outliers exist within many populations and they could possibly represent the unique lineage bearers that might easily pass 'unnoticed' if the ethnic identifiers are erroneously enforced as population identifiers. Among the Turkana, for example, it would be vital to further examine and note the apparently divergent sub tribes like the Ngibotook, Ngilukumong, Ngimaesorokho and even the Ngisiger. The use of ancestry informative markers would certainly help matters in such cases by assigning the various samples to their respective ancestry backgrounds more clearly (McKeigue, 2005).

The use of language, culture and economic activities as population identifiers can only be indicative but not definitive and we thence suggest the use of sampling sites' regional names or even the Global Positioning System (GPS) coordinates instead as they might be more applicable. We as well do recommend that while referring to any samples used in a study, one should remember that they're possibly not representative of the entire population from which they were obtained and thus should only be taken as indicative of the resident diversity within the population under study. We can, however, never emphasise enough the importance of continued sampling as well as analysis so as to enhance our knowledge of the nature of variations, be it linguistic, cultural genetic or phenotypic, present within existing populations. It is only through such continuous efforts that most of the variations (especially the rare variation) within populations will be uncovered and its effect probably appreciated.

To sum up, we note that ethnic labels like language, culture, economic activities etc. are not accurate population identifiers and hence their continued use and or application as such should be reconsidered and taken only as indicative but not conclusive.

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