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"The Map of the Mexican's Genome": overlapping national identity, and population genomics

Ernesto Schwartz-Marín · Irma Silva-Zolezzi

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Abstract This paper explores the intersections between national identity and the production of medical/population genomics in Mexico. The ongoing efforts to construct a Haplotype Map of Mexican genetic diversity offers a unique opportunity to illustrate and analyze the exchange between the historic-political narratives of nationalism, and the material culture of genomic science. Haplotypes are central actants in the search for medically significant SNP's (single nucleotide polymorphisms), as well as powerful entities involved in the delimitation of ancestry, temporality and variability (www.hapmap.org). By following the circulation of Haplotypes, light is shed on the alignments and discordances between socio-historical and bio-molecular mappings. The analysis is centred on the comparison between the genomic construction of time and ethnicity in the laboratory (through participant observation), and on the public mobilisation of a "Mexican Genome" and its wider political implications. Even though both: the scientific practice and the public discourse on medical/population genomics are traversed by notions of "admixture", there are important distinctions to be made. In the public realm, the nationalist post-revolutionary ideas of Jose Vasconcelos, as expressed in his Cosmic Race (1925), still hold sway in the social imaginary. In contrast, admixture is treated as a complex, relative and probabilistic notion in laboratory practices. I argue that the relation between medical/population genomics and national identity is better understood as a process of re-articulation (Fullwiley Social Studies of Science 38:695, 2008), rather than coproduction (Reardon 2005) of social and natural orders. The evolving process of re-articulation conceals the novelty of medical/population genomics, aligning scientific facts in order to fit the temporal and ethnic grids of

E. Schwartz-Marín (✉)
EGENIS ESRC—Centre for Genomics in Society, Exeter University, Exeter, UK
e-mail: es265@ex.ac.uk
URL: www.genomicsnetwork.ac.uk/egenis

I. Silva-Zolezzi
National institute of Genomic Medicine (INMEGEN), Mexico, Mexico
e-mail: izolezzi@inmegen.gob.mx.com
URL: www.inmegen.gob

"Mestizaje". But it is precisely the social and political work, that matches the emerging field of population genomics to the pre-existing projects of national identity, what is most revealing in order to understand the multiple and even subtle ways in which population genomics challenges the historical and identitarian frames of a "Mestizo" nation.

Keywords Population genomics · Mestizo identity · Haplotypes · Nationalism · Ethnography

> "Por mi raza hablará el espíritu [The Spirit shall speak for my race]", Motto of The Autonomous National University of Mexico (UNAM), by Jose Vasconcelos UNAM 2009 [1920-21]).
>
> "Mestizaje in the context of nation making is a 20th century post-revolutionary ideology (Gutierrez 1998: 293)".

Almost a century has gone by, and the role of Vasconcelos in the construction of the official scripts of Mexican identity is undeniable.[1] At the dawn of the 20th century "the Mexican elite strongly felt the political need to answer negative European racial mythologies with mythologies of their own (Stepan 1991:145)". Jose Vasconcelos was one of the most prominent intellectual characters in post-revolutionary Mexico, acknowledged amongst other deeds, for the enhancement of the Mexican Educational System, and for his controversial presidential candidacy in 1929. Amongst his many achievements, the most perdurable and famous one, has been his ideological contribution to a national imaginary known as Mestizaje.

During his time as a public officer and Mexican Secretary of Education (1921–24), he and a group of elite intellectuals were capable of creating the foundations of a National-Mestizo Identity. This National Mestizo Identity has spread throughout the country, especially by means of the national educational system, and Mexican patriotic symbols (Gutierrez 1998:292). The title of Vasconcelos' seminal publication, the "Cosmic Race" (1925) has become a keyword regarding *Mestizaje* (Barba 2009a, b). The adjective "Cosmic" refers to the synthesis of a dialectic racial process, in which old racial stocks will fuse into one definitive race that agglomerates the best qualities of all, hence: "...the future race, will not be a fifth or a sixth race, destined to prevail

[1] Although Jose Vasconcelos was not the one to start branding the "Mestizo" as the new widely accepted identity of the Mexican republic (see: Basave 2002), his ideas are a fundamental reference in the twentieth century construction of Mestizaje. To talk about the construction of Mestizaje as an all-encompassing identitarian discourse, would mean to address a cultural process that spans to various centuries in Mexico, and Latin America.

Mestizaje in Mexico has been widely studied by anthropologists and social scientists (Basave 2002; Stepan 1991; Gutierrez 1998; Navarrete 2005; Moreno Figueroa 2007; López-Beltran 2007). Mestizaje—as nation making—can be studied and reconstructed in the intellectual work of seminal political thinkers of Mexico (for an historical approach see: Basave Benitez 2002), or through the lenses of eugenic and racial projects in order to consolidate political, national, and cultural identities in Latin America (Stepan 1991).This paper adds to the existing literature on Mestizaje, by studying its impact on the interpretation of Mexican population research. The work of Lopez-Beltran and Vergara (2010) also explores the relation of Mestizaje, from an historical and philosophical perspective, rather than ethnographic.

over their ancestors; what is going to come out of it, is the definitive race, the synthesis race or the integral race. (Vasconcelos 1925; translation made by the author) <Online version in: http://www.filosofia.org/aut/001/razacos.htm; last consulted 29/July/2009>".

Many Mexicans recognise themselves as Mestizos,[2] a product of the clash of two cultures: the Indigenous and the Spanish. The product of this biological and cultural fusion, is considered by Vasconcelos, as both, a future oriented national project in which racial divisions will eventually disappear (claims of universalism); and a dominant ethno-racial identity that could join in one category different ethnic and cultural backgrounds (claims of unity).

The Universal and Unitary claims, are therefore fundamental characteristics of the Mexican ethnoscape, read as a Mestizo Narrative. In Mexico, *Mestizaje* has become a homogenising discourse, a response to the anxieties of diversity and fragmentation that unfolded after the Mexican Revolution; akin to the creation of a benefactor state and to a unified national project (Tenorio 2010).

Regarding the role of *Mestizaje* as a National identity, we will refer to a specific post-revolutionary notion of admixture, re-produced by Mexican intellectuals and politicians in the first half of the twentieth century. On the other hand, it is important to mention the work of Natividad Gutierrez (1998:294), who identifies *Mestizaje* as a way to romanticise the encounter between Spaniards and Indigenous, and delimit the space of national culture in Mexico. The construction of these cultural and national boundaries has had profound implications in the way ethno-racial[3] diversity is approached inside the country:

> ...the imaginary of Mestizaje has obscured our eyes...no one has been preoccupied by the admixture of indigenous peoples... It has made it difficult to see ourselves as a diverse country... diversity was a problem for national integration... it was not until now, that we are starting to value diversity... that we don't see it as a problem (Tenorio 2010).

The problematic relation between admixture as a homogeneous national identity and ethnic diversity in Mexico, are synthesized by Juan Pedro Viqueira's (2010) comments: "...the great problem of *Mestizaje* is that it has led us to a terrible dualism... postulating two homogeneous groups: Mestizos and an Indigenous

[2] To refer to the Mestizo as a clear identity amongst Mexicans is not easy, since many Mexicans would not clearly recognize themselves as Mestizos or Mestizas, even when directly questioned about their ethnic or racial identities (Moreno Figueroa 2007). The boundaries of Mestizo biology in Mexico are difficult to delimit.

Census from the XIX century show a massive growth of self identified Mestizos in Mexico (23% of the total population in 1808, was considered mestizo, this number increased to 43% in 1885, while the indigenous population diminished from 60% in 1808, to 38% in the same time lapse).Such an increase could only be explained through a catastrophe of enormous dimensions—just affecting indigenous communities—, combined with a disproportionate and gigantic reproduction of Mestizos (Navarrete 2005). In fact the study argues that the enormous and expedient growth of the Mestizo group is better explained by the inclusion in the Mestizo category of people formerly included under the indigenous brand.

[3] Following Brubackers (2009) we find it difficult to draw clear boundaries between race and ethnicity, so we prefer to use ethno-racial as a general term, different from the genethnicities produced in the laboratories, or *Mestizaje* as nation making. As we continue through the paper we use the term "Mextizaje", to talk about the re-articulation between genethnicities and Mestizaje, and we keep using the term ethno-racial in general and vernacular grounds.

minority [...] what we have to learn is to value diversity, within diversity (Viqueira 2010)". The duality between the Indigenous and the Mestizos also rests on a fundamental time partition, since Mexican history is marked by both, a cultural and biological new subject, the Mestizo: "The deep roots of our nationality are in the Indian past, the point at which our history begins. It was a glorious past, brought to a halt by the Conquest. Since then, the real Mexican, the Mestizo, has arisen (Bonfil Batalla in Underiner 2004: 29)".

The novelty of Mestizaje depends on the millenary status of indigenous communities, in contrast with the promising future of "The Cosmic Race"; therefore for Vasconcelos the uprising of an admixed race would be the end of racial divisions. In this scheme the indigenous past of Mexico is just but one step towards the final racial emancipation (Vasconcelos 1925). As a question of historical record, Mestizaje, as ethno-racial admixture or hybridisation, can be roughly traced back 500 years ago, when various indigenous nations were conquered by Spaniards.[4] On the other hand as a matter of national identity *Mestizaje* is an ongoing emancipatory process.

"Mextizaje" and laboratory ethnography

The intersections between a popular and romanticised version of *Mestizaje* in Mexico, and the production of biogenetic identities in the medical/population genomics laboratory of the Mexican Institute of Genomic Medicine (INMEGEN), are presented in this article. The conflation between Mexican national identity, and the notion of admixture as a product of population genomics research, is what we call "**Mex**tizaje". We have found that the dynamics of "**Mex**tizaje" have resulted to be tensions between two incommensurable, yet intertwined, temporal and identitarian frameworks; usually read as if they were mirrors of each other.

The first temporal and identitarian framework is derived from an interpretation of Mexican history, filtered by a dominant and widely spread notion of national identity that we link to post-revolutionary ideas (Gutierrez 1998:292). The second framework is the product of interpretations of genetic variability produced in the population genomics laboratory, mediated by haplotypes. A haplotype is a sequence of DNA bases in the same chromosome, which remains relative stable through various generations.[5]

In order to analyse these two time frames and identities, we have elaborated on the politics of time proposed by Nancy Krieger (2005). Understood as the way in which mostly unconscious beliefs and implicit assumptions feed into choices of time scale, shaping scientific questions (2005: 2157). Additionally we use the politics of time in conjunction with the notion of re-articulation used by Duana Fullwiley (2008) to describe the relation between race and genomics.

Duana Fullwiley (2008) argues that the relation between race and biogenetic identities runs contrary to the notion of coproduction "understood as the simultaneous coming into

[4] This is a static notion of admixture in Mexico, in 500 hundred years admixture has taken many shapes and flavours. An historical example of the dynamics and mobility of racial admixture in the "Castas System" of the Colonial period can be found in López-Beltran (2007).

[5] In Burchard's lab it is around 10 generations (Fullwiley 2008:716), but inside INMEGEN's population genomics lab the reference is always to 20 generations or more.

being of societal arrangements and scientific ideas and practices (Reardon in Fullwiley 2008: 698)". Fullwiley's notion of re-articulation depicts of tautological relation, in which seemingly neutral DNA reinforces those centuries-old categories of race, and vice versa.

Fullwiley's ethnography of admixture mapping in Burchard's Laboratory present us with a culturally specific re-articulation of race and genomics, in which pre-existing racial categories serve as first principles to construct genomic difference. The belief amongst scientists in this laboratory about the existence of 3 well defined racial groups (Native Americans, Europeans, and Africans), are fundamental to support the idea that the differential contribution of genomic race, can explain disease risk in admixed populations of Mexican and Puerto Rican origin.

Mexican genomics follows a similar path to that of re-articulation. This emerging scientific field reactivates national identitarian projects, in order to frame the political significance of medical genomics for public health and beyond (see: Jiménez-Sánchez 2002a, b, 2003a, b, 2009). Yet, contrary to the good old-fashioned but at the same time modern dilemma in which familiar paradigms of race resurface unquestioned and reinforced (Fullwiley 2008: 699), in the laboratory of population genomics of the INMEGEN, there is room for problematisation and uncertainty (in comparison to a popular notion of Mexican origins).

In fact those problematisations challenge, even though not publicly, a dominant interpretative repertoire which maps specific historical, rhetorical and ethnic logics as natural properties of admixture in Mexico. The construction of a Mexican genomic diversity project does not simply mirrors the history of admixture in the country. Therefore, there are no unbroken circuits that run from genomic identity to racial-national identity in the laboratory of population genomics of the INMEGEN.

To analyse "**Mex**tizaje" is to reveal the confrontations between two identitarian frameworks: the popular vs. the biogenetic one, conflated as a single historical and natural process. To bring forth the tensions at the core of this conflation, it is necessary to compare the production of genethnicities (Thacker 2005: 162–3),[6] with wider interpretations of scientists, medics and bioethicists. Who in order to legitimate, dispute or make sense of the production of genomic cartographies, implicitly involve unconscious beliefs; borrowing time frames, scales of explanation, and identities that reinforce "what we already know... about admixture in Mexico".[7]

In the case of a genomic cartography, the time frame of analysis is inseparable from the interpretation of a population's genetic structure and diversity. Consequently, the politics of time (Krieger 2005) in Mexican genomics is strongly linked to the process of re-articulation (Fullwiley 2008), and/or coproduction (Reardon 2005) embedded in population genomics and the interpretation of biogenetic identities. In the Mexican case, both, coproduction and re-articulation are complementary. Natural orders can be articulated to pre-existing racial orders, but in the laboratory, haplotypes and genetic variants do not behave exactly as expected, therefore these resistances bring forth spaces in which coproduction is possible.

[6] "Bioinformatics—an apparent neutral technical tool—thus becomes manifestly political, negotiating how race and ethnicity will be configured through the filter of biotech, constituting unique type of *genethnicity* (Thacker 2005:163)."

[7] This line is borrowed from an informal chat with researchers in the INMEGEN, to defend the project. But the same argument is used by critical voices of the project..."what does this project tells us... that we did not already know".

The comparison, between the popularised and biogenetic versions of Mestizaje, is the product of a long and ongoing dialogue inside the population genomics laboratory of the INMEGEN. For over a year and a half, both, ethnographer and genomic scientist, have exchanged and debated different points of view. Some of those discussions have turned out to be grounds for common reflection. It might even seem strange that Irma Silva Zolezzi is both, author and subject of study. This duplicity is due to the fact that both, ethnographer and key informant recognise their complementary role in the production of an argument.[8]

We ask for certain interdisciplinary tolerance from our readers. This tolerance is fundamental, since we will be moving back and forth, from the realm of population genomics technical interpretations, to the realm of sociological and cultural interpretations. Although this journey is mainly the product of laboratory ethnography and elite interviews with scientists, some pieces of this article might ask from the reader to engage with diffuse notions of national identity that are hard to pin down. These notions are circulating explicitly or implicitly, amongst a reduced group of researchers in contact with genomics, especially involved with haplotypes, or genomic scientists involved in biomedical and/or socio-political projects. We have chosen our informants based on their role as critics or endorsers of population genomics in Mexico, and their role in the production of the Mexican HapMap, or at least their close interaction with medical/population genomics (most of them either work in the INMEGEN, or are specialist in the area).

The first section presents the interpretative repertoires mobilised in order to dispute "Mexican Uniqueness" between expert groups- and its genomic representations in mass media. Subsequently we explore the relations and heuristic approaches in order to read time and ethnicity through haplotypes. We have to pay close attention to the interpretation of genetic diversity, specifically to haplotypes study. First and foremost, because haplotypes are strategic mediators in order to find probable genetic variations related to disease. But most importantly, because through their interpretation we make evident the way in which "**Mex**tizaje" permeates the understanding of genetic identities.

Finally we contrast the nationalist interpretative repertoires informed by *Mestizaje*, used by some scientists and medics, with the material culture that produces and analyzes genethnicities in the laboratory of medical/population genomics of the INMEGEN. We do this in order to bring forth some of the common strategies and tactics deployed to align bio-genetic, and ethno-historical narratives in Mexico.

Mapping Mexican "Uniqueness"

> My recalcitrant scepticism obliged me to read the note. Is it possible to achieve in Mexico what hasn't been possible to achieve anywhere else in any other moment in History? Is it possible that the scientists that posses Mexican birth

[8] This paper invariably mixes genomic and social science, even though we agree on the main arguments of the paper, we have contributed in different ways and areas of expertise. The sociological interpretation is the sole responsibility of the first author and part of his PhD dissertation; while the genomic explanations, illustrations and much more intimate knowledge of haplotypes has been produced by Irma Silva Zolezzi.

The idea for this paper was born from many discussions in the population genomics laboratory of the INMEGEN, sharing insights and ideas with each other. We have used pseudonyms, except when explicitly asked to use the name of the informant; in some cases we have used a pseudonym even when we had permission to use the researcher's name.

> certificates enhanced with little eagles have found our national identity in a gene? (Author's translation)
>
> ¿El Genoma Mexicano? El Moro, 2006, Septiembre: <http://morisimo.blogspot.com/2006/09/genoma-mexicano.html>

Maps, valuable instruments for those that need orientation, provide a manageable graphical representation, of a space that would be otherwise, inaccessible. Nevertheless maps also draw paths, naturalising spaces that could be explored in multiple ways. Cartography represents, but also frames certain characteristics and not others, it makes evident certain roads and not others, it puts emphasis in certain marvels, labyrinths and monuments, and not others. The deep and constant political work of maps is stabilised through a representation of a world that looks orderly and comprehensible. Maps as political devices make the assumptions, contingencies and logics under which they were built, as a matter of public concern. In the age of population genomics, maps of molecular markers are the decodification of historical trajectories, national narratives, and ethno-molecular compositions, as well as the source of a future oriented economy of knowledge (Jiménez-Sánchez 2002a).

A genomic cartography is a description of common genetic variability within a group or population.[9] Through the aggregation of a mass of individuals, common genetic diversity arises, which is not only directed to inform about the presence or not of certain genetic variants, but also (and most commonly) of their relative frequency in a certain population. One of the principal objectives of mapping Mexican genomic diversity was to describe how indigenous ancestry has contributed to the "unique" genetic makeup of Mestizos; due to the fact their admixed origins are different from other populations in the international HapMap:

> Mexico has a population of *unique* genomic makeup as a result of its history. As of February 14, 2000, Mexico had a total of 97,483,412 inhabitants, occupying the 11th place among the most populated nations on earth, with an annual population growth rate of nearly 1.58%. The vast majority of the Mexican population emerged from a mixture between Meso-American native groups and Spaniards (Jiménez-Sánchez 2002a: 32, emphasis added)

The Mexican Genome Diversity Project (MGDP) was conceived as an exceptional opportunity for the development of medical genomics in Mexico. In 2005 when the MGDP was officially launched by the INMEGEN, the International HapMap project had not included Mexican Americans or admixed populations in their study. The availability of samples from different regions of Mexican territory was an asset. In comparison with the 90 Yoruba samples used in the International HapMap to represent African ancestry; 300 hundred samples from distant geographical regions in Mexico seemed to be a much more comprehensive group: "...if you compare 300 individuals representing all of the country, against 90 representing all of Africa in the international Hap Map; thanks to the decrease in

[9] There are plenty of questionings around what constitutes a population (see: Reardon 2005; M'charek 2000). Yet none of those questionings, even when the scientists in the lab are well aware of them, change the practical use of populations as a representation of a cultural and biological community: this delimitation can be done through their genotypes, or other characteristics as language, mobility, phenotypes and as many qualities and categories in which you can divide the living entities in the world (which of course make it a very problematic concept).

the cost of the technology, we have as many SNPs as the Hap Map... so we have a great coverage (Jiménez-Sánchez 2009)".

The MGDP was also directed towards justifying the cost-benefit of constructing a National Genomic platform; instead of using a combination of existing (i.e. mapped) ancestral populations. In order to grasp the consequences and importance of endorsing a genomic notion of "Uniqueness", we have to explain, and summarize four basic assumptions and successful statements of INMEGEN's political framing—to fund the creation of the institute from 1999 to 2004—inside the Mexican Congress[10]:

1. Mexican migratory history and its complex ethnic composition, make it impossible to import the genomic knowledge of Mexicans, and its future medical applications (2003a, b).

2. If in any case it is possible to import this knowledge, it would only make Mexicans more dependent on foreign countries. If developed internally, it would generate huge healthcare savings, and even better, it would become the seed for an economy based on knowledge (Frenk-Mora 2001, 2004, 2009; Jiménez-Sánchez 2004, 2002a, b).

3. Since Mexicans and other admixed populations were not included in the original International HapMap project; creating a Haplotype map would not only be useful for Mexicans, but also for other Latin American populations with a similar migratory history (i.e. ancestry; Jiménez-Sánchez 2002a).[11]

4. Thanks to the exponential progress of sequencing technologies, reading certain parts of the genome through haplotypes and tag SNP's will reduce the costs of sequencing disease related mutations. Of course until technology is so cheap, that whole genomes can be read instead of haplotypes (Soberon 2009).

During the negotiations to create the National Institute of Genomic Medicine in Mexico (INMEGEN) and its flagship project "The Mexican Genome Diversity Project",[12] debates on the reality of race were not really controversial; since such debates did not even take place (1999–2004). This lack of debate does not obey to an explicit public agreement amongst Mexican scientists on the biological truth or falsity of race; it is much better explained by the conjunction of two decisive factors: The first is that during the negotiation to create this institution, the main political concern was cloning (ACI 2002), and not racism or biological reification. The second one is that the political framing of population genomics in Mexico took

[10] INMEGEN was the first of the twelve national institutes of health to be discussed democratically in Mexico, inside both chambers of Mexican congress. Successful negotiations gave the lobbying group 120 million dollars plus private donations in order to develop genomic medicine in the country.

[11] Haplotypes are also fundamental in order to support the central idea of a "Mexican Uniqueness" in the service of medical research: "Shared haplotype analysis was used as a tool to indirectly estimate tag SNP transferability between HapMap to Mexican population and between Mexican subpopulations. An indication that a haplotype map for Mexicans could be useful for tag SNP selection is that the use of any combination of two Mexican subpopulations as a reference provided better coverage than using the combination of all HapMap populations (Silva-Zolezzi et al. 2009:5)".

[12] In the paper we use the "Map of the Mexican's Genome", and the "Mexican Genome Diversity Project", to name the genotyping efforts in order to describe the genetic structure of Mestizo populations of Mexican origin. We use the first name to make reference to the marketing and communication efforts to promote the scientific project, and the "diversity project" refers to its common usage inside the laboratory.

advantage of an already accepted and popular notion of biological and cultural Mexicanhood: *Mestizaje* (Lopez-Beltran and Vergara 2010; Schwartz 2008, 2009).

The branding of Mexican biological uniqueness coexisted until recently[13] without problems with the rejection of the scientific basis for racial categories, proposed by the HGP organizers, who as a matter of fact were amongst the international supporters of this genomic project in Mexico (Jiménez-Sánchez 2002a). Five years afterwards, the once fruitful and unproblematic framing of medical/population genomics, has become the battle ground for an academic dispute about the existence of a "Mexican Uniqueness".

Dr. Elias (Pseudonym)—Mexican Pioneer in population genetics—has severely criticised the endeavour using a contingent repertoire (see: Mccann-Mortimer et al. 2004). One of the constant critiques to INMEGEN's project arises from the representativeness of this genomic cartography. Public critical scientist, as Dr. Elias, mobilises the great diversity of the mestizo category, in combination with long standing socioeconomic/ethnic barriers in the Mexico, in order to exemplify a sampling bias:

> ... If you go to any private university in the country you will find a predominant European ancestry—over 70% most surely—, but if you go to UNAM (Mexico's National University) European ancestry will hardly reach 50 or 40% [...]...I don't have any doubt their measures of genetic markers are right [...] the doubt arises when they say this is the genetic structure of Aguascalientes, or whatever... this is a country of free circulation [...] I don't think their samples are representative enough to assure it.

Even though the MGDP was designed to become a biomedical tool intended to capture common variability, and not a map representing the whole genetic diversity in the country, fierce criticism has arisen.[14] There are also some sceptic voices coming from the field of Bioethics and public policy, Laura (Pseudonym) an influential national bioethicist summarised her scepticism, by interrogating INMEGEN's initial promises:

> ... I also listen to contradictions in.....in the declarations on press...one of the arguments to defend the INMEGEN, and the Mexican HapMap and so on, it is because we cannot buy it from anyone. Because the information coming out

[13] New Director General of the INMEGEN, Dr. Xavier Soberon Mainero, who was recently interviewed in a national newspaper in Mexico said, as soon as he took office:

> I am going to call it Genomic Knowledge of Mexican Populations, because there has been certain confusion and controversy about: I am Mexican, but my genome is not being studied, since I am from Eskimo origins, but I am Mexican? Well then let's call it populations (Soberon in Saavedra 2009)

Of course such declaration was not the product of agreement or discussion between genomic scientists and/or bioethicists either. I read it as a response to continuous critique made by the scientific community, toward what many of my scientist-informants see as a misleading reification of Mexican nationality.

[14] Most of the lay opposition has also paid attention on the lack of representativeness of the mapping project, combined with its exaggerated nationalist marketing Anon 2009, available in: (www.cuestionableinmegenblogspot; Edu 2006).

> from it is only useful for those who create it.... then if we don't do it ourselves we are doomed... then... It would not be useful even if everyone else, end up doing the map of their populations... and then I hear the Director General saying, that this was so important that the other populations in Latin America could benefit from it... and I said how?!! If we could not benefit from them [existing maps], how others are going to benefit from ours...I feel a lot of inconsistency.

As a response to criticism coming from expert groups, composed of population geneticists and bioethicists, the so called "Map of the Mexicans' Genome"[15] was defended by former Director General of the INMEGEN, Gerardo Jimenez-Sanchez (October 2009), in order to backup the initial public framing:

> ***G.J.S***—We defined in the paper... with numbers!! That none of the other maps cover us satisfactorily... and that any combination of two Mexican states covers us better, between 96 and 97%...
>
> *E.S*—Yes, and as more distance exists it is better... Sonora and Guerrero...
>
> ***G.J.S***—Yes, exactly... So we demonstrated that effectively, we cannot import genomic medicine... we demonstrated that we can do a map, and we have the capacities, to do it rapidly, in time and put it in the web... we demonstrated that we can!!

On one side empiricist, impersonal and quantitative accounts are deployed in order to emphasize the scientificity of the project, and the validity of the initial public statements (Gerardo Jimenez-Sanchez). And we also find contingent repertoires, to underline the inconsistencies of science communication, biased sampling, or inflated promises in the service of public manoeuvring: "...he [Gerardo Jimenez] said what he had to say in order to get the funding, but all he said is nothing but future projections, much exaggerated ones (Dr. Elias)".

Facing criticism Dr. Gerardo Jiménez Sánchez, former Director General, said: "... they might be jealous and afraid... to know that a bunch of young scientists did a map, they could not do... in more than 30 years of studying Mexican populations". Even though the same type of interpretative repertoires used by the opposing parties around the concept of race in the confrontations of the HGP, are mobilised in the confrontations generated by the "Map of Mexicans' Genome"; in contrast with the debates in the USA, none of the expert groups disputing "Mexican Uniqueness" interpret these discordances as the product of a racist ideology or discrimination.

A strong work of demarcation between race and populations has given genomic entrepreneurs and laboratory scientists enough space to talk about an underlying national biology and/or particular set of Mexican genetic markers. These demarcations help them to avoid any engagement with the thorny debates around the biological "reality" of race, ethnicity or the less charged use of ancestry. In the

[15] Public communication of the project in the INMEGEN, has substituted the "Map of the Mexicans' Genome", for the newly coined term by the Director General, Xavier Soberon Mainero, "Map of the Genomic knowledge of Mexican Populations" (see: http://genomamexicanos.inmegen.gob.mx/).

arena of Mexican Genomics, race is strictly avoided, in and out of the laboratory, except to state that genomics has shown that races don't exist.[16]

"Pop" genomics and the "Cosmic Race"

When mass media first engaged with genomics, the ethno-racial composition of Mexico suffered a drastic racial reconfiguration. One of the most widely distributed newspapers in the country "El Reforma" reported that Mexicans were the combination of 35 races (Alcantara 2007a, b): "Doctor [Jimenez Sanchez] highlighted that due to race, there is a pronounced difference between the populations of various states within the country. In Sonora they have the highest prevalence of European genes, 58%, while in Guerrero, their population presents a major index of African genes, 22% (translation made by the author, emphasis added)".[17]

Natividad Gutierrez (1998) has named the national valorisation of *Mestizaje* as "Mestizoism", since this is not the only national narrative of Mexico. There are many other historical events and indigenous foundational narratives that remain obscured by the dominant Mestizo identity. The marketing and divulgation of medical/population genomics in Mexico, mirrors a constant exaltation of "Mestizoism". Mass media celebrating the public release of the article published in PNAS, entitled "Analysis of the Mexican Mestizo populations to develop genomic medicine in Mexico (Silva-Zollezi et al. 2009)" is a good example to illustrate such phenomena.

The nation building process that began with Mexican independence in 1810 and its reshaping in the 19th and 20th centuries draws heavily from indigenous cultural capital (Gutierrez 1998:292–294). Still today Mestizoism can be read and seen in the article appearing in the QUO magazine, after the massive launching of the Mexican Diversity Project, entitled "The Mexican Genome: Uncovering the secrets of the Cosmic Race".

[16] After a series of seminars between jurists and scientists in Mexico, the consensus that emerged was that the concept of race was to be avoided, in order to leave space for the concept of human geographic variation (March, 2008). Researchers that were in the event, told me that the question of race was never a topic for debate, the event was a continuous presentation of experts from various fields, that endorsed the idea that race was an unfounded category.

So we could say that this institutional effort, added very little to any open discussion of the topic, what is true is that all of the scientists involved in population genetics or genomics, that I have interviewed, prefer the word ancestry, over race. In the case of other scientist who use ancestry categories for their research, but who are not familiar with the discussions in the field they might not see any difference, even when they prefer to use ethnicity or ancestry.

[17] There, she made a terrible mistake... ehhh... because really there are no 35 races, what happens there, is that, well... we human beings share almost the 99.8%, which is exactly the same between, independently of what region or population we belong.....Now what the INMEGEN is observing is that inside that 0.2% that gives us our individuality, taking that .2% as a 100%, there is a 35% of that .2%... in which we differ from the rest of the populations of the Hap Map, so there is not 35 races, not the 35% of all our genome, it is only from the part that gives us our individuality, which is a 0.2%, from which a 35% of that segment is the one we have different with respect to the Caucasians, Africans and Asians (March, 2008).

This article is just but one of the many mediatic and popular references to an ethno-social imaginary synthesized by Vasconcelos.[18] One of the examples of how Mestizoism appropriates and reconverts a national indigenous heritage is fully visible in the image appearing in the cover of the magazine. An Aztec "Eagle" warrior, wearing a special feathered head decoration while surrounded by a double helix depicting the colours of the Mexican flag:

Mexican DNA and Aztec "Eagle" Warrior[19]

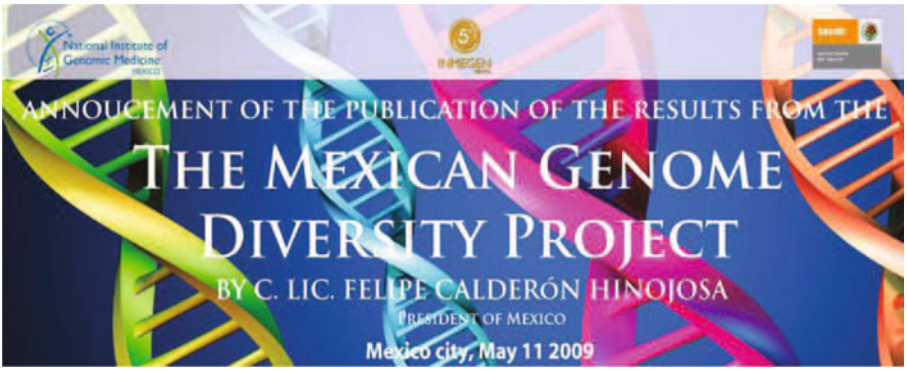
The foot note of the image reads: "The decodification will help us understand better the genetic architecture, product of the Mestizaje between Spaniards and people from pre-Columbian Mesoamerica". But most astonishing was the official communication of the project by the National Institute of Genomic Medicine (INMEGEN), who branded it as "The Map of Mexicans' Genome".

Such a name had been enhancing my ethnographic curiosity for many months, so as soon as I arrived to Mexico, I started a 3 h discussion about the existence of "The Mexican Genome" with Volkovak and Altair, INMEGEN's ELSI researchers. My very first "finding" in the field came as I said goodbye to Altair, who was still passionate with his arguments: "I recommend you to read the Cosmic Race of Vasconcelos—he kind of whispered across the room—to

[18] Two years before a dominical supplement entitled it: "The Genes of Mexico (anon. 2007)".

[19] Used with permission of QuO magazine editor and the corporative group Expansion (appeared in the cover of June 2009). Image taken from: http://www.cnnexpansion.com/actualidad/2009/06/04/genoma-destapa-diferencias-de-mexicanos, last consulted on 10-01-18 (Picture production: Max Olvera. Picture postproduction: Luis Delfín.)

understand what genomics and the Mestizo is all about (field notes, August 2008)"[20,21]



Everyone raised in Mexico—especially in Mexico City as us—has heard the motto of Mexican National University (UNAM) created by Vasconcelos "Por mi raza hablará el espíritu" [The Spirit shall speak for my race], even though very few of us are aware of the profound racist underpinnings of his thought (Meyer 2009). Vasconcelos version of "constructive miscegenation" has its limits, basically the overwhelming importance he gives to biological race in social life (Stepan 1991: 145); as well as his adherence to the belief that each race has essential temperaments and psycho-social dispositions (see: Vasconcelos 1925).

The universal and unitary characteristics intervening in the construction of *Mestizaje*—as nation making—have proven its obdurate character: "The idea of the cosmic race has proven highly resistant to demythologization. It has tended to be taken at face value rather than examined critically, as though a commitment with the mestizo meant an acceptance of all and every race in the nation, or even a devaluation of racial biology in Mexican history (Stepan 1991: 145)". Almost 1 year after our initial discussion about the existence of a Mexican Genome, I confronted Altair and his admiration of the "Cosmic Race" (Field notes September 2009):

> E.S—Have you really read the Cosmic Race?—The response was clear and strong—
>
> **Altair—**I have not only read it, I know it by heart!!
>
> E.S—[...] But you know, it is pretty racial, even essentialist in its approach to racial types... I don't know if you are aware of those connotations?
>
> *Volkovak*: Come on Altair... that is true!!

[20] Following Altair's advice I read Vasconcelos' "Cosmic Race" (1958), the reading was a surprise, his references to a Hyperborean race, the old forgotten Lemurians, both of them linked to an occultist cosmogony (most probably taken from Theosophy and Masonry, also see: Didier Tisdael Jaén prologue of Vasconcelos Cosmic Race) were particularly amusing, especially since Altair is a proud (although ideologically eclectic) Christian missionary in his free time.

[21] This image is taken from INMEGEN's web page (www.inmegen,gob.mx). This was also the image used as scenario for the official announcement of the Mexican Genome Map in the presidential residence.

Altair—You know I really like it, with its essentialist tones and everything... I like it... it is not racism, but integration and fraternity!!!

Until then I had not experienced the strength and resilience of *Mestizaje*—explicitly—in any discussion with my informants. Dominant notions of *Mestizaje* still hold sway in the Mexican imaginary, particularly in the media representation of biological Mexicanhood.

Contemporary critiques of *Mestizaje* in Mexico think about it as: "...a tricky theory... a way to erase races, without erasing racism (Aguilar 2010)". What is true is that the universal and unitary characteristics of Mestizaje are still part or the popular understanding of Mexican origins, making it difficult to recognize the racial underpinnings of this national identity. Even though very few informants, such as Altair, make explicit reference to Vasconcelos' work or to national *Mestizaje* as the framework to understand genomic medicine, I have found the logics of the Mestizo identity intertwined with the interpretative repertoires used in genomic research.

Reading time and ethnicity through haplotypes

Haplotypes are particular combinations of genetic variants in the same chromosome that travel together and remain relatively stable through various generations. These DNA arrangements have become central actants (Latour 2004) in the search for medically significant SNP's[22] (single nucleotide polymorphisms); as well as powerful entities involved in the delimitation of ancestry, population's temporality and variability.

As medical and cost/benefit devices, haplotypes, are pivotal to find meaningful genetic variations related to disease, without having to read the whole genome of a patient. For molecular anthropology, genetic diversity (i.e. haplogroups, haplotypes, mutation rates, AIM's and SNP's)[23] has been linked to populations' temporality, ethnic boundaries, ancestral lineages (like in the Cohanim haplotype; Abu El-Haj 2004; Thomas et al. 1998) and evolutionary narratives (Sommers 2008).

To understand the role of haplotypes in contemporary genomics, we need to understand first the notion of Linkage Disequilibrium (LD), understood as the probability that a combination of certain genetic polymorphisms is non-randomly associated at two or more loci (Slatkin 2008); in population genomics patterns of LD are strongly related to a population history. Events such as genetic drifts, and bottlenecks transform the patterns of linkage disequilibrium; a drastic reduction in population size (bottlenecks), generally make some haplotypes disappear, increasing LD as a result.

[22] Association Studies: These studies will be aimed to identify haplotypes in Mexican patients, and their association to multifactorial traits such as variation in drug response. This strategy can contribute to identifying captive markets within the Mexican population (Jiménez-Sánchez 2002a: script directed to the pharmaceutical industry and other private investors)

[23] For a sharp and detailed ethnographic account on the construction of ancestry markers and admixture mapping, as tools in the search for racial differences in US health research, see: Fullwiley 2008. Basically in the population genomics lab AIM's are those SNP's with a relatively high frequency, compared to other populations of the International HapMap (i.e. European, African and Asian).

Therefore haplotype length, and haplotypic diversity, are linked to population's temporality "Haplotype blocks vary somewhat among human populations—they tend to be somewhat shorter in African populations (Slatkin 2008; HapMap 2003, 2009)".[24] Haplotype blocks with less variability[25] and higher LD, are a sign of a younger population, while haplotypes with lower LD, and higher variability are read as a sign of an older population; since recombination necessarily implies more time. Therefore in molecular anthropology, Africans are the ones understood as the oldest population, using as a starting point anthropological and paleontological studies (also see: Sommers 2008).

For many of our informants haplotypes are incontrovertible proofs of continental/ethnic origin, which cannot be misleading or ambivalent. Yet haplotypes and their interpretation remain confusing and distant for many "experts" in the field of genomic medicine, who are not interacting with them on a daily basis (i.e., in the laboratory). Even for some scientists and physicians working inside the INMEGEN, the interpretation and constitution of haplotypes, remains obscure. Dr. Max, a physician with some training in medical genomics-in charge of top administrative functions inside the INMEGEN—told me that: "haplotypes are constituted of little coloured squares, which represent different continental groups... like the red ones are Indigenous, the grey ones are European... and so on.... you know. The computer gives you that information right away!!"

As a matter of fact those "red, grey and white ethnic squares" represent linkage disequilibrium (LD or a non random association of two or more alleles, in this case SNP's). Of course these squares are not informative of ethnicity or biogenetic identities by themselves. As you can notice in the graphic representation of haplotype blocks, the colour of the little squares, change according to the higher or lower probability of finding any combination of two SNP's together (e.g. red = high probability; white/grey = low or very low probability). The patterns of linkage disequilibrium (LD) differ from population to population,[26] providing a tool for researchers interested in identifying specific markers (known as tag SNP's) that may act as reporters of other highly associated polymorphisms (Frazer et al. 2009).

As an example in Fig. 1b, the middle haplotype (block 2), covering SNP's 10 to 22, depicts a high (LD) between SNP's 10, 11, 12, so by genotyping any of these three SNP's you will immediately know the other two. The first two combinations are CTA, and the combination of the other two haplotypes is TCG. So if you

[24] As modern humans spread throughout the world, the frequency of haplotypes came to vary from region to region through random chance, natural selection, and other genetic mechanisms. As a result, a given haplotype can occur at different frequencies in different populations, especially when those populations are widely separated and unlikely to exchange much DNA through mating. Also, new changes in DNA sequences, known as mutations, have created new haplotypes, and most of the recently arising haplotypes have not had enough time to spread widely beyond the population and geographic region in which they originated (International HapMap: http://www.hapmap.org/originhaplotype.html.en, last consulted August 17 2009, International HapMap 2003)

[25] Possible haplotypic alleles or different combinations of SNP's within a haplotype block.

[26] ...haplotypes seen outside Africa tend to be subsets of the haplotypes inside Africa. In addition, haplotypes in non-African populations tend to be longer than in African populations, because populations in Africa have been larger through much of our history and recombination has had more time there to break up haplotypes (HapMap web page).

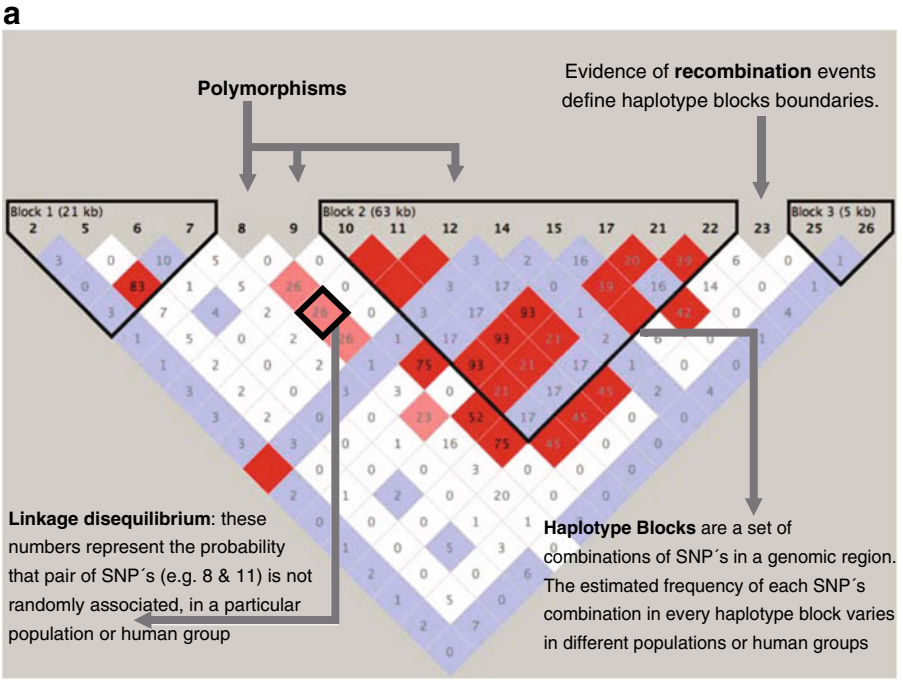


Fig. 1 **a** Haplotype blocks. Images used with permission of Irma Silva-Zolezzi, Head of the Population Genomics laboratory. **b** Variability within haplotype blocks. **c** Principal component analysis graph of Mestizo populations. Image used with permission of Proceedings of the National Academy of Sciences (PNAS), taken from (Silva-Zolezzi 2009: figure B:6). **d** Comparison between Haplotype blocks between Mexican Mestizos, Indigenous and Europeans. The map shows a comparison between the haplotype blocks of three populations (*1*) CEU—European of the International Hap Map, (*2*) Zapotecos—used in the Mexican Hap Map,—as the representatives of indigenous diversity—(*3*) Mestizos from Guanajuato also used in the Mexican Hap Map. The Zapotecos from Oaxaca (*2*), are the ones that show longer haplotype blocks, while the Mestizos from Guanajuato (*3*) are in between the European and Indigenous diversity. According to Haplotypes alone, the Mestizos are an older population than the Zapotecos (and therefore have shorter haplotypes)

genotype SNP 12, you will know that depending on the allele, either A or G, it will be accompanied by CT or TC respectively. Patterns of LD (the basis for the construction of haplotypes) are also used as arguments in favour of mapping certain populations, since their genetic characteristics—as larger chromosomal areas—could

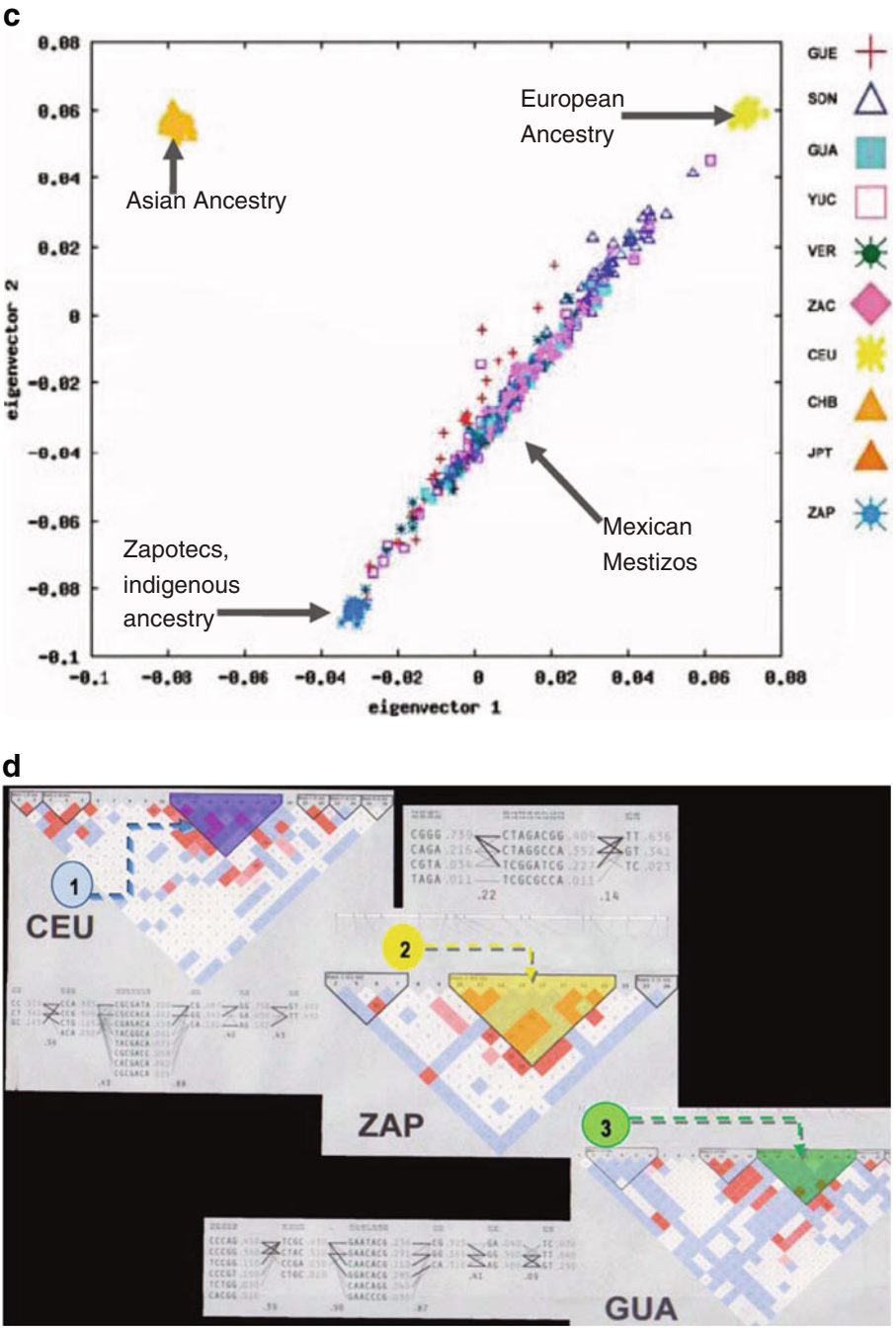


Fig. 1 (continued)

make the search for medically relevant SNP's easier or even feasible (Alkes et al. 2007; Silva-Zolezzi et al. 2009):

> Recently admixed populations such as African-Americans and Latino ethnic groups are known to have *areas of* LD (linkage disequilibrium) that can extend over large chromosomal regions due to allele frequency differences between the ancestral populations. This increased LD among admixed populations can facilitate mapping complex traits in an approach generally referred to as admixture mapping (cf. Burchard in Fullwiley 2008: 716).

The previous quote used to endorse admixture mapping, is not mentioning that compared to Europeans, one of the "ancestral" ethnic groups of African-Americans, the admixed population has more haplotypic diversity, and shorter haplotype blocks (see: Gabriel et al. 2002: 2226–28). Therefore the areas of LD of African-Americans are a lot more similar to Yoruba than to European samples. If we extend this comparison to other ancestral populations, such as the Asian (composed of Japanese & Chinese samples of the HapMap), we would find again that the admixed Afro-Americans have shorter haplotype blocks. Consequently in the case of Afro-Americans, the idea that their LD can extend to large chromosomal areas, will be completely misleading except when compared to Yorubas, the most diverse population of the HapMap.[27]

We should be careful not to naturalise time and admixture too fast, without being aware of its implications, or that certain assertions go against most of the specialised literature on the topic (Zhu et al. 2004; Gabriel et al. 2002; Wall and Pritchard 2003). Since recombination is not only a temporal phenomenon in relation to the historic-sexual mating of the "ancestral populations", but also a question of genetic/hereditary time, the notion of "**Mex**tizo" haplotypes in the next section will better illustrate this temporal duality.

The construction and delimitation of haplotypes is mediated through algorithms, probability and statistical tests (Gabriel et al. 2002). The contested boundaries of haplotype blocks (Zhu et al. 2004), and the questioning of their fundamental assumptions (Terwilliger and Hiekkalinna 2006) is one of many examples showing the controversial and fluctuating properties of human variation after the HGP. The production of genethnicities in human genomics is not fixed, it dwells on relative and probabilistic frequencies of certain genotypes; yet their circulation and translation as mediators between bio-genetic and ethno-racial identities in Mexico draws heavily from the popular notion of a dominant Mestizo identity. Mestizaje functions as a cultural filter to make genomic science meaningful in many ways (i.e. to support the project, to claim sovereignty (Schwartz 2008, 2009) or to question its representativeness).

[27] For the moment it is important to note that the difference in LD and haplotype blocks between admixed populations and its parental populations, according to population genomics models, would most of the time occupy a middle ground between ancestors. So certain admixed populations as the Afro-Americans would turn to have more haplotypic diversity and lower LD than most populations in the HapMap, with exception of the HapMap Yorubas. Therefore to say that they have larger LD areas would be misleading if we don't specify, compared to what ancestral population. The time of admixture, is not the decisive factor when talking about haplotype blocks, or areas of linkage disequilibrium, except when you read genetic variability as a one to one mirror, with history.

Indigenous and "Mextizo" haplotypes

Inside INMEGEN Population Genomics laboratory, the existence of a "Genomic Map of Mexicans" fades away when it comes to talk to talk about the "Diversity Project". Whenever the first name is used, it is to make reference to its political or marketing connotations. In comparison to the unitary Mestizo narrative, the way in which diversity is represented in the strong visual and probabilistic laboratory culture, comprises multiple concomitant ways to visualise admixture. Mestizos can become a cline along two clusters; one representing Europeans (CEU: coming from 30 US trios with central and western European ancestries) and the other cluster representing indigenous or Amerindians (AMI: coming from 30 Zapotecos). Despite the fact that studying indigenous genetic contribution (traduced in the lab as AMI-Amerindian ancestry-) is fundamental to the emergence of the Genomic Mestizo, it can only be understood in comparison to other "ancestral" populations (i.e. Asian (EA), African (YRI) and European(CEU) as represented in the international HapMap).

Mestizos can also be presented as a specific composite of ancestral percentages "in this model their mean ancestries (SD±) were 0.552±0.154 AMI, 0.418±0.155 EUR, 0,018±0.035 for AFR and 0.012±0.018 EA (Silva Zolezzi et al. 2009:2)". The Mestizo category can also be disaggregated to compare differential contributions of ancestry in different states of the country, differences in heterozigocity and haplotype diversity; or it can be put together to show common variability and AIM's (ancestry informative markers). Most importantly the majority of these molecular movements fit into existing knowledge, historical records (African Slaves entry points) and known indigenous population densities (Silva-Zolezzi et al. 2009:5).

In the field of genomics, genethnic distinctions are differentials in the frequencies of certain genetic variants between studied (i.e., mapped) populations (Fig. 1c, presents the principal vectors of variation). One curious (even anecdotal) piece of information in the laboratory related to haplotypic distinctions between indigenous and Mestizos, can reveal the tactics to articulate natural and social orders in Mexican Genomics arena. Irma Silva-Zolezzi explains the indigenous contribution and its relation to diversity, as follows: "It is kind of paradoxical that by the presence of indigenous ancestry, the variability of Mestizo populations is reduced in genomic terms, when compared to European populations".

The lesser haplotypic diversity coming from indigenous genetic heritage confers some of its specific genetic characteristics to the Mestizo population; like unique allelic frequencies, or the 89 private SNP's not found in any other population of the International Hap Map (Silva-Zolezzi et al. 2009:4). One of the curious characteristic of "Mestizo" haplotypes is their counter intuitive bio-temporality. Even though they are historically the youngest population in the country (Mestizo genealogy can be roughly traced to 500 years ago, with the symbolic and reproductive alliance between la Malinche and Hernan Cortes), their haplotypes are more diverse and (LD) areas are shorter than indigenous ones.

We had always considered this discordance interesting. Yet it was not until a discussion in the laboratory on the 15th of May, 3 days after the presidential

presentation of "The Map of the Mexicans' Genome"[28]; that we really acknowledged the importance of such discordance to understand the re-articulation of population genomics with the Mestizo identity.

After the Friday's seminar in the laboratory, a very interesting discussion on variability and temporality began. The authors of this paper were discussing how 90 Yorubas could be representative of the most diverse population in the world—Irma Silva-Zolezzi a little bit mad—answered to the question of her co-author: "so now you are going to play Dr. Elias game around sampling and representativeness right?"[29] We laughed, and she continued to explain to all of us the difficulties of making a haplotype map of African populations:

> Making a traditional map of African diversity would be incredibly difficult, and might not even cover a good deal of the African diversity...Yet Africans—she emphasized—might become interesting as the new target of commercial/medical genomics, since populations with larger haplotypes have helped researchers to identify genomic regions in which to re-sequence genotypes and refine specific candidate SNP's; and the smaller haplotypes of Africans could make the search easier.

Leonardo, the bio-informatician interrupted the chat, saying "yes the boxes in the African genome are smaller, and as populations become younger the haplotypes (boxes) are bigger". Irma and I recovered the example of mestizo populations in which the haplotypes are smaller than the indigenous ones, going against the common sense of the mestizo as a younger population. It was precisely in the middle of the conversation that I remembered this piece of the interview; I had with Dr. X (pseudonym) a top Scientist/Politician of the Mexican genomic community almost 10 months before the discussion in Laboratory:

> **Dr. X**—They are, they are... pure indigenous, let's say... how do I know? We already ran their genome, and we could take those that are (pause) let me say... pure... in the sense that...that... they are not mixed. Because you can identify those that are not mixed from the ones that are mixed...
>
> ES—With the Haplotypes...?
>
> **Dr. X—**Of course!!...you say here no, no... The ones that are already mixed, since they are recent admixtures, then the blocks are very big, when the genome is mixed (clapping) you find yourself with very big blocks. If many generations have passed and the genome has been recombined, the blocks are very little, so they are very difficult to identify. But 500 years, identifying blocks... but them, if they are mixed, they mixed two or three generations ago,

[28] The article published in PNAS (Silva-Zolezzi et al. 2009) was celebrated by Mexican President Felipe Calderon in the Presidential Residence with a very serious State ceremony. The ones of us who took part in the event discussed various weeks around this topics, for the laboratory crew and the ones who were directly involved in its production it became a door for discussion and further reflection on the topic.

[29] The discussion over the Mexican HapMap representativeness and reliability, is one of the fundamental critiques to genomic mapping; coming from geneticist, and philosophers of science specially Carlos Lopez-Beltran, Edna Suarez and Francisco Vergara (all of them from UNAM, and the group of critical genomics in which Ernesto Schwartz participates see Book: The Mexican Genome, Lopez-Beltran (ED) forthcoming), and lay critics.

> so the admixture is very grotesque (clapping)!!! Imagine that the Indigenous were the brown genome, and the European, Mestizos or whoever is green genome and you mix as they are mixed 50% and 50% (clapping) it is very obvious!!! You notice they are... and if they mixed four generations ago, it is the same, the difference is too grotesque!! But if you go with the Africans that have so many generations the blocks are so little that you cannot identify who is who, talking about admixture...

The use of words as grotesque or pure in order to qualify—or to visually describe—admixture, are amongst other interesting aspects of this piece. But what is striking is that one top scientist/politician involved with the constitution of medical genomics; interprets the genomic boundary between the Mestizo and indigenous identity, following historical criteria, that goes against the fundamental logic of molecular anthropology and population genomics (cf. Gabriel et al. 2002; Zhu et al. 2004; Frazer et al. 2009).

In the previous segment, Dr. X is not only inverting, but using a basic shared knowledge of population genomics—Africans are older—in order to reinforce (consciously or not) the temporal divisions on which "Mestizaje" rests. As if the molecular anthropological stories of admixture (like the Mexican one) followed this pattern (i.e. Mestizos are younger and therefore they should have larger haplotype blocks). Approached through a syllogism the argument makes a lot of sense:

Older populations have shorter haplotype blocks- **Basic thesis of Molecular Anthropology.**
Amerindians are older than Mestizos- **Fundamental notion in Mexican History.**
Therefore Amerindians should have shorter haplotype blocks than Mestizos- **Alignment of genethnicities to fit Mexican History**

The counter intuitive story told by Haplotypes is hard to understand in and out of the laboratory. When discussing this "scientific curiosity" with Elisa—a laboratory technician at Illumina/Population genomics laboratory—she argued:

> No...No Zapotecos are older, how can they be younger. It does not make sense, is endogamy, not temporality. I still think that the Zapotecos are older, than the Mestizos... it relates to endogamy, not time. They are older; they were here before the Mestizos.

The social-political template, on which Indigenous and Mestizo identities are built, definitely permeates the approach and understanding of population genomics. Discordances or "curiosities", as the time story told by haplotypes, render visible the continuous efforts to make sense of population genomics, in not so new, and apparently, not so problematic terrains.[30] Another example of how time frames

[30] Reinforcing "what we already know" about demography, folk categories or ethnicity, would seem to be a safe way to avoid critiques or disagreement. Even though since its design the project of the Mexican Genome diversity project has been heavily criticised (Ribeiro 2005, 2008); now with its public announcement, critique and praise has dramatically increased (see: anon <www.cuestionableinmegen.blogspot.com>).

intervene in the interpretation of biogenetic identities can be found in Dr. Elias, population geneticist, explanation on how he differentiated between Indigenous and Mestizos individuals in his famous genetic studies: "well indigenous populations have been here for a very long time, before the Spaniards.... and the Mestizos are the new ones..."

Medical/population genomics is a young and very fragmented disciplinary field; as an example medical doctors working in genomics use the gen-ethnic labels without really knowing how they were produced. Public scientists and top officers inside the institute, as the ones I have interviewed for this article, are not really trained in population genomics. The much reduced number of specialists in population genomics and medicine in Mexico are the product of organisational efforts such as the INMEGEN, or are still to graduate from the BA in Genomic Science of Mexico's National University (UNAM). Irma Silva-Zolezzi (human geneticist) knowledge about population genomics has been the result of an intense 5 year process of experimentation and autonomous learning in order to develop a map of common genetic variability in Mexico; rather than the product of formal training in the area of population genomics.

Once, that is said, it would be understandable that public figures in the field, make sense of knowledge gaps by making reference to popular and uncontested notions of Mexicanhood such as Mestizaje. Nevertheless, we think that the use of haplotypes and genetic variability, in order to reinforce what we already know about Mexican origins, reveals something much more interesting than the "ignorance" of notorious scientist in Mexico. What the confrontation between these two identities (popular vs. genomic) reveal, is the work of alignment or calibration that remains hidden, since it is re-articulation (Fullwiley 2008:617) or made to fit into century old notions of Mexican origins.

Popular assumptions of ethnicity deeply solidified in the imaginary of lay citizens, journalists and scientists alike, are not only deployed in order to sell the benefits of genomic science. The crisscrossing of national identity and biomolecular identities can be traced down to the very interpretation of genetic mapping. For STS scholars there might be no surprise in discovering that in the terrain of "neutral" DNA "Mextizaje" mediates the understanding of genetic groupings in Mexico; the same way it reveals race as—*les Américains*—know it in other cultural coordinates (Fullwiley 2008:706).

Unfortunately one of the aspects that these simplistic calibrations/re-articulations leave behind is the complexity and multiplicity involved in the emergence of this techno-scientific field. Making flat, what is really complex, and reproducing received knowledge, instead of problematising and exploring emergent properties and contradictions. Many of our informants would say such flattening is beneficial for science communication and political negotiations

Discussion

By following the circulation of haplotypes, temporality and ethnicity in Mexican genomics arena, we can disclose assumptions embedded in the apparently evident and unproblematic understanding of admixture in Mexico. The fundamental tactics

of Mexican politics of time (Krieger 2005) are akin to Fullwiley's notion of re-articulation, since a national identitarian narrative—*Mestizaje*—has been reiteratively projected in order to frame the political, medical and ethno-racial properties of population genomics. On the other hand the analysis of specific tactics of naturalisation (M'charek 2005) and reinscription are made clear by paying close attention to co-emergence (Reardon 2005) or co-production (Jasanoff 2005). We should think of these two approaches—coproduction and re-articulation—as complementary in the analysis of genethnicities, its production, and translation throughout the different social worlds of the post-genomic era.

Amanda M'charek (2000) work on forensic DNA, showing the transformation of populations in its trips between the laboratory and the courtroom, is an example of the malleable and probabilistic qualities of biogenetic identities. These characteristics allow different identities to coexist, depending on which parcel—as well as how many markers—of the genome you are studying. Biogenetic identities that even when are the products of "ancestral" populations that coincide with longstanding racial classifications do not necessarily stand in a tautological relation with the ethnic landscape, in this particular case Mestizaje.

In the field of public policy and science communication the rather flexible and ambivalent nationalist discourse on *Mextizaje*, has allowed genomic entrepreneurs and lobbyists to frame the idea to found a new science based on the knowledge of populations, their demographic history and their genetic uniqueness. The partial connections between a population and its uniqueness, disclose the impossibility to import this knowledge from any other country, as well as the moderated feasibility of using the same technical knowledge in order to map other Latin American countries that have a similar demographic history. Bringing to life a strategic ambivalence (even if a contested one), which is able to reinforce a nationalistic and an international—expanding discourse at the same time.

Although the ambivalent constitution of Mestizaje has allowed experts in the field to gloss over the debate on race; taking advantage of the dominant national identity, which departs from the cultural/reproductive encounter of the Spaniards and the indigenous communities. The way in which Mestizaje travels into the realm of medical and anthropological laboratory genomics produces discordances between the temporality of historical and biogenetic maps. Time itself has been stabilised in such a way (old Indigenous vs. new Mestizos), that certain basic characteristics of genomic variability (haplotypic length, diversity and linkage disequilibrium areas), are interpreted in order to reinforce what we already know about "admixture" (even when such common sense knowledge goes against seminal works in the discipline).

The impact of those assumptions might add to nothing, but a scientific "curiosity", or a lack of a nuanced understanding of the material culture of population genomics (by Mexican public scientists and leading experts). Yet we think such discordances can become a starting point to ask ourselves about the confrontation between a relative, probabilistic and sometimes (as in the case of admixture) counter intuitive construction of genethnicities; with a much more stable, rigid and romanticised version of national identity in Mexico and beyond.

When facing a more or less rigid identity, the role of genomic science would be either to confirm or challenge official historical records and national narratives. The case of the Lembas, an African tribe (Thomas et al. 1998; Abu El-Haj 2004) is one

of such examples, in which the presence of a specific modal haplotype in the expected frequency amongst the Bubas—Lembas priestly clan—has produced a reconsideration of their claims of Jewish origin. In the case of Mestizaje, debate and public reflection on the tension between these two approaches (rigid vs. relative/probabilistic) to genomic science and identity formation, could build nuanced and multilayered understandings of national and group identities. Identitarian notions, which pay serious attention to the material production of genethnicities and its implications, would have to be much more flexible in order to incorporate plurality and mapping discordances (i.e. genetic temporality vs. historical temporality) into their embedded scientific/political statements.

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Dr. X, Mexican Genomic Scientist and public expert in the field, Mexico City 2008.
Dr. Gerardo Jimenez-Sanchez, Former Director General and co-founder of the INMEGEN, 2008, and October 2009
Dr. Laura, National Bioethicists, Mexico City 2009
Dr. Elias, Biomedical Researcher, Mexico City 2008
Dr. Max, INMEGEN's top official, Mexico City 2009
Dr. March, Former Head of Research of the INMEGEN, and current head of public communication of science, Mexico City 2008
Dr. Xavier Soberon Mainero, Mexico City 2009