Population in Fragments: Inclusion, Risk, and the Anticipatory Universality of Postcolonial Genomics

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Abstract: In recent years, genomic medicine has invited critical attention for its potential to include diverse population groups and therefore expand the clinical relevance of global genome databases in diagnosing diseases. Population geneticists across the Global South demand being included in this process by translating their national populations into geneticized fragments that move back and forth between laboratories, databases and sites of diagnosis and care. Taking the case of postcolonial India, this article explores how the scientific universality of genomics becomes contested, only to produce an 'anticipatory universality' oriented towards public-health futures. Drawing on Ruha Benjamin's concept of 'postcolonial genomics', my argument is three-fold. First, I critique analyses that have explained population genetic studies in India as an exercise in fostering nationalism, showing instead that geneticists are increasingly interested not in the 'Indian' population as a whole, but rather in its 'fragments'. Second, through a case study of the Lambadas in Telangana, I show how the material formation of these fragments highlights the limits of genomic universality, where the haplotype[1] is treated as the ultimate fact in tracing both ancestry and disease risk. Third, I argue that it is partly due to the financial dependence of postcolonial geneticists on state bureaucracies that they enact an 'anticipatory universality' for genomics, which, even if severely limited and often harmful in the present, promises to be universally applicable in the future.
[postcolonial genomics, inclusion, scientific universality, geneticization, caste and tribe, anticipatory futures]

In the summer of 2022, I was sitting in the office of Dr. Vinod Scaria, a leading Indian geneticist known for belonging to the team that sequenced the first 'Indian genome' in 2009. As an ethnographer interested in how genomics is making inroads into India's public-health programmes, I had landed in Scaria's office through a series of media reports following the state of affairs in genome sequencing and surveillance. Since 2015, Scaria's lab, based at a leading government-funded institute of genomics,[2] had been working as part of a collaborative team of geneticists, clinicians and public-health experts with the aim of using genomics to identify rare and undiagnosed diseases and

1 A haplotype is a set of alleles that are inherited together on a single chromosome. Once they have accumulated from both paternal (Y-chromosome) and maternal lineage (traced through mt-DNA) it can be used to identify both ancestry and disease susceptibility through specific combinations of genetic markers. An allele is a variant of a sequence of nucleotides found at a particular location on the DNA molecule.

2 https://www.igib.res.in/, Accessed March 25th, 2023.

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develop public-health solutions for genetic disorders. While speaking about genomics and its utility in meeting public-health needs, Scaria recalls the most celebrated finding of the consortium: the discovery of the novel 'Nalband' mutation.

In 2015, Shamsudheen KV, then a PhD student working in Scaria's lab, came across a media report that was as intriguing as it was tragic. In the city of Agra, Uttar Pradesh, Mohammad Nazir, a father of eight, had written a petition to the President of India pleading for six of his children to be euthanized. The reason was a 'mystery' disease that had caused them to become progressively paralysed below the neck, rendering them unable to carry out daily tasks independently. As the undiagnosed condition gradually reduced their quality of life, managing their physical needs became increasingly unaffordable for the family. For the parents, euthanasia was the last resort; they wanted to put themselves and their children out of their misery.

Suspecting a genetic condition, Scaria's team decided to collect blood samples not only from the affected family but also their immediate neighbours, who belonged to the same ethnic community, identified as the Nalband. The Nalband are a group of Sunni Muslims spread across parts of India, Pakistan and Iran whose history in India can be traced back to the 15th and 16th centuries, when the first Nalband migrated to present-day north India from present-day Iran. Scaria and his team spent two years sequencing the whole exomes[3] of both affected and unaffected individuals from the community to trace 'the tapestry of genetic relatedness' (Koshy, *The Hindu* 2017).

Ultimately, the team was able to find the novel and rare mutation on chromosome 21, close to the MLC 1 gene, that causes a debilitating neurological condition called megalencephalic leukoencephalopathy with subcortical cysts (MLC). Having identified the exact mutation, the geneticists reached out to the children's clinician, who put them on prophylactics as part of a targeted therapy that improved their quality of life in the absence of a cure. Talking to me in his office, Scaria zooms back to the crucial role of population genetics in enabling disease diagnosis, especially when rare, unidentified, mutations are involved. 'Population genetics is the baseline for medical genetics', he said:

> India has about 4000 endogamous communities who have their own specific marriage practices, which makes them genetically distinct. In the last seven years, we have found many communities who are prone to certain diseases.

Because they had not found this mutation in any other Indian population group, Scaria continued: 'we concluded that the Nalband were a "founder population" for this specific mutation on MLC 1, which we named the "Nalband mutation".'

Scaria's comments reveal a common practice among geneticists to identify founder populations for specific disease mutations and concentrate public-health screening on

3 An exome is a protein-coding region on a genome. Whole exome sequencing is a common, more cost-effective method of detecting mutations on the selected DNA sequence compared to whole genome sequencing.

those identified as such. This article explores how geneticists in India mobilize the universality of genomics to craft populations and make them available for public-health interventions. In doing so, the geneticists not only include themselves in the global knowledge production of genomics, but also claim inclusion for Indian population groups in disease gene databases, a move that promises to improve diagnosis and ultimately therapeutics closer to home. To achieve this, they see it as their task to decipher the genetic ancestry of India's population, which is not only diverse and unique but also under-represented in genome databases worldwide.

As the case of the Nalband shows, genomic medicine ties together questions of genetic ancestry and incidence of disease in such a way that one becomes the 'baseline' for the other. While genomic medicine depends on global regimes of knowledge, its practices take on particular expressions in places where state-funded research institutes and public health rather than market-driven privatized medicine are the dominant sites of diagnosis, care and innovation in medical technologies. Anthropologist Ruha Benjamin captures this configuration of research and medicine under the label of 'postcolonial genomics', a particularly public health-oriented form of genomics that has emerged in postcolonial states and that requires practitioners to calibrate their research in ways that 'can simultaneously advance the science, foster public support, and produce health and economic goods' (Benjamin 2009:343). Some of these concerns are implicit in the naming of MLC 1 as the 'Nalband mutation', which simultaneously inscribes an Indian group as the origin of a genetic marker, contributes to gene disease databases by adding a novel rare mutation, and frames the Nalband as potential subjects of public-health interventions.

Extending Benjamin's insights while decentring the nation in a social-scientific critique of genomics, this article contributes to this special issue by asking how universality is produced and contested through articulations of population in the postcolonial contexts where populations are always already marked by colonial knowledge regimes. Drawing on scholarship in anthropology and science and technology studies (STS), this article addresses three interlinked questions. First, if populations in human genetics, as elsewhere, are not given but turned into biological and social entities (Bangham and Chadaverein 2014; Gannett and Greisemer 2004), what purpose do they serve for the practitioners of science? Second, how do classificatory practices advanced by population geneticists shape how populations are interpreted in public health interventions? And third, what kinds of inclusions and exclusions come into effect once they re-inscribe populations as biological entities?

Methodology

The article is based on thirteen months of ethnographic fieldwork from 2021 to 2023 in laboratories, clinics and a teaching institute for human genetics in the south Indian

city of Hyderabad, supplemented by interviews with prominent geneticists, then based in Delhi.[4] I draw on my interaction with geneticists, their own publications, and my discursive and ethnographic engagement with one particular ethnic group in the state of Telangana, the Lambadas, who were identified as a high-risk group for thalassemia, one of the inherited blood diseases (IBDs) that were the focus of my fieldwork. IBDs are fast becoming routinized in India's genetic surveillance programmes, which seek to reduce the burden of these diseases and are often directed at lower-caste and tribal groups, who supposedly are at higher risk of being affected by them. In section iii), I draw on my interactions with laboratory technicians, genetic counsellors and clinicians, who repeatedly articulated this risk towards the Lambadas. My own positionality as an upper-caste researcher also allowed me access to many families, including Lambadas who were receiving state-subsidized care for thalassemia.

Postcolonial Genomics: Whose Genomes, Whose Diseases?

The recent development of public health-oriented genomics in postcolonial states accompanies calls for diversifying existing genome databases to include groups of non-European ancestry. Indeed, under-representation of the non-European genome has been a running concern in several studies (Chambers et al. 2014; Fatumo et al. 2022; Landry et al. 2018; Jain et al. 2021; Wu et al. 2019). Notably, such calls are often led by practitioners who themselves belong to these very excluded groups, thus contesting simple binaries between the scientific researcher of the Global North and the research subjects of the Global South (Lyons et al. 2017; Kowal, Radin and Reardon 2013; Anderson 2009).

Thus, scientists from the postcolonial world become important political actors within the global knowledge hierarchy. A bias towards people of European ancestry in global genome databases, they argue, limits the benefits of clinical findings to reach those from diverse ancestral backgrounds. Following such calls for diversity, conscious attempts are being made to move away from the extractive nature of human genome projects of the past.[5] Ethical concerns raised during the Human Genome Diversity Project (HGDP) and the following HapMap project criticised that DNA samples collected from indigenous and other non-White communities were only incorporated

4 Well-known scientists working in labs in the two cities have collaborated on various national genome projects, such as the Indian Genome Variation Consortium, or Indigen, which sequenced 1008 individuals in India for the first time, and more recently the Genome India project, which planned to sequence 10.000 genomes by the end of 2023.

5 See the section entitled 'Diversity, Equity and Inclusion at NHGRI' on the webpage of the US-based National Human Genome Research Institute: https://www.genome.gov/about-nhgri/leadership-initiatives/Diversity-Equity-and-Inclusion-at-NHGRI. Accessed March 25th, 2023.

in so far as they furthered the differences in ancestry and haplogroup analysis, not because they addressed specific health needs of those from the communities (Radin 2018; Reardon 2009).

Critical engagement with new genetics and genomics has thus argued that the shift from racial types to populations, ancestry and DNA frequencies has not led to the abandonment of race and racialization in science and medicine (Fujimura and Rajagopal 2011; Fullwiley 2011; Haraway 1997; M'charek, Schramm, and Skinner 2014; Montoya 2007; Reardon 2009). Rather, it has brought into effect what Nadia Abu-el Haj (2007) has termed the 'genetic re-inscription of race'. As risk and 'ethnoracial' differences are increasingly being calculated at the molecular level, they also become profitable commodities in the bioeconomy, giving rise to a concept of race that is no longer reducible to the object of twentieth-century eugenics (ibid.). Claims that non-European genomes are under-represented then become part of the same kind of 'vital politics' (Rose 2001) that gave purchase to the demands of ethnic minorities and women of colour in western countries to be included in medical research (Epstein 2009). This politics renders genomic medicine a universalist project that constantly accumulates more and more different genomes.

Ultimately, as genetic technologies become more widely used in establishing one's 'true' identity, it is not just race that becomes re-inscribed in genetic terms, but also religion, nationality, ethnicity and even citizenship (Burton 2018; Tamarkin 2014; McGonigle 2021; Mukharji 2023; Schramm, Skinner and Rottenburg 2012). Against this backdrop, genomics in India presents an important case study for 1) its aspirations to participate in global science regimes and be included in disease gene databases; 2) its particular deployment of admixture and endogamy, which tends to ascribe genetic risk to historically marginalized groups; and 3) its orientation towards public-health solutions.

Attending to these aspirations, discursive and material practices and motivations, my argument in the following sections is three-fold. First, I challenge scholarly analyses that have explained population genetics in India as an exercise in fostering nationalism. By contrast, I argue that the geneticization of admixture and endogamy have led to the fragmentation of the national population, and that it is these fragments that are currently at the forefront of genomic medicine. Second, through a case study of the Lambadas in Telangana, I illustrate how the population fragments are constituted in an epistemic and linguistic environment pertaining to risk, which in turn proclaims the limits of genomic universality in which haplotypes are taken to be objective facts. Finally, I explore how aspirations to translate genomic knowledge across public-health domains anticipates the universal applicability of genomics to future health governance.

Between Admixture and Endogamy: The Indian Population and its Fragments

While India did not participate in the Human Genome Project, transnational networks forged by a few Indian geneticists had already started investigating the genetic basis of the Indian population in the 1990s. Among these early internationally trained geneticists was the late Dr Lalji Singh, popularly known as the 'father of DNA fingerprinting' in India. While Singh in many ways pioneered DNA-based population studies, it was his long-time collaborator, Dr Kumarasamy Thangaraj, who took the lead after the former's untimely death in 2016. During my brief re-visit to Hyderabad in 2023, I had the chance to meet Dr Thangaraj, who is now a leading population geneticist in India, and is based at the Centre for Cellular and Molecular Biology (CCMB).

In recounting their journey to publishing their famous 2009 paper in *Nature*, entitled 'Reconstructing Indian population history', Thangaraj noted how it all began with a workshop on DNA fingerprinting organized by Singh in 1994. One of the workshop participants was Edwin Southern, the British biologist whose research lead to the invention of the Southern Blot test.[6] Southern informed and encouraged Singh and Thangaraj to collaborate with another British geneticist, Chris Tyler Smith, who was at the time working on Y-chromosome polymorphism and applying it to understanding migration patterns in human evolution. Singh and Thangaraj complemented this research with their own studies of both Y-chromosome and mitochondrial DNA markers in selected Indian population groups to include 'heterogeneity in the network analysis' and 'population specific haplotypes and alleles'[7] (Thangaraj, Ramana, and Singh 1999).

Their broad inclusion of a diversity of origins was followed by a series of population-specific studies, particularly of the Great Andamanese, who were first studied as India's 'vanishing population', a group that the researchers later hypothesized were the first modern humans to have migrated out of Africa (Thangaraj et al. 2003). 'This paper published in *Science* got so much attention and eventually made David (Reich) reach out to us. Then we started collaborating with him,' Thangaraj told me while recalling the journey towards the 2009 publication. The publication was significant not only because it was led by David Reich, the prestigious population geneticist based at Harvard Medical School who had carried out similar investigations in other parts of the world,

6 The Southern Blot test is an essential technique used in electrophoresis to separate DNA fragments from any sample that tests it against a DNA sequence probe, and thus offers quantification of which sequence is more prominent in a sample. It is also widely used in detected single-gene disorders whose mutations have been deciphered and are known.

7 When geneticists speak of 'population-specific haplotypes' that can identify disease-gene linkages, they are referring to haplotypes inherited over generations due to endogamy.

but also because it had the potential to reframe highly contested debates around caste and indigeneity in India's public and intellectual discourse.[8]

The Reich et al. study (2009) suggested that population groups in India show high levels of variation, as well as 'a gradient of proximity with West Eurasians' (Reich et al. 2009:491), which they called the 'Indian cline'. Following the logic of 'population specific haplotypes', the geneticists hypothesized that different groups have different proportions of ancestry from two somewhat distinct founder groups, whom they named the 'Ancestral North Indians' (ANI) and 'Ancestral South Indians' (ASI). The two clusters, ANI and ASI, were themselves conceptualized as 'models' rather than as homogenous. The authors go as far as to add a disclaimer about the modelling of these clusters:

> We caution that 'models' in population genetics should be treated with caution. While they provide an important framework for testing historical hypotheses, they are oversimplifications. For example, the true ancestral populations of India were probably not homogeneous as we assume in our model but instead were likely to have been formed by clusters of related groups that mixed at different times. However, modelling them as homogeneous fits the data and appears to capture meaningful features of history. (Reich et al. 2009:492)

In his study of Latin American genomics, Peter Wade (2017) argues that constructions of purity and mixture are co-produced. While the *mestizaje* or mixed-race identity is the national norm in Latin America, particularly in Brazil, indigenous people figure as 'relatively pure' and are made to stand in as ancestral populations for present-day humans. In the broad context of genetic studies, then, the Andamanese emerge as 'pure' but also as different from the ancestral populations of the present-day peoples of India. The Reich et al. study in fact denies ascribing homogeneity even to the ancestral populations, while presenting the ANI and ASI as homogenous models. In this context, these researchers' use of the 'Indian cline' is interesting precisely because in evolutionary genetics a 'cline' differs conceptually from a 'class' (Fujimura et al. 2014). While the latter is seen as a set of static characteristics that carries the spectre of pure races, a cline describes a pattern of biological variation against which one can measure the expression of particular traits.

While most groups cluster along the Indian cline, according to these researchers, the ancestry of six 'outlier groups' reflected considerable differences from the Indian

8 These debates particularly revolved around what had come to be known in India's public discourse as the Aryan Migration Theory. These studies posited genetic incursions in reconstructing evolutionary migration, the 'peopling' of India, the introduction of agriculture, the spread of languages, and social stratifications based on ethnic, racial or caste lines, and that have either directly referred to the Aryan migration as a historical event or taken one or the other position in the debate (Cavalli-Sforza 2001; Bamshad et al. 2001; Wells et al. 2001; Sahoo et al. 2006; Indian Genome Variation Consortium 2008; Reich et al. 2009).

cline. These were Siddi with African ancestry, the Nayishi and Ao Naga, who cluster close to the Chinese, the Great Andamanese and the Onge, who have some parts of ASI ancestry but none of ANI, and the Chenchu, a tribal group from present day Andhra Pradesh and Telangana who were found to be closer to Native Australians. This classification of 'outliers' points to a similar tendency in the study of 'religious isolates' that Projit Mukharji (2023) observed in his historical account of race science in India. Mukharji notes that in the immediate aftermath of decolonization, Indian researchers conducting blood variation studies framed groups such as the Cochin Jews, Muslims and Parsis as having migrated to India from elsewhere. Unlike North American contexts, where the dominant figure of genetic difference is indigeneity, Mukharji makes a case for how 'exogeneity' defined genetic difference in the Indian context, in turn legitimizing national territorial belonging. Pertinent to the definition of the 'religious isolate', however, was a biohistorical notion of endogamy that enabled the group's isolation before and after migration. Indeed, endogamy was the defining element that enabled caste, tribe, religion or any 'group' to be studied as a biological 'population'.

The genome mapping studies of more recent years have taken this biohistorical construction of endogamy for granted while re-directing their interest towards improved diagnoses of disease. In that capacity, the dominant articulation of population in postgenomic studies are those of admixture and endogamy. Both of these forms are again reflected in another foundational study conducted by the Indian Genome Variation Consortium (IGVC), which sought to further disease-gene explorations in Indian populations. While it classified its population sample according to language, geography and ethnicity, grouping on the basis of ethnicity showed 'significant differentiation' (IGVC 2008:8). The study concluded its published report with the following statement:

> We note that the people of India are referred as 'Indian' in many population genetic studies. The implication of such usage is that the Indian population is genetically homogeneous, which, as the results of our study indicate, is evidently not true. However, we have also shown that it is possible to identify large clusters of ethnic groups that have substantial genetic homogeneity. (IGVC 2008:17)

This finding of 'substantial genetic homogeneity' within ethnic groups came at the same time as findings of variation across national genetic populations. STS scholar Banu Subramaniam (2019) has criticized this configuration in population genetic studies to suggest the formation of 'an indigenous nation transnationally bound'. According to her, what unites genetic studies reconstructing population history, genetic explanations of caste differences and the discovery of disease by banking Indian DNA is an ideological discourse of 'bionationalism', that is, an imagined community brought together on the basis of shared biological ancestry. The notion of bionationalism also concurs with Benjamin's (2009) observation that postcolonial genomics in India has made use of the particular rhetoric of nationalism summarized in the age-old adage of 'unity in diversity'.

While regimes of bionationalism continue to inform knowledge practices in postcolonial genomics, my interest here is slightly different. Without eschewing criticism, I want to take seriously my interlocutors' claims that calibrating populations in a way that geneticizes admixture and endogamy can aid in testing individuals for identified or candidate genes, and eventually set up public-health programmes. Following these public-health orientations in postcolonial genomics, it is clear that what geneticists are increasingly interested in is not so much the 'Indian' population itself but what, following Partha Chatterji (1993), can be called its 'fragments'. For Chatterji, if the postcolonial nation was not a single imagined community but was rather constituted differently through its various regions, castes, religions, histories etc., the supposed universality of the nation state as a form of political authority was called into question.

In a similar vein, approaching postcolonial genomics through the lens of nationalism occludes the material, epistemic and linguistic environments in which populations are fragmented, particularly for the purposes of developing public-health programmes. Those who have highlighted a similar fragmentation of the national population have noted how the 'molecularization of categories of belonging' (Egorova 2009:7) engenders hierarchical knowledge regimes that allow researchers to accept claims of self-identification that fit into their research design and goals and reject those that do not (ibid.; Mukharji 2023). Still others have highlighted how the calibration of endogamous populations in both the Global North and Global South become national resources in the global market of genomics R&D and further the creation of biocapital (Sundar Rajan 2006; Tupasela 2021). Advancing such granular analyses, I elaborate on how 'populations in fragments' are articulations of risk that are regional and place-based, and thus unsettle the universality of genomic medicine.

Materializing the Fragments: The Case of the Lambada in Telangana

> After admixture in the last 2000–4000 years, in the last 2000 years, everybody is following endogamy. So, we wanted to look at the effects of endogamy, not only in India, but in South Asia like Pakistan, Sri Lanka etc. Then we realized that one-third of the populations that we had analysed are expected to carry population specific disease, or rare diseases. In fact, we found quite a few disease mutations that are exclusive to certain groups. So once we identify the mutation, screen the population, do prenatal diagnosis, then only we can see the disease burden reducing. The impact can only be seen after two to three generations. (Thangaraj, K., personal interview, 2023)

From my conversations with both Scaria and Thangaraj and in their own publications, it was abundantly clear that an active need to translate research findings into public-health solutions underwrites the practice of genomics in India. In this context, endogamy is

posited as the main factor that has determined genetic drift and population stratification in recent evolutionary history of South Asia, as the above quote by Thangaraj suggests. Endogamous marriage practices are seen to produce a founder effect that gives rise to smaller population subsets as they become differentiated from the larger group, leading to what geneticists call 'inbreeding'. An extreme form of such inbreeding occurs when the group practices consanguinity: reproducing within the bloodline by practising cousin marriages. However, this interpretation of social norms defining genetic norms assumes that the norm is the same everywhere and is always obeyed. Such claims in genetics are deeply troubling, not only because they reify the social boundaries of intergroup relations into biological difference, but also because they ignore forms of marital and caste admixture that have always existed and continue to do so, as historians of South Asia have argued (Egorova 2009; Mukharji 2023; Thapar 2014).

When I asked Thangaraj if endogamy is also used as a model (referring to the quote from his own publication cited above), rather than a norm that is universally practiced, his answer was a resounding 'no'. Emphasizing that within India and other parts of South Asia caste endogamy is almost always followed, his implicit suggestion was that biological reproduction takes place within the caste group. When I persisted with the question of whether the norms of endogamy are always followed, Thangaraj's reply was more assertive: 'Even if two people may not say that they are related, we can check if they come from the same ancestors.' Ascribing an infallible authority to DNA, he concluded, 'Haplotype is the ultimate fact.'

Without reiterating the critique of endogamy in South Asia that historians have put forward with sufficient evidence, I ask what happens when populations move out of the realm of models to become fragments marked by risk. I illustrate this with a case study of the Lambada, a marginalized community whom I encountered during my fieldwork on genetic screening programmes in the city of Hyderabad, southern India. As they become fragmented in postcolonial genomics, populations are neither pure social entities of caste, ethnicity or religion, nor biological entities of population groups demarcated by shared ancestry. Rather, I contend that fragments emerge when 'genomic articulations' (Tallbear 2013) of caste and ethnicity meet 'demographic articulations' of genetic risk. By demographic articulations, I am referring to epistemic practices that pursue non-genetic factors such as those of fertility, marriage, birth and migration to predict or explain risk. In what follows, I demonstrate how this fragmentation of Lambada as a population bound by risk materializes and is experienced on the ground.

The Lambadas are a traditionally nomadic community whose members are today spread across multiple states in India. Their major occupation in the pre-colonial and colonial periods was transporting goods like grains and salt, sometimes over very long distances. In the pre-independence princely state of Hyderabad, the Lambada served as major caravan traders and merchants from at least the 17th century, according to historical accounts (Bhukya 2010; Vaditya 2019). The introduction of railways in British India effectively destroyed their source of livelihood, leading to widespread dispossession and a transition to peasantry. This transition from a nomadic to a settled life

was, however, accompanied by periods when the Lambadas were known to indulge in dacoity (banditry), particularly in times of drought and famine. In response to their 'rebellious' behaviour, the British colonial state classified the Lambada as 'criminal tribes' under the Criminal Tribes Act 1871, a law whose underlying logic was that criminal behaviour tends to be hereditary in nature.

The postcolonial Indian state 'de-notified' the previously criminal tribes but re-classified them as 'habitual offenders' under the Habitual Offenders Act 1957. Members of these tribal groups continued to be identified as such until as recently as 2007, when the UN Committee on the Elimination of Racial Discrimination asked India to repeal the act and rehabilitate all the enlisted tribes. The Lambada, however, through a series of political and social assertions, were included in the 'Scheduled Tribes' provision of the Indian Constitution in 1971 by the then united state of Andhra Pradesh (of which Hyderabad was the capital till 2014). This inclusion is seen by many Lambada to have granted them much needed political representation and opportunities for upward social mobility.

Recounting this social history of the Lambada is crucial in situating their current inclusion in genetic research and screening programs as a 'high-risk' group for thalassemia, an inherited blood disorder that leads to perpetually low levels of haemoglobin in the blood and thus creates dependence on regular blood transfusions, reducing the quality of life in multiple ways. Although internally diverse in terms of class, education and status groups, many Lambada continue to live in poverty, lacking access to proper health care and education, while many Lambada women particularly have become easy targets of indiscriminate surgical operations, rendering them one of the most 'bioavailable' groups in the region (Cohen 2007; Mamidi and Pulla 2013).

During my fieldwork in Hyderabad, I met numerous experts, including doctors, nurses, medical geneticists, genetic counsellors, lab technicians and biological anthropologists, who repeatedly mentioned the Lambada in the context of thalassemia and their burden on the state of Telangana. When I asked them how the Lambada were identified as a high-risk group, I was given several answers. While many just held that opinion without backing it up with any particular evidence, one of the major factors cited by geneticists and clinicians was the high incidence of parental consanguinity found in the community. According to this explanation, the Lambadas predominantly followed the practice of cross-cousin marriage, which leads to an increased risk of birth defects over generations. This claim also rested on a long history of anthropological studies of tribal customs that was often accompanied by an anxiety towards 'high rates of inbreeding' in southern India (Roy Choudhury 1976; Saheb and Naik 1983; Sanghvi 1996).

A strong connection between genetic risk and marital practices was also the finding of a recent study conducted by a team of geneticists, clinicians and biological anthropologists in the state of Telangana (Rao et al. 2021). The study suggested that, while thalassemia is prevalent in 31 out of 33 ethnic groups in the state, five of them show a considerably higher rate of incidence for the disease, citing consanguinity as

one of the risk factors. Ultimately, they identified five high-risk groups, namely the Lambada, Sunni Muslims, Mala, Madiga and Mudiraj, all of whom are designated tribal, religious and caste minorities respectively by Telangana state. The researchers used the method of tracing the pedigrees of existing patients, recording the unaccounted deaths of family members, their places of birth and their marriages, which included calculating marital distance and the type of marriage tradition followed. Based on their findings, the study also recommended genetic screening to be concentrated on the identified groups, as well as 'high-risk districts' in the state.

In respect of other explanations, though less often invoked than consanguinity, the biological anthropologists and molecular geneticists I met at the teaching institute noted that it was because of their long history of migration that the Lambadas may have been exposed to regular outbreaks of malaria. As a result of natural selection, they developed the thalassemia-causing mutation, which also provides natural immunity against the parasite (Roberts and Williams 2003). This line of reasoning draws a causal link between the risk of a disease mutation and the geographical area in which the community is known to reside. While the Lambada were only known to have settled in their present location in recent years, other tribal groups were also assumed to share the risk of thalassemia because they lived in heavily forested regions where the incidence of malaria was considered a routine public-health problem (Corrêa et al. 2017; Rambabu 2016). This group of experts used the tribal identity of the Lambada as an example to propose further genetic screening of other tribal groups in the state.

Finally, one overarching factor often mentioned was that the low levels of literacy and awareness in the community made them ignorant of their own health conditions. The Lambada often delayed visits to hospitals, did not 'maintain' their haemoglobin levels and thus their overall health, and were generally non-compliant even when asked to follow their strict diet and medication routines. Even though this was not an explanation for risk, this line of reasoning was followed by the clinicians and genetic counsellors to predict the incidence of the disease in unreported cases. At their worst, such reasoning forecloses any possible benefits of genomic or demographic articulations, as they become caste-based articulations of risk that denigrate the whole community. One moment from my field particularly exemplified this when a clinician juxtaposed the community's recent upward mobility to their health status, remarking, 'These Lambada trouble us a lot! They are so good with their money, but when it comes to their health, they don't pay any heed.'

As scholarship on social medicine in India has observed, complaints about non-complying patients are often informed by entrenched notions of caste and class, especially when providers themselves come from upper-caste backgrounds (Nayar 2007; Thapa et al. 2021). Contrary to such complaints, the numerous Lambada families whom I met in Hyderabad were receiving state-subsidized treatment for thalassemia and complying with their own genetic surveillance by asking family members to be tested for the disease. However, they were unsure why they carried the risk of the disease. As one Lambada couple whose child was thalassemia-affected asked me, 'Why do

you think we got this disease? We are both Lambada, but we are not cousins. We did not get married within the family. Why, then, is our child affected by it?'

The case of the Lambada in Telangana reveals the multiple ways in which the fragmentation of the Indian population becomes operational in a wider epistemic and linguistic landscape, and why it exceeds genomic articulations of population that DNA-based population studies provide the basis for. While population geneticists take recourse to the language of modelling, and rightly so, they can generate deeply stigmatizing effects when they project their data back on to communities. These effects are particularly intensified when a community historically criminalized by the colonial and postcolonial state is unilaterally diagnosed as at risk. As part of state-led genetic-screening programmes, more and more Lambada are currently being recruited to be tested, a trend which studies like Rao et al. (2021) only exacerbate. However, as I observed in the city of Hyderabad, those found to be affected by the condition are eventually asked to travel to the capital city from faraway regions to receive blood transfusions to manage their health condition. Infrastructure and inequalities of health between different regions of the state remain so glaring that a new gap emerges between diagnostics and therapeutics.

The Anticipatory Universality of Postcolonial Genomics

What does the context of postcolonial India reveal about the universality of genomics? First, it pushes us to ask difficult questions about the universal applicability of genomics that geneticists from non-Euro-American contexts have been affirming in their demands for inclusion. While genomic medicine aims to become more universal by accumulating different genomes, postcolonial realities on the ground, as illustrated in the case of the Lambada, sound the limits of its universal applicability, and in turn force us to ask to whom it is applicable. Does genomic knowledge apply to the Lambada, or does the knowledge of the Lambada apply to genomics?

Furthermore, it reveals how knowledge practices also emerge at the edges of scientific universality. In population genetics, population-specific haplotypes are seen as the key that unlocks the mysteries of disease mutations transmitted down the generations. And yet, in their translation from the lab to the clinic or the health camp, the iterability of the haplotype is possible only through recourse to risk articulations that exceed genetic factors. Much like DNA fragments in the lab that require the addition of reagents to be extracted, isolated and intervened in, as well as moved out of laboratories (Latour and Woolger 1987), population fragments require something other than genomic articulations to come into existence and become mobile entities.

Finally, in this case the Lambada become a fragment not only because they are an ethnic group but also because they are an ethnic group at risk, which is understood to be actualized in vital processes of marriage, birth, fertility and migration. These

contingent demographic articulations of risk become scripted on to the colonial and postcolonial state's classification of them as a 'criminal tribe' and are crucial to sustaining their health surveillance on the ground. At the same time, these articulations also enable their inclusion into disease gene databases by breaking them into mobile population fragments. The Lambada were recently included in the GenomeAsia Phase2 database one of the 'South Asian medical cohorts' (Wall, Sathirapongsasuti and Gupta et al. 2023). In other words, population fragments that emerge within postcolonial genomics anticipate the universal applicability of genomics, hoping that it will be relevant in the future, even as they sound the limits of its actuality.

Discussing the anticipatory dimension of contemporary technoscience, Adams, Murphy and Clarke (2009) propose that anticipation has an epistemic value as actuarial practices of science are replaced by speculative forecasts which then animate the present for further optimization and preparedness. Given its public-health orientations, postcolonial genomics enacts such anticipatory logics not only in the way it articulates the Indian population and its fragments, but also in how it frames its research agendas to make them amenable to health bureaucracies. I briefly share a snippet of my conversation with Vinod Scaria that exemplified these anticipatory logics. A highlight of my conversation was how Scaria described genomics as helping to develop solutions for public health in a country that is highly stratified in terms of its population structure and resources. Scaria was painfully aware of this social stratification not only among all citizens, but also between different federal governments:

> Place also matters. If you go to Uttar Pradesh or Bihar, and tell the government to do newborn screening[9], no one is going to listen to you. For them, diarrhoea is a bigger problem. Their infant mortality rate is from fifty years back. But in a state like Tamil Nadu or Kerala, their infant mortality has reached global standards … attending to genetic disease burdens will significantly improve their metrics.[10] So, governments have an incentive here.

Thus, apart from identifying risk populations and disease genes that would be given a priority in public health programmes, Scaria had introduced the third factor of place. However, this was not the 'place' of high-risk districts that we encountered in the Rao et al. study (2020). This was the 'place' of well-performing state bureaucracies that could afford and be interested in translating genomic knowledge for public health. 'So,

9 Newborn genetic screening is a set of laboratory techniques aimed to test a series of genetic conditions in a newborn. Typically, the tests are performed on a blood spot collected through a heel prick in an infant. For further information, see: https://www.genome.gov/genetics-glossary/Newborn-Genetic-Screening Accessed March 25th, 2023. While newborn screening is becoming more routinised in India, there are no nation-wide guidelines for the same.

10 Scaria compares UP and Bihar, which often perform poorly on human development indices such as life expectancy and disease mortality with Tamil Nadu and Kerala, two of the leading states in those same indices.

you're saying that genomics is not for everyone?' I ask him. 'It will be … just not yet.' Situating genomics in the realm of statecraft, Scaria's concern implicitly demonstrated the accountability of geneticists like him working in publicly funded institutions for the state. Even when state bureaucracies are interested in investing in public-health programmes such as newborn screenings, it is the task of geneticists to demonstrate the value of such programmes through association studies that identify risk populations and diseases. 'It's better to show the government that these people actually exist, rather than showing them data', Scaria added.

Thus, genomics in its present technoscientific form in India was 'not yet' applicable to everyone because of limited resources, the inequality in health standards and metrics, and the lack of incentives for states that lag behind. 'But it will be' because of improvements in its technology, scale of use, and cost efficiency. But more importantly, because it is anticipated that as more and more populations become risk fragments and are included in disease gene databases, it will become easier to identify what kind of diseases afflict what kind of people, leading to the further specification of public-health programmes. This specification will then bypass any need for iterative studies that construct model cohorts to represent those actually at risk or affected by diseases.

Scaria's response of 'not yet, but it will be' suggests a gradual scaling up of genomic studies and brings the argument of anticipation centre-stage. In many ways, this goal of making genomic medicine universal by accumulating different genomes is driven to make its applications more specific, targeted and precise. Even though the grounds of postcolonial India delimit and visibilize the harms of this universality, postcolonial genomics continues to enact an 'anticipatory universality' to see results in the present. This anticipatory universality was directed towards transforming genomics into not only a universal technoscience but also a universal technopolitical form, ready for deployment in future health governance.

Conclusion: Anticipating Inclusion, Articulating Exclusion

If universality is necessarily unfinished and mobilized by actors to fulfil their particular agendas, as the introduction of this special issue suggests, then it is precisely the unfinished state of genomics that postcolonial geneticists mobilize in order to include not only themselves but also the populations they fragment into globally circulating knowledge regimes. While disease gene databases form one end of this material archive of inclusion, which promises to capture the universality of humanity and make medical genomics applicable for all, postcolonial geneticists such as those in India are also accountable to state bureaucracies for developing public-health programmes. In this article, I have detailed the discursive terrains, epistemic practices and linguistic environments in which population groups in India that are taken to be 'genetically

homogenous' materialize as risk-carrying fragments and become mobile entities circulating between the lab, the clinic and the database.

Following the work of Indian geneticists and their positioning in transnational networks of population and medical genetics, I ask whether bionationalism is the most appropriate or most timely intervention for describing the discursive terrain in which science is practised. Rather, I take their claims of under-representation to be symptomatic of a larger shift in medical, health and scientific research towards the pursuit of inclusion. And yet inclusion does not mean the same thing for the geneticists and the populations they fragment. As I argued through the case study of the Lambada, their inclusion in genetics research and public-health programmes comes at the cost of reiterating historical stigmas, a process that therefore goes beyond the universal authority of haplotypes in articulating disease risk. Ultimately, the inclusion of populations in disease databases and geneticists' agendas in health bureaucracies highlights a new kind of discursive formation that I have referred to as an 'anticipatory universality'. By deferring the applicability, benefits and established methodology into the future, postcolonial genomics can justify the exclusions brought about by its current technoscientific limitations. As such, the Lambada of Telangana are testament to what happens if globally circulating scientific regimes are not accompanied by place-based ethical norms. More pertinently for this special issue on 'universality in pieces', this case reminds us of the 'postcolonial hybridities and heterogeneity' (Anderson 2009:389) of regimes of knowledge, to which I hope this article contributes.

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