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► **To cite this version:**

Pradiptajati Kusuma, Nicolas Brucato, Murray P Cox, Philippe Grangé, Denis Pierron, et al.. The Austronesian dispersal over the Indo-Pacific region. International Symposium on Austronesian Diaspora, Jul 2016, Bali, Indonesia. hal-04741634

HAL Id: hal-04741634

<https://hal.science/hal-04741634v1>

Submitted on 17 Oct 2024

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The Austronesian Dispersal Over the Indo-Pacific Region

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Introduction

Island Southeast Asia, hosting more than 25,000 islands, has been a region of a dense maritime network since 8,000 years ago. It favoured the development of long distance seafaring technologies, the main instrument of the Austronesian expansion - one of the most widespread human migration. This expansion started about 5,000 years ago with the spread of agricultural populations; it probably originated in Taiwan and reached distant locations, such as Rapa Nui in the Pacific Ocean and Madagascar through the Indian Ocean [1,2]. This created a diverse modern range of Austronesian populations across vast Oceans, with their own cultural traits and genetic heritage across vast Oceans. To better understand the differential Austronesian genetic impact on populations from the Indo-Pacific region, we have started a project to reconstruct their population biological history, using genetic, epigenetic and epidemiological markers, on more than 5,000 individuals from the different regions in the Indian Ocean rim and Island Southeast Asia.

Materials and Methods

Samples: Saliva and/or blood samples collected from Indonesia, East Africa, and Papua New Guinea (PNG) individuals (red and green circles; Figure 1).

Genetic markers: Mitochondrial DNA, Y-chromosome, and autosomal genome-wide SNP (Illumina Omni 5 and Omni Express SNP arrays).

Epigenetic markers: Typed with Illumina Human Methylation 450 chip and analyzed in correlation with genetic markers.

Epidemiological markers: Host genetic adaptation mechanism against malaria (Southeast Asian Ovalocytosis, SAO), HTLV-1 and HHV-8 viruses.

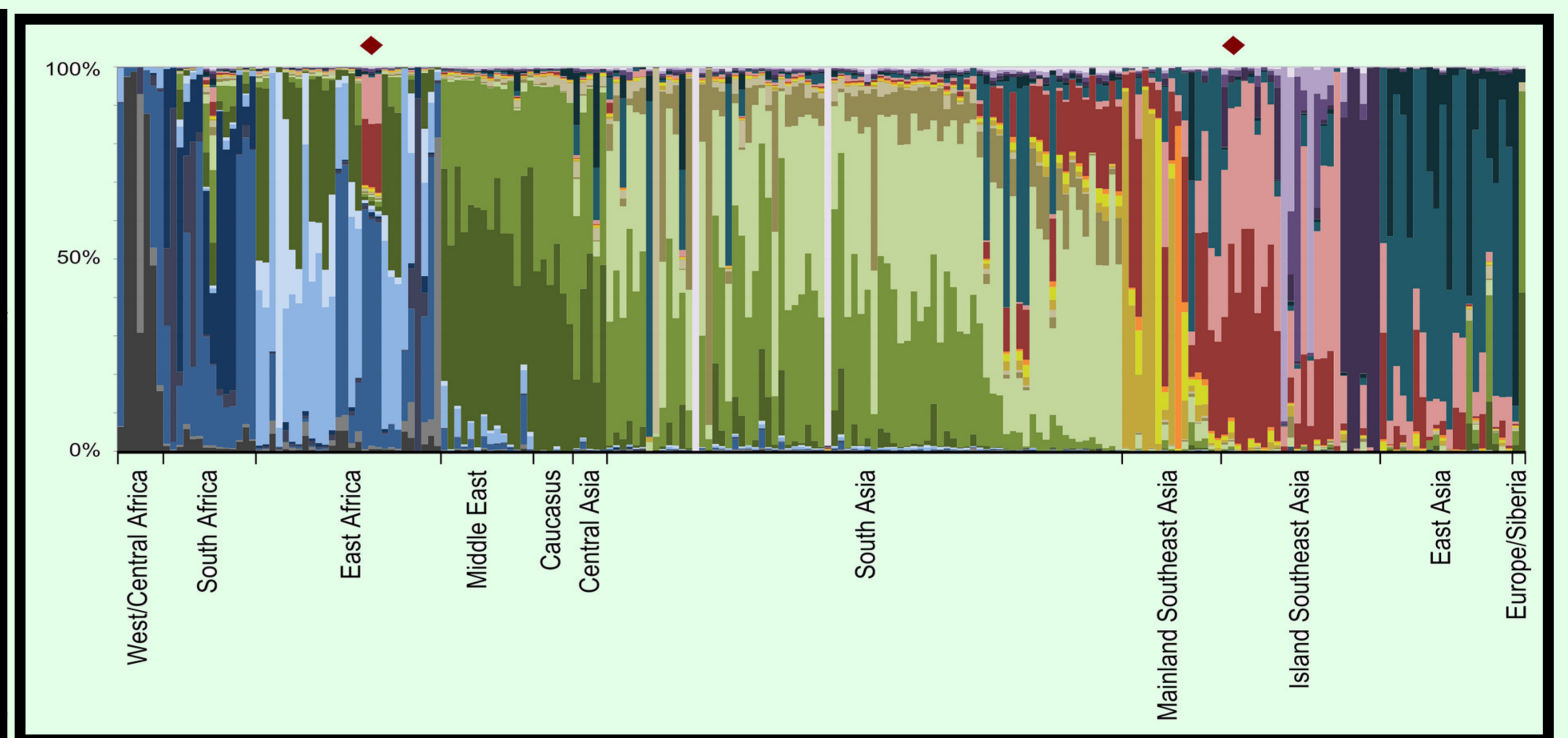
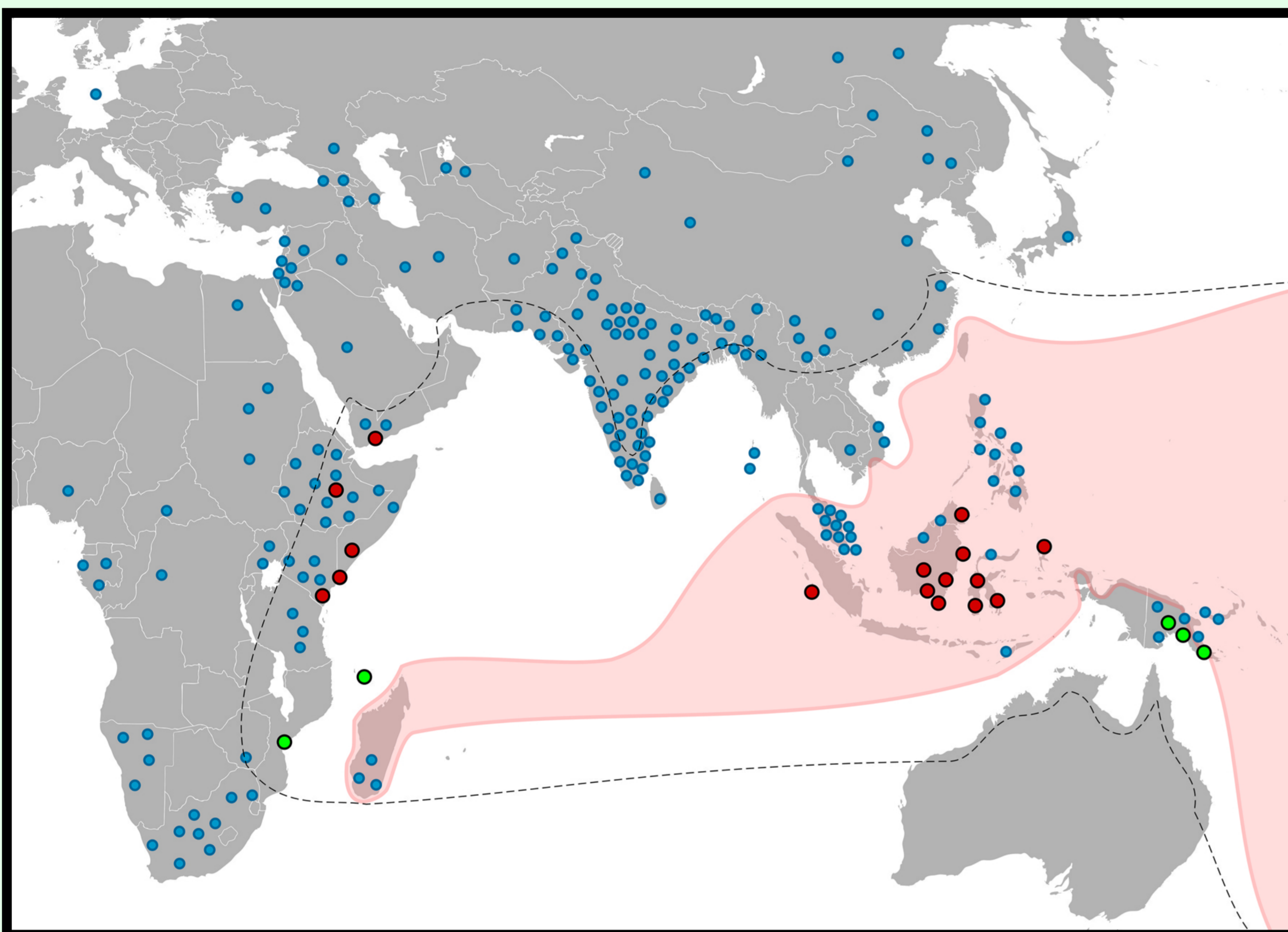
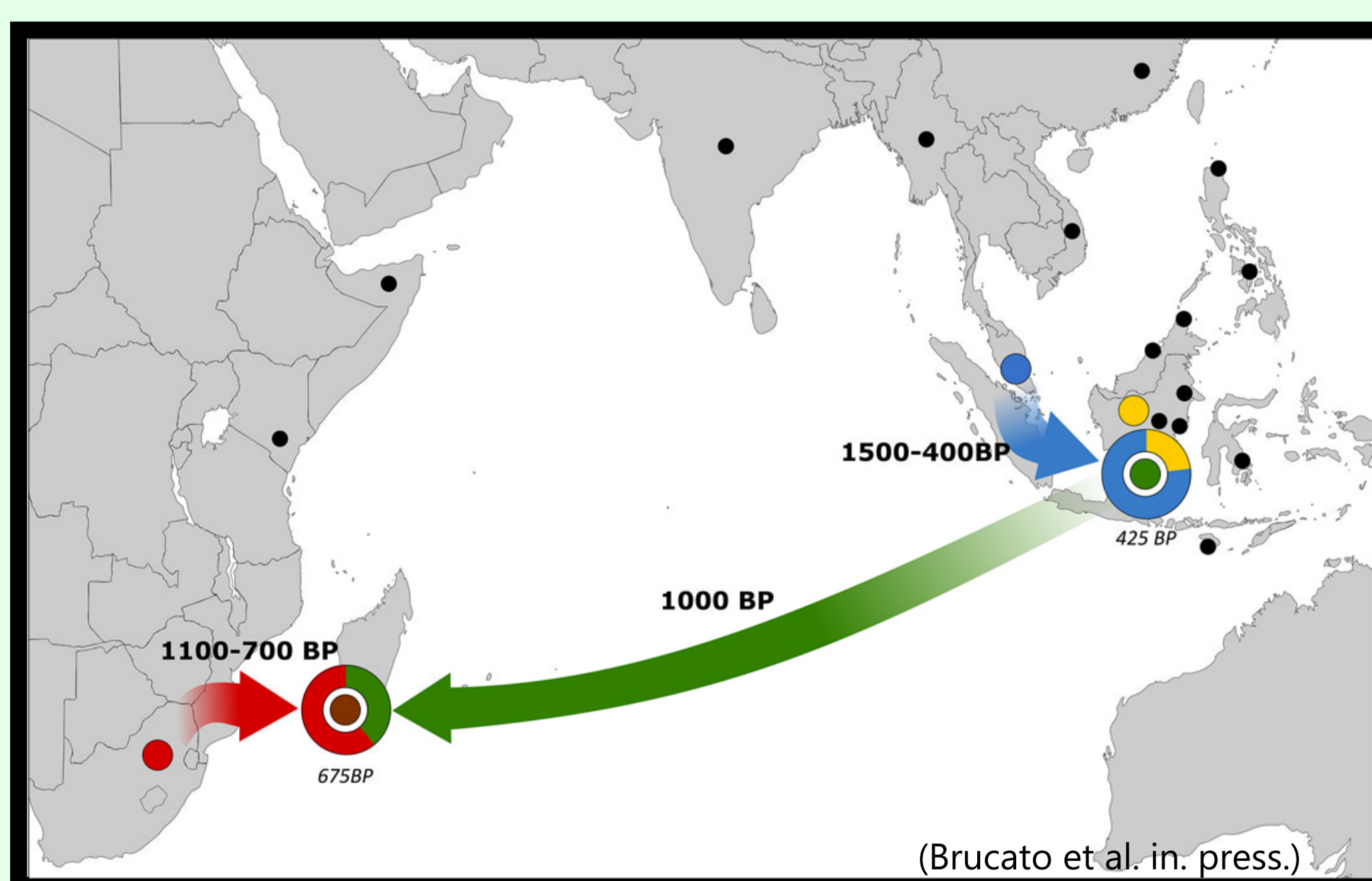


Figure 1 (left). Map showing the geographical distribution of the Austronesian language (pink area), and areas of documented archaeological/historical contact between Southeast Asian / Austronesian speakers with other populations across Pacific and Indian Oceans (dashed lines). **Red circles** - current populations under study; **green circles** - new populations in ongoing sampling campaign; and **blue circles** - comparative populations from published studies. **Figure 2 (above)** shows the genetic background complexity of worldwide populations, visualized by an ADMIXTURE plot. Austronesian genetic influence (red and pink colors) is observed in Island Southeast Asia (ISEA) cluster and East Africa / Madagascar (marked by red diamonds icon).

RESULTS AND PERSPECTIVES

Madagascar was settled by Indonesian people from South Borneo

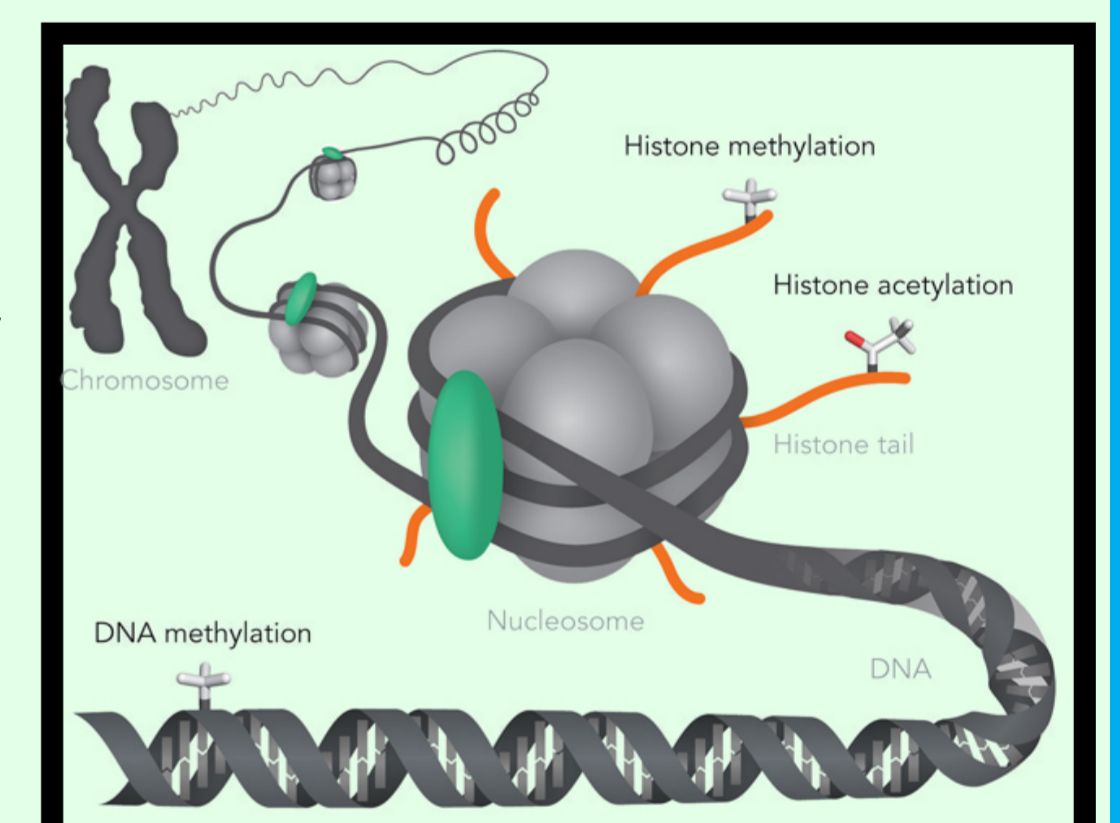


We generated genome-wide data from Southeast Borneo populations, including the Ma'anyan, a population whose language is the closest to the Malagasy language, along with the Banjar and other indigenous Borneo populations. We incorporated published data compiled from populations across the Indian Ocean region. We find strong support for an origin of the Asian ancestry of Malagasy among the Banjar people, but interestingly not from their linguistic sibling, the Ma'anyan. The Banjar ethnic group emerged from the presence of a Malay

Empire trading post in Southeast Borneo, which favoured admixture between the Malay and an autochthonous Borneo group, the Ma'anyan. Reconciling genetic, historical and linguistic data, we show that **the Banjar, in Malay-led voyages, were the most probable Asian source in the founding of the Malagasy gene pool**, estimated to migrate 1,000 ybp. This long-standing question, about the mysterious Asian origin of Malagasy people, has finally been decrypted step by step, through our scientific project [3,4,5,6].

Population Epigenetics : Biological adaptation after major migration and admixture events

The epigenome is at the intersection between the genome and the environment, acting as the mediator of the biological plasticity. Regulating gene expression, it defines a dynamic biological layer giving to the cell and the organism a high reactivity to any kind of stress (e.g. diet or infectious diseases). The diverse migratory events that conducted human populations in highly different locations forced each individual to adapt rapidly to new environments (climates, pathogens, etc.), a phenomenon mainly driven by epigenetic variation. Moreover, admixture events between highly differentiated genomes can potentially imbalance the genetic expression, creating a new epigenetic profile.

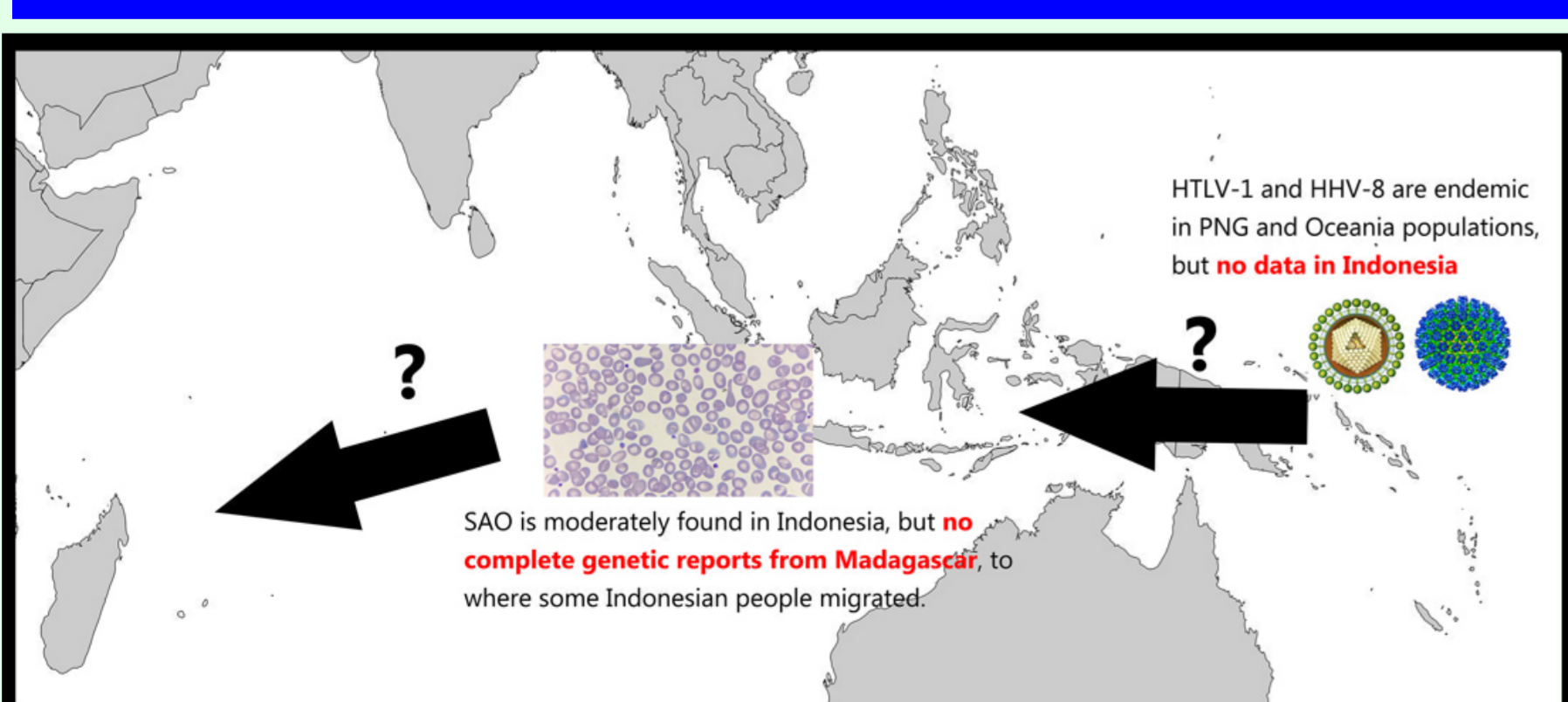


(image courtesy of <http://horizondiscovery.com>)

The current technological improvements (i.e. chip, NGS) led us to conduct an epigenetic study to explore two venues based on the identification of common/discordant patterns of genomic and epigenomic diversity between populations:

- 1/ Can we define the **epigenetic variation due to drastic environmental changes** such as the one occurring after major migrations?
- 2/ What is the **impact of admixture** between different genomic background on epigenetic variation?

Diseases signature as migration markers



Humans migration is often followed with the spread of diseases (parasites, bacteria, viruses). Studying the genetic diversity of a disease and its distribution we can reconstruct its origin and dispersal route, and therefore the migration route of populations. We are investigating the genetic diversity of HTLV-1 and HHV-8 viruses in PNG and Oceania populations, and screening its distribution in Indonesia

see whether these viruses were brought to Oceania through the Austronesian expansion process. Furthermore, we are studying the connection between Indonesia and East Africa through the population genetic adaptation mechanism against malaria (i.e. SAO) that is commonly found in Indonesia, but not yet detected in East Africa. This will complement the genetic evidence that supports Indonesian population, particularly the people of South Borneo, as the ancestral population of the Malagasy.

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Acknowledgments

We thank the Eijkman Institute for Molecular Biology (Jakarta, Indonesia) for accommodating the sampling program in Indonesia. This research was supported by French ANR grant number ANR-14-CE31-0013-01 (grant OceaAdapto to F-X.R.), the French Ministry of Foreign and European Affairs (French Archaeological Mission in Borneo (MAFBO) to F-X.R.), and the French Embassy in Indonesia through its Cultural and Cooperation Services (Institut Français en Indonésie).

