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The Austronesian Advantage: Natural Selection and Linguistic Diversity

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Abstract: The "Austronesian advantage" suggests that Austronesian-speaking populations in Melanesia are resistant to tropical splenomegaly syndrome, a medical condition linked to chronic exposure to malaria. This hypothesis was proposed by Kevin M. Kelly in his 1988 dissertation, a subsequent 1990 paper, and a 1993 paper co-published with Jeffrey Clark. I now update the Austronesian advantage hypothesis with additional linguistic, anthropological, and genetic data. I find that cultural adaptations cannot fully explain the Austronesian expansion. Rather, the Austronesian advantage, a classic example of natural selection, completes the picture by connecting the Austronesian expansion with greater reproductive success. I also strengthen the Austronesian advantage hypothesis with data from Tibet. The correlation between language expansion and natural selection extends well beyond the Austronesian world.

Keywords: Austronesian languages; Papuan languages; linguistic anthropology; natural selection

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1. Introduction

According to statistics from to the World Health Organization, malaria killed about 400,000 people in 2017 [1]. Turning to the historical record, the disease may have appeared in the ancient Chinese texts as early as 6700 years ago. Additional historical documentation comes from ancient India, Egypt, Greece, Rome, and Mesopotamia [2,3].

One historical misconception about malaria associates the source of the affliction with swamps. Hence, the term "malaria" comes from Italian and means "bad air." Modern science now identifies malaria as an infection caused by a parasite from the genus *Phasmodium*, a single-cell microorganism. Interestingly, modern understanding of malaria stems from the work of several researchers who worked independently over a 100-year period (1880–1982) in an effort to map the lifecycle of the *Phasmodium* parasite [3]. From these efforts we know that the female Anopheles mosquito spreads the microorganism while feeding on human blood. An infected individual is bitten by the mosquito and the *Phasmodium* parasite is carried away inside the salivary gland of the mosquito. Transmission occurs when the mosquito feeds on an infected individual and transfers the *Phasmodium* parasite into a new human host who is not infected. Accordingly, modern efforts to combat malaria focus on insecticides and other measures to prevent the Anopheles mosquito from breeding as well mosquito netting and other measures that block the mosquitos from biting people. Anti-malarial drugs are also used to prevent and treat the disease.

Gamma globulin represents a genetic marker that has a strong association with the immune system. The anthropologist Kevin M. Kelly, in his 1988 dissertation [4] and in a 1990 paper published in *Current Anthropology* [5], discusses gamma immunoglobulin polymorphisms found among the Austronesian and Papuan populations of Melanesia. The 1990 paper rejects a simple link between these polymorphisms and the geographic origins of both populations. Rather, according to the researcher, these polymorphisms are linked to natural selection and more specifically, resistance to malaria. He supports this position with the distribution pattern of Austronesian and Papuan populations. The Austronesians are found within the low-lying coastal regions where Malaria is prevalent.

Papuans (non-Austronesians), on the other hand, inhabit the highlands where the affliction is far less prevalent.

Kelly coauthored a study with Jeffrey T. Clark in 1993 [6] that evaluated gamma immunoglobulin polymorphisms gathered from Austronesians and Papuans of Melanesia. Much of the data came from New Guinea. Within this area of the world, Austronesians and Papuans are equally susceptible to contracting malaria. Rather, the Austronesian advantage is linked to resistance against tropical splenomegaly syndrome, later known as hyperreactive malarious splenomegaly, a massive and fatal enlargement of the spleen that occurs as the result of chronic exposure to malaria (see also Kelly's 1990 [5], 1996 [7], and 1999 [8] publications for additional details). As such, natural selection has given Austronesians an evolutionary advantage that assures greater reproductive success in malaria-infested regions.

Discussions of the Austronesian languages have generally focused on cultural adaptations that mediated the expansion of this language family. I would like to suggest that evolutionary adaptation, and more specifically, the Austronesian advantage, should also be part of the discussion. I intend to resurrect Austronesian advantage and defend it with additional linguistic, anthropological, and genetic data. In doing so I suggest that cultural adaptations, such as agriculture and navigational skills, only provide a partial explanation for the Austronesian expansion. Evolutionary adaptation completes the picture by connecting the Austronesian expansion with greater reproductive success. I also strengthen the Austronesian advantage hypothesis with data from Tibet. The correlation between natural selection and linguistic variation extends well beyond the Austronesian world.

2. Origins of Austronesian

The Austronesian language family occupies a large corner of the global linguistic tapestry with more than twelve hundred languages and 324 million speakers [9]. This language family has two main branches, Formosan and Malayo-Polynesian. Formosan consists of twenty languages found on the island of Taiwan. Malayo-Polynesian, on the other hand, consists of 1236 languages that have a north to south geographic distribution from Taiwan to New Zealand, and a west to east distribution from Madagascar to Rapa Nui (Easter Island). The Oceanic sub-branch of Malayo-Polynesian follows the diversification of Austronesian in Oceania. Examples of Oceanic languages include Fijian, Samoan, Maori, and Hawaiian.

The Formosan branch of the Austronesian language family represents the linguistic signature of Taiwanese aboriginals as well as a linguistic relic of the prehistoric Dapenkeng culture. The Dapenkeng migrated to Taiwan from the East Asian mainland about 55,000 years ago. For almost 1000 years the Dapenkeng were hunter-gatherers. Their subsistence strategy included the harvesting of marine resources. Then, they adopted agriculture and began to cultivate foxtail millet and rice [10]). About 4000 years ago, as the result of soil depletion and population pressure (Bellwood 2005: 135) [11], agriculture and Austronesian-speaking farmers spread from Taiwan to the Philippines.

3. The Lapita Expansion

The evolution of the Malayo-Polynesian language branch follows the Austronesian expansion out of Taiwan. From an archaeological perspective, the expansion follows the migration of the Lapita culture. Evidence of this tradition comes from the archaeological record and a unique style of pottery. The Lapita culture initially expanded southwards through the Philippines to Borneo. From Borneo, a second Austronesian expansion occurred around 3400 years ago, with some migrating westwards in the direction of Malaysia, while others migrated eastwards in the direction of New Guinea. By around 3000 years ago the Lapita culture began to spread across eastern Indonesia and Papua New Guinea. Then, by around 2000 years ago, the Lapita culture reached western Oceania. Finally, by around 1250 AD, after colonizing many of the islands of central and eastern Oceania, the Lapita cultural expansion terminated in New Zealand [12].

Homo sapiens colonized present-day Papua New Guinea about 50,000 years ago [13]. The term "Papuan" represents a broad cultural and linguistic description of their descendants. When the Austronesians arrived in New Guinea about 3000 years ago, they encountered the Papuans. The genetic evidence suggests that the Austronesian and Papuans formed a new population. Genetic evidence for admixture consists of Y-chromosome mutations that evolved in situ among the Papuans as well as mutations that represent genetic relics of the Lapita expansion. This new admixed population then carried the Lapita culture and Oceanic languages eastwards across the Pacific Ocean.

From a Y-chromosome perspective, the genetic relics of the initial out-of-Taiwan Austronesian expansion are the O1a-M307, O1a-M110, and O2a-B451 mutations [14–16]. The C-M208, M1a-P34, and S1a-M245 mutations are characteristic of Papuan populations [17–20]. A simple genetic model of the Oceanic expansion would draw an analogy to a city bus with a long route that began in Taiwan and ended in New Zealand. In Taiwan, passengers with the O1a-M307, O1a-M110, and O2a-B451 mutations started the journey. On New Guinea, passengers with C1-M208, M-256, and S-B254 mutations climbed aboard the bus. In western Oceania, the passengers from Taiwan reached the end of their journey. The passengers from Papua New Guinea rode the bus to the end of the line.

4. Austronesian and Cultural Adaptations

Based on the number of speakers and its vast geographic distribution, Austronesian is indeed a significant linguistic "heavyweight" within the global tapestry of linguistic variation. As such, some researchers have explored cultural adaptations that may have facilitated this expansion of language and culture. Donohue and Denham [21], for example, correlate the success of Austronesian with trade networks that were controlled by Austronesian-speaking populations. According to Blust (2013: 11–17), these trade networks flourished because of technological advantages, such as outrigger canoes, as well as advanced navigational skills that eventually carried the Austronesians over vast stretches of open water [22]). However, correlating the so-called success of Austronesian with trade is problematic because trade does not necessarily produce a reproductive advantage. In other words, Austronesian behaves much like language families that co-expanded with early agriculture, such as Niger-Congo or Sino-Tibetan. These languages thrived and survived because agriculture can support much higher population density than hunting and gathering. Population pressure then pushed languages and farming beyond a putative homeland.

Bellwood (2005: 141) explains the importance of agriculture and its role in the Austronesian expansion. He writes that most Austronesian-speaking populations practice agriculture and that without it, the Austronesians could not have colonized Oceania [11]. In short, agriculture appears to be a far more crucial component of the Austronesian success story than just trade networks and technology. As explained earlier, Austronesian agriculture began with rice and millet cultivation on Taiwan. However, as explained by Bellwood (2005: 130–139) [11] and Blust (2013: 6–7) [22], when the Austronesian expansion reached Borneo, climatic conditions no longer supported the cultivation of grain crops. At this point the Austronesians began to cultivate tubers and tree crops that flourish on islands in Southeast Asia and Oceania. Tubers include taro and yams. Examples of tree crops are sugar cane, bananas, pandanus, breadfruit, sago palm, canarium nuts, and coconuts. Nevertheless, correlating the success of Austronesian with tuber and tree crop agriculture also seems problematic. Papuans also cultivated these crops. Why, then, would agriculture have been hugely successful for Austronesians, and moderately successful for Papuans?

5. Evolutionary Adaptation

As previously explained, *Homo sapiens* colonized New Guinea about 50,000 years ago. During the Holocene, which began about 11,000 years ago, the Papuans began to congregate in the central highlands of this island. A recent study (Gaffney et al. 2021) suggests that when the Holocene transition occurred on Papua New Guinea, humans had depleted

much of the large game food resources in the lowlands. To acquire protein, hunter gatherers adapted and began to harvest small game. They conducted hunting forays into the highlands to acquire possums, fruit bats, and other similar sized animals. These short incursions into the highlands eventually resulted in permanent occupation of the region [23].

Malaria avoidance, as previously suggested, also offers a potential explanation for Holocene migration into the central highlands as the prevalence of this affliction diminishes at greater altitude. Support for this position stems from differing patterns of agricultural activity among Papuans and Austronesians. The transition to agriculture began among the Papuans of the central highlands about 10,000 years ago [24]. Meanwhile, the coastal lowlands of New Guinea remained sparsely populated until the arrival of the Austronesians about 3000 years ago. Within the coastal lowlands, the Austronesians eventually became successful farmers [5,25].

To understand the correlation between natural selection and the success of Austronesian agriculture within the lowland coastal region of New Guinea, I return to the 1993 study by Clark and Kelly [6]. Both researchers compared gamma globulin polymorphisms from Austronesian and non-Austronesian populations on New Guinea. Gamma globulin was examined because the marker has a strong association with the immune system. The researchers were able to identify a specific polymorphism characteristic of lowland Austronesian-speaking populations who are resistant to tropical splenomegaly syndrome, which as noted previously, is a massive and fatal enlargement of the spleen that occurs as the result of chronic exposure to malaria. They also identified another polymorphism associated with highland Papuan groups, populations that are more susceptible to this affliction.

Clark and Kelly [6] offer several salient points that strengthen the "Austronesian advantage." Anopheles mosquitos, the vector that transmits the *Phasmodium* parasite to humans, thrive in the wet and swampy lowlands of New Guinea, whereas they are far less prevalent in the highlands. Lowland coastal agriculture, on the other hand, further intensifies the spread of malaria by creating habitat that facilitates the breeding cycle of these mosquitos. Additionally, lowland coastal agriculture creates permanent human settlements that provide a host population for the *Phasmodium* parasite. Thus, the Austronesians had an evolutionary adaptation that enabled them to farm the malaria-infested coastal areas of New Guinea, whereas such activity for Papuans would have been lethal. Taking this a step further, this a classic example of natural selection.

Clark and Kelly [6] also suggest that admixture between Austronesians and Papuans created a new population that inherited a resistance to tropical splenomegaly syndrome. This conclusion is consistent with recent previously introduced Y-chromosome data that support admixture between Papuans and the lowland Austronesian farmers on New Guinea. Taking this a step further, their children not only inherited an evolutionary adaptation but an Austronesian language as well.

As previously suggested, malaria avoidance conveniently explains why the Papuans occupied the highlands of New Guinea at the onset of the Holocene. The prevalence of malaria diminishes with altitude. However, this also presupposes the presence of malaria on New Guinea before the arrival of the Austronesians. Such an argument seems plausible based on a recent study of the *Plasmodium vivax* organism, the species of the *Plasmodium* parasite that has plagued the Austronesian world. Loy et al. (2018) report a close genetic relationship between *Plasmodium vivax* parasites that infect chimps and gorillas in Africa and the *Plasmodium vivax* parasites that infect people in Southeast Asia. Based on this observation, the researchers suggest that when people left Africa, between 100,000 and 70,000 years ago, the *Plasmodium vivax* organism essentially hitched a ride with the humans. Extending this idea further, *Homo sapiens* and *Plasmodium vivax* co-expanded into Papua New Guinea about 50,000 years ago [26].

Again, as previously suggested, natural selection explains the success of Austronesian lowland agriculture on New Guinea. At this point it should be emphasized that the Austronesian advantage may well have evolved before the Austronesians arrived on New Guinea. Researchers recognize twelve epidemiological zones of malaria where people

have endured chronic long-term exposure to the affliction. The expansion of Austronesian falls within Malaysian and Australasian epidemiological zones. Combined, both zones include the Philippines, Indonesia, the Malay Peninsula, Indonesia, West Timor, and Papua New Guinea (Arrow and Gelbrand 2004: 142–143 and Table 6-1) [2]. Perhaps the process of natural selection began in mainland China, or on Taiwan, or in the Philippines, or on Borneo.

6. Tibeto-Burman

The Austronesian advantage is not an isolated phenomenon. Cultural and evolutionary adaptation also helps to explain the position of Tibeto-Burman languages within the global tapestry of language variation. From a linguistic perspective, Tibeto-Burman languages are a branch within the Sino-Tibetan language family. According to Ethnologue, the Tibeto-Burman branch consists of 442 languages that are organized within twelve different subbranches [9]. Tibeto-Burman languages are predominately found in the East Asian countries of China and Myanmar (Burma), and the South Asian countries of India, Nepal, Bhutan, and Bangladesh. A reliable estimate for the number of Tibeto-Burman speakers could not be found. The number is probably less than 100 million.

From an archaeological perspective, the starting point for a discussion of Tibeto-Burman languages begins with the Tibetan Plateau in China. The initial expansion of Tibeto-Burman languages correlates well with the cultivation of barley on the Tibetan plateau beginning about 3600 years ago. Unlike other grain crops, barley tolerates the cold and dry climate that is associated with the high altitude of this region [27]. In addition to the cultivation of barley, which is a cultural adaptation, an evolutionary adaptation also explains the success of Tibeto-Burman languages. The Tibetan Plateau lies at an average altitude of 4000 m above sea level. Here, hypoxia and altitude sickness pose a significant health danger. People from lower altitudes can, over time, become acclimated to living at high altitude. Nevertheless, Tibetans have an evolutionary adaptation that allows them to utilize the deleted oxygen level more efficiently that those who have moved to Tibet from a lower altitude [28]. A recent study (Yang et al. 2017) compared the genomes of about 3000 Tibetans with 7000 non-Tibetans from East Asia. The study was able to isolate the adaptation to nine different loci of the human genome [29].

7. Conclusions

Researchers who explore language variation often focus on cultural adaptations that mediate language expansions, such as agriculture and trade networks. Evolutionary adaptations must also be part of the discussion. The Austronesian advantage provides especially robust support for this position. Moreover, the Austronesian advantage is not an isolated case. Tibetans, for example, possess a unique evolutionary adaptation that enables them to survive at extreme altitude. This adaptation helps to explain the position of Tibeto-Burman languages within the global tapestry of languages. Finally, it is important to emphasize that the correlation between evolutionary adaptation and language may provide innovative research opportunities in the future. For example, the Duffy negative mutation may present a future research opportunity to explore linguistic diversity in Africa. This mutation is prevalent among populations on this continent and is associated with resistance to malaria. Similarly, the SLC24A5 gene may present a future research opportunity to explore linguistic diversity in western Eurasia. This evolutionary adaption is linked to more efficient vitamin D synthesis at higher latitudes.

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References

1. World Health Organization. Malaria Fact Sheet. Available online: https://www.who.int/news-room/fact-sheets/detail/malaria (accessed on 23 August 2019).
2. Arrow, K.J.; Panosian, C.; Gelband, H. (Eds.) *Saving Lives, Buying Time: Economics of Malaria Drugs in an Age of Resistance*; Institute of Medicine (US) Committee on the Economics of Antimalarial Drugs; National Academies Press: Washington, DC, USA, 2004. Available online: https://www.ncbi.nlm.nih.gov/books/NBK215638/ (accessed on 16 January 2019).
3. Cox, F.E. History of the discovery of the malaria parasites and their vectors. *Parasites Vectors* **2010**, *3*, 5–9. [CrossRef]
4. Kelly, K.M. The Biological Significance of Melanesian GM Distribution: Selection and the GM Hypothesis. Ph.D. Thesis, University of Illinois, Urbana, IL, USA, 1988.
5. Kelly, K.M. GM polymorphisms, linguistics affinities, and natural selection in Melanesia. *Curr. Anthropol.* **1990**, *31*, 201–219. [CrossRef]
6. Clark, J.T.; Kevin, M.K. Human genetics, paleoenvironments, and malaria: Relationships and implications for the settlement of Oceania. *Am. Anthropol.* **1993**, *95*, 612–630. [CrossRef]
7. Kelly, K. IGHG3 G and the Pathogenesis of Hyperreactive malarious splenomegaly. *Med. Hypotheses* **1996**, *46*, 135–139. [CrossRef]
8. Kelly, K.M. Malaria and Immunoglobulins in Pacific Prehistory. *Am. Anthr.* **1999**, *101*, 806–809. [CrossRef]
9. Simons, G.F.; Charles, D.F. (Eds.) *Ethnologue: Languages of the World*, 21st ed.; SIL International: Dallas, TX, USA, 2018. Available online: http://www.ethnologue.com (accessed on 24 March 2019).
10. Hung, H.-C.; Mike, T.C. Foragers, fishers and farmers: Origins of the Taiwanese Neolithic. *Antiquity* **2014**, *88*, 1115–1131. [CrossRef]
11. Bellwood, P. *First Farmers: The Origins of Agricultural Societies*; Blackwell Publishing: Malden, MA, USA; Oxford, UK; Carlton, VIC, Australia, 2005.
12. Horsburgh, K.A.; McCoy, M.D. Dispersal, isolation, and interaction in the islands of Polynesia: A critical review of archaeological and genetic evidence. *Diversity* **2017**, *9*, 37. [CrossRef]
13. Oppenheimer, S. Out-of-Africa, the peopling of continents and islands: Tracing uniparental gene trees across the map. *Philos. Trans. R. Soc. B Biol. Sci.* **2012**, *367*, 770–784. [CrossRef] [PubMed]
14. Mirabal, S.; Herrera, K.J.; Gayden, T.; Regueiro, M.; Underhill, P.A.; Garcia-Bertrand, R.L.; Herrera, R.J. Increased Y-chromosome resolution of haplogroup O suggests genetic ties between the Ami aborigines of Taiwan and the Polynesian Islands of Samoa and Tonga. *Gene* **2012**, *492*, 339–348. [CrossRef] [PubMed]
15. Trejaut, A.J.; Poloni, E.S.; Yen, J.-C.; Lai, Y.-H.; Loo, J.-H.; Lee, C.-L.; He, C.-L.; Lin, M. Taiwan Y-chromosomal DNA variation and its relationship with Island Southeast Asia. *BMC Genet.* **2014**, *15*, 77. [CrossRef] [PubMed]
16. Wei, L.-A.; Yan, S.; Teo, Y.-I.; Huang, Y.-U.; Wang, L.-I.; Yu, G.; Saw, W.-O.; Ong, R.T.-W.; Lu, Y.; Zhang, C.; et al. Phylogeography of Y-chromosome haplogroup O3a2b2-N6 reveals patrilineal traces of Austronesian populations on the eastern coastal regions of Asia. *Public Libr. Sci. One* **2017**, *12*, e0175080. [CrossRef] [PubMed]
17. Mona, S.; Tommaseo-Ponzetta, M.; Brauer, S.; Sudoyo, H.; Marzuki, S.; Kayser, M. Patterns of Y-Chromosome Diversity Intersect with the Trans-New Guinea Hypothesis. *Mol. Biol. Evol.* **2007**, *24*, 2546–2555. [CrossRef] [PubMed]
18. Mona, S.; Grunz, K.E.; Brauer, S.; Pakendorf, B.; Castrì, L.; Sudoyo, H.; Marzuki, S.; Barnes, R.H.; Schmidtke, J.; Stoneking, M.; et al. Genetic Admixture History of Eastern Indonesia as Revealed by Y-Chromosome and Mitochondrial DNA Analysis. *Mol. Biol. Evol.* **2009**, *26*, 1865–1877. [CrossRef] [PubMed]
19. Karafet, T.M.; Hallmark, B.; Cox, M.; Sudoyo, H.; Downey, S.; Lansing, J.; Hammer, M.F. Major East-West Division Underlies Y Chromosome Stratification across Indonesia. *Mol. Biol. Evol.* **2010**, *27*, 1833–1844. [CrossRef] [PubMed]
20. Delfin, F.; Myles, S.; Choi, Y.; Hughes, D.; Illek, R.; van Oven, M.; Pakendorf, B.; Kayser, M.; Stoneking, M. Bridging Near and Remote Oceania: mtDNA and NRY Variation in the Solomon Islands. *Mol. Biol. Evol.* **2011**, *29*, 545–564. [CrossRef]
21. Donohue, M.; Tim Denham, T. Farming and language in Island Southeast Asia: Reframing Austronesian history. *Curr. Anthropol.* **2010**, *51*, 223–256. [CrossRef]
22. Blust, R. *The Austronesian Languages*, revised, ed.; Asia-Pacific Linguistics Research School of Pacific and Asian Studies, The Australian National University: Canberra, Australia, 2013. Available online: pacling.anu.edu.au/materials/Blust2013Austronesian.pdf (accessed on 27 February 2019).
23. Gaffney, D.; Summerhayes, G.R.; Luu, S.; Menzies, J.; Douglass, K.; Spitzer, M.; Bulmer, S. Small game hunting in montane rainforests: Specialised capture and broad spectrum foraging in the Late Pleistocene to Holocene New Guinea Highlands. *Quat. Sci. Rev.* **2021**, *253*, 106742. [CrossRef]
24. Denham, T.; Haberle, S.; Lentfer, C.; Fullagar, R.; Field, J.; Therin, M.; Porch, N.; Winsborough, B. Origins of Agriculture at Kuk Swamp in the Highlands of New Guinea. *Science* **2003**, *301*, 189–193. [CrossRef]
25. Schapper, A. Farming and the Trans-New Guinea family: A consideration. In *Language Dispersal beyond Farming*; Martine, R., Alexander, S., Eds.; John Benjamins Publishing Company: Amsterdam, The Netherlands, 2017; pp. 155–181.
26. Loy, D.E.; Plenderleith, L.J.; Sundararaman, S.A.; Liu, W.; Gruszczyk, J.; Chen, Y.-J.; Trimboli, S.; Learn, G.H.; MacLean, O.; Morgan, A.; et al. Evolutionary history of human Plasmodium vivax revealed by genome-wide analyses of related ape parasites. *Proc. Natl. Acad. Sci. USA* **2018**, *115*, E8450–E8459. [CrossRef]
27. Zhang, D.; Dong, G.; Wang, H.; Ren, X.; Ha, P.; Qiang, M.; Chen, F. History and possible mechanisms of prehistoric human migration to the Tibetan Plateau. *Sci. China Earth Sci.* **2016**, *59*, 1765–1778. [CrossRef]

28. Tianyi, W.; Kayser, B. High altitude adaptation in Tibetans. *High Alt. Med. Biol.* **2006**, *7*, 193–208.
29. Yang, J.; Jin, Z.-I.; Chen, J.; Huang, X.-I.; Li, X.; Liang, Y.-U.; Mao, J.-I.; Chen, X.; Zheng, Z.; Bakshi, A.; et al. Genetic signatures of high-altitude adaptations in Tibetans. *Proc. Natl. Acad. Sci. USA* **2017**, *114*, 4189–4194. [CrossRef] [PubMed]