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Genetics

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## Writing Assignment #4

Genetics is essential because it may ensure that particular groups of people, species, or populations can adapt to changing environmental conditions. Apart from dealing with environmental factors, genetic variety gives them the capacity to fend off new illnesses and outbreaks. Low genetic diversity, on the other hand, may make a species more vulnerable to biotic and abiotic stressors like illness and drought, putting it at danger of extinction in the long term. The human genome contains instructions for regulating gene expression, which differs from cell type to cell type and individual to individual. Denisovans are a mysterious species only known from ancient DNA samples and remnants of that DNA shared by ancient hominids and Homo sapiens via interbreeding. People who currently reside in Southeast Asian islands, Papua New Guinea, and Australia bear the brunt of their genetic mark. According to genetic data, the Philippine Negrito ethnic group has the greatest Denisovan heritage of any ethnic group. According to a new study, indigenous people known as the Ayta Magbukon derive about 5% of their DNA from Denisovans. Recent large-scale investigations have defined the genome's regulatory function across a wide range of cell types, each from a modest sample size. Understanding the activities of healthy tissues and the biological origins of complex characteristics and illnesses has been aided by measuring how gene regulation and expression differ between individuals. However, because these investigations were done on a small number of cell types that are easily accessible, their value in understanding regulatory biology and human health is restricted. We define patterns of tissue specificity, compare local and distal effects, and assess the functional characteristics of the genetic effects based on the discovered genetic effects. We also show how multi-tissue, multi-individual data may be utilized to discover genes and pathways that are impacted by human illness-associated variation, allowing for a mechanistic understanding of gene regulation and disease genetics. "Denisovans may have genetically encompassed H. luzonensis and two other fossil hominids found on different Southeast Asian islands, H. floresiensis on Flores and H. erectus on Java, Teixeira suspects. H. floresiensis, or hobbits, survived from at least 100,000 years ago to around 60,000 years ago (SN: 6/8/16). H. erectus arrived on Java about 1.6 million years ago and died out between 117,000 and 108,000 years ago." According to the research, Ayta Magbukon people had somewhat more Denisovan ancestry than other Philippine Negrito groups because they married with East Asian migrants to the island less often about 2,281 years ago. They matched the ancient DNA of

Denisovans and Neanderthals with that of 1,107 people from 118 ethnic groups in the Philippines, including 25 Negrito tribes. The DNA was then compared to that obtained earlier from modern-day Papua New Guinea highlanders and Indigenous Australians. This article relates to genetics because in virtually every situation, your gene version will raise or decrease your chances of a certain consequence such as being fat, but this outcome is not guaranteed. Other genetic and environmental factors, such as how much you eat and exercise, also contribute to your final outcome. The fragments remaining after this frenzy of molecular slicing would all be the same length if everyone's DNA was the same. However, there are repeating regions of DNA that differ significantly between people. As a result, the lengths of my chopped fragments are unlikely to be identical to yours. Scientists may state with high confidence that a match between a DNA profile obtained at a crime scene and the profile of a suspect is not due to chance by combining multiple of these variable sites in the genome. The likelihood of two unrelated persons sharing the same profile varies on how many variable DNA regions you utilize, but it's usually one in a few. Source:

- ENCODE Project Consortium. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *The Washington Post* 447, 799–816 (2007)
- J.C. Teixeira *et al.* Widespread Denisovan ancestry in Island Southeast Asia but no evidence of substantial super-archaic hominin admixture. *Nature Ecology & Evolution*. Vol. 5, May 2021, p. 616. doi: 10.1038/s41559-021-01408-0.