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Polygenic Influences and the Origins of Human Creativity

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Abstract

Though genome-wide association studies (GWAS) have identified specific genetic variants linked to creativity, it remains unclear if these variants are distributed evenly across global populations and what that implies about how biology and creative achievement interact. Comparing these variants across populations was important because population history, migration, and genetic drift shaped how creativity-linked alleles are distributed, offering insight into how biology may have subtly intersected with cultural expression. This study compared allele frequencies of twenty creativity-associated variants across East Asian, European, and African populations. Population data were pulled from the 1000 Genomes Project, accessed through the Ensembl genome browser (Allen, 2022), and gene expression data were pulled from the GTEx portal. A threshold of ten percent allele frequency difference was applied to ensure meaningful cross-continental contrasts were identified, and a stricter threshold of thirty percent was applied to explore the strongest contrasts. Nineteen out of twenty variants exceeded the ten-percent threshold between at least one comparison, while six out of twenty exceeded the thirty-percent threshold. This level of divergence indicated that creativity-linked variants were highly structured by population history rather than evenly distributed worldwide. Several variants, such as rs10223052-A and rs59841088-A, demonstrated a notable divergence across populations, particularly in brain-expressed and nerve-expressed genes tied to neurodevelopment and cognitive functions. These results supported the view of creativity as a polygenic trait, shaped by the cumulative contribution of numerous variants. Population-level genetic differences may have contributed, alongside culture and experiences, to the persistence of distinctive artistic traditions across human history.

Keywords: Creativity, Allele frequency, Population genetics, Art history, Neurogenetics, Cultural diversity

1. Introduction

Creativity, often celebrated as a hallmark of expression encompassing all forms of art, music, and innovation, is widely regarded as a universal yet culturally contingent feature that defines humanity. Across ancient civilizations, artistic expression has emerged in profoundly distinct forms, reflecting different regional values, access to materials, and ideas. East Asian art has traditionally prioritized harmony, balance, and naturalism, using techniques such as ink wash painting or calligraphy to emphasize suggestive minimalism and abstraction. In contrast, European art, particularly during the Renaissance, portrays realism, religious ideals, and illusionistic depth. Meanwhile, African cultures portray geometric patterns, symbolic motifs, and stylized representations, often incorporating these elements into ritual performances, music, or storytelling. These vastly divergent art forms suggest not only differences in artistic style but also possible variations in the cognitive and genetic processes that shape them (Clarke, 2006; The Metropolitan Museum of Art, 2000; Team, 2024).

While environmental influences such as education, cultural exposure, and socioeconomic opportunity play a role in shaping creative achievement, emerging evidence from the field of genetics has suggested that biological factors may also contribute to individual variance in creativity. Specifically, genome-wide association studies (GWAS), which scan the genome to identify links between variants and specific traits, have begun to identify specific single-nucleotide polymorphisms (SNPs), which are single base-pair changes in DNA that vary among individuals, associated with creative achievement (Abid, 2025; Cerezo, 2025; Du, 2024). Creativity was not explored as a philosophical principle in these studies. Rather, it was viewed as a quantifiable output such as writing a book, composing a piece of music, or producing art.

These findings raised important questions about the role of genetics in creativity, as well as how the distribution of creativity-linked genetic variants may have differed across global populations. Human gene alleles were not evenly distributed. Factors such as historical migrations, population bottlenecks, genetic drift, and adaptation had all shaped the allele frequencies we observe in modern groups. Therefore, variation of more complex traits such as creativity may have occurred at different rates between populations. Such variation provided the opportunity to explore whether genetic predispositions toward creative achievement might have aligned with cultural and historical differences in artistic expression.

Despite growing interest in the genetics of creativity, no prior research has compared the global distribution of creativity-associated variants across multiple continental groups. This gap established the novelty of the present study and motivated the cross-population analysis.

In this study, the primary focus was to compare the allele frequency distribution patterns of twenty creative achievement-associated variants between East Asian and European populations. The East Asian group included the Japanese in Tokyo (JPT) and the Han Chinese in Beijing (CHB), while the European group included the Iberian (IBS) and Tuscan (TSI) populations. These comparisons were chosen for their clear geographic and cultural distinctions and the richness of their artistic histories. The East Asian-European contrast also served as a logical baseline because these regions have well-studied, highly distinct artistic traditions that allow biological variation to be interpreted within deep cultural contexts. By examining whether genetic differences aligned with these diverse traditions, this study seeks to uncover how biological variation may have contributed to different cultural expressions.

However, the scope of this research extended beyond an East Asian-European binary. African populations, specifically the Mende in Sierra Leone (MSL) and the Yoruba in Ibadan (YRI), were included as reference groups to determine whether cross-continental divergence was broader than the baseline comparison and to contextualize allele frequency variation in groups with the deepest global genetic diversity. After gathering allele frequency data and completing the analysis, it was clear that these comparisons allowed for a unique interpretation of what such differences may have meant in understanding the biological underpinnings of creative diversity across human populations.

In summary, this study investigated whether the genetic make-up of creativity varied across global populations by analyzing allele frequencies and expression quantitative trait locus (eQTL) gene expression patterns in East Asian, European, and African groups. The purpose of this study was to explore how differences in creativity-associated variations influenced or explained the emergence of culturally distinct artistic traditions. Furthermore, it aimed to bridge neurobiology and art history as co-influencing fields of study and added to the broader discussion of how biology and culture worked together to shape the human capacity for creative expression.

2. Material and Methods

A genome-wide search for creativity-associated variants was conducted using the GWAS Catalog (Abid, 2025), a publicly available database of gene associations. The reported trait used for filtering was “creative achievement”, which was defined as tangible, real-world creative accomplishments. From the resulting dataset, the top twenty most statistically significant single-nucleotide polymorphisms (SNPs) were selected based on their p-values, all originating from one published GWAS study (Du, 2024). This study was selected because it is currently the only large-scale GWAS that has examined creative achievement using publicly accessible SNP-level data. Other creativity- or artistry-related genetic studies either did not meet genome-wide significance thresholds, did not release variant-level statistics, or examined broader personality constructs rather than creative output. For each SNP, the reported effect allele, its direction of effect on creative achievement (unit increase or decrease in creative achievement), and the allele frequencies of the six target populations were recorded in a data table. In addition to analyzing the frequencies, this study investigated whether each variant had an expression quantitative trait locus (eQTL) relationship with a gene using data from the GTEx portal (GTEx Consortium, 2015).

Data for allele frequencies were obtained from the 1000 Genomes Project and accessed through the Ensembl genome browser. The data were retrieved from Ensembl release 114, May 2025. Frequencies were examined for multiple subpopulations (JPT, CHB, IBS, TSI, MSL, YRI) to assess consistency within continental regions. However, the main analysis was conducted at the continental level for East Asian (EA), European (EU), and African (AFR) groups as this paper focused on comparing patterns in a broader sense. Subpopulation differences were addressed in the discussion section.

Each SNP was cross-referenced with the GTEx Portal to note potential expression quantitative loci (eQTL) relationships with genes and to assess their biological relevance to creative achievement. These eQTLs indicated whether a variant influenced expression levels of nearby genes, and this gene expression was analyzed with an emphasis on brain and nervous system tissues. These specific tissues were chosen for further analysis given their heightened relevance to cognitive function and creativity. Tissue-specific eQTLs were recorded and interpreted based on their known gene functions, with many of them being heavily involved in neural connectivity, brain development, and neuroplasticity. Not all eQTL results were recorded; only those that appeared most frequently and showed consistent associations across tissues were included in the final dataset.

To analyze meaningful differences, two thresholds were applied: a threshold of ten percent difference in effect allele frequency was utilized to identify general global variation, and a threshold of thirty percent was used to analyze the most pronounced divergences. These thresholds were selected based on prior work in population genetics demonstrating that differences of 10% or more often reflect non-random population structure shaped by migration, drift, or selection, while differences of 30% or more typically indicated strong differentiation across continental groups (e.g., 1000 Genomes Project Consortium, 2015). No multiple-testing correction or additional effect-size criterion was applied because the purpose of these thresholds was descriptive rather than inferential–they served as heuristic markers to classify allele frequency differences, not as statistical significance cutoffs. Variants with frequency differences greater than or equal to ten percent between any two continental populations were considered notable and further analyzed in the Results section. In practical terms, a ten-percent difference indicates a modest but meaningful shift in how common an allele is between populations, whereas a thirty-percent difference reflects a large divergence that is unlikely due to random fluctuations. Because this study relied on descriptive population comparisons rather than inferential statistics, no formal hypothesis tests or multiple-testing corrections were applied; instead, the ten-percent and thirty-percent thresholds served as practical effect-size markers indicating when differences were large enough to be biologically meaningful.

Table 1. eQTL Associations for Creativity-Associated Variants

Variant	eQTL Gene
rs1487441-G	No eQTL found
rs34034116-C	RBM6; ACTL11P; AMT; CAMKV
rs10223052-A	ERCC8; ELOVL7
rs448809-G	MEF2C-AS2; ENSG00000250377
rs68119843-A	No eQTL found
rs11678979-T	AFF3
rs11793831-G	No eQTL found
rs11691869-C	AFF3
rs9964724-C	ENSG00000285940
rs7581162-T	No eQTL found
rs62098013-G	DCC
rs12130762-G	PTGER3; ENSG00000269933
rs7601502-G	ERBB4
rs9537814-T	No eQTL found
rs531139717-C	No eQTL found
rs59841088	HAUS4; RBM23; PRMT5-DT; ENSG00000279656
rs2880052-G	CAMKMT
rs9783478-A	PPFIA2
rs72757186-T	No eQTL found
rs2240857-T	ENSG00000233264; GLCCI1

3. Results

All twenty variants analyzed are presented above in Table 2. Out of the top twenty most significant creative achievement-associated variants, nineteen displayed allele frequency fluctuations greater than ten percent between at least one pairwise comparison. Only the variant rs-12130762-G remained stable across all groups.

Table 2. Top 20 Creativity-Associated Variants Across Global Populations

Variant	Effect Allele (Direction)	P-Value
rs1487441-G	G: decrease	4 x 10^-23
rs34034116-C	C: increase	3 x 10^-18
rs10223052-A	A: increase	6 x 10-13
rs448809-G	G: increase	4 x 10^-12
rs68119843-A	A: decrease	5 x 10^-12
rs11678979-T	T: decrease	7 x 10^-12
rs11793831-G	G: decrease	4 x 10^-11
rs11691869-C	C: decrease	9 x 10^-11
rs9964724-C	C: decrease	2 x 10^-10
rs7581162-T	T: increase	2 x 10^-10
rs62098013-G	G: increase	4 x 10^-10
rs12130762-G	G: decrease	7 x 10^-10
rs7601502-G	G: increase	7 x 10^-10
rs9537814-T	T: increase	9 x 10^-10
rs531139717-C	C: increase	1 x 10^-9
rs59841088	A: decrease	2 x 10^-9
rs2880052-G	G: increase	2 x 10^-9
rs9783478-A	A: decrease	5 x 10^-9
rs72757186-T	T: decrease	5 x 10^-9
rs2240857-T	T: increase	6 x 10^-9

Six variants exceeded the thirty-percent threshold, demonstrating particularly strong divergences. rs11691869-C (AFF3) was more frequent in Africans (0.983) than East Asians (0.455). rs11793831-G (AFF3) was more common in Africans (0.904) than East Asians (0.533). rs10223052-A (ERCC8/ELOVL7) was more frequent in East Asians (0.513) compared to Africans (0.039). rs2880052-G (CAMKMT) showed a difference between East Asians (0.675) and Europeans (0.369). rs11678979-T (AFF3) was more frequent in Europeans (0.719) than East Asians (0.439). Finally, rs62098013-G (DCC) was nearly fixed in Africans (0.990) and East Asians (0.967) but lower in Europeans (0.657).

Several other variants displayed differences in the range of twenty to thirty percent. rs1487441-G differed between East Asians (0.578) and Africans (0.801). rs34034116-C (RBM6 and related genes) was more common in East Asians (0.879) than Europeans (0.579). rs68119843-A was more frequent in Africans (0.700) than East Asians (0.421). rs448809-G (MEF2C-AS2) was more common in Africans (0.672) than East Asians (0.393). rs9537814-T appeared more often in Africans (0.971) compared to Europeans (0.767).

The remaining variants displayed smaller but measurable divergences above ten percent across at least one population comparison. These included rs9964724-C, rs7581162-T, rs7601502-G (ERBB4), rs531139717-C, rs59841088-A (HAUS4/RBM23/PRMT5-DT), rs9783478-A (PFFIA2), rs72757186-T, and rs2240857-T

In summary, the dataset demonstrates a continuum of differentiation. The ten-percent threshold was used to identify wider divergences, while the thirty-percent threshold isolated six variants (rs11691869-C, rs11793831-G, rs11678979-T, rs10223052-A, rs2880052-G, and rs62098013-G) as the most significant divergences across populations for further analyses.

4. Discussion

The results of this study confirmed that genetic variants linked to creative achievement were not evenly distributed across human populations. Nearly all variants showed allele frequency differences exceeding ten percent, which suggests that genetic variations relevant to creativity were rampant, influenced and structured by population history. Furthermore, six of these variants exceeded an even stricter thirty-percent threshold, which demonstrated the strongest divergences with biological and environmental significance. These high-contrast variants were of particular interest as they mapped to genes with clear neural functions, suggesting biological pathways through which creativity may be influenced. These numerical differences represent absolute contrasts in effect-allele frequency between populations, measured as the difference in the proportion of chromosomes carrying the allele in each group. They serve as descriptive indicators of uneven distribution rather than causal evidence of how genetics influences creativity.

In East Asian and European populations, there were strong divergences in variants linked to maintaining and metabolizing the nervous system. For example, rs10223052-A (ERCC8 and ELOVL7) and rs2880052-G (CAMKMT) were much more prominent in East Asians compared to Europeans. ERCC8 played a role in transcription-coupled DNA repair, particularly in neurons under metabolic stress, while ELOVL7 extended fatty acid chains involved in neural membranes. (Distelmaier, 2025) CAMKMT methylated proteins involved in calcium signaling, which was a crucial process for synaptic plasticity (Database$_1$, 2025). Together, these genes supported cognitive endurance, learning efficiency, and adaptability. One possible interpretation was that these pathways conceptually aligned with artistic traditions in East Asia, which emphasized repetition, minimalism, and symbolism as seen in sumi-e ink paintings, Zen gardens, and calligraphy. (Team, 2024) In contrast, European populations showed lower frequencies of these variants and instead carried alleles more associated with intermediate or balanced neural regulation. (The Metropolitan Museum of Art, 2000) This finding could have paralleled artistic traditions in Europe that prioritized anatomical realism, scientific observation, and perspective paintings, as exemplified by Renaissance masters such as Michelangelo and Leonardo da Vinci.

African populations showed enrichment for AFF3 variants (rs11691869-C, rs11793831-G, rs11678979-T), which regulated transcription during neural development (Database$_2$, 2025). These variants exhibited the largest divergences in frequency, with rs11691869-C diverging by more than 0.5 between East Asians and Africans. AFF3 was involved in regulating gene expression in cortical neurons, suggesting a link to flexibility in brain wiring. The prevalence of these variants in African groups may have contributed to a deviation in cognitive tendency, orienting with artistic traditions that emphasized abstraction, ritualistic performances, improvisation, and oral storytelling. (Clarke, 2006) This higher prevalence aligned with artistic traditions such as Yoruba mask-making, Mende storytelling, and diverse rhythmic musical performances that integrated ritual and community participation. These high-contrast variants demonstrated the largest divergences, but creativity, like most complex traits, was unlikely to be influenced by a few large-effect loci alone.

Moderate variants also supported the understanding of creativity as a polygenic trait. Multiple SNPs, such as rs1487441-G, rs34034116-C, rs68119843-A, rs9964724-C, rs7581162-T, rs7601502-G, rs9537814-T, rs531139717-C, rs9783478-A, rs72757186-T, and rs2240857-T, displayed frequency differences in the ten- to twenty-five-percent range. While none were considered extremely significant as they did not exceed the thirty-percent threshold or presented strong eQTL associations in brain or nerve tissue, their presence reinforced the view that many smaller genes accumulated and interacted with cultural and environmental conditions. Taken together, these moderate variants affected and expanded the genetic interpretation of creativity, even if they were individually less significant. This

Table 3. Allele Frequencies for Creativity-Associated Variants (With Averages)

Variant	EA	EUR	AFR
rs1487441-G	JPT: 0.644 CHB: 0.586 AVG: 0.578	IBS: 0.495 TSI: 0.481 AVG: 0.491	MSL: 0.765 YRI: 0.796 AVG: 0.801
rs34034116-C	JPT: 0.827 CHB: 0.903 AVG: 0.879	IBS: 0.500 TSI: 0.603 AVG: 0.579	MSL: 0.718 YRI: 0.773 AVG: 0.745
rs10223052-A	JPT: 0.596 CHB: 0.539 AVG: 0.513	IBS: 0.318 TSI: 0.350 AVG:0.338	MSL: 0.018 YRI: 0.005 AVG: 0.039
rs448809-G	JPT: 0.529 CHB: 0.432 AVG: 0.393	IBS: 0.463 TSI: 0.519 AVG: 0.440	MSL: 0.653 YRI: 0.648 AVG: 0.672
rs68119843-A	JPT: 0.447 CHB: 0.432 AVG: 0.421	IBS: 0.453 TSI: 0.402 AVG: 0.418	MSL: 0.759 YRI: 0.755 AVG:0.700
rs11678979-T	JPT: 0.490 CHB: 0.422 AVG: 0.439	IBS: 0.701 TSI: 0.687 AVG: 0.719	MSL: 0.682 YRI: 0.769 AVG: 0.743
rs11793831-G	JPT: 0.538 CHB: 0.456 AVG: 0.533	IBS: 0.607 TSI: 0.640 AVG: 0.568	MSL: 0.935 YRI: 0.917 AVG: 0.904
rs11691869-C	JPT: 0.510 CHB: 0.447 AVG: 0.455	IBS: 0.654 TSI: 0.636 AVG: 0.648	MSL: 0.982 YRI: 0.991 AVG: 0.983
rs9964724-C	JPT: 0.202 CHB: 0.204 AVG: 0.203	IBS: 0.322 TSI: 0.374 AVG: 0.332	MSL: 0.418 YRI: 0.403 AVG: 0.409
rs7581162-T	JPT: 0.188 CHB: 0.301 AVG: 0.258	IBS: 0.626 TSI: 0.589 AVG: 0.575	MSL: 0.559 YRI: 0.403 AVG: 0.487
rs62098013-G	JPT: 0.962 CHB: 0.947 AVG:0.967	IBS: 0.631 TSI: 0.720 AVG: 0.657	MSL: 1.000 YRI: 1.000 AVG: 0.990
rs12130762-G	JPT: 0.995 CHB: 1.000 AVG: 0.999	IBS: 0.907 TSI: 0.944 AVG: 0.916	MSL: 1.000 YRI: 1.000 AVG: 0.999
rs7601502-G	JPT: 0.990 CHB: 0.956 AVG: 0.943	IBS: 0.836 TSI: 0.776 AVG: 0.742	MSL: 0.900 YRI: 0.940 AVG: 0.927
rs9537814-T	JPT: 0.837 CHB: 0.869 AVG: 0.896	IBS: 0.776 TSI: 0.790 AVG: 0.767	MSL: 0.976 YRI: 0.977 AVG: 0.971
rs531139717-C	JPT: 0.861 CHB: 0.879 AVG: 0.924	IBS: 0.752 TSI: 0.762 AVG: 0.714	MSL: 0.971 YRI: 0.986 AVG: 0.970
rs59841088	JPT: 0.837 CHB: 0.743 AVG:0.803	IBS: 0.617 TSI: 0.598 AVG: 0.604	MSL: 0.541 YRI: 0.532 AVG:0.555
rs2880052-G	JPT: 0.553 CHB: 0.660 AVG: 0.675	IBS: 0.397 TSI: 0.332 AVG: 0.369	MSL: 0.624 YRI: 0.764 AVG: 0.702
rs9783478-A	JPT: 0.375 CHB: 0.490 AVG: 0.473	IBS: 0.640 TSI: 0.668 AVG: 0.656	MSL: 0.341 YRI: 0.407 AVG: 0.415
rs72757186-T	AVG: 1.000	AVG: 0.750	AVG: 0.940
rs2240857-T	JPT: 0.788 CHB: 0.762 AVG: 0.750	IBS: 0.907 TSI: 0.897 AVG: 0.861	MSL: 0.853 YRI: 0.884 AVG: 0.895

observation mirrored patterns seen in other polygenic traits, such as height, intelligence, and educational attainment, where hundreds of variants of small effect size combined to influence a trait. Creativity likely followed a similar model, with large-effect variants setting a baseline and smaller variants fine-tuning the behavior. Additionally, these moderate SNPs may have interacted with cultural and environmental variables in ways that could not be captured by allele frequencies only. For example, the higher presence of rs34034116-C in East Asians may not have determined their creativity directly, but in the context of East Asian educational traditions reinforcing discipline, it may have amplified cultural pathways of expressiveness.

Europeans frequently held intermediate allele frequencies, often positioned between East Asian and African distributions. For example, variant rs59841088-A (HAUS4/RMB23/PRMT5-DT) was more common in East Asia (0.803) than in Europe (0.604), and less frequent in Africa (0.555). This intermediary position may have reflected Europe's demographic history as a crossroads of cultural and genetic synthesis, shaped by migration, trade, and intellectual exchanges across the Mediterranean, Silk Road, and later colonial networks. These historical interactions not only influenced the genetic backgrounds of settlers but also led to the emergence of hybrid artistic traditions. European art often drew influence from other regions; for instance, Renaissance art incorporated rediscovered classical Greek and Roman ideas alongside mathematical and astronomical advances transmitted by Islamic scholars. This history suggested that Europe's genetic profile corresponded with Europe's cultural blending, and that its creativity reflected both internal and external influences.

Though this study emphasized comparison on the continental level, variation on the subpopulation level added to this discussion of creativity as polygenic. For example, within East Asia, rs10223052-A was slightly higher in JPT (0.596) than CHB (0.539), and rs59841088-A was almost ten percent higher in JPT than CHB. Within Europe, rs11678979-T was marginally more prevalent in IBS (0.701) than TSI (0.687). Within Africa, internal groups displayed larger contrasts, which was consistent with the deeper population structure observed throughout African history. Specifically, the Yoruba in Ibadan (YRI) and the Mende in Sierra Leone (MSL) often differed substantially: rs2880052-G (CAMKMT) differed by ~0.14 between (YRI: 0.764, MSL: 0.624), and rs7581162-T differed by ~0.16 (YRI: 0.403, MSL: 0.559). These results demonstrated that within-continent heterogeneity, particularly in Africa, was equally substantial. The data also aligned with Africa's evolutionary history, as the continent contained the oldest and most diverse human lineages, whereas non-African groups were the result of founder effects and genetic bottlenecks. These contrasts show that relying on continental averages can mask meaningful structure within populations, and that some of the strongest genetic gradients occur within continents rather than between them.

Stable alleles such as rs12130762-G reinforced creativity as a universal trait. Despite the population-level allele frequency differences, some variants were observed globally, which was consistent with the role of creative achievement as a shared human capacity. The presence of conserved variants served as a reminder that though differences in allele frequencies may have nudged populations toward certain tendencies, creativity as a whole remained a fundamental part of the human condition. From the anthropological record, it was evident that art emerged in all known societies, from Paleolithic cave paintings in Europe to the symbolic mask carvings and figures in Africa to jade congs in East Asia.

Limitations of this study must also be acknowledged. First, data from the GWAS catalog represented statistical associations, not direct causation. The creative phenotype used, "creative achievement", encompassed observable outcomes such as producing art or writing a book, but it may not have captured all forms of creativity across cultures. Second, though this analysis averaged subpopulation frequencies to represent East Asian, European, and African groups to cover diversity in a broader sense, this approach inevitably masked the finer details that existed within each region. For example, African populations were especially diverse, and the subpopulation-level variation between Mende and Yoruba groups revealed noteworthy internal differences. Finally, it was undeniable that cultural, environmental, and historical influences played profound roles in influencing the emergence of art styles, meaning that genetics offered only part of the explanation.

Further research should expand to underrepresented populations in South Asia, the Americas, and Oceania to broaden the scope of analysis and capture a more global picture of creativity's genetic underpinnings. Incorporating epigenetic data could have helped clarify how environmental pressures, such as education, nutrition, and stress, altered gene expression connected with creativity. Longitudinal studies could have tracked how polygenic scores interact with lived experiences, helping to explain how creativity emerged and changed across a lifetime. Finally, interdisciplinary collaboration between geneticists, anthropologists, and art historians was essential as genes alone could not explain art. These results needed to be contextualized and responsibly interpreted to avoid deterministic misapplications.

Through these findings, broader implications arose. The uneven distribution of creative achievement-associated variants suggested that population genetics may have provided subtle predispositions that, in interaction with environment and culture, influenced the emergence of different artistic traditions across human history. While genetics was unable to account fully for artistic traditions alone, allele frequency differences may have helped explain why distinct creative modes of thinking (East Asian minimalism, European realism, and African abstraction) persisted across world regions into divergent styles observed today.

5. Conclusion

This study analyzed twenty genetic variants associated with creative achievement across East Asian, European, and African populations. Nineteen exceeded the ten-percent threshold, and six exceeded a stricter thirty-percent threshold. East Asian populations showed higher frequencies for variants related to neural metabolism and maintenance. African populations demonstrated higher frequencies for variants relevant to transcriptional regulation. European populations generally acted as an in-between group. Subpopulation-level variations further underscored the role of local demographic histories. Creativity remained a universal human trait, but its genetic makeup was globally unevenly distributed, which allowed us to better understand the diversity of artistic traditions worldwide.

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