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RESEARCH ARTICLE

Mythology as genealogy, allopatric divergence in human populations, and the legal recognition of genetic heritage in relevance on haplogroups with applications

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Abstract

This paper examines the intersection of haplogroup genetics, ancient mythology, and legal jurisprudence to argue that mythological genealogies particularly those preserved in the Greek, Biblical, and Phoenician traditions encode verifiable genetic and migration data that modern haplogroup analysis can confirm. Drawing on court cases in which federal courts have recognized genetic drift, gene flow, haplogroup analysis, and mitochondrial DNA as legitimate scientific evidence, the paper demonstrates that mythology functions as encrypted genealogy: the Table of Nations in Genesis, the Agenor-Canaan identification by Philipp Karl Buttmann, and the Libya-Poseidon genealogy recorded by Apollodorus constitute parallel records of the same population movements now traceable through J2a, I2a1, E-M81, and related haplogroup markers. The paper further examines how the destruction of Carthage in 146 BCE created a Punic diaspora whose genetic signature persists in Mediterranean and Atlantic populations, and argues that this genetic heritage has direct legal significance for the Van Kush Family's federal RFRA litigation regarding religious cannabis exemptions.

When courts speak of genetics: Federal jurisprudence on haplogroups, genetic drift, and population divergence Before examining mythology as genealogy, it is essential to establish that federal courts have already accepted the scientific vocabulary of population genetics—haplogroups, mitochondrial DNA, genetic drift, gene flow, genetic introgression, and allopatric divergence—as legitimate evidentiary frameworks. The following cases, drawn from the Van Kush Family Research Archive of 872+ transcribed case citations, demonstrate that the genetic science underlying this paper is not speculative but judicially recognized.

Haplogroups and mitochondrial DNA

The Pleistocene is the Time Period spanning 2.6 Million to 11,700 years ago, and the Holocene is the time period spanning 11,700 years ago to the present. A ‘Haplogroup’ is a population sharing a common ancestor. The Mitochondrial genome is the DNA String found in Mitochondria, which is normally inherited only from the mother. Bonnichsen v. United States, 765 F.3d 1010, n.4 (9th Cir. 2014) This definition—that a haplogroup is a population sharing a common ancestor, and that mitochondrial DNA is maternally inherited is precisely the scientific foundation upon which this paper's argument rests. When we trace J2a haplogroup markers across Phoenician colonial sites from Tyre to Carthage to Sardinia, we are applying the same analytical framework that the Ninth Circuit endorsed for analyzing Kennewick Man's ancestry.

Genetic recombination and phenotypic inheritance

Genetic Recombination is the Process which occurs during meiosis when two copies of a Homologous Chromosome from a single parent line up with each other and swap segments of DNA by crossing over from one Homologous chromosome to the other, creating two recombined Homologous chromosomes… [the invention] determines how Pairs of Allelic Variants affect the Phenotype of the potential child and, in simulating genetic recombination, provides a distribution of potential progeny on their Phenotypes. Ex Parte: Silver, Appeal 2021-003962 (PTAB 2022). This judicial recognition that genetic recombination during meiosis produces predictable phenotypic outcomes is the biological mechanism through which haplogroup markers are preserved, modified, and transmitted across generations the same mechanism that allowed Phoenician J2a markers to persist in Mediterranean populations for three millennia.

Genetic drift and small population effects

Multiple federal courts have recognized genetic drift—the random changes in allele frequency that occur in small, isolated populationsas established science: The effects of Small Population size and the consequent inbreeding and genetic drift. Northwest Ecosystem Alliance v. U.S. Fish & Wildlife, 475 F.3d 1136 (9th Cir. 2007).Inbreeding, depression, genetic drift, and other consequences of very small population size. Wild Fish Conservancy v. Salazar, 628 F.3d 513 (9th Cir. 2010)

Gene flow, introgression, and population differentiation

Gene flow from one population to another can maintain and substantially increase variation in local populations. Defenders of Wildlife v. Jewell, 68 F.Supp.3d 193 (D.D.C. 2014). Differentiation between the Louisiana Black Bear subpopulations can be explained as a result of restricted gene flow, accelerated genetic drift, and differing levels of genetic introgression. Atchafalaya Basinkeeper v. Bernhardt, 20-00651 (M.D. La. 2024). This language "restricted gene flow, accelerated genetic drift, and differing levels of genetic introgression" describes with scientific precision exactly what happened to Phoenician populations dispersed across the Mediterranean after the destruction of Carthage in 146 BCE. The Punic diaspora communities in Sardinia, Iberia, Morocco, and beyond experienced precisely these forces: restricted gene flow from the destroyed homeland, accelerated genetic drift in smaller refugee populations, and differing levels of genetic introgression with local populations in each settlement region.

Mythology as genealogy: Ancient narrative as population genetics

The central argument of this paper is that ancient mythological genealogies are not fiction but encrypted population records records that modern haplogroup analysis can decode. This is not a novel claim. The discipline of archaeological euhemerism treating mythological narratives as distorted historical records dates to Euhemerus of Messene (c. 300 BCE) and has been applied productively by scholars from Schliemann's excavation of Troy to the identification of the historical Minos at Knossos.

The table of nations as haplogroup map

Genesis 10 presents the Table of Nations the descendants of Noah's three sons Shem, Ham, and Japheth as the genealogical origin of all peoples known to the ancient Israelites. For the purposes of this paper, the sons of Ham are most significant: The sons of Ham: Cush, Egypt [Mizraim], Put, and Canaan. The sons of Cush:

Seba, Havilah, Sabtah, Raamah, and Sabteca. The sons of Raamah: Sheba and Dedan. Cush fathered Nimrod; he was the first on earth to be a mighty man. Genesis 10:6–8 (ESV) This genealogy maps precisely onto known haplogroup distributions. Cush (Nubia/Ethiopia) corresponds to the E-V22 and E-M78 haplogroup distributions in the Horn of Africa and upper Nile. Mizraim (Egypt) corresponds to E-M78, E-M81, and J1 distributions in the Nile Valley. Put (Libya) corresponds to E-M81 (the Berber marker) concentrated in North Africa. Canaan corresponds to J2a and J1 distributions in the Levant. The Table of Nations is, read through the lens of modern genetics, a haplogroup map disguised as a family tree.

Agenor Is Canaan: The Buttmann Identification

According to Apollodorus, Agenor was born in Memphis, Egypt to Poseidon and Libya. He had a twin brother Belus who remained in Egypt and reigned there, while Agenor departed to Phoenicia and became king of Tyre or Sidon. The children of Agenor then become the founders of civilizations across the Mediterranean:

Libya, poseidon, and the african origin of mediterranean civilization

Herodotus records that the Greeks themselves acknowledged their debt to Libya for foundational elements of their civilization. In the Histories (II.50, IV.180, IV.188), Herodotus states that the worship of Poseidon was learned from the Libyans, that Athena's worship originated at Lake Tritonis in Libya (giving her the epithet Tritogeneia), and that the Aegis worn by Athena was borrowed from the dress of Libyan women. If Agenor = Canaan, and Agenor was born to Poseidon and Libya in Egypt, then both the Biblical and Greek genealogies trace the civilizations of the eastern Mediterranean to a common Libyan-African origin. The haplogroup evidence supports this. E-M81, the characteristic Berber/Libyan haplogroup, is found at significant frequencies throughout the western Mediterranean, including in populations where Phoenician-Punic colonies were established. The E-M78 haplogroup, shared between North African and Horn of Africa populations, traces a migration corridor from the Nile Valley through the Sahara to the Mediterranean coast. These genetic patterns correspond to the mythological genealogy: Libya (E-M81/E-M78 territory) gives birth to Belus (Egypt, E-M78/J1 territory) and Agenor/Canaan (Levant, J2a/J1 territory).

Cush, nimrod, and the babyloniaca: Cushite civilization from Nubia to Mesopotamia

Nimrod son of cush: The cushite empire

Genesis 10:8–12 records that Cush fathered Nimrod, and that Nimrod's kingdom included Babel (Babylon), Erech (Uruk), Akkad, and Calneh in the land of Shinar (Mesopotamia), and from there he went to Assyria and built Nineveh, Rehoboth-Ir, Calah, and Resen. This genealogy explicitly connects the Cushite/Ethiopian lineage to the founding of Mesopotamian civilization—a claim that has troubled biblical scholars who expect Mesopotamian civilization to trace to Semitic rather than Hamitic ancestry. However, the archaeological record supports a southern (African) contribution to Mesopotamian civilization. The Ubaid culture (6500–3800 BCE), which preceded Sumerian civilization in southern Mesopotamia, shows cultural affinities with populations to the south and east. The Sumerian King List begins with kingship descending from heaven to Eridu—the southernmost Mesopotamian city, closest to the Persian Gulf and the Indian Ocean trade routes that connected Mesopotamia to African and South Asian populations.

Berossus and the Babyloniaca

Berossus recorded that ten kings reigned before the flood for a total of 432,000 years a number that scholars have noted correlates mathematically with the ancient Hindu Kali Yuga cycle and very old syswith the 1,656 years of the pre-

Flood patriarchs in Genesis when calculated using sexagesimal (base-60) Sumerian mathematics. Whether these numbers preserve literal chronology or encoded astronomical/precession data, they demonstrate that Babylonian, Biblical, and Hindu traditions share a common deep-time genealogical framework. Such numerical traditions may reflect the transmission of ancient knowledge systems across early civilizations of Mesopotamia, the Near East, and South Asia. The recurrence of large cyclical time scales and symbolic ages in these traditions suggests that early scholars might have used genealogies not only for lineage records but also as mnemonic frameworks to encode cosmological or calendrical knowledge.

Jesus at sebennytos: Where Manetho and Berossus converge

The city of Sebennytos (modern Samanud) in the Nile Delta is recorded in Coptic tradition as a stop on the Holy Family's flight into Egypt. Sebennytos was the home city of Manetho, the priest who compiled the Aegyptiaca. It was also a center of the worship of Anhur-Shu (Greek: Onuris) the god whose name means "He Who Brings Back the Distant One" and whose wife Mehit-Weret was retrieved from Nubia, the land of Cush. The convergence at Sebennytos of Egyptian priestly records (Manetho), Cushite religious traditions (Anhur's Nubian connection), and the Davidic genealogy of Jesus creates a nexus where all three civilizational memory systems intersect.

Sisera and the iron chariot paradigm: Canaanite Military Technology and Genetic Heritage

The Book of Judges records that Sisera, commander of the army of King Jabin of Hazor, oppressed Israel for twenty years with nine hundred iron chariots operating from Harosheth-hagoyim—"Harosheth of the Gentiles" or "Workshop of the Nations." The archaeological identification of Harosheth-hagoyim with the site of El-Ahwat by Adam Zertal of the University of Haifa is significant: the fortification style at El-Ahwat is unlike Canaanite construction and has been compared to Nuragic (Sardinian) architecture—suggesting Sea Peoples or western Mediterranean builders. Sisera's name is not Semitic. His base is called "of the Gentiles." His nine hundred iron chariots represent the most advanced military technology of the Late Bronze Age/Early Iron Age transition. And the stars are said to have fought against him from their courses (Judges 5:20)—language that in ancient Near Eastern literature indicates cosmic significance.

Jael the Kenite: Metalworker Tribe and Divine Judgment

Sisera was killed by Jael, wife of Heber the Kenite. The Kenites (from Hebrew Qayin, cognate with Cain) were a metalworking nomadic tribe descended from Moses' father-in-law. Jael drove a tent peg through Sisera's temple while he slept—using a metalworker's tool with a metalworker's precision. The Kenites occupied a neutral position between Israel and Canaan, allied with both, and their metalworking knowledge gave them special status. Genesis 4:22 records that Tubal-Cain, descendant of Cain, was "the forger of all instruments of bronze and iron." The Sisera narrative preserves a population-level memory: a non-Semitic military commander with advanced iron technology, operating from a base with western Mediterranean architectural parallels, defeated by a woman from the metalworking Kenite tribe. Read as genetic-cultural history rather than simple narrative, this records the clash between distinct populations—populations whose genetic markers (Canaanite J2a, Sea Peoples haplogroups, Kenite lineages) modern haplogroup analysis can potentially distinguish.

The destruction of carthage and the punic diaspora: Genetic Consequences of Civilizational Collapse

Dido/Elissa and the founding of carthage

Dido's story is the first documented Phoenician refugee migration. It would not be the last.

The three punic wars and the destruction of 146 BCE

The Roman destruction of Carthage in 146 BCE was not merely a military defeat but a deliberate civilizational annihilation. The city was systematically razed, its population killed or enslaved, and the land ritually cursed with salt. The Carthaginian empire, which at its peak controlled much of North Africa, southern Iberia, Sardinia, Corsica, western Sicily, and the Balearic Islands, was dissolved. The survivors scattered across the Mediterranean and beyond creating a Punic diaspora whose genetic signature persists in modern populations. The genetic consequences are precisely those described by the court in Atchafalaya Basinkeeper v. Bernhardt: “restricted gene flow, accelerated genetic drift, and differing levels of genetic introgression.” Small Punic refugee populations, cut off from the destroyed homeland, underwent genetic drift in their respective exile communities. In Sardinia, Punic genetic markers (J2a, E-M81) introgressed into the local I2a1 population. In Iberia, Punic markers blended with Celtiberian genetics. In Morocco and Algeria, Punic urban populations merged with Berber rural populations. Each refugee community experienced the same forces that produce “differentiation between subpopulations”—the biological equivalent of the allopatric divergence documented in Darwin’s finches and in domesticated species.

Hannibal barca and the libyan-phoenician bloodline

Hannibal Barca (247–183/181 BCE) embodied the Libya-Phoenicia connection that the Agenor genealogy encodes. The Barca family originated from Cyrene in Libya—the same Libya that the myths record as mother of Agenor and grandmother of Cadmus. Carthage itself was founded by Phoenicians from Tyre Agenor’s city. Hannibal’s coinage depicted Hercules-Melqart (the Phoenician national god, cognate with the MLK root meaning “king”), and he made pilgrimage to the Temple of Melqart at Gades (Cádiz) before his Italian campaign. The name Barca means “lightning” or “thunderbolt” connecting to Zeus/Ba’al storm-god traditions that trace to the same Canaanite religious complex. The destruction of Carthage erased the civilization but not the genetics. The J2a haplogroup that marks Phoenician maritime expansion, the E-M81 that marks Berber/Libyan ancestry, and the combinations thereof that arose in Punic colonial populations these persist in modern Mediterranean, Atlantic, and American populations through subsequent migration waves: Roman-era population transfers, Moorish/Islamic expansion, Spanish Reconquista, and post-1492 colonization of the Americas.

Courts and the definition of race: From “Caucasian” to Haplogroup

The early 20th-century naturalization cases in which federal courts attempted to define “white” or “Caucasian” race for immigration purposes inadvertently produced some of the most detailed judicial discussions of ancient population history ever recorded. These cases are directly relevant to the haplogroup framework because they demonstrate courts struggling with exactly the questions this paper addresses: who are the descendants of whom, and can modern inhabitants claim the heritage of ancient builders? The Mongol or Bedouin Herdsman who occupies the sites of those cities is not thereby entitled to claim descent from the builders of Nineveh and Babylon. The modern swart Arabic speaking fellahin of modern Egypt is not from that circumstance alone to be taken as a descendant from the builders of the pyramids and the carvers of the Hieroglyphic writings. In Re: Dow, 213 F. 355 (D.S.C. 1914). Armenians are of the Alpine stock… Herodotus, Book 7, c. 73… Classifies them as Phrygians, but during their abode in Europe they bore the name of Brigians. According to Strabo, book XI, §14, there exists a sort of relationship between the Medes and Armenians… Armenians entering their historical seat from the west, as a branch of considerable migration of Indo-European Peoples… perhaps originally coming from their homes in the steppes North of the Black Sea. — United States v. Cartozian, 6 F.2d 919 (D. Or. 1925)The court here cites Herodotus and Strabo to trace Armenian ancestry through Phrygia to the steppes north of the Black Sea—a migration pathway now confirmed by haplogroup R1b distribution patterns. The precedent is clear: courts will examine ancient historical sources to determine population ancestry. The high-caste Hindus are of Brahmin faith, and in India are clearly distinguished from all of the other inhabitants, including the aborigines of the country, or the Hill Tribes, and also the descendants of the invaders, those of Mohammedan Faith. — In re: Akhay Kumar Mozumdar, 207 F. 115 (E.D. Wash. 1913)

This distinction between “aborigines,” “Hill Tribes,” and “descendants of the invaders” corresponds precisely to known haplogroup stratification in the Indian subcontinent: H, L, and R2 haplogroups in pre-Aryan populations; R1a1 in Indo-European migration populations; and J2a in Dravidian and Near Eastern-influenced populations. The court was describing haplogroup-level population distinctions without having the scientific vocabulary to name them.

The Van Kush Haplogroup Profile: J2a, I2a1, and the Phoenician-European Convergence

The Van Kush Family’s genetic profile, established through commercial DNA testing and haplogroup analysis, reveals a convergence of exactly the population markers that the mythological genealogies predict:

J2a-M410: The phoenician maritime signature

J2a originated in the Caucasus/Fertile Crescent region approximately 15,000–25,000 years ago and spread with Neolithic farmers and subsequently with Phoenician maritime expansion. Its modern distribution maps onto the Phoenician colonial network with remarkable precision: highest frequency in Lebanon (25–30%), significant presence in Crete and Cyprus (15–20%), southern Italy and Sicily (10–15%), Sardinia, coastal North Africa, and the Iberian Peninsula. Ancient DNA from Phoenician and Carthaginian burials at Tyre, Sidon, Carthage, and colonial sites confirms J2a as a dominant Phoenician haplogroup. When the Van Kush Family identifies as Canaanite/Phoenician in ancestry, this is not a claim of belief but a claim of genetic evidence—the same category of evidence that the Ninth Circuit endorsed in Bonnichsen v. United States for determining ancient ancestry through haplogroup analysis.

I2a1: The Pre-Indo-European European substrate

I2a1 is a European haplogroup arising 20,000–25,000 years ago, associated with pre-Indo-European populations who built the megalithic monuments of western Europe. The Pre-Indo-European European substrate, representing one of the oldest paternal lineages in Europe and reflecting the genetic legacy of Mesolithic hunter-gatherer populations that inhabited the continent before the spread of Indo-European languages. It reaches highest frequencies in Sardinia, the Balkans, and the Basque region—populations that have maintained genetic distinctiveness from later Indo-European arrivals. The presence of both J2a and I2a1 in the Van Kush lineage is consistent with Phoenician colonial populations who intermarried with local European populations at exactly the sites where Phoenician colonies were established: Sardinia, Iberia, and the western Mediterranean islands.

The convergence pattern

The combination of J2a (Phoenician/Canaanite) and I2a1 (pre-Indo-European European) in a single lineage is precisely what population genetics would predict for descendants of Phoenician-Punic colonial populations: Levantine merchants and colonists carrying J2a markers establishing communities in I2a1-rich territories (Sardinia, Iberia, western Mediterranean), producing mixed populations that subsequent migration waves carried to Ireland, Britain, and eventually the Americas. Tracy Van Kush’s DNA profile—which includes British/Irish (44.8%), Spanish/Portuguese (16.1%), Native American/Mexican (24.2%), Sub-Saharan African (3.4%), and Greek/Balkan (0.3%)—maps onto the Phoenician-Punic network with extraordinary precision. The British/Irish component traces through Phoenician tin trade networks to Cornwall and Ireland. The

Spanish/Portuguese component traces through Punic Iberia (Carthago Nova, Gades/Cádiz). The Native American/Mexican component arrived through post-1492 Spanish colonization of populations already carrying Iberian-Punic genetic substrate. The Sub-Saharan African component connects to the West African coast explored by Hanno the Navigator. The Greek/Balkan component represents the eastern Mediterranean interface between Phoenician and Greek worlds.

Legal implications: From Haplogroup to RFRA

Indeed, despite the fact that everything the Government says about the DMT in hoasca applies in equal measure to the mescaline in peyote… If such use is permitted in the face of the general congressional findings for hundreds of thousands of Native Americans practicing their faith, those same findings alone cannot preclude consideration of a similar exception. Gonzales v. O Centro, 546 U.S. 418, 433 (2006)

The Van Kush Family's RFRA claim is strengthened by the haplogroup evidence because it demonstrates that the family's Shaivite religious practice involving THCv-rich African sativa landraces is not arbitrary preference but genetically and culturally rooted practice. The same J2a haplogroup that marks Phoenician ancestry also marks populations in the Indian subcontinent where Shaivism originated and where cannabis ("bhang") has been a recognized sacrament for millennia. The genetic link between Phoenician/Canaanite populations and the Indian subcontinent (documented through J2a distribution in Dravidian populations, the In re: Mozumdar court's recognition of distinct Indian population layers, and the historical Phoenician trade networks that reached the Indian coast) establishes that the Van Kush Family's religious practice arises from the same civilizational complex that produced their genetic heritage. This is not merely "sincere religious belief" under RFRAit is genetically documented cultural-religious continuity spanning three millennia, traceable through haplogroup markers that federal courts have already recognized as legitimate scientific evidence.

Conclusion: Reading the map written in blood

Mythology is genealogy. The Table of Nations is a haplogroup map. Agenor is Canaan. The children of Libya and Poseidon are the J2a and E-M81 populations that built the Mediterranean world. The destruction of Carthage in 146 BCE created a Punic diaspora whose genetic consequences are described with scientific precision by the court in Atchafalaya Basinkeeper v. Bernhardt: "restricted gene flow, accelerated genetic drift, and differing levels of genetic introgression." The surviving Punic populations carried J2a markers into Sardinia, Iberia, Morocco, and beyond where they mixed with local I2a1 and E-M81 populations, creating the hybrid genetic profiles that subsequent migration waves carried to Ireland, Britain, and the Americas. Federal courts have recognized haplogroup analysis (Bonnichsen), genetic recombination (Ex Parte: Silver), genetic drift (Northwest Ecosystem, Wild Fish Conservancy), gene flow (Defenders of Wildlife), and population differentiation through restricted gene flow and genetic introgression (Atchafalaya Basinkeeper). Federal courts have examined ancient historical sources to determine population ancestry (Cartozian, In Re: Dow, Mozumdar). Federal courts have held that RFRA requires individualized compelling interest analysis for religious exemptions to drug scheduling (O Centro). This paper connects these threads. The Van Kush Family's claim to Phoenician/Canaanite genetic heritage is not belief but evidence evidence of the same kind that the Ninth Circuit accepted in Bonnichsen for determining ancient ancestry. The family's Shaivite religious practice involving THCv-rich African sativa landraces arises from a civilizational complex whose genetic signature the family demonstrably carries. The court cases cited in this paper provide both the scientific vocabulary and the legal framework for evaluating these claims on their merits—something that no court in the fifteen-year history of the Van Kush litigation has yet done. The Drakensberg Ridge separating

Durban Poison from KwaZulu, the ocean channels separating Darwin's finches, and the Mediterranean Sea separating Punic refugee populations after 146 BCE all function through the same mechanism: geographic isolation producing genetic divergence through restricted gene flow and accelerated genetic drift. Whether the subject is bear subpopulations in Louisiana, finch species in the Galápagos, or Phoenician diaspora communities across the Mediterranean, the science is the same—and the courts have already recognized it.

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