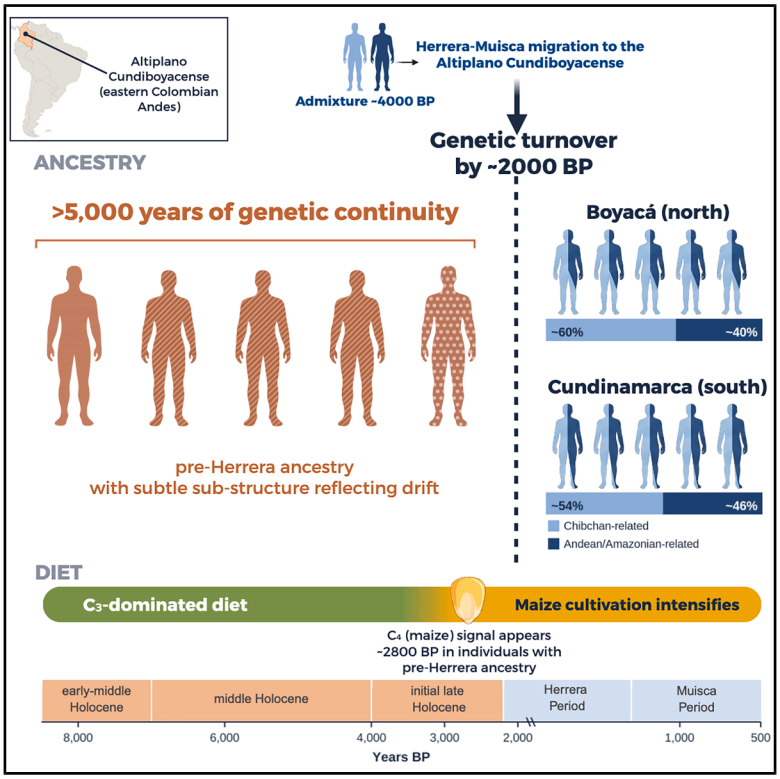
Cell

Subsistence transition preceded population turnover in the eastern Colombian Andes

Graphical abstract



Highlights

- 212 ancient genomes span 7,000 years in the eastern Colombian Andes
- Pre-Herrera genetic continuity for more than 5,000 years with no external gene flow
- C_4-enriched diets detected ~2,800 BP are decoupled from later population replacement
- People with Chibchan/Amazonian-Andean ancestry replaced the local gene pool by ~2,000 BP

Authors

Kendra Sirak, Miguel Delgado, Angélica Viviana Triana Vega, ..., Nadin Rohland, Lars Fehren-Schmitz, David Reich

Correspondence

kendra_sirak@fas.harvard.edu (K.S.), medelgado@unicauca.edu.co (M.D.), reich@genetics.med.harvard.edu (D.R.)

In brief

Ancient DNA data and stable isotope data from the eastern Colombian Andes reveal that C_4-enriched resources were incorporated into local food webs during five millennia of genetic continuity and that a later population turnover introduced people with ancestry admixed between that found in Chibchan-related groups and that found at the Amazonian-Andean interface.

Sirak et al., 2027, Cell *190*, 1–15
January 21, 2027 © 2026 Elsevier Inc. All rights are reserved, including those for text and data mining, AI training, and similar technologies.
https://doi.org/10.1016/j.cell.2026.10.010

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

Cell

CellPress

Article

Subsistence transition preceded population turnover in the eastern Colombian Andes

Kendra Sirak,[1,2,21,*] Miguel Delgado,[3,4,5,*] Angélica Viviana Triana Vega,[6] Sebastián Rivas,[7] Pedro Argüello,[8] Ana María Boada,[9] Javier Rivera-Sandoval,[10] Germán Peña,[11] Carl Langebaek,[12] Juan Pablo Ospina,[12] Sonia Archila,[12] Saúl Alberto Torres Orjuela,[12] Martha Beatriz Mejía Cano,[12] Freddy Rodríguez Saza,[13] Alison Barton,[1,2] Kim Callan,[2,14] Elizabeth Curtis,[2,14] Trudi Frost,[2,14] Lora Iliev,[2,14] Aisling Kearns,[2] Jack Kellogg,[2,14] Ann Marie Lawson,[2,14] Lijun Qiu,[2,14] J. Noah Workman,[2] Matthew Mah,[2,14,15] Mariam Nawaz,[2,14] Gregory Soos,[2,14] Alexander Cherkinsky,[16] Carla S. Hadden,[16] Keith M. Prufer,[17,18] Swapan Mallick,[2,14,15] Nadin Rohland,[2] Lars Fehren-Schmitz,[19,20] and David Reich[1,2,14,15,*]

[1]Department of Human Evolutionary Biology, Harvard University, Cambridge, MA 02138, USA
[2]Department of Genetics, Harvard Medical School, Boston, MA 02115, USA
[3]Departamento de Antropología, Facultad de Ciencias Humanas y Sociales, Universidad del Cauca, Popayán, Colombia
[4]Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Buenos Aires, República Argentina
[5]División Antropología, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, La Plata, República Argentina
[6]Instituto de Geología, Universidad Nacional Autónoma de México, Mexico City, Mexico
[7]Sistema de Cultura, Arte, y Patrimonio, UNIMINUTO, Bogotá, Colombia
[8]Escuela de Ciencias Sociales, Universidad Pedagógica y Tecnológica de Colombia, Tunja, Colombia
[9]Department of Anthropology, University of Pittsburgh, Pittsburgh, PA 15260, USA
[10]Departamento de Antropología, Universidad Nacional de Colombia, 111321 Bogotá, Colombia
[11]Instituto de Ciencias Naturales, Universidad Nacional de Colombia, 111321 Bogotá, Colombia
[12]Departamento de Antropología, Universidad de los Andes, 111711 Bogotá, Colombia
[13]PhyloGenomicsUD, Grupo de Investigación MATTOPO, Programa Académico de Biología, Facultad de Ciencias Matemáticas y Naturales, Universidad Distrital Francisco José de Caldas, Bogotá, Colombia
[14]Howard Hughes Medical Institute, Harvard Medical School, Boston, MA 02115, USA
[15]Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA
[16]Center for Applied Isotope Studies, University of Georgia, Athens, GA 30602, USA
[17]Department of Anthropology, University of New Mexico, Albuquerque, NM 87131, USA
[18]Center for Stable Isotopes, University of New Mexico, Albuquerque, NM 87131, USA
[19]UCSC Paleogenomics, Department of Anthropology, University of California, Santa Cruz, Santa Cruz, CA 95064, USA
[20]University of California, Santa Cruz Genomics Institute, University of California, Santa Cruz, Santa Cruz, CA 95064, USA
[21]Lead contact
*Correspondence: kendra_sirak@fas.harvard.edu (K.S.), medelgado@unicauca.edu.co (M.D.), reich@genetics.med.harvard.edu (D.R.)
https://doi.org/10.1016/j.cell.2026.10.010

SUMMARY

The Altiplano Cundiboyacense in the eastern Colombian Andes preserves one of the Americas' most continuous archaeological sequences, recording cultural and demographic change. We generated genome-wide data from 212 individuals spanning over 7,000 years, including early-middle and middle Holocene hunter-gatherers, initial late Holocene groups with mixed economies and the earliest isotopic evidence of maize consumption, and increasingly sedentary Herrera and Muisca populations. Individuals predating the Herrera Period form a lineage that persisted for five millennia, structured by drift in small groups without external gene flow. Two individuals dating ~2,800 years before present (BP) retain autochthonous ancestry while showing isotopic signatures consistent with maize consumption, decoupling subsistence change from population replacement. The emergence of Herrera culture ~2,200 BP coincided with a sharp genetic break by ~2,000 BP, which reflects migration by people descended from admixture ~4,000 BP between groups with Chibchan- and Amazonian-Andean-related ancestries. Herrera and Muisca Period individuals show north-south genetic substructure paralleling archaeological differentiation.

All rights are reserved, including those for text and data mining, AI training, and similar technologies.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

INTRODUCTION

Northwest South America is the main gateway into the continent from Central America and has been an important setting for demographic and cultural transformations throughout the Holocene. Within this region, some of the best-documented archaeological sequences are found in present-day Colombia where human occupation is documented by the late Pleistocene (~13,000 years before present, BP) when groups equipped with diverse lithic technologies and broad-spectrum economies exploited the open environments that formed during the transition from a warm and wet climate to cooler and drier conditions.[1–9] Over time, they settled diverse landscapes including the coastal Caribbean lowlands, the Orinoco and Amazon River basins, the inter-Andean valleys, and the Altiplano Cundiboyacense.

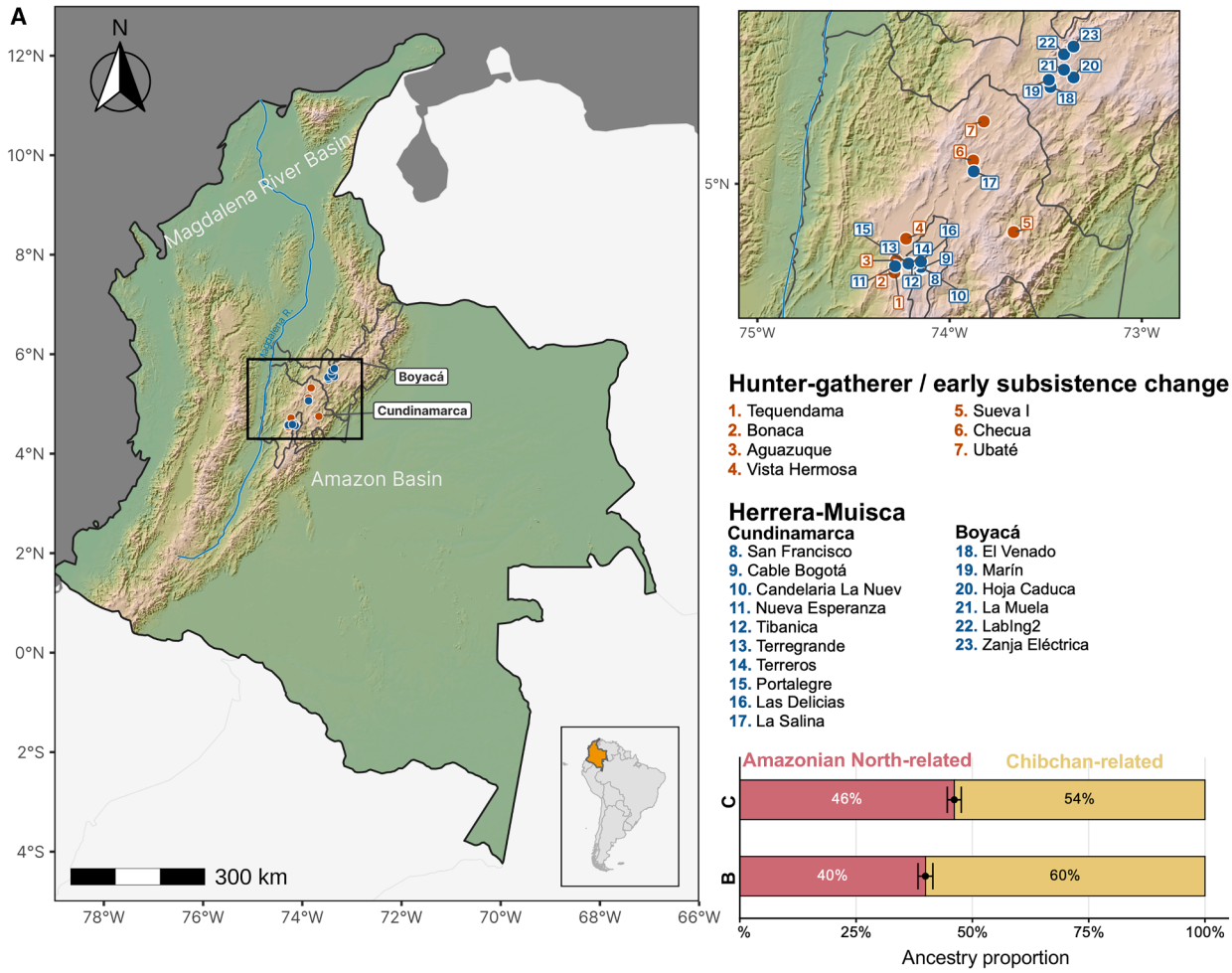
The Altiplano Cundiboyacense—a high-altitude plateau in the Eastern Cordillera of the northern Andes that includes the Sabana de Bogotá in the south and the highlands of Boyacá in the north—has archaeological evidence of human habitation since the late Pleistocene,[4,5,10,11] although the earliest skeletal remains date to the early-middle Holocene (10,000–7,000 BP). This was a period of climatic amelioration that may have fostered demographic expansion, generalized diets and economies, and interregional exchange among hunter-gatherer groups.[1,6,12–14] People relied mostly on C_3 plants that dominated highland Andean environments with flexible use of animal protein.[13,15,16] Warmer and drier conditions during the middle Holocene (7,000–4,000 BP, the hypsithermal interval) have been linked to the fragmentation of forested areas and possible demographic contraction and dispersals of resident hunter-gatherers.[12,17] Zooarchaeological[18] and isotopic[13] evidence indicates a continued exploitation of C_3 plants and an increased emphasis on guinea pig (*Cavia* sp.) and to a lesser extent white-tailed deer (*Odocoileus virginianus*). Archaeobotanical evidence from middle Holocene sites including Checua, Aguazuque, and Tequendama (Data S1, section 1) documents a broad-spectrum subsistence economy centered on high-Andean tubers and legumes, with limited incorporation of maize (*Zea mays*) at Checua evidenced by starch grains recovered from plant-processing tools and human dental calculus.[19] The cooler and wetter conditions of the early initial late Holocene (4,000–2,500 BP) facilitated shifts in subsistence practices, which included the earliest isotopic evidence of C_4-enriched resources in human diets.[1,8,13,20–22] Some research has proposed population continuity from the late Pleistocene through the arrival of sedentary farmers on the Altiplano Cundiboyacense in the later initial late Holocene (~2,200 BP), citing the persistence of the Abriense lithic industry and attributing craniodental changes to *in situ* adaptation.[21,23–28] Other research suggests that non-local people migrated to the region during the middle Holocene and mediated dietary shifts and craniofacial changes.[1,13,17,22,29,30] Exchange networks linking the Sabana de Bogotá with the Middle Magdalena Valley, Atlantic coast, Cauca Valley, and southwestern Colombia could have been conduits for cultural transformation and gene flow,[15,17,23,31,32] while the appearance of C_4-enriched resources in local food webs could reflect population dispersals across these networks.[29]

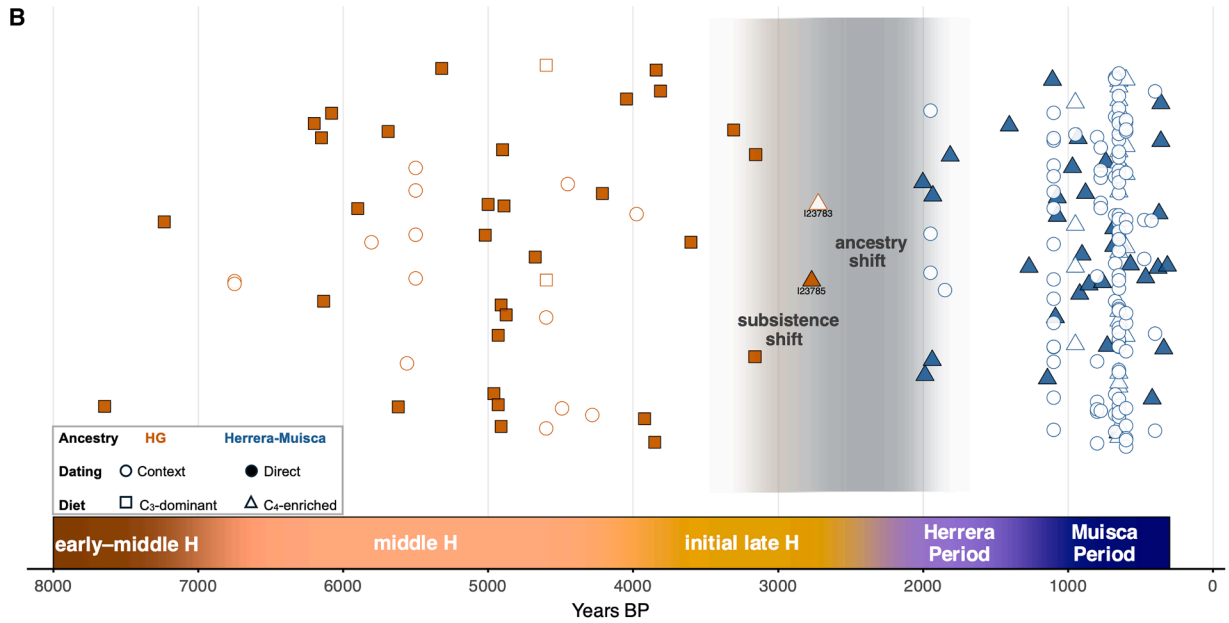
Around 2,500 BP, there is archaeological evidence of emerging complex sedentary societies on the Altiplano Cundiboyacense, and ~2,200–1,300 BP is known as the Herrera Period.[33,34] It is characterized by longer-term occupations, cultivation of maize along with other crops on the most fertile soils,[34] and ceramic production. Archaeological, skeletal, and ancient DNA data suggest that the ancestors of Herrera populations migrated to the region and connect the incoming population to the spread of Chibchan speakers from lower Central America.[35–37] Based on typological similarities between the earliest Herrera pottery tradition (Mosquera rojo inciso) on the Altiplano Cundiboyacense and the Arrancaplumas tradition from the Magdalena River Valley, some archaeologists have hypothesized that Herrera ancestors entered South America and moved southward via the Magdalena River Valley, thus establishing the Arrancaplumas tradition in the lowlands before 2,500 BP and expanding to the Sabana de Bogotá via the Magdalena River corridor between 2,500–2,000 BP, after which they maintained connections with communities who remained there.[38,39] However, Arrancaplumas also shares affinities with Mosquera triturada, another variant of early Herrera pottery found on the Altiplano Cundiboyacense, thus inviting further evaluation of migratory models based on ceramic evidence.[38]

In the final late Holocene (1,200–500 BP), cultural and sociopolitical transformations led to what is known archaeologically as the Muisca Period.[33] Studies of skeletal and dental morphology[17,26,27,29,30,40,41] and ancient DNA[5,37] document a close biological relationship between Herrera and Muisca Period people, suggesting population continuity despite cultural shifts.[30] The Herrera and Early Muisca Periods were characterized by sustained population growth,[34] a shift in settlement patterns to larger and denser household clusters,[42] and changes in social organization,[43,44] while the Late Muisca Period was characterized by further population growth,[34] the expansion of chiefly sociopolitical organization, growth in trade networks, craft specialization, and the expansion of settlements near fertile agricultural fields.[34,45] At the time of Spanish contact, multiple large and socially complex Muisca chiefdoms participated in shared religious ceremonies, alliances, and conflicts,[43] spoke Chibchan dialects, and practiced avunculocal post-marital residence and matrilineal political succession.[43,44]

Although the Altiplano Cundiboyacense has yielded abundant human skeletal material suitable for paleogenomic investigation, genome-level ancient DNA from the region remains limited. A previous study[37] demonstrated that people of the Herrera and Muisca Periods were genetically distinct from a group who lived ~6,000 BP; however, a sampling gap between ~6,000 and 2,000 BP prevented resolution of when, how abruptly, and in association with which subsistence or cultural changes this ancestry shift occurred. Three hypotheses remain to be tested: (1) the ancestry transition occurred in the middle Holocene during a period primarily featuring C_3 plant economies; (2) it occurred in the initial late Holocene when the earliest clear isotopic signal of C_4-enriched resources appears in human diets; or (3) it was associated with the appearance of the Herrera culture.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010





(legend on next page)

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

RESULTS

We generated genome-wide data by enriching for ~1.4M single-nucleotide polymorphisms (SNPs) across the genome and mitochondrial genome and report results for 212 individuals with data meeting ancient DNA authenticity standards (Figure 1; Data S1, section 1; Data S2, Table S1). We also generated direct radiocarbon (^{14}C) dates on bone samples and stable isotope data for 47 individuals with ancient DNA data (Data S1, section 2; Data S2, Table S2). In what follows, we use "BP" for chronological periods and calibrated calendar-year ranges (cal. BCE or cal. CE) when referring to ^{14}C dates. Based on archaeological evidence, strata (layer) dates, or direct ^{14}C dates on bone samples, we divided 49 individuals associated with Holocene hunter-gatherer or early subsistence transition contexts into three temporal categories: early-middle Holocene, dating 7,000 BP or older (n = 2); middle Holocene, dating ~7,000–4,000 BP (n = 33); and initial late Holocene, dating ~4,000 BP or more recent (n = 14) (Data S2, Table S1). These temporal divisions mark intervals characterized by climatic, cultural, or biological shifts and have been used in previous work.[5,13,17,30] A total of 163 individuals were associated with Herrera or Muisca contexts, including 9 from the Herrera Period (~2,200–1,300 BP) and 154 dating to the final late Holocene (~1,200–500 BP), encompassing both the Early and the Late Muisca Periods. We co-analyzed these data with 21 previously published genomes from Colombia.[37]

We used principal component analysis (PCA) as in Kennett et al.[46] (Figures 2A, S1, and S2). Ancient people from the Altiplano Cundiboyacense fall into two clusters. The "HG (hunter-gatherer) Cluster" includes all individuals predating the Herrera Period, spanning over 5,000 years (from Sueva I, I28092, directly dated to 6,567–6,437 cal. BCE, to Aguazuque, I23785, dated to 983–835 cal. BCE), and overlaps with some published ancient South Americans. The "Herrera-Muisca Cluster" is shifted toward, but does not overlap, present-day Chibchan speakers from Costa Rica and ancient Panamanians of similar ancestry (hereafter "Chibchan-related ancestry"). All Herrera and Muisca Period individuals—directly dated as early as ~2,000 BP (I23725 from Nueva Esperanza, 46 cal. BCE–69 cal. CE)—fall in this cluster, thus indicating a complete ancestry shift by this time and suggesting Herrera-to-Muisca Period population continuity. One outlier (>15k SNPs), the Late Muisca male I10932, is shifted toward the HG Cluster and other South Americans.

We grouped individuals from the Altiplano Cundiboyacense relative to known genetic diversity in the Americas with *qpWave* (Data S1, section 3). Using a multistep approach, we found relative genetic homogeneity among most individuals in the "HG Cluster" upon PCA within the limits of our resolution. We grouped these people for some analyses as Colombia_SB_HG ("SB" denotes the Sabana de Bogotá and "HG" denotes pre-Herrera-associated ancestry), excluding two individuals whose *qpWave* model fits did not support inclusion in the merged group (Data S1, sections 3 and 4; Data S2, Table S3) and one lower-coverage first-degree relative of another individual.

PCA, *qpWave*, and a distance-based neighbor-joining tree based on inverted pairwise outgroup-f_3 statistics all support genetic discontinuity between pre-Herrera and Herrera-Muisca Period individuals, indicating a major ancestry shift. While Herrera and Muisca contexts cluster separately from pre-Herrera individuals (Figure 2C; Data S2, Table S4), they are largely homogeneous aside from a few exceptions (Data S1, section 3). The most pronounced PCA outlier, I10932, shows reduced affinity to other Herrera-Muisca Period individuals in *qpWave*, particularly for Chibchan-related ancestry (Data S1, section 4; Data S2, Tables S4–S8). *qpWave* detected no temporal substructure at multi-period sites (Data S1, section 3). A few site-level f_4 comparisons reached nominal significance; most notably, the Herrera Period group at Nueva Esperanza showed reduced allele sharing with many Indigenous American populations relative to the same site's Muisca groups—a pattern that does not recur elsewhere and most likely reflects drift in a small group rather than gene flow. Overall, we found no compelling evidence for demic movement as the primary driver of cultural transformation between the Herrera and Muisca Periods (Data S2, Table S9). We collectively refer to individuals post-dating 2,000 BP as "Herrera-Muisca Period groups."

In the neighbor-joining tree, most Herrera-Muisca Period groups form a shared cluster with geographic substructure separating the southern Altiplano (present-day Cundinamarca) from the northern Altiplano (present-day Boyacá) (Figure 2C); we defined these as two regional groups, "Colombia_Cundinamarca" and "Colombia_Boyacá," and focus below on them and Colombia_SB_HG. A few sites did not cluster regionally, specifically La Salina (in Cundinamarca but oriented toward Boyacá; Figure 1A) and Purnia (Santander). These are discussed in Data S1, section 4.

Five millennia of population continuity on the Sabana de Bogotá

Leveraging time-series data from 56 pre-Herrera Period individuals spanning more than five millennia, we asked: (1) do the genetic relationships among the pre-Herrera groups of the Sabana de Bogotá reflect structure arising from drift, or is there evidence for the entrance of non-local ancestry during this time? And (2) what is the genetic relationship between these people and other ancient Central and South Americans?

Figure 1. Overview of ancient individuals with genome-level data generated in this study

(A) Map of Colombia showing the study region in the eastern Colombian Andes. Pre-Herrera Period sites and Herrera-Muisca Period sites are labeled in orange and blue, respectively. The present-day departments of Cundinamarca and Boyacá are outlined and labeled. The top right image is a zoomed regional map with numbers corresponding to the site list below. The lower right image summarizes ancestry proportions for Herrera-Muisca Period regional groups from Cundinamarca (C) and Boyacá (B) inferred with *qpAdm*, showing inferred proportions of Amazonian North-related and Chibchan-related ancestry in coral and gold, respectively. Error bars indicate ±1 SE.

(B) Timeline illustrating the temporal distribution of samples and shifts in subsistence strategy and ancestry that took place during the Holocene (H). I23783 and I23785 from Aguazuque, who have a genetic profile consistent with pre-Herrera ancestry and isotopic values indicative of consuming C_4-enriched resources, are labeled. The legend is on the lower left of the plot.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

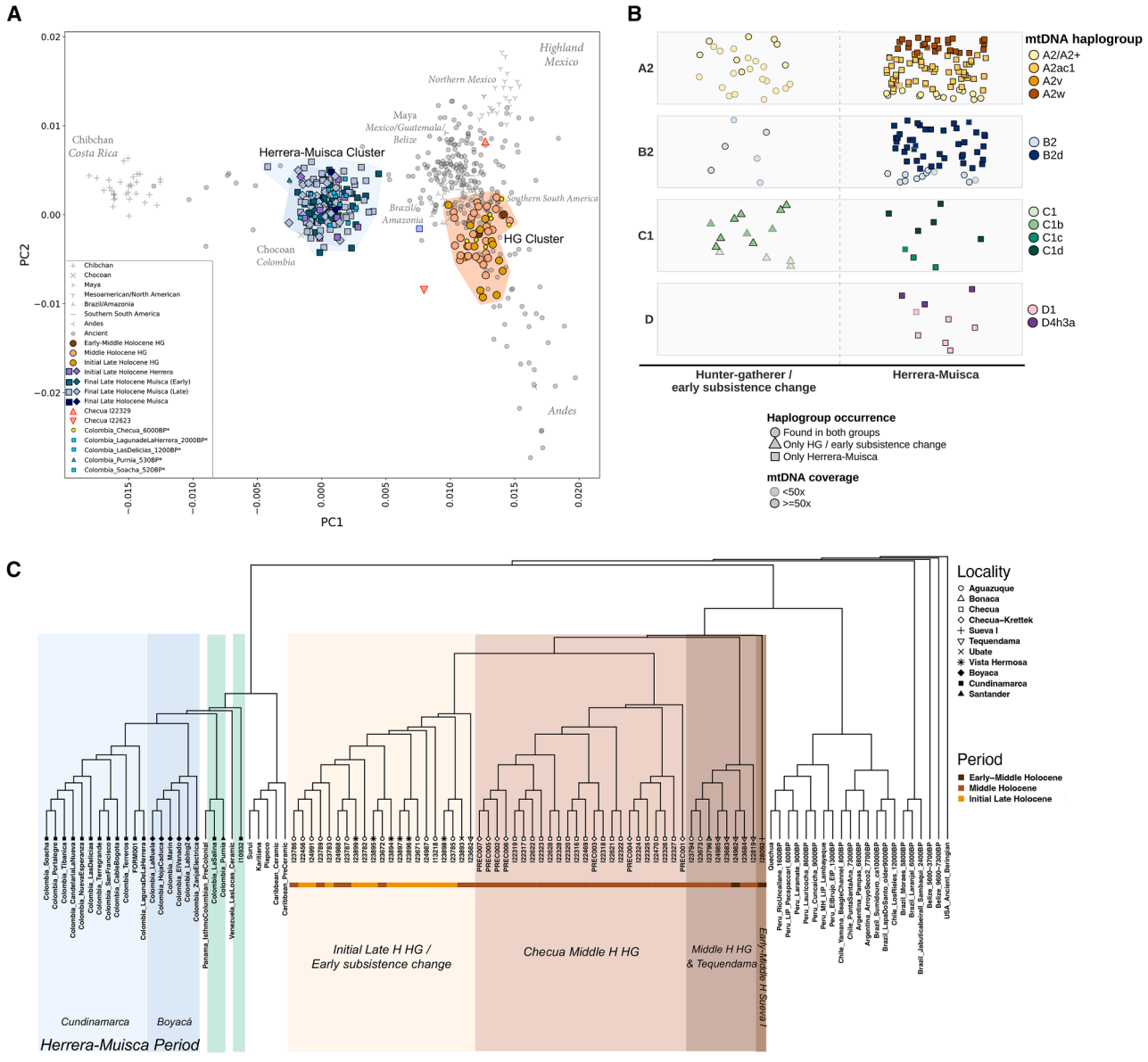


Figure 2. Genome-wide and uniparental evidence for population turnover on the Altiplano Cundiboyacense

(A) PCA showing ancient individuals from the Altiplano Cundiboyacense projected onto axes of genetic variation defined by present-day American populations. Reference data are in gray (see Figure S2 for legend). Data generated in this study and published ancient Colombian data[37] are represented by large and small colored symbols, respectively. An asterisk next to a sample name in the legend indicates publication in Krettek et al.[37] A red outline identifies two low-coverage PCA outliers (<15k SNPs) and a blue outline indicates a PCA outlier of sufficient coverage. For the Herrera-Muisca Cluster, a square symbol indicates an individual is from a site in Cundinamarca, a diamond indicates an individual is from a site in Boyacá, and a triangle indicates an individual is from Santander.

(B) Mitochondrial DNA (mtDNA) haplogroups for ancient individuals grouped by period and broad maternal lineage. HG/early subsistence-change individuals are on the left and Herrera-Muisca Period individuals are on the right. Data are in Data S2, Table S18.

(C) Distance-based tree constructed from pairwise inverse outgroup-f_3 statistics. Shading highlights major subclades discussed in the text. Herrera-Muisca contexts are in blue (sites from Cundinamarca in light teal and sites from Boyacá in light royal blue) and green (outliers), while pre-Herrera contexts are in yellow-brown (initial late Holocene group in yellow, Checua Middle Holocene HG group in light brown, Middle Holocene HG and Tequendama group in brown, and Sueva I HG in dark brown). Symbols indicate archaeological locality (top legend), and colored bars indicate chronological period (bottom legend). Data are in Data S2, Table S4.

In the neighbor-joining tree (Figure 2C), pre-Herrera individuals from the Sabana de Bogotá form a distinct genetic clade within broader Central and South American variation,[37] structured into subclades by time and geography. The oldest individual (I28092, 6,567–6,437 cal. BCE) is the most basal, lacking drift shared by later individuals and anchoring the earliest Holocene diversity in the region. The remaining pre-Herrera individuals fall into three subclades: one grouping early-middle and

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

middle Holocene Tequendama with Bonacá and some Aguazuque individuals; a site-specific Checua clade; and a third linking most middle Holocene Aguazuque individuals (as well as one each from Ubaté and Tequendama) with all initial late Holocene individuals (Vista Hermosa and Aguazuque), thus reflecting continuity at Aguazuque over time and some genetic diversity in the middle Holocene. I22318 and I23671, flagged as subtly distinct in *qpWave*, cluster with other individuals from their same site and period.

We next tested whether this substructure reflects external gene flow or drift among groups sharing common ancestry. f_4-statistics of the form f_4(Yoruba, *IndigenousAmerican_Test*; *Colombia_SB_HG_SubClade1*, *Colombia_SB_HG_SubClade2*) are overwhelmingly indistinguishable from zero, as they show no asymmetric allele sharing with external populations; significant values (|Z| up to 8.8) instead reaffirm substructure among the pre-Herrera subclades, which is driven mainly by the basal early-middle Holocene individual from Sueva I (Data S2, Table S10). Outgroup-f_3 values are similarly uniform across subclades (Data S2, Table S11; Figure S3). Together, these results indicate genetic continuity on the Sabana de Bogotá from the early-middle through the initial late Holocene, with substructure reflecting accumulated drift within a shared ancestral population rather than the introduction of external ancestry.

These patterns of internal substructure are consistent with the small effective community sizes of 245–292 people (95% confidence interval fitted via the likelihood profile) that we infer for pre-Herrera groups, thus reflecting the strong drift expected in small, isolated communities. Despite evidence for a very small ancestral pool, close-kin unions were not pervasive. Only 9 pre-Herrera individuals out of 31 tested have any runs of homozygosity (ROH) > 20 cM, a pattern indicating recent parental relatedness (Data S2, Table S12; Figure S4). Consistent with a small, enduring community, we identify a three-generation family buried at Checua spanning ~3,765–3,630 calBCE with reproductive partners I22622 and I22323 buried together (the latter, a female, representing the only primary burial),[47] while their son (I22317) and his daughter (I22319) were co-buried as part of a separate triple burial (Data S1, section 5).

The ancestry of pre-Herrera people on the Sabana de Bogotá derives wholly from the Southern Native American (SNA) expansion into South America, with no Spirit Cave- or UPopA (Mixe)-related affinity beyond that observed in other Central and South American populations (Data S2, Table S13; Figure S5).[48,49] f_4-statistics of the form f_4(Yoruba, Colombia_SB_HG; *IndigenousAmerican_Test1*, *IndigenousAmerican_Test2*) show that Colombia_SB_HG shares significantly less genetic drift with ancient North American and Mesoamerican groups than with Central and South American ones, to which it is broadly symmetrically related (Data S2, Tables S11 and S14). A weak but consistent signal of elevated allele sharing with a few ancient Peruvian groups (Peru_LIP_Pacapaccari_600BP and Peru_MH_LIP_Lambayeque) is most parsimoniously explained by shared deep northern Andean ancestry given their large temporal separation. Together, these results indicate that Colombia_SB_HG is a deeply diverging South American lineage that made little to no detectable genetic contribution to any sampled population in the Americas.

We confirm the basal positioning and distinctiveness of Colombia_SB_HG with *qpGraph* by systematically exploring possible admixture graph topologies and evaluating how well each graph fits observed *f*-statistics (Data S1, section 6). Colombia_SB_HG represents a distinct lineage that branches from the primary SNA ancestry underlying most South American populations, which dispersed rapidly into and throughout the continent,[50] thus underscoring both their early divergence from and their broader connection to the initial peopling of South America.

Asynchronous shifts in subsistence and ancestry

Two individuals from Aguazuque—I23785 (directly dated to 983–835 cal. BCE) and I23783 (from a context dated 968–807 cal. BCE)[20]—have genetic profiles entirely consistent with local pre-Herrera Period ancestry (Data S2, Tables S3 and S15), yet they exhibit dietary isotope signatures ($\delta^{13}C$) reflecting a substantive contribution from C_4-enriched resources (Figure 3; Data S1, section 2; Data S2, Table S2). Given the limited availability of wild C_4 plants in the high-altitude Andean environment[22,51,52] and faunal isotope data[22,53] from early-middle and middle Holocene Tequendama and Aguazuque indicating that C_4 plants were not a considerable part of animal diets, elevated $\delta^{13}C$ values in these individuals most likely reflect a human-mediated shift in local food webs driven by changes in subsistence strategies. Archaeobotanical evidence of maize starch grains on lithic tool surfaces and in dental calculus from the region identifies maize as the most parsimonious C_4 source, which is consistent with its well-documented presence on the Sabana de Bogotá and its substantially greater dietary role there by the initial late Holocene,[8,13,21,22,54] and in contrast to its role as a minor, non-staple component of a diversified plant diet at middle Holocene Checua[19] (Data S1, section 2). Our joint genomic and isotopic data therefore decouple the early appearance of maize on the Sabana de Bogotá[19] and its isotopically detectable incorporation into human diets[8,13,21,22] from the ancestry turnover that took place between pre-Herrera and Herrera-Muisca Periods. This suggests early cultivation was adopted or developed within genetically continuous local populations rather than introduced by population replacement. Such a pattern could reflect the circulation of crops, knowledge, or practices through broader interregional interaction spheres.[55]

While pre-Herrera Period-associated ancestry persisted for more than 5,000 years, by at least 2,000 BP, the population living on the Altiplano Cundiboyacense was genetically distinct from the people who lived in the region for many prior millennia. Consistent with Krettek et al.,[37] our data from individuals associated with Herrera-Muisca Period contexts form a distinct cluster in PCA and in a neighbor-joining tree, and are differentiated from pre-Herrera Period individuals in *qpWave*, thus indicating a clear ancestry shift and suggesting that the local gene pool was largely, if not entirely, replaced. Consistent with this interpretation, no Herrera-Muisca Period group shows significantly greater affinity to Colombia_SB_HG than any other, as expected under a replacement scenario (Data S2, Table S14), and ancestry modeling fits no Colombia_SB_HG-like ancestry component in the models for any Herrera-Muisca Period group (Data S1,

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

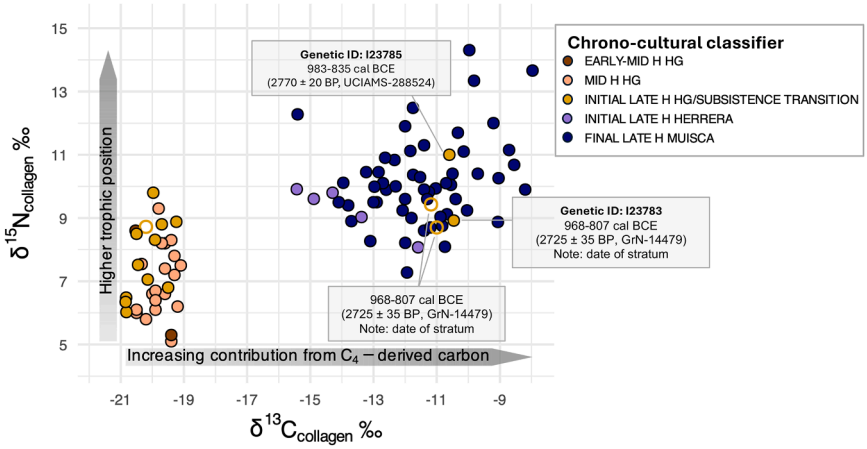


Figure 3. Isotopic measurements on collagen extracted from human bone samples

Scatterplot of $\delta^{13}C_{collagen}$ versus $\delta^{15}N_{collagen}$ for individuals with isotopic and ancient DNA data in our dataset (Data S2, Table S2) together with previously published isotopic information (Data S1, section 2). Points colored by chrono-cultural classifier (H for Holocene). Filled symbols indicate individuals with both isotopic and genomic data; unfilled symbols indicate individuals with isotopic data only.[21] A horizontal gray arrow indicates increasing $\delta^{13}C$ values toward the right, interpreted as increasing contribution from C_4-enriched resources, and a vertical gray arrow highlights increasing $\delta^{15}N$ values upward, interpreted as higher trophic position. Individuals with $\delta^{15}N$ values exceeding 13‰ are interpreted as likely breastfeeding infants; elevated $\delta^{15}N$ at this magnitude reflects trophic enrichment from consuming breast milk, which occupies a higher trophic level than the mother's diet, rather than a dietary signal intrinsic to the individual. Excluding these infants, Herrera-Muisca Period individuals cluster at elevated $\delta^{15}N$ relative to pre-Herrera people, which is consistent with a coupled system of increased maize cultivation and guinea pig husbandry during Herrera-Muisca times (Data S1, section 2). Four individuals from initial late Holocene Aguazuque, two with genomic data and one with a direct ^{14}C date from bone, who have a diet incorporating C_4-enriched resources, are labeled.

section 7), together indicating that the ancestry shift reflects population replacement rather than admixture.

To characterize the ancestry that replaced the pre-Herrera gene pool, we computed statistics of the form f_4(Yoruba, *Test*; Colombia_SB_HG, *Colombia_HerreraMuisca*) and find that, relative to pre-Herrera Colombian hunter-gatherers and early food producers, Herrera-Muisca Period people share significantly more alleles with Central American Chibchan-related populations (|Z| up to 18.1) as well as with some Amazonian groups or those with Amazonian-related affinities, which includes those with so-called "Amazonian North" affinity who live on the eastern slopes of the northern Andes in present-day Colombia and Ecuador and speak Andean languages but are traditionally associated with the Amazonian cultural domain[56] (Figures S6A and S7A; Data S2, Tables S16 and S17). These patterns suggest that multiple ancestry components differentiate pre-Herrera and Herrera-Muisca Period people.

Mitochondrial DNA (mtDNA) also indicates a demographic shift, with Herrera-Muisca groups introducing previously unobserved matrilines (Figure 2B; Data S2, Table S18). Although all individuals carry deeply rooted American maternal lineages,[57] the sub-lineages differ markedly. Pre-Herrera individuals are dominated by A2-derived lineages (A2 + [64], A2 + [64] + @16111, A2 + [64] + 16189) alongside B2 and C1, particularly C1b. Herrera-Muisca individuals show a major shift: A2ac1 becomes the most frequent A2 sub-lineage and B2d the dominant B2 sub-lineage; C1b is absent; and A2w, C1c, C1d, D1, and D4h3a appear (although previous work[58] reported D4h3a in a pre-Herrera individual from Checua, we do not observe this lineage prior to the Herrera-Muisca-associated ancestry shift). Although broad A2, B2, and C1 lineages occur across both contexts, the finer-scale mtDNA composition changes substantially, thus indicating that the Herrera-Muisca maternal gene pool was not simply a continuation of the pre-Herrera one. Haplogroups A2w and B2d, the latter estimated to have emerged ~2,900 BP,[59] serve as useful uniparental markers for the Chibchan-related component of the ancestry shift documented here,[5,48,60–62] whereas D1 and D4h3a—lineages more frequent in Amazonian and eastern Andean groups—point to additional complexity. Y chromosome haplogroups (Data S2, Table S1) are less informative here, as Q-branch lineages predominate across Indigenous American populations with limited phylogeographic resolution at the sub-haplogroup level. We next reconstruct the genome-level ancestry of Herrera and Muisca Period people.

Herrera-Muisca groups expanded and developed genetic substructure after forming by admixture ~4,000 BP

Previous work showed that by 2,000 BP, local ancestry on the Sabana de Bogotá was replaced by ancestry connected to Central America associated with the Herrera ceramic complex, which persisted through the Muisca Period.[37] Post-2,000 BP people of the Altiplano Cundiboyacense were assessed as being genetically intermediate between ancient Panamanians (used as a proxy for people carrying so-called "Chibchan-related ancestry") and other Central and South Americans, but a source for the latter ancestry was unidentified.[37]

With hapROH, we infer community sizes growing from ~555–900 individuals in the Herrera Period to ~1,005–1,162 in the Muisca Period (95% confidence intervals from likelihood profiles; these values reflect the gene pool contributing to sampled individuals over recent generations, not the size of the regional population). This continuous growth aligns with archaeological evidence for demographic increase, expanding food production, technological specialization, and larger, more socially stratified societies across the Herrera and Muisca Periods.[34,43,63] Three Muisca Period individuals from Marín, Portalegre, and El Venado are the offspring of close-kin unions, exhibiting 385–406 cM of ROH > 4 cM and 226–255 cM of ROH > 20 cM (Data S2, Table S12; Figure S8). While these values document the occurrence of consanguineous unions, the absence of a broader shift

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

toward an elevated ROH suggests that unions of close kin were rare despite the acceptance of cross-cousin marriage within the Muisca kinship system.[43,64,65] We identify several "families" comprising closely related individuals (up to 3rd-degree relatives), which includes one connecting the sites of Tibanica, Portalegre, and Candelaria La Nueva (Data S1, section 5).

While Herrera-Muisca Period people form a relatively homogeneous genetic group relative to other ancient and modern Americans, the internal substructure among Herrera and Muisca Period groups observed in the neighbor-joining tree (Figure 2C) aligns with archaeologically attested cultural differences between the southern Muiscas (Cundinamarca) and northern Muiscas (Boyacá), with the latter associated with greater cosmopolitanism and possibly more connectivity to Amazonia. This finding of geographic-based substructure is consistent with cultural indicators, like burial practices, which have been found to differ between northern and southern Muisca groups.[66] f_4-statistics assessing allele-sharing asymmetries between the Herrera-Muisca groups and other Indigenous American populations are mostly indistinguishable from zero, consistent with their overall homogeneity (Figures S6B and S7B; Data S2, Tables S5 and S6). Weak signals link Colombia_Boyacá to Chibchan-related groups and Colombia_Cundinamarca to Amazonian North-related groups, though near the limits of *f*-statistic resolution, and I10932 shows less allele sharing with Chibchan-related groups, consistent with its distinct profile. Overall, these results suggest that Herrera-Muisca Period groups across the Altiplano Cundiboyacense were shaped less by distinct migration pulses than by varying proportions of shared ancestries and geographically structured patterns of interaction.

Herrera-Muisca Period groups show a marked excess of shared drift with Central American Chibchan-related populations (proxied by ancient Panamanians[48] and present-day Cabécar) relative to other American groups tested (Data S2, Tables S19 and S20). However, the two Chibchan-related proxies share significantly more drift with each other than either does with Herrera-Muisca Period groups ($|Z| > 10.9$; Data S2, Table S21), which is consistent with continued drift within the Chibchan clade after its divergence from the Herrera-Muisca lineage and/or later admixture into the Herrera-Muisca lineage alone. Reciprocally, a broad range of Indigenous American groups share significantly more drift with Herrera-Muisca people than with Central American Chibchan speakers (Data S2, Tables S22–S25). Groups showing this pattern include deep South American lineages (Brazil, the Andes, and the Southern Cone), as expected from post-divergence drift; weaker signals from Intermediate-Period Peruvians, Caribbean-related, and Mesoamerican groups may reflect deep shared ancestry, later gene flow, or an ancestry layer absent from Chibchan populations. Among all tested groups, present-day populations carrying "Amazonian North" ancestry[56] show the strongest and most specific affinity to ancient Herrera-Muisca Period people relative to Chibchan-related groups. Collectively, these results reject a simple clade relationship between Central American Chibchan speakers and Herrera-Muisca people, thus indicating that the latter carry ancestry beyond that shared with Chibchan speakers.

We modeled Herrera-Muisca ancestry with *qpAdm*. Single-source models, including Chibchan-related proxies, were strongly rejected ($p < 0.05$), supporting multiple ancestry components (Data S1, section 7). We fit the Herrera-Muisca groups as a mixture of Chibchan-related ancestry (proxied by ancient Panamanians) and northwest Amazonian/Andean-related ancestry, proxied by the Kichwa Orellana of the eastern Andean slopes, who carry the "Amazonian North" profile that split ~4,000 years ago from the "Amazonian Core" ancestry of the central Amazon Basin.[56] We find consistent support for both ancestries, with subtle regional variation in their proportions. We fit Colombia_Cundinamarca as having 53.8% ± 1.5% Chibchan-related and 46.2% ± 1.5% Amazonian North-related ancestry ($p = 0.95$), and Colombia_Boyacá as having 60.1% ± 1.6% Chibchan-related and 39.9% ± 1.6% Amazonian North-related ancestry ($p = 0.24$; Figure 1A; Data S1, section 7). With DATES, we estimated this admixture to have occurred on average 136 ± 15 generations (3,944 ± 435 years) before these individuals lived ($Z = 9.0$) (Figure S9; estimates for each regional group separately were qualitatively similar, see Data S2, Table S26). This ancient admixture date implies that the genetic foundation of Herrera and Muisca Period populations was established prior to their archaeological prominence in the eastern Colombian highlands.

DISCUSSION

Genome-wide data from 212 individuals from the Altiplano Cundiboyacense spanning 7,000 years allow us to reconstruct population history at a temporal and spatial resolution not previously attainable.

The ancestry of pre-Herrera Period people from the Sabana de Bogotá forms a distinct lineage that is nevertheless deeply connected to the broader peopling of South America. There was population continuity on the Sabana de Bogotá over five millennia, with no evidence of gene flow from genetically distinct populations despite shifts in subsistence during this time. The observed substructure reflects the accumulation of genetic drift in small communities, which were possibly influenced by environmental shifts such as the rising temperatures and decreased humidity of the middle Holocene that resulted in habitat fragmentation and reduced the availability of key resources, including animals (deer and guinea pigs) and plants.[4,17,67] Changes in resource exploitation strategies, mobility, and social networks, potentially increasing isolation, may be reasons why some early hunter-gatherer lineages are not reflected in later groups. Some substructure may be directly connected to patterns of mobility and site use; for example, the site-specific genetic clustering at Checua is consistent with the archaeological record at the site, where sporadic early visits gave way from ~7,500 BP to repeated, more intensive occupations with constructed floors, hearths, dense faunal and lithic assemblages, and human burials.[19,47]

There are abundant data supporting the early introduction of maize to Andean South America. In regions of Colombia like the Middle Cauca River Basin (western central Colombian Andes), analysis of pollen, starch grains, and phytoliths from tools indicates processing of maize seed likely for direct consumption as early as ~7,000 BP,[31,68,69] while maize grains have been identified in the intra-Andean basin of Duitama between 3,680–2,610

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

BP[70] and in the calculus of individuals dating ~4,900 BP from Checua.[19] While it is well-evidenced that a C_3-to-C_4 transition occurred during the initial late Holocene,[8,13,21,54] a central contribution of our work is demonstrating that the incorporation of maize as a meaningful component in local food webs occurred independently of the major change in ancestry. The two individuals (I23783 and I23785) from Aguazuque, who are genetically indistinguishable from other pre-Herrera Period people yet were consuming enough C_4-derived resources to be reflected as an isotopic shift, provide genomic support for the incorporation of C_4 plants into subsistence systems by resident populations well before the ancestry turnover associated with Herrera-Muisca Period people. While the abruptness of the C_3-to-C_4 dietary transition in Figure 3 partly reflects the scarcity of individuals from the ~3,800–2,000 BP transitional window rather than a truly instantaneous shift, the broader published isotopic record from the region (not restricted to individuals with genomic data) documents additional individuals dating to ~3,300–2,200 BP[13] with intermediate $\delta^{13}C$ values, which is consistent with a gradual dietary uptake of C_4 resources within the resident population. The pre-Herrera populations of the Sabana de Bogotá were evidently active participants in subsistence diversification, suggesting well-established socioeconomic networks.

Our results confirm the finding of a major genetic turnover occurring on the Altiplano Cundiboyacense[37] while refining the dates of this event to 2,800–2,000 BP. Bioarchaeological evidence from cranial and dental morphology independently supports discontinuity between pre-Herrera and Herrera-Muisca Period individuals,[27,30,40,41] consistent with replacement rather than continuity. A possibility is that paleoclimatic and paleoenvironmental changes may have led to reduced occupation of the Altiplano prior to the arrival of Herrera Period people.[17] Under this scenario, incoming populations would have encountered less pressure from local populations, facilitating expansion with limited admixture. While our genomic data support a population replacement, future research should clarify why pre-Herrera-related ancestry is nearly absent in the Herrera-Muisca Periods and whether incoming groups had an earlier, limited presence enabling cultural contact before population displacement.

Consistent with previous work,[37] we find that the ancestors of Herrera-Muisca Period people carried Chibchan-related ancestry and an additional component absent from the gene pool of Chibchan-speaking groups. Based on available genomic data—which include limited information from individuals with Amazonian ancestry—this ancestry is best characterized as having Amazonian-Andean affinities and is best proxied by the "Amazonian North" genetic profile observed today in the Andean foothills of Ecuador and Colombia, regions that maintain cultural and demographic connections with the Amazon Basin.[56] We infer that the admixture event forming this gene pool took place ~4,000 BP—well before the appearance of these groups on the Altiplano Cundiboyacense and coincident with the linguistic evidence for the diversification of Chibchan languages and spread of Chibchan speakers throughout the Isthmo-Colombian sphere[36,71]—thus implying that the genetic foundations of Herrera and Muisca populations formed outside this region. While the location where this admixed ancestry profile formed is unknown, regions that could have served as stages for interaction include the Magdalena River Valley or the eastern piedmont of the Cordillera Oriental with its adjacent Llanos/Orinoquía foothills—the latter encompassing the Muisca's proximate social sphere. Nevertheless, the ethnohistoric homeland of Herrera-Muisca society remains the Altiplano Cundiboyacense, which should be distinguished from the unresolved question of where the admixed ancestry profile characterizing the Herrera-Muisca Period population was initially formed.

We infer an increase in effective community size from the Herrera Period to the Late Muisca Period, in line with archaeological and isotopic evidence of sustained population growth during this time,[34,42,44,72] which was plausibly fueled by a coupled system of intensifying maize cultivation and guinea pig husbandry.[9] Supporting this, paleoenvironmental reconstructions confirm a significant human impact on the regional landscapes at this time.[73–75] Herrera-Muisca Period people represent a largely homogeneous yet internally structured genetic cluster, which shows a minor differentiation between northern and southern groups that parallels archaeological distinctions in material culture, burial practices, and connection networks,[66,76–78] including documented differences in body position, tomb shape, and the trajectory of social differentiation that date back to the Herrera Period.[66] This is consistent with culturally and geographically mediated differences in external contact and gene flow throughout the Altiplano Cundiboyacense.

Several centuries ago, the eastern Colombian Andes were home to multiple large Muisca chiefdoms whose renown and wealth attracted Spanish invaders. The region was incorporated into the colonial domain in 1537, ending Indigenous political autonomy on the Sabana de Bogotá. Nevertheless, descendant communities continue to inhabit the region today, and ancient DNA offers a means to reconstruct the history of the people who have shaped and reshaped its genetic and cultural landscape for millennia.

Limitations of the study

The data we report increase the regional ancient DNA sample size substantially, but several limitations should be acknowledged. First, sampling remains uneven, particularly between ~2,800–2,000 BP, when the ancestry turnover occurred, while our inference that the pre-Herrera gene pool was largely, if not entirely, replaced rests on the absence of a detectable admixture signal between pre-Herrera and Herrera-Muisca Period groups. Presently, we cannot distinguish genuine reproductive isolation from an early admixture signal that was subsequently diluted by continued gene flow. More ancient DNA data from this period may resolve whether the transition was abrupt, involved short-lived admixture between established and incoming groups, or varied across communities. Second, ancient genomic data from Amazonia and the eastern Andean slopes remain very limited, so the non-Chibchan component of Herrera-Muisca Period ancestry is approximated by a present-day genetic profile rather than by a contemporaneous ancient source. Consequently, the ancient population that contributed to this ancestry and the geographic location of the admixture event cannot be identified, and reported affinities should be regarded as approximate pending the recovery of relevant ancient genomes. Third,

our interpretation of a meaningful maize-based dietary shift among pre-Herrera people derives from the C_4-enriched isotopic values of two individuals from Aguazuque; because bulk stable-carbon isotopes reflect C_4 input generally rather than maize specifically, this attribution depends on the assumption that wild C_4 resources were scarce in the high-altitude Andean environment. Microbotanical evidence together with isotopic data from additional individuals would aid in confirming the dietary source and establishing the extent of the shift.

RESOURCE AVAILABILITY

Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the lead contact, Kendra Sirak (kendra_sirak@fas.harvard.edu).

Materials availability

Open science principles require making all data used to support the conclusions of a study maximally available, and we support these principles here by making fully publicly available not only the digital copies of molecules (the sequences) but also the molecular copies (the DNA libraries themselves, which constitute molecular data storage). Researchers who wish to carry out deeper sequencing of libraries published in this study should make a request to the lead contact. We commit to granting reasonable requests as long as the libraries remain preserved in our laboratories, with no requirement of inclusion as collaborators or co-authors on any resulting publications.

Data and code availability

Data generated in this study have been deposited in the European Nucleotide Archive (ENA: PRJEB110479) and are publicly available. This paper does not report any original code.

ACKNOWLEDGMENTS

We thank the Instituto Colombiano de Antropología e Historia (ICANH); Museo Nacional de Colombia; Instituto de Ciencias Naturales, Universidad Nacional de Colombia; Universidad de los Andes; Universidad Pedagógica y Tecnológica de Colombia (UPTC); and El Departamento de Estudios Sociales, INGETEC, for permissions and support for this project. We thank Nicole Adamski, Kristin Stewardson, and Fatma Zalzala for ancient DNA laboratory work, and Brendan Culleton and Laurie Eccles for radiocarbon dates and isotope analysis and for discussions about those data. S.A., J.P.O., and M.B.M.C. developed the archaeological research program in the Checua River valley, excavating several sites and conducting archaeobotanical and archaeothanatology studies, among other analyses. K.S. and M.D. acknowledge support from the National Geographic Society. D.R. acknowledges support from the National Institutes of Health (HG012287); the John Templeton Foundation (grant 61220); from J.-F. Clin; from the Allen Discovery Center, a Paul G. Allen Frontiers Group-advised program of the Paul G. Allen Family Foundation; and from the Howard Hughes Medical Institute. The author-accepted version of this article—that is, the version not reflecting proofreading and editing and formatting changes following the article's acceptance—is subject to the Howard Hughes Medical Institute (HHMI) Open Access to Publications policy, as HHMI lab heads have previously granted a nonexclusive CC BY 4.0 license to the public and a sublicensable license to HHMI in their research articles. Pursuant to those licenses, the author-accepted manuscript can be made freely available under a CC BY 4.0 license immediately upon publication. M.D. dedicates this paper to the memory of Franz Xaver Faust (1953–2025), a beloved friend and teacher.

AUTHOR CONTRIBUTIONS

Conceptualization, K.S., M.D., L.F.-S., and D.R.; writing—original draft, K.S.; writing—review and editing, K.S., M.D., and D.R. with the input of all other co-authors; resources—archaeological materials assembly and descriptions, S.R., A.V.T.V., P.A., A.M.B., J.R.-S., G.P., C.L., J.P.O., S.A., S.A.T.O., M.B.M.C., and F.R.S.; project administration, K.S. and M.D.; methodology—sampling, K.S., M.D., and L.F.-S.; methodology—laboratory work, K.C., E.C., T.F., L.I., J.K., A.M.L., L.Q., J.N.W., and N.R.; methodology—data processing and curation, A.K., M.M., S.M., M.N., G.S., and D.R.; methodology—radiocarbon dates and isotope data, A.C., C.S.H., and K.M.P.; formal analysis, K.S. and A.B.; visualization, K.S.; supervision, D.R.; funding acquisition, K.S., M.D., and D.R.

DECLARATION OF INTERESTS

The authors declare no competing interests.

DECLARATION OF GENERATIVE AI AND AI-ASSISTED TECHNOLOGIES IN THE MANUSCRIPT PREPARATION PROCESS

During the preparation of this work, the authors used Claude (Anthropic) and ChatGPT (OpenAI) to improve the readability and language of the manuscript. The lead author reviewed and edited the content and is responsible for its accuracy in the published article.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

- KEY RESOURCES TABLE
- EXPERIMENTAL MODEL AND STUDY PARTICIPANT DETAILS
  - Ancient Individuals
- METHOD DETAILS
  - Ethical Considerations
  - Sampling of ancient individuals
  - Ancient DNA data generation, bioinformatics, and quality control
  - Dataset assembly
  - Radiocarbon (^{14}C) dates and isotope data
- QUANTIFICATION AND STATISTICAL ANALYSIS
  - Population structure overview with PCA
  - Analyses of genetic ancestry
  - Ancestry modeling
  - Inferring relationships and community sizes
  - Estimation of admixture dates
  - Use of Artificial Intelligence (AI)

SUPPLEMENTAL INFORMATION

Supplemental information can be found online at https://doi.org/10.1016/j.cell.2026.10.010.

Received: February 18, 2026
Revised: July 30, 2026
Accepted: October 5, 2026

REFERENCES

1. Cárdenas, F. (2002). Datos sobre la Alimentación Prehispánica en la Sabana de Bogotá, Colombia (Instituto Colombiano de Antropología e Historia).
2. Aceituno, F.J., Loaiza, N., Delgado-Burbano, M.E., and Barrientos, G. (2013). The initial human settlement of Northwest South America during the Pleistocene/Holocene transition: Synthesis and perspectives. Quat. Int. *301*, 23–33. https://doi.org/10.1016/j.quaint.2012.05.017.
3. Delgado, M., Aceituno, F.J., and Loaiza, N. (2015). Multidisciplinary studies on the human-environment interaction during the initial peopling of the Americas. Quat. Int. *363*, 1–3. https://doi.org/10.1016/j.quaint.2015.01.040.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

4. Delgado, M., Aceituno, F.J., and Barrientos, G. (2015). 14C data and the early colonization of northwest South America: a critical assessment. Quat. Int. *363*, 55–64. https://doi.org/10.1016/j.quaint.2014.09.011.

5. Delgado, M., Rodríguez, F., Kassadjikova, K., and Fehren-Schmitz, L. (2021). A paleogenetic perspective of the Sabana de Bogotá (Northern South America) population history over the Holocene (9000–550 cal BP). Quat. Int. *578*, 73–86. https://doi.org/10.1016/j.quaint.2020.08.031.

6. Aceituno, F.J., and Loaiza, N. (2015). The role of plants in the early human settlement of Northwest South America. Quat. Int. *363*, 20–27. https://doi.org/10.1016/j.quaint.2014.06.027.

7. Borrero, L.A. (2015). Moving: Hunter-gatherers and the cultural geography of South America. Quat. Int. *363*, 126–133. https://doi.org/10.1016/j.quaint.2014.03.011.

8. Delgado, M. (2021). Patterns of dietary diversity in Holocene north-west South America: new insights from Bayesian stable isotope mixing models. Antiquity *95*, 1027–1042. https://doi.org/10.15184/aqy.2021.56.

9. Lord, E., Collins, C., deFrance, S., LeFebvre, M.J., Pigière, F., Eeckhout, P., Erauw, C., Fitzpatrick, S.M., Healy, P.F., Martínez-Polanco, M.F., et al. (2020). Ancient DNA of guinea pigs (*Cavia* spp.) indicates a probable new center of domestication and pathways of global distribution. Sci. Rep. *10*, 8901. https://doi.org/10.1038/s41598-020-65784-6.

10. Prates, L., Politis, G.G., and Perez, S.I. (2020). Rapid radiation of humans in South America after the last glacial maximum: A radiocarbon-based study. PLoS One *15*, e0236023. https://doi.org/10.1371/journal.pone.0236023.

11. Delgado, M. (2021). Early Neotropical hunter-gatherers and the dynamics of the initial peopling of Northern South America. Quat. Int. *578*, 1–4. https://doi.org/10.1016/j.quaint.2021.02.033.

12. Delgado, M. (2015). Variación dental y craneofacial en el norte de los Andes durante el Pleistoceno y el Holoceno: su relevancia para la discusión de la colonización temprana de Sudamérica. PhD thesis (Universidad Nacional de La Plata).

13. Delgado, M. (2018). Stable isotope evidence for dietary and cultural change over the Holocene at the Sabana de Bogotá region, Northern South America. Archaeol. Anthropol. Sci. *10*, 817–832. https://doi.org/10.1007/s12520-016-0403-3.

14. Piperno, D.R., and Pearsall, D.M. (1998). The Origins of Agriculture in the Lowland Neotropics (Academic Press). https://doi.org/10.1016/B978-012557180-7/50002-3.

15. Nieuwenhuis, C. (2002). Traces on Tropical Tools: a Functional Study of Chert Artefacts from Preceramic Sites in Colombia (Archaeological Studies Leiden University, Volume 9) (Leiden University Press).

16. Nieuwenhuis, C. (1998). Unattractive but effective: unretouched pointed flakes as projectile points? A closer look at the Abriense and Tequendamiense artefacts. In Explorations in American Archaeology. Essays in Honor of Wesley R. Hurt, M. Plew, ed. (University Press of America), pp. 133–163.

17. Delgado Burbano, M.E. (2012). Mid and Late Holocene population changes at the Sabana de Bogotá (Northern South America) inferred from skeletal morphology and radiocarbon chronology. Quat. Int. *256*, 2–11. https://doi.org/10.1016/j.quaint.2011.10.035.

18. Zorro-Luján, C.M. (2019). La ocupación humana del Altiplano Cundiboyacense en el periodo precerámico: Una aproximación desde la zooarqueología. PhD thesis (Universidad de los Andes).

19. Archila, S., Groot, A.M., Ospina, J.P., Mejía, M., and Zorro, C. (2021). Dwelling the hill: Traces of increasing sedentism in hunter-gatherers societies at Checua site, Colombia (9500–5052 cal BP). Quat. Int. *578*, 102–119. https://doi.org/10.1016/j.quaint.2020.07.040.

20. Correal Urrego, G. (1990) Aguazuque. Evidencia de Cazadores, Recolectores y Plantadores en la Altiplanicie de la Cordillera Oriental (Fundación de Investigaciones Arqueológicas Nacionales, Banco de la República).

21. van der Hammen, T., Correal Urrego, G., and van Klinken, G.J. (1990). Isótopos estables y dieta del hombre prehistórico en la Sabana de Bogotá (un estudio inicial). Bol. Arqueol. FIAN *5*, 3–11.

22. Ziegler, M.J., Robinson, M., Aceituno, F.J., Morcote-Ríos, G., Becerra-Valdivia, L., Carleton, W.C., Iriarte, J., and Roberts, P. (2025). Human dietary diversity in the Colombian Andes at the terminal Pleistocene-late Holocene sites Tequendama and Aguazuque. iScience *28*, 111624. https://doi.org/10.1016/j.isci.2024.111624.

23. Correal Urrego, G., and van der Hammen, T. (1977). Investigaciones Arqueológicas en los Abrigos Rocosos del Tequendama: 12.000 Años de Historia del Hombre y Su Medio Ambiente en la Altiplanicie de Bogotá (Fondo de Promoción de la Cultura del Banco Popular).

24. Correal Urrego, G. (1990). Evidencias culturales durante el Pleistoceno y Holoceno de Colombia. Rev. Arqueol. Am. *1*, 69–89.

25. Neves, W.A., Hubbe, M., and Correal, G. (2007). Human skeletal remains from Sabana de Bogotá, Colombia: A case of Paleoamerican morphology late survival in South America? Am. J. Phys. Anthropol. *133*, 1080–1098. https://doi.org/10.1002/ajpa.20637.

26. Rodríguez Cuenca, J.V., and Vargas, C. (2010). Evolución y tamaño dental en poblaciones humanas de Colombia. Rev. Acad. Colomb. Cienc. Exactas Fis. Nat. *34*, 423–439. https://doi.org/10.18257/raccefyn.34(133).2010.2461.

27. Rodríguez Cuenca, J.V. (2007). La diversidad poblacional de Colombia en el tiempo y el espacio: estudio craneométrico. Rev. Acad. Colomb. Cienc. Exactas Fis. Nat. *31*, 321–346. https://doi.org/10.18257/raccefyn.31(120).2007.2343.

28. Rodríguez Cuenca, J.V. (1992). Características físicas de la población prehispánica de la cordillera Oriental: implicaciones etnogenéticas. Maguaré *8*, 7–45.

29. Delgado, M. (2012). Dental and craniofacial diversity in the northern Andes, and the early peopling of South America. In Southbound: Late Pleistocene Peopling of Latin America, L. Miotti, M. Salemme, N. Flegenheimer, and T. Goebel, eds. (Center for the Study of the First Americans, Texas A&M University), pp. 33–38.

30. Delgado, M. (2017). Holocene population history of the Sabana de Bogotá region, Northern South America: An assessment of the craniofacial shape variation. Am. J. Phys. Anthropol. *162*, 350–369. https://doi.org/10.1002/ajpa.23124.

31. Aceituno, F.J., and Loaiza, N. (2007). Domesticación del bosque en el Cauca medio colombiano entre el Pleistoceno final y el Holoceno medio. BAR International Series 1654 (Archaeopress).

32. López, C. (2008). Landscape Development and the Evidence for Early Human Occupation in the Inter-Andean Tropical Lowlands of the Magdalena River, Colombia (Syllaba Press).

33. Boada, A.M., and Cardale, M. (2017). Cronología de la Sabana de Bogotá (Comparative Archaeology Database, University of Pittsburgh). http://www.cadb.pitt.edu/muiscacrono/muiscacrono.pdf.

34. Langebaek, C.H. (1995). Arqueología Regional en el Territorio muisca: Estudio de los Valles de Fúquene y Susa (University of Pittsburgh Latin American Archaeology Publications).

35. Hoopes, J.W. (2005). The emergence of social complexity in the Chibchan world of southern Central America and northern Colombia, AD 300–600. J. Archaeol. Res. *13*, 1–47. https://doi.org/10.1007/s10814-005-0809-4.

36. Constenla Umaña, A. (1991) Las Lenguas del Área Intermedia: Introducción a Su Estudio Areal (Editorial Universidad de Costa Rica).

37. Krettek, K.-L., Casas-Vargas, A., Mas-Sandoval, A., Alvis, L.A., Reiter, E., Madero, J.M., Urban, M., Vargas, J.C.N., Usaquén, W., Rodríguez Cuenca, J.V., et al. (2025). A 6000-year-long genomic transect from the Bogotá Altiplano reveals multiple genetic shifts in the demographic history of Colombia. Sci. Adv. *11*, eads6284. https://doi.org/10.1126/sciadv.ads6284.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

38. Peña León, G.A. (2010). Arrancaplumas, un yacimiento de antiguos pescadores en los raudales del río Magdalena (Colombia). PhD thesis (Universidad Autónoma de Madrid).

39. Cifuentes Toro, A. (1993). Arrancaplumas y Guataquí: dos periodos arqueológicos en el valle medio del Magdalena. Bol. Arqueol. FIAN *8*, 3–88.

40. Rodríguez Cuenca, J.V. (2001). Craneometría de la población prehispánica de los Andes orientales de Colombia: diversidad, adaptación y etnogénesis. Implicaciones para el poblamiento americano. In Los Chibchas: Adaptación y Diversidad en los Andes Orientales de Colombia (Universidad Nacional de Colombia and Colciencias), J.V. Rodríguez Cuenca, ed., pp. 251–310.

41. Rodríguez Flórez, C.D., and Colantonio, S.E. (2015). Biological affinities and regional microevolution among pre-Hispanic communities of Colombia's Northern Andes. Anthropol. Anz. *72*, 141–168. https://doi.org/10.1127/anthranz/2015/0454.

42. Boada Rivas, A.M. (1999). Organización social y económica en la aldea muisca de El Venado valle de Samacá, Boyacá. Rev. Colomb. Antropol. *35*, 118–145. https://doi.org/10.22380/2539472X.1320.

43. Langebaek, C.H. (2019). Los Muiscas: La Historia Milenaria de un Pueblo Chibcha (Debate).

44. Boada, A.M. (2025). Archaeology of the Bogotá Chiefdom and Its Predecessors. In Memoirs in Latin American Archaeology, No. 30 (University of Pittsburgh).

45. Boada Rivas, A.M. (2018). Control sobre tierras, sistemas de camellones, canales y mano de obra durante el periodo prehispánico en la sabana de Bogotá, Colombia. Latin Am. Antiq. *29*, 660–680. https://doi.org/10.1017/laq.2018.44.

46. Kennett, D.J., Lipson, M., Prufer, K.M., Mora-Marín, D., George, R.J., Rohland, N., Robinson, M., Trask, W.R., Edgar, H.H.J., Hill, E.C., et al. (2022). South-to-north migration preceded the advent of intensive farming in the Maya region. Nat. Commun. *13*, 1530. https://doi.org/10.1038/s41467-022-29158-y.

47. Ospina, J.P., and Archila, S. (2021). Marking graves and intruding on the dead: An archaeothanatological analysis to unveil posthumous experiences of death and remembrance at the site of Checua, Colombia (7580–5052 cal BP). Quat. Int. *578*, 120–130. https://doi.org/10.1016/j.quaint.2020.07.042.

48. Capodiferro, M.R., Aram, B., Raveane, A., Rambaldi Migliore, N., Colombo, G., Ongaro, L., Rivera, J., Mendizábal, T., Hernández-Mora, I., Tribaldos, M., et al. (2021). Archaeogenomic distinctiveness of the Isthmo-Colombian area. Cell *184*, 1706–1723.e24. https://doi.org/10.1016/j.cell.2021.02.040.

49. Moreno-Mayar, J.V., Vinner, L., de Barros Damgaard, P., de la Fuente, C., Chan, J., Spence, J.P., Allentoft, M.E., Vimala, T., Racimo, F., Pinotti, T., et al. (2018). Early human dispersals within the Americas. Science *362*, eaav2621. https://doi.org/10.1126/science.aav2621.

50. Posth, C., Nakatsuka, N., Lazaridis, I., Skoglund, P., Mallick, S., Lamnidis, T.C., Rohland, N., Nägele, K., Adamski, N., Bertolini, E., et al. (2018). Reconstructing the Deep Population History of Central and South America. Cell *175*, 1185–1197.e22. https://doi.org/10.1016/j.cell.2018.10.027.

51. Mora, G., and Pratt, L.M. (2002). Carbon isotopic evidence from paleosols for mixed C3/C4 vegetation in the Bogota Basin, Colombia. Quat. Sci. Rev. *21*, 985–995. https://doi.org/10.1016/S0277-3791(01)00079-8.

52. Boom, A., Mora, G., Cleef, A.M., and Hooghiemstra, H. (2001). High altitude C4 grasslands in the northern Andes: relicts from glacial conditions? Rev. Palaeobot. Palynol. *115*, 147–160. https://doi.org/10.1016/S0034-6667(01)00056-2.

53. Triana Vega, A.V., and Pérez Crespo, V.A. (2022). Variación ambiental en los sitios arqueológicos del Holoceno temprano y medio de Tequendama y Aguazuque, Colombia. Bol. Soc. Geol. Mex. *74*, A140622. https://doi.org/10.18268/BSGM2022v74n3a140622.

54. Tessone, A., Colonese, A.C., Delgado, M.E., Pezo-Lanfranco, L., Santana-Sagredo, F., and Barberena, R. (2026). Isotopes and human organizational diversity in South America. J. Archaeol. Sci. *186*, 106460. https://doi.org/10.1016/j.jas.2025.106460.

55. Mejía Cano, M.B. (2018). Uso de recursos vegetales en grupos de cazadores-recolectores (ca. 9000–3000 ap), del norte de la Sabana de Bogotá: análisis arqueobotánico de fitolitos y almidones en artefactos líticos y cálculo dental. Master's thesis (Universidad de los Andes).

56. Barbieri, C., Barquera, R., Arias, L., Sandoval, J.R., Acosta, O., Zurita, C., Aguilar-Campos, A., Tito-Álvarez, A.M., Serrano-Osuna, R., Gray, R.D., et al. (2019). The Current Genomic Landscape of Western South America: Andes, Amazonia, and Pacific Coast. Mol. Biol. Evol. *36*, 2698–2713. https://doi.org/10.1093/molbev/msz174.

57. Perego, U.A., Angerhofer, N., Pala, M., Olivieri, A., Lancioni, H., Hooshiar Kashani, B., Carossa, V., Ekins, J.E., Gómez-Carballa, A., Huber, G., et al. (2010). The initial peopling of the Americas: a growing number of founding mitochondrial genomes from Beringia. Genome Res. *20*, 1174–1179. https://doi.org/10.1101/gr.109231.110.

58. Díaz-Matallana, M., Gómez Gutiérrez, A., Briceño, I., and Rodríguez Cuenca, J.V. (2016). Genetic analysis of Paleo-Colombians from Nemocón, Cundinamarca provides insights on the early peopling of northwestern South America. Rev. Acad. Colomb. Cienc. Exactas Fis. Nat. *40*, 461–483. https://doi.org/10.18257/raccefyn.328.

59. Behar, D.M., van Oven, M., Rosset, S., Metspalu, M., Loogväli, E.-L., Silva, N.M., Kivisild, T., Torroni, A., and Villems, R. (2012). A "Copernican" Reassessment of the Human Mitochondrial DNA Tree from its Root. Am. J. Hum. Genet. *90*, 675–684. https://doi.org/10.1016/j.ajhg.2012.03.002.

60. Tamm, E., Kivisild, T., Reidla, M., Metspalu, M., Smith, D.G., Mulligan, C.J., Bravi, C.M., Rickards, O., Martinez-Labarga, C., Khusnutdinova, E.K., et al. (2007). Beringian standstill and spread of Native American founders. PLoS One *2*, e829. https://doi.org/10.1371/journal.pone.0000829.

61. Achilli, A., Perego, U.A., Bravi, C.M., Coble, M.D., Kong, Q.-P., Woodward, S.R., Salas, A., Torroni, A., and Bandelt, H.-J. (2008). The Phylogeny of the Four Pan American MtDNA Haplogroups: Implications for Evolutionary and Disease Studies. PLoS One *3*, e1764. https://doi.org/10.1371/journal.pone.0001764.

62. Morales-Arce, A.Y., Hofman, C.A., Duggan, A.T., Benfer, A.K., Katzenberg, M.A., McCafferty, G., and Warinner, C. (2017). Successful reconstruction of whole mitochondrial genomes from ancient Central America and Mexico. Sci. Rep. *7*, 18100. https://doi.org/10.1038/s41598-017-18356-0.

63. Rivas, S., Calderón, D., Marulanda, C., Mendoza, L.F., Scott, G.R., Poulson, S.R., and Delgado, M. (2024). Stable isotopes and paleodiet of the ancient inhabitants of Nueva Esperanza: A late Holocene site from Sabana de Bogotá (Colombia). Int. J. Osteoarchaeol. *34*, e3244. https://doi.org/10.1002/oa.3244.

64. Gamboa Mendoza, J.A. (2013). El Cacicazgo muisca en los Años Posteriores a la Conquista: del Psihipqua al Cacique Colonial, 1537–1575 (Instituto Colombiano de Antropología e Historia).

65. Villamarin, J.A., and Villamarin, J.E. (1975). Kinship and Inheritance among the Sabana de Bogotá Chibcha at the Time of Spanish Conquest. Ethnology *14*, 173–179. https://doi.org/10.2307/3773088.

66. Argüello García, P.M. (2020). Cambios en las prácticas funerarias prehispánicas en el altiplano Cundiboyacense (centro de Colombia) desde el periodo Precerámico al Muisca Tardío. Un análisis exploratorio. Bol. Antropol. *35*, 40–71. https://doi.org/10.17533/udea.boan.v35n60a04.

67. Vélez, M.I., Hooghiemstra, H., Metcalfe, S., Wille, M., and Berrío, J.C. (2006). Late Glacial and Holocene environmental and climatic changes from a limnological transect through Colombia, northern South America. Palaeogeogr. Palaeoclimatol. Palaeoecol. *234*, 81–96. https://doi.org/10.1016/j.palaeo.2005.10.020.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

68. Aceituno, F.J., and Loaiza, N. (2014). Early and Middle Holocene evidence for plant use and cultivation in the Middle Cauca River Basin, Cordillera Central (Colombia). Quat. Sci. Rev. *86*, 49–62. https://doi.org/10.1016/j.quascirev.2013.12.013.

69. Aceituno, F.J., and Loaiza, N. (2018). The origins and early development of plant food production and farming in Colombian tropical forests. J. Anthropol. Archaeol. *49*, 161–172. https://doi.org/10.1016/j.jaa.2017.12.007.

70. Gómez, A., Berrío, J.C., Hooghiemstra, H., Becerra, M., and Marchant, R. (2007). A Holocene pollen record of vegetation change and human impact from Pantano de Vargas, an intra-Andean basin of Duitama, Colombia. Rev. Palaeobot. Palynol. *145*, 143–157. https://doi.org/10.1016/j.revpalbo.2006.10.002.

71. Constenla Umaña, A. (2012). Chibchan languages. In The Indigenous Languages of South America: a Comprehensive Guide, L. Campbell and V. Grondona, eds. (De Gruyter), pp. 391–440. https://doi.org/10.1515/9783110258035.391.

72. Argüello, P. (2023) Tunja Prehispánica: Estudio de los Patrones de Asentamiento (Editorial de la Universidad Pedagógica y Tecnológica de Colombia-UPTC).

73. Vélez, M.I., Salgado, J., Delgado, M., Patiño, L.F., Bird, B., Escobar, J.H., and Fajardo, S. (2024). Humans and climate in ritualized landscapes, the case of Lake Tota in the eastern highlands of Colombia. Holocene *34*, 1587–1597. https://doi.org/10.1177/09596836241266408.

74. van Geel, B., and van der Hammen, T. (1973). Upper Quaternary vegetational and climatic sequence of the Fuquene area (Eastern Cordillera, Colombia). Palaeogeogr. Palaeoclimatol. Palaeoecol. *14*, 9–92. https://doi.org/10.1016/0031-0182(73)90064-3.

75. van der Hammen, T., and González, E. (1965). A pollen diagram from "Laguna de la Herrera" (Sabana de Bogotá). Leidsche Geol. Meded. *32*, 183–191.

76. Argüello, P. (2015). Subsistence economy and chiefdom emergence in the Muisca area: a study of the Valle de Tena. PhD thesis (University of Pittsburgh).

77. Fajardo Bernal, S. (2016). Prehispanic and colonial settlement patterns of the Sogamoso Valley. PhD thesis (University of Pittsburgh).

78. Escallón, M.F. (2004). Decoración, Cronología y Territorio: un Estudio Comparativo de la Cerámica Herrera del Altiplano Cundiboyacense. Master's thesis (Universidad de los Andes).

79. Alpaslan-Roodenberg, S., Anthony, D., Babiker, H., Bánffy, E., Booth, T., Capone, P., Deshpande-Mukherjee, A., Eisenmann, S., Fehren-Schmitz, L., Frachetti, M., et al. (2021). Ethics of DNA research on human remains: five globally applicable guidelines. Nature *599*, 41–46. https://doi.org/10.1038/s41586-021-04008-x.

80. Ávila-Arcos, M.C., de la Fuente Castro, C., Nieves-Colón, M.A., and Raghavan, M. (2022). Recommendations for sustainable ancient DNA research in the global south: Voices from a new generation of paleogenomicists. Front. Genet. *13*, 880170. https://doi.org/10.3389/fgene.2022.880170.

81. Kowal, E., Weyrich, L.S., Argüelles, J.M., Bader, A.C., Colwell, C., Cortez, A.D., Davis, J.L., Figueiro, G., Fox, K., Malhi, R.S., et al. (2023). Community partnerships are fundamental to ethical ancient DNA research. HGG Adv. *4*, 100161. https://doi.org/10.1016/j.xhgg.2022.100161.

82. Pinhasi, R., Fernandes, D., Sirak, K., Novak, M., Connell, S., Alpaslan-Roodenberg, S., Gerritsen, F., Moiseyev, V., Gromov, A., Raczky, P., et al. (2015). Optimal Ancient DNA Yields from the Inner Ear Part of the Human Petrous Bone. PLoS One *10*, e0129102. https://doi.org/10.1371/journal.pone.0129102.

83. Hansen, H.B., Damgaard, P.B., Margaryan, A., Stenderup, J., Lynnerup, N., Willerslev, E., and Allentoft, M.E. (2017). Comparing Ancient DNA Preservation in Petrous Bone and Tooth Cementum. PLoS One *12*, e0170940. https://doi.org/10.1371/journal.pone.0170940.

84. Pinhasi, R., Fernandes, D.M., Sirak, K., and Cheronet, O. (2019). Isolating the human cochlea to generate bone powder for ancient DNA analysis. Nat. Protoc. *14*, 1194–1205. https://doi.org/10.1038/s41596-019-0137-7.

85. Sirak, K., Fernandes, D., Cheronet, O., Harney, E., Mah, M., Mallick, S., Rohland, N., Adamski, N., Broomandkhoshbacht, N., Callan, K., et al. (2020). Human auditory ossicles as an alternative optimal source of ancient DNA. Genome Res. *30*, 427–436. https://doi.org/10.1101/gr.260141.119.

86. Sirak, K.A., Fernandes, D.M., Cheronet, O., Novak, M., Gamarra, B., Balassa, T., Bernert, Z., Cséki, A., Dani, J., Gallina, J.Z., et al. (2017). A minimally-invasive method for sampling human petrous bones from the cranial base for ancient DNA analysis. BioTechniques *62*, 283–289. https://doi.org/10.2144/000114558.

87. Rohland, N., Glocke, I., Aximu-Petri, A., and Meyer, M. (2018). Extraction of highly degraded DNA from ancient bones, teeth and sediments for high-throughput sequencing. Nat. Protoc. *13*, 2447–2461. https://doi.org/10.1038/s41596-018-0050-5.

88. Rohland, N., Harney, E., Mallick, S., Nordenfelt, S., and Reich, D. (2015). Partial uracil–DNA–glycosylase treatment for screening of ancient DNA. Philos. Trans. R. Soc. Lond., B Biol. Sci. *370*, 20130624. https://doi.org/10.1098/rstb.2013.0624.

89. Gansauge, M.-T., Aximu-Petri, A., Nagel, S., and Meyer, M. (2020). Manual and automated preparation of single-stranded DNA libraries for the sequencing of DNA from ancient biological remains and other sources of highly degraded DNA. Nat. Protoc. *15*, 2279–2300. https://doi.org/10.1038/s41596-020-0338-0.

90. Rohland, N., and Reich, D. (2012). Cost-effective, high-throughput DNA sequencing libraries for multiplexed target capture. Genome Res. *22*, 939–946. https://doi.org/10.1101/gr.128124.111.

91. Kapp, J.D., Green, R.E., and Shapiro, B. (2021). A fast and efficient single-stranded genomic library preparation method optimized for ancient DNA. J. Hered. *112*, 241–249. https://doi.org/10.1093/jhered/esab012.

92. Maricic, T., Whitten, M., and Pääbo, S. (2010). Multiplexed DNA sequence capture of mitochondrial genomes using PCR products. PLoS One *5*, e14004. https://doi.org/10.1371/journal.pone.0014004.

93. Fu, Q., Hajdinjak, M., Moldovan, O.T., Constantin, S., Mallick, S., Skoglund, P., Patterson, N., Rohland, N., Lazaridis, I., Nickel, B., et al. (2015). An early modern human from Romania with a recent Neanderthal ancestor. Nature *524*, 216–219. https://doi.org/10.1038/nature14558.

94. Mathieson, I., Lazaridis, I., Rohland, N., Mallick, S., Patterson, N., Roodenberg, S.A., Harney, E., Stewardson, K., Fernandes, D., Novak, M., et al. (2015). Genome-wide patterns of selection in 230 ancient Eurasians. Nature *528*, 499–503. https://doi.org/10.1038/nature16152.

95. Haak, W., Lazaridis, I., Patterson, N., Rohland, N., Mallick, S., Llamas, B., Brandt, G., Nordenfelt, S., Harney, E., Stewardson, K., et al. (2015). Massive migration from the steppe was a source for Indo-European languages in Europe. Nature *522*, 207–211. https://doi.org/10.1038/nature14317.

96. Rohland, N., Mallick, S., Mah, M., Maier, R., Patterson, N., and Reich, D. (2022). Three assays for in-solution enrichment of ancient human DNA at more than a million SNPs. Genome Res. *32*, 2068–2078. https://doi.org/10.1101/gr.276728.122.

97. Davidson, R., Roca-Rada, X., Ravishankar, S., Taufik, L., Haarkötter, C., Collen, E., Williams, M.P., Webb, P., Mahmud, M.I., Djami, E.N.I., et al. (2025). Optimized in-solution enrichment of over a million ancient human SNPs. Genome Biol. *26*, 190. https://doi.org/10.1186/s13059-025-03622-6.

98. Li, H., and Durbin, R. (2009). Fast and accurate short read alignment with Burrows–Wheeler transform. Bioinformatics *25*, 1754–1760. https://doi.org/10.1093/bioinformatics/btp324.

99. 1000 Genomes Project Consortium, Auton, A., Brooks, L.D., Durbin, R.M., Garrison, E.P., Kang, H.M., Korbel, J.O., Marchini, J.L., McCarthy,

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

S., McVean, G.A., et al. (2015). A global reference for human genetic variation. Nature *526*, 68–74. https://doi.org/10.1038/nature15393.

100. Korneliussen, T.S., Albrechtsen, A., and Nielsen, R. (2014). ANGSD: analysis of next generation sequencing data. BMC Bioinform. *15*, 356. https://doi.org/10.1186/s12859-014-0356-4.

101. Huang, Y., and Ringbauer, H. (2022). hapCon: estimating contamination of ancient genomes by copying from reference haplotypes. Bioinformatics *38*, 3768–3777. https://doi.org/10.1093/bioinformatics/btac390.

102. Fu, Q., Mittnik, A., Johnson, P.L.F., Bos, K., Lari, M., Bollongino, R., Sun, C., Giemsch, L., Schmitz, R., Burger, J., et al. (2013). A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes. Curr. Biol. *23*, 553–559. https://doi.org/10.1016/j.cub.2013.02.044.

103. Nakatsuka, N., Luisi, P., Motti, J.M.B., Salemme, M., Santiago, F., D'Angelo del Campo, M.D., Vecchi, R.J., Espinosa-Parrilla, Y., Prieto, A., Adamski, N., et al. (2020). Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. Nat. Commun. *11*, 3868. https://doi.org/10.1038/s41467-020-17656-w.

104. Raghavan, M., Steinrücken, M., Harris, K., Schiffels, S., Rasmussen, S., DeGiorgio, M., Albrechtsen, A., Valdiosera, C., Ávila-Arcos, M.C., Malaspinas, A.-S., et al. (2015). Genomic evidence for the Pleistocene and recent population history of Native Americans. Science *349*, aab3884. https://doi.org/10.1126/science.aab3884.

105. Nakatsuka, N., Lazaridis, I., Barbieri, C., Skoglund, P., Rohland, N., Mallick, S., Posth, C., Harkins-Kinkaid, K., Ferry, M., Harney, É., et al. (2020). A Paleogenomic Reconstruction of the Deep Population History of the Andes. Cell *181*, 1131–1145.e21. https://doi.org/10.1016/j.cell.2020.04.015.

106. Barquera, R., Del Castillo-Chávez, O., Nägele, K., Pérez-Ramallo, P., Hernández-Zaragoza, D.I., Szolek, A., Rohrlach, A.B., Librado, P., Childebayeva, A., Bianco, R.A., et al. (2024). Ancient genomes reveal insights into ritual life at Chichén Itzá. Nature *630*, 912–919. https://doi.org/10.1038/s41586-024-07509-7.

107. Bergström, A., McCarthy, S.A., Hui, R., Almarri, M.A., Ayub, Q., Danecek, P., Chen, Y., Felkel, S., Hallast, P., Kamm, J., et al. (2020). Insights into human genetic variation and population history from 929 diverse genomes. Science *367*, eaay5012. https://doi.org/10.1126/science.aay5012.

108. Bongers, J.L., Nakatsuka, N., O'Shea, C., Harper, T.K., Tantaleán, H., Stanish, C., and Fehren-Schmitz, L. (2020). Integration of ancient DNA with transdisciplinary dataset finds strong support for Inca resettlement in the south Peruvian coast. Proc. Natl. Acad. Sci. USA. *117*, 18359–18368. https://doi.org/10.1073/pnas.2005965117.

109. de la Fuente, C., Ávila-Arcos, M.C., Galimany, J., Carpenter, M.L., Homburger, J.R., Blanco, A., Contreras, P., Cruz Dávalos, D., Reyes, O., San Roman, M., et al. (2018). Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia. Proc. Natl. Acad. Sci. USA. *115*, E4006–E4012. https://doi.org/10.1073/pnas.1715688115.

110. Fernandes, D.M., Sirak, K.A., Ringbauer, H., Sedig, J., Rohland, N., Cheronet, O., Mah, M., Mallick, S., Olalde, I., Culleton, B.J., et al. (2021). A genetic history of the pre-contact Caribbean. Nature *590*, 103–110. https://doi.org/10.1038/s41586-020-03053-2.

111. Ferraz, T., Suarez Villagran, X., Nägele, K., Radzevičiūtė, R., Barbosa Lemes, R., Salazar-García, D.C., Wesolowski, V., Lopes Alves, M., Bastos, M., Rapp Py-Daniel, A., et al. (2023). Genomic history of coastal societies from eastern South America. Nat. Ecol. Evol. *7*, 1315–1330. https://doi.org/10.1038/s41559-023-02114-9.

112. Lindo, J., Haas, R., Hofman, C., Apata, M., Moraga, M., Verdugo, R.A., Watson, J.T., Viviano Llave, C., Witonsky, D., Beall, C., et al. (2018). The genetic prehistory of the Andean highlands 7000 years BP though European contact. Sci. Adv. *4*, eaau4921. https://doi.org/10.1126/sciadv.aau4921.

113. Mallick, S., Li, H., Lipson, M., Mathieson, I., Gymrek, M., Racimo, F., Zhao, M., Chennagiri, N., Nordenfelt, S., Tandon, A., et al. (2016). The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature *538*, 201–206. https://doi.org/10.1038/nature18964.

114. Moreno-Mayar, J.V., Potter, B.A., Vinner, L., Steinrücken, M., Rasmussen, S., Terhorst, J., Kamm, J.A., Albrechtsen, A., Malaspinas, A.-S., Sikora, M., et al. (2018). Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. Nature *553*, 203–207. https://doi.org/10.1038/nature25173.

115. Nägele, K., Posth, C., Iraeta Orbegozo, M., Chinique de Armas, Y., Hernández Godoy, S.T., González Herrera, U.M., Nieves-Colón, M.A., Sandoval-Velasco, M., Mylopotamitaki, D., Radzeviciute, R., et al. (2020). Genomic insights into the early peopling of the Caribbean. Science *369*, 456–460. https://doi.org/10.1126/science.aba8697.

116. Nakatsuka, N., Holguin, B., Sedig, J., Langenwalter, P.E., Carpenter, J., Culleton, B.J., García-Moreno, C., Harper, T.K., Martin, D., Martínez-Ramírez, J., et al. (2023). Genetic continuity and change among the Indigenous peoples of California. Nature *624*, 122–129. https://doi.org/10.1038/s41586-023-06771-5.

117. Popović, D., Molak, M., Ziółkowski, M., Vranich, A., Sobczyk, M., Vidaurre, D.U., Agresti, G., Skrzypczak, M., Ginalski, K., Lamnidis, T.C., et al. (2021). Ancient genomes reveal long-range influence of the pre-Columbian culture and site of Tiwanaku. Sci. Adv. *7*, eabg7261. https://doi.org/10.1126/sciadv.abg7261.

118. Prüfer, K., Racimo, F., Patterson, N., Jay, F., Sankararaman, S., Sawyer, S., Heinze, A., Renaud, G., Sudmant, P.H., de Filippo, C., et al. (2014). The complete genome sequence of a Neanderthal from the Altai Mountains. Nature *505*, 43–49. https://doi.org/10.1038/nature12886.

119. Rasmussen, M., Anzick, S.L., Waters, M.R., Skoglund, P., DeGiorgio, M., Stafford, T.W., Rasmussen, S., Moltke, I., Albrechtsen, A., Doyle, S.M., et al. (2014). The genome of a late Pleistocene human from a Clovis burial site in western Montana. Nature *506*, 225–229. https://doi.org/10.1038/nature13025.

120. Scheib, C.L., Li, H., Desai, T., Link, V., Kendall, C., Dewar, G., Griffith, P.W., Mörseburg, A., Johnson, J.R., Potter, A., et al. (2018). Ancient human parallel lineages within North America contributed to a coastal expansion. Science *360*, 1024–1027. https://doi.org/10.1126/science.aar6851.

121. Skoglund, P., Mallick, S., Bortolini, M.C., Chennagiri, N., Hünemeier, T., Petzl-Erler, M.L., Salzano, F.M., Patterson, N., and Reich, D. (2015). Genetic evidence for two founding populations of the Americas. Nature *525*, 104–108. https://doi.org/10.1038/nature14895.

122. Villa-Islas, V., Izarraras-Gomez, A., Larena, M., Campos, E.M.P., Sandoval-Velasco, M., Rodríguez-Rodríguez, J.E., Bravo-Lopez, M., Moguel, B., Fregel, R., Garfias-Morales, E., et al. (2023). Demographic history and genetic structure in pre-Hispanic Central Mexico. Science *380*, eadd6142. https://doi.org/10.1126/science.add6142.

123. Lazaridis, I., Patterson, N., Mittnik, A., Renaud, G., Mallick, S., Kirsanow, K., Sudmant, P.H., Schraiber, J.G., Castellano, S., Lipson, M., et al. (2014). Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature *513*, 409–413. https://doi.org/10.1038/nature13673.

124. Patterson, N., Moorjani, P., Luo, Y., Mallick, S., Rohland, N., Zhan, Y., Genschoreck, T., Webster, T., and Reich, D. (2012). Ancient admixture in human history. Genetics *192*, 1065–1093. https://doi.org/10.1534/genetics.112.145037.

125. Reich, D., Patterson, N., Campbell, D., Tandon, A., Mazieres, S., Ray, N., Parra, M.V., Rojas, W., Duque, C., Mesa, N., et al. (2012). Reconstructing Native American population history. Nature *488*, 370–374. https://doi.org/10.1038/nature11258.

126. Bronk Ramsey, C. (2009). Bayesian analysis of radiocarbon dates. Radiocarbon *51*, 337–360. https://doi.org/10.1017/S0033822200033865.

127. Reimer, P.J., Austin, W.E.N., Bard, E., Bayliss, A., Blackwell, P.G., Bronk Ramsey, C., Butzin, M., Cheng, H., Edwards, R.L., Friedrich, M., et al. (2020). The IntCal20 Northern Hemisphere radiocarbon age calibration

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

curve (0–55 cal kBP). Radiocarbon *62*, 725–757. https://doi.org/10.1017/RDC.2020.41.

128. Bozzi, D., Broomandkhoshbacht, N.Z., Delgado, M., Buikstra, J.E., Amorim, C.E.G., Kassadjikova, K., Estrada, M.P., Greub, G., Rascovan, N., Šmajs, D., et al. (2026). A 5500-year-old *Treponema pallidum* genome from Sabana de Bogotá, Colombia. Science *391*, eadw3020. https://doi.org/10.1126/science.adw3020.

129. Triana, A.V. (2019). Dieta y acceso a recursos determinadas a partir del sexo en grupos de cazadores recolectores de la sabana de Bogotá durante el Holoceno temprano y medio. PhD thesis (Universidad de los Andes).

130. Archila, S., and Langebaek, C. (2015). Dieta y Uso de Recursos Vegetales de una Población Humana de Hace 5000 Años en los Andes Orientales de Colombia, el Caso de Ubaté. Final report (Universidad de los Andes).

131. Gascuel, O. (1997). BIONJ: an improved version of the NJ algorithm based on a simple model of sequence data. Mol. Biol. Evol. *14*, 685–695. https://doi.org/10.1093/oxfordjournals.molbev.a025808.

132. Weissensteiner, H., Pacher, D., Kloss-Brandstätter, A., Forer, L., Specht, G., Bandelt, H.-J., Kronenberg, F., Salas, A., and Schönherr, S. (2016). HaploGrep 2: mitochondrial haplogroup classification in the era of high-throughput sequencing. Nucleic Acids Res. *44*, W58–W63. https://doi.org/10.1093/nar/gkw233.

133. Schönherr, S., Weissensteiner, H., Kronenberg, F., and Forer, L. (2023). Haplogrep 3 – an interactive haplogroup classification and analysis platform. Nucleic Acids Res. *51*, W263–W268. https://doi.org/10.1093/nar/gkad284.

134. Olalde, I., Mallick, S., Patterson, N., Rohland, N., Villalba-Mouco, V., Silva, M., Dulias, K., Edwards, C.J., Gandini, F., Pala, M., et al. (2019). The genomic history of the Iberian Peninsula over the past 8000 years. Science *363*, 1230–1234. https://doi.org/10.1126/science.aav4040.

135. Ringbauer, H., Novembre, J., and Steinrücken, M. (2021). Parental relatedness through time revealed by runs of homozygosity in ancient DNA. Nat. Commun. *12*, 5425. https://doi.org/10.1038/s41467-021-25289-w.

136. Chintalapati, M., Patterson, N., and Moorjani, P. (2022). The spatiotemporal patterns of major human admixture events during the European Holocene. eLife *11*, e77625. https://doi.org/10.7554/eLife.77625.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Biological samples		
212 newly reported ancient individuals	This paper	N/A
Deposited data		
Sequencing data for 212 newly reported ancient individuals	This paper	ENA: PRJEB110479
Critical commercial assays		
Twist Ancient Human DNA Panel	Twist Bioscience	104305
Twist High Concentration Mitochondrial Panel	Twist Bioscience	104562
HiSeq X Ten Reagent Kit v2.5	Illumina	FC-501-2521
NextSeq 500/550 High Output Kit v2.5	Illumina	FC-404-2002
NovaSeq S4 300 cycles	Illumina	20028312
NovaSeq X 10B 300cycles	Illumina	20085594
NovaSeq X 25B 100cycles	Illumina	20125967
NovaSeq X 25B 300cycles	Illumina	20104706
Software and algorithms		
DReichLab/ADNA-Tools	https://github.com/dReichLab/ADNA-Tools	N/A
DReichLab/adna-workflow	https://github.com/dReichLab/adna-workflow	N/A
OxCal v.4.4	https://c14.arch.ox.ac.uk/oxcal.html	N/A
EIGENSOFT v.7.2.1	https://github.com/DReichLab/EIG	N/A
BWA v.0.7.15	https://github.com/lh3/bwa	N/A
Picard MarkDuplicates v.2.17.10	http://broadinstitute.github.io/picard/	N/A
ADMIXTOOLS v.7.0	https://github.com/DReichLab/AdmixTools	N/A
ADMIXTOOLS2 v.2.0	https://github.com/uqrmaie1/admixtools	N/A
DATES v.4702	https://github.com/priyamoorjani/DATES	N/A
hapROH v.0.3a4	https://github.com/hringbauer/hapROH	N/A
HaploGrep2	https://github.com/seppinho/haplogrep-cmd	N/A
HaploGrep3	https://github.com/genepi/haplogrep3	N/A
hapConX	https://github.com/hringbauer/hapROH	N/A
contamMix v1.0-12	https://github.com/plfjohnson/contamMix	N/A
ANGSD	https://github.com/ANGSD/angsd	N/A
R v.4.4.2	https://www.r-project.org/	N/A
Chemicals, peptides, and recombinant proteins		
2X HI-RPM hybridization buffer	Agilent Technologies	5190-0403
Herculase II Fusion DNA Polymerase	Agilent Technologies	600679
Pfu Turbo Cx Hotstart DNA Polymerase	Agilent Technologies	600412
50% PEG 8000	Anatrace	OPTIMIZE-82100ML
0.5M EDTA (pH8.0)	BioExpress	E177
Sera-Mag™ SpeedBead Carboxylate-Modified Magnetic Particles	Cytiva Life Sciences	65152105050250
silica magnetic beads	G-Biosciences	786-916
10X T4 RNA Ligase Buffer	New England Biolabs	B0216L
Bst DNA Polymerase 2.0, large frag.	New England Biolabs	M0537
UGI	New England Biolabs	M0281
USER enzyme	New England Biolabs	M5505

(*Continued on next page*)

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

Continued

REAGENT or RESOURCE	SOURCE	IDENTIFIER
50% PEG 8000	New England Biolabs	
Buffer PB	QIAGEN	19066
Buffer PE concentrate	QIAGEN	19065
1M Tris-HCl (pH8.0)	Thermo Fisher Scientific	AM9856
1M NaOH	Sigma-Aldrich	71463
20% SDS	Sigma-Aldrich	5030
3M Sodium Acetate (pH5.2)	Sigma-Aldrich	S7899
5M NaCl	Sigma-Aldrich	S5150
Ethanol	Sigma-Aldrich	E7023
Guanidine hydrochloride	Sigma-Aldrich	G3272
Isopropanol	Sigma-Aldrich	650447
PEG-8000	Sigma-Aldrich	89510
Proteinase K	Sigma-Aldrich	P6556
Tween-20	Sigma-Aldrich	P9416
Water	Sigma-Aldrich	W4502
10X Buffer Tango	Thermo Fisher Scientific	BY5
50X Denhardt's solution	Thermo Fisher Scientific	750018
AccuPrime Pfx Polymerase (2.5U/μL)	Thermo Fisher Scientific	12344032
ATP	Thermo Fisher Scientific	R0441
dNTP Mix	Thermo Fisher Scientific	R1121
Dynabeads MyOne Streptavidin C1 beads	Thermo Fisher Scientific	65002
FastAP (1U/μL)	Thermo Fisher Scientific	EF0651
GeneAmp 10X PCR Gold Buffer	Thermo Fisher Scientific	4379874
Human Cot-1 DNA	Thermo Fisher Scientific	15279011
Klenow Fragment (10U/μL)	Thermo Fisher Scientific	EP0052
Maxima Probe qPCR 2xMM	Thermo Fisher Scientific	K0233
Maxima SYBR Green kit	Thermo Fisher Scientific	K0251
Salmon sperm DNA	Thermo Fisher Scientific	15632-011
SSC Buffer (20X)	Thermo Fisher Scientific	AM9770
T4 DNA Ligase	Thermo Fisher Scientific	EL0012
T4 DNA Ligase, HC (30U/μL)	Thermo Fisher Scientific	EL0013
T4 DNA Polymerase	Thermo Fisher Scientific	EP0062
Equinox Library Amp Mix, 96 rxn	Twist Bioscience	104108
T4 Polynucleotide Kinase	Thermo Fisher Scientific	EK0032

EXPERIMENTAL MODEL AND STUDY PARTICIPANT DETAILS

Ancient Individuals

Descriptions of the archaeological contexts of the ancient individuals analyzed in this study are provided in Data S1, section 1.

METHOD DETAILS

Ethical Considerations

The analysis of ancient DNA has the potential to have strong impacts on communities that are geographically, culturally, or biologically related to this research. We adhered to the guidelines established by the Colombian institution responsible for archaeological heritage, the Instituto Colombiano de Antropología e Historia (ICANH) in accordance with globally applicable recommendations for ancient DNA work,[79] which call for obtaining required permissions, complying with local regulations, minimizing the impact of sampling on collections of human remains, and incorporating interdisciplinary and regionally diverse perspectives into ancient DNA work.

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

We were informed by ongoing discussions about equitable ancient DNA research particularly in the Global South, which emphasize that ancient DNA research is strengthened by involving local institutions in the research process, building equitable research partnerships, sharing knowledge and resources, and engaging with local communities where appropriate.[80,81]

Herrera and Muisca descendant communities continue to inhabit the region today, so our team has involved the communities that could be affected by this work, not only seeking permission but also guidance on dissemination and impact. During the course of this work, we met with, consulted, shared information with, and learned from local community members in Colombia, specifically around the Sabana de Bogotá, including both academic and non-academic and Indigenous and non-Indigenous communities. We conducted outreach efforts, connecting with these stakeholders through presentations and interviews held at the Instituto Colombiano de Antropología e Historia (ICANH) in Bogotá on November 28, 2023, and meetings and discussions with the local communities affiliated with La Corporación Universitaria Minuto de Dios (Uniminuto) in Bogotá on December 1, 2023. Some of the results presented here were shown at the 2024 Colombian Congress of Archaeology in Santa Marta, Colombia. Following these meetings, M.D. continues to update these audiences on research progress, ensuring that this work has the support, benefits from the insight, and involves the participation of local academic partners and community members.

Sampling of ancient individuals

Skeletal material screened for ancient DNA was sampled, exported, and analyzed with full permission from Instituto Colombiano de Antropología e Historia (ICANH). This project proceeded under archaeological intervention license number 8270 issued to M.D. on August 20, 2019. Samples were taken from skeletal materials curated at different institutions: Museo Nacional de Colombia; Instituto de Ciencias Naturales, Universidad Nacional de Colombia; Universidad de los Andes; Universidad Pedagógica y Tecnológica de Colombia (UPTC); and El Departamento de Estudios Sociales, INGETEC. Descriptions of the archaeological sites from which the skeletal material in this study derives are in Data S1, section 1.

Ancient DNA data generation, bioinformatics, and quality control

When sampling human skeletal material for this work, we prioritized skeletal elements recognized to be especially DNA-rich.[82–85] When skulls were complete, we generated powder from the cochlea by approaching it from the cranial base.[86] In other cases, we generated powder from bone and tooth samples[84] in ancient DNA clean room facilities at Harvard Medical School (Boston), the University of Vienna (Vienna), or the University of California, Santa Cruz (Fehren-Schmitz Lab, UCSC Paleogenomics) (Data S2, Table S27). DNA was extracted from powder using a method optimized for retaining small DNA fragments.[87] From the DNA extracts, we prepared truncated dual-barcoded double-stranded libraries[88] or full-length dual-indexed single-stranded libraries.[89] We produced DNA libraries from 238 unique individuals, sometimes multiple libraries per sample. All libraries were produced at Harvard Medical School, except for one library each for I23786 and I23795 which were produced at UCSC Paleogenomics. For all libraries (ds.half and ss.USER), we used *Escherichia coli* UDG (in the enzyme mix "USER" from NEB), which removes uracils (except when a deaminated cytosine was methylated) and cuts DNA strands at abasic sites, but inefficiently cuts terminal dephosphorylated uracils, thereby leaving C-to-T 'damage' characteristic of aDNA. For all double-stranded libraries we replaced MinElute columns for reaction clean-ups with magnetic silica beads and Qiagen buffer PB and used SPRI beads instead of MinElute columns for PCR cleanup at the end of library preparation.[90] We added two seven-base-pair (bp) indexing barcodes to the truncated adapters of each double-stranded library (for shotgun sequencing to the library or after enrichment) and thereby completed the adapter sites for sequencing (it is not necessary to add these barcodes to single-stranded libraries, which are already indexed and adapter sites are completed from library preparation). At UCSC Paleogenomics, USER-treated DNA extracts were used to prepare dual-indexed single-stranded libraries.[91]

We enriched the libraries using one of the following strategies: 1) for sequences overlapping mtDNA[92] and approximately 1.2 million nuclear targets ("1240k") simultaneously[93–95]; or 2) using the Twist Ancient Human DNA Panel[96] (Twist Bioscience) for approximately 1.4 million SNPs. The Twist reagent includes all SNPs in the "1240k" capture set and has been shown to generate data that are fully co-analyzable with shotgun sequencing data[96] and shows no evidence of allelic bias.[97] To generate paired-end reads, enriched libraries were sequenced on the Illumina NextSeq500 instrument for 2x76 cycles or on the Illumina HiSeq X Ten or NovaSeq instrument for 2x101 (300 cycles kits) or 2x61 (100 cycles kits) cycles. Indices were read with 2x7 cycles (double-stranded libraries) or 2x8 cycles (single-stranded libraries).

The resulting read pairs were separated using library-specific barcode pairs (for double-stranded libraries) or index pairs (for single-stranded libraries) and merged prior to alignment. We retained reads that showed no more than one mismatch between the forward and reverse base if base quality was at least 20, or three mismatches if base quality was less than 20. A custom toolkit (available at https://github.com/DReichLab/ADNA-Tools) was used for merging and trimming adapters and barcodes. Merged sequences were mapped to the human reference genome version (hg19) and the Reconstructed Sapiens Reference Sequence (RSRS)[59] using the samse command of the Burrows-Wheeler aligner[98] (v.0.7.15). Duplicate sequences were removed following alignment using the Picard MarkDuplicates tool (v.2.17.10; http://broadinstitute.github.io/picard/). For variant calling, we used an adaptive pseudohaploid approach. We estimated error rates empirically, assuming that monomorphic sites in 1000 Genomes data[99] are truly monomorphic, and then stratified these error rate estimates by library type, SNP bases (variant or reference), read position, strand, and mapping and base quality, with the base positions more than 10 bases from the 5′ or 3′ end being considered central and merged. These error rates are determined from the sample BAM, allowing for an unbiased adaptive pulldown procedure. Because at a (C,T) SNP the

estimated error *E*(C,T) for C->T may be very different from E(T,C) for T->C, we use a symmetric function *S* and calculate (for example) S=max[*E*(C,T),*E*(T,C)]. We threshold *S* with a parametric value of 0.02 and bases with *S* below this value go into a pileup of reliable bases out of which a random base is selected. The error achieved is smaller than the threshold, which is an upper bound on the error of each potential base that contributes to the pileup.

From the resulting data, we excluded any individuals covered at <15,000 SNPs on the 1240k capture set and excluded or flagged individuals as potentially contaminated if the C->T substitution rate was less than 3% in UDG-treated libraries or less than 10% in non-UDG-treated libraries, the lower bound for ANGSD[100] or hapConX[101] was >0.01, the mtDNA consensus match upper bound estimated using contamMix v1.0-12[102] was <0.90, or the sex ratio was intermediate between 0.05–0.3 (Data S2, Table S1). Twenty-four individuals were excluded based on coverage or evidence of contamination and two individuals (I23670 and I23795) were excluded because direct radiocarbon dates on the sampled bones were inconsistent with the chronological context of the sites to which they had been attributed. One individual from first-degree relative pairs was excluded from population genetics analysis when the data were grouped; in all cases, we retained the higher-coverage individual. Library information is in Data S2, Table S27.

Dataset assembly

We merged data from 212 individuals passing quality control checks into a co-analysis dataset of previously published data from ancient and present-day individuals[37,46,48–50,103–122] whose genomes had been shotgun sequenced or enriched for sequences covering a canonical set of ~2M SNPs,[96] which includes targeted SNPs as well as off-target sites (commonly captured because of physical proximity). We refer to this as the '2M' dataset. We also merged the data with Affymetrix Human Origins (HO) SNP genotyping data,[56,121,123,124] which allows us to leverage data from a more genetically diverse range of present-day Indigenous American populations. We refer to this as the '2M.HO' dataset. For PCA, we merged these data with a dataset of modern Indigenous American populations genotyped on an Illumina SNP array using unmasked and unadmixed individuals only.[125] We refer to this as the '2M.Illumina' dataset. The populations included in our co-analysis datasets are listed in Data S2, Table S28.

Radiocarbon (^{14}C) dates and isotope data

We report 53 direct radiocarbon (^{14}C) dates on bone or tooth fragments from 51 individuals generated using accelerator mass spectrometry (AMS) (Data S2, Table S1). Forty-nine dates correspond to 47 individuals with genetic data passing quality control and analyzed as part of this work (Data S2, Table S2). Most dates were generated at the Pennsylvania State University (PSU) Radiocarbon Laboratory (PSUAMS; n = 26, with sample preparation and chemistry for four samples performed at the University of New Mexico (UNM) Center for Stable Isotopes (CSI)), while others were generated at the University of Georgia (UGA) Center for Applied Isotope Studies (CAIS) (UGAMS; n = 2), the University of California, Irvine's (UCI) W. M. Keck Carbon Cycle Accelerator Mass Spectrometer Facility (UCIAMS; n = 11), and at the Woods Hole Oceanographic Institution's National Ocean Sciences Accelerator Mass Spectrometry (NOSAMS; n = 14). Dates for I28092 were generated at both PSU and UCI, and we report the statistically combined date obtained in OxCal[126] (v.4.4) using the Combine() function (figures in Data S1, section 1). This is possible because agreement indices (Acomb = 121.5%; χ^2 test, df = 1, T = 0.209) indicate statistical consistency between the two measurements. We calibrated ^{14}C ages in OxCal[126] (v4.4) using the IntCal20 Northern Hemisphere curve[127] and report 95.4% CI calibrated radiocarbon ages. For 22 additional individuals, we report genomic data here while ^{14}C dates for these individuals were previously reported.[19,23,128–130] In the absence of direct dates for individuals with genomic data, we inferred dates based on context dates from archaeological strata (layers) or based on archaeological context information.

For 47 individuals with genome-wide data passing quality control and direct ^{14}C dates generated for this work, we also report dietary isotope information (Data S2, Table S2). Dietary isotope data were generated for 19 individuals following sample preparation and chemistry at PSU with measurement at Yale University's Analytical and Stable Isotope Center (YASIC; n = 13) or Penn State's LIME facility (n = 6), for 18 at CSI, for 10 at UCI, and for one at CAIS. Dietary isotope data for I28092 were generated at both PSU/YASIC and UCI, producing nearly identical δ^{13}C and δ^{15}N values. Details of isotope analysis can be found in Data S1, section 2. Stable isotope analyses were performed on a targeted subset of individuals from the genomic dataset. Sampling prioritized individuals with suitable skeletal material and sufficient preservation for reliable measurements and emphasized temporal and archaeological contexts most relevant to the subsistence and ancestry transitions explored in this study.

QUANTIFICATION AND STATISTICAL ANALYSIS

Population structure overview with PCA

To visualize population structure, we carried out Principal Component Analysis (PCA) using smartpca v.18721 with the options 'lsqproject: YES' to project ancient individuals and 'newshrink: YES' to remap the points for the individuals used to generate the PCA axes to the positions where they would be expected to fall if they had been projected, thereby allowing the projected and non-projected individuals to be co-visualized. We first generated a worldwide PCA with eigenvectors computed using present-day Yoruba, French, and Han Chinese individuals to check for non-Indigenous American ancestry in the 212 ancient Colombian individuals reported in this work (Figure S1). We then used the 2M.Illumina dataset and projected ancient individuals onto eigenvectors computed using 12 individuals from four present-day American populations (Maleku, Zapotec, Teribe, Aymara) as in ref. [46]. We

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

identify three PCA outliers, although only one (I10932) is covered at more than 15k SNPs (the remaining two individuals have lower SNP coverage, and their placement on PCA is likely to reflect limited data rather than genuine ancestry differences).

Analyses of genetic ancestry

We computed outgroup f_3-statistics as f_3(A, B; Yoruba) using *qp3pop* (v.701) in ADMIXTOOLS[124] with the option 'inbreed: YES' to investigate the genetic distance between pairs of individuals or groups (Data S2, Table S4). To create Figure 2C, we visualized relative genetic affinities by converting f_3 values to distances by taking their inverse ($1/f_3$) and building a distance tree using *R* (v4.4.2) and the package *ape*. We rooted the tree with USA_Ancient_Beringian.SG. To summarize relative genetic affinity, we used the BIONJ algorithm,[131] a distance-based method that follows the same agglomerative scheme as neighbor-joining (NJ) and is designed to reduce sensitivity to noise. The tree is interpreted as a visualization of genetic affinities rather than a formal demographic model. We excluded two pre-Herrera Period individuals with fewer than 50,000 SNPs covered on the 2M dataset (I22329 and I22623) and grouped Herrera and Muisca Period individuals by site with the exception of five individuals who were lower-coverage first-degree relatives of another individual in the dataset. We analyzed two individuals whom we assessed as being genetically distinct using *qpWave* (I10932 and FORM001) separately (Data S1, sections 3 and 4). To optimize visualization, we applied Grafen's branch length transformation to standardize tip heights, followed by a power transform of node heights (exponent = 0.5) to expand the scale near the leaves while preserving the overall topology. This approach improves resolution of shallow divergences and makes fine structure among closely related samples more visible.

We computed f_4-statistics using *qpDstat* (v.1160) from ADMIXTOOLS[124] with 'f4mode: YES' and 'inbreed: YES.' In all cases where an outgroup was required, we used Yoruba. Standard errors were from a jackknife procedure with units consisting of 5 cM blocks. Results are in Data S2, Tables S5–S10, S13–S17, S19–S25, S29, and S31.

We assessed genetic homogeneity with pairwise *qpWave* (v.1600) to test cladality between pairs of individuals or groups in our analysis dataset. We used 'inbreed: NO', 'allsnps: YES' and set Han as 'basepop' for all qpfstats calculations. We used the 2M.HO dataset to ensure that our reference set contained a consistent data type. We provide a step-by-step description of *qpWave* analyses in Data S1, section 3. Additional results are in Data S2, Tables S3, S30, and S32.

We called mtDNA haplogroups using HaploGrep2[132] (Data S2, Table S18) and re-examined in greater detail the mtDNA haplogroup calls of I22456, I22628, I23879, I22622, I22495, and I22497 with HaploGrep3.[133] We determined Y chromosome haplogroups using both targeted SNPs and off-target sequences that aligned to the Y chromosome based on comparisons to the Y chromosome phylogenetic tree with YFull 12.03 (https://www.yfull.com/). We provide two notations for Y chromosome haplogroups in Data S2, Table S1. The first uses a label based on the terminal mutation, while the second describes the associated branch of the Y chromosome tree based on the nomenclature of the International Society of Genetic Genealogy (http://www.isogg.org).

Ancestry modeling

We used the *qpAdm* (v.2092) framework[95] to model ancestry and estimate ancestry proportions for ancient Colombian individuals. *qpAdm* uses f_4-statistics to detect shared drift between a target individual or group of individuals and possible admixing source proxies relative to a set of differentially related outgroup populations (the 'reference set'). It evaluates whether a target can be plausibly modeled as descending from a common ancestor of one or more source populations and produces estimates of ancestry proportions from one or more proxy sources. Models associated with $p>0.05$ are assessed as being consistent with the data. We used 'inbreed: NO', 'allsnps: YES' and set Han as 'basepop' for all *qpfstats* calculations. Additional details are in Data S1, section 7.

We used the '*find_graphs()*' function in the ADMIXTOOLS2 software to identify admixture graphs that fit observed *f*-statistics. This function tries to find the best-fitting graph topologies for a set of *f*-statistics. We began with 500 or 1,000 different random graphs each time and searched graph space to find an optimal graph once per random initialization. We used USA_Ancient_Beringian.SG as an outgroup and included in our models a subset of ancient populations selected from those evaluated in our f_4-statistic analyses. We filtered graphs to include only those with Z-score < 3.0 and evaluated fit also based on log-likelihood (LL) score, where low LL scores indicate a better fit. We assessed graphs that included 0–3 mixture events, and present graphs with 2 admixture events as this is the category of graphs with the fewest admixture events that still fits the data. Multiple locally optimal graphs that fit the data were found, and all of them share key features. Multiple graphs being found is not surprising given the complexity of graph space and the fact that admixture graphs are simplifications of an underlying true history which is inevitably more complicated; the goal of admixture graph fitting here is simply to show that the proposed model is plausible. The graphs presented exhibit a good statistical fit and are biologically and historically reasonable. Additional details are provided in Data S1, section 6.

Inferring relationships and community sizes

We tested genetic relatedness between every pair of individuals reported in this study following the method described in ref. [134]. We additionally analyzed shared genomic segments on the X chromosomes of individuals I22495 and I22497, who were initially assessed as father-son, using *hapROH*.[135] A father-son relationship would be unexpected given evidence of matrilineal kinship in Muisca communities. Details of this analysis are in Data S1, section 5.

For 181 individuals (31 pre-Herrera, 9 Herrera, and 141 Muisca Period individuals) with data from at least 300,000 SNPs overlapping a core set of 2M targeted SNPs, we applied the software *hapROH* to call ROH (Data S2, Table S12) and estimate effective population size (N_e). In the main manuscript we report *Ne* as the 95% confidence interval (CI) fitted via the likelihood profile. For the

Please cite this article in press as: Sirak et al., Subsistence transition preceded population turnover in the eastern Colombian Andes, Cell (2027), https://doi.org/10.1016/j.cell.2026.10.010

estimate of the sizes of hunter-gatherer/early food producer communities reported in the main manuscript, we used 28 individuals after excluding 3 with a sum total > 50 cM of ROH > 20 cM. We repeated analyses using 14 individuals from middle Holocene Checua who had a sum total < 50 cM of ROH > 20 cM and obtained a slightly lower but qualitatively similar estimate of 207–262 individuals (95% CI) for this site. For the estimate of community sizes during the Herrera Period, we used all 9 individuals as none had a sum total > 50 cM of ROH > 20 cM. For the estimate of community sizes during the Muisca Period, we used 132 individuals after excluding 9 with a sum total > 50 cM of ROH > 20 cM.

Estimation of admixture dates

We ran the software *DATES*[136] (v. 4702) with binsize: 0.001, maxdis: .20, qbin: 10, a random seed, and jackknife: YES. This method *measures* the decay of ancestry covariance to infer the time since mixture and estimates jackknife standard errors. Data are in Data S2, Table S26.

Use of Artificial Intelligence (AI)

Generative AI tools (OpenAI's ChatGPT (GPT-5.5 Thinking) and Anthropic's Claude) were used during the preparation of figures for this study to assist with writing and refining R code used to generate Figures 1–3 and S4–S7. All code outputs were critically reviewed, revised, and verified by the lead author prior to inclusion.