

MicroEvol



Evolution et dynamiques des populations
pyrénéennes : Vallée de Vicdessos

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? : Place des Pyrénées françaises dans les différentes phases de peuplement du SO Europe

Comparaison des populations modernes à partir des marqueurs uni-parentaux.

Définition moléculaire ++: séquençage total de l'ADN mitochondrial
nouveau Kit Y-chromosome (soumis)

« POOL PYRENEEN »



« PARTICULARISME
DE VICDESSOS »

« autochtone », « contacts »

Micro-structuration liée au contexte montagnard : avantages et désavantages liés à la cette structuration et aux effets de la dérive génétique

Méthode - généralités

Obtention des accords du Comité d’Ethique et du Ministère (DC-2011)
Information à la population

Échantillonnage

Volontaires, Consentements éclairés, Prélèvements salivaires anonymisés
Pas d’apparentement premier/deuxième degrés
Grand-mère maternelle (mtDNA - > 100 ind) et/ou Grand père paternel
(Chromosome Y -> 60 ind) né.e.s dans la Vallée

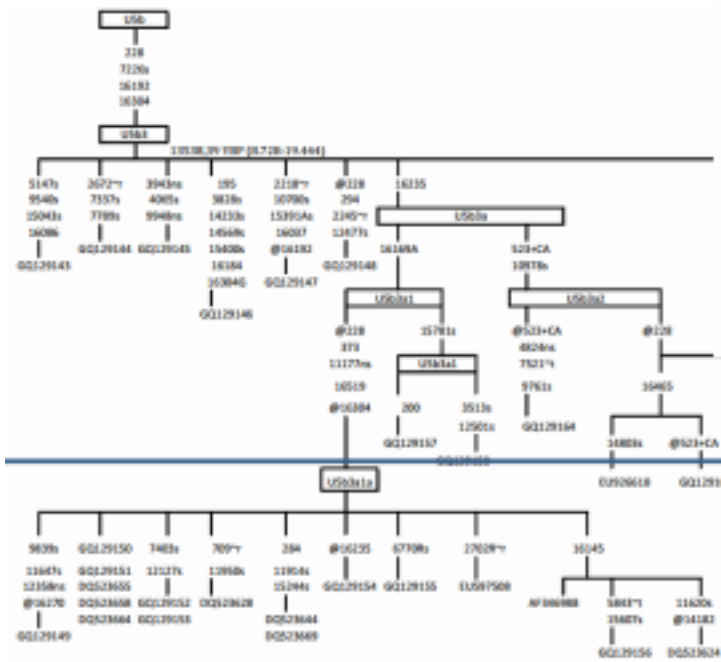
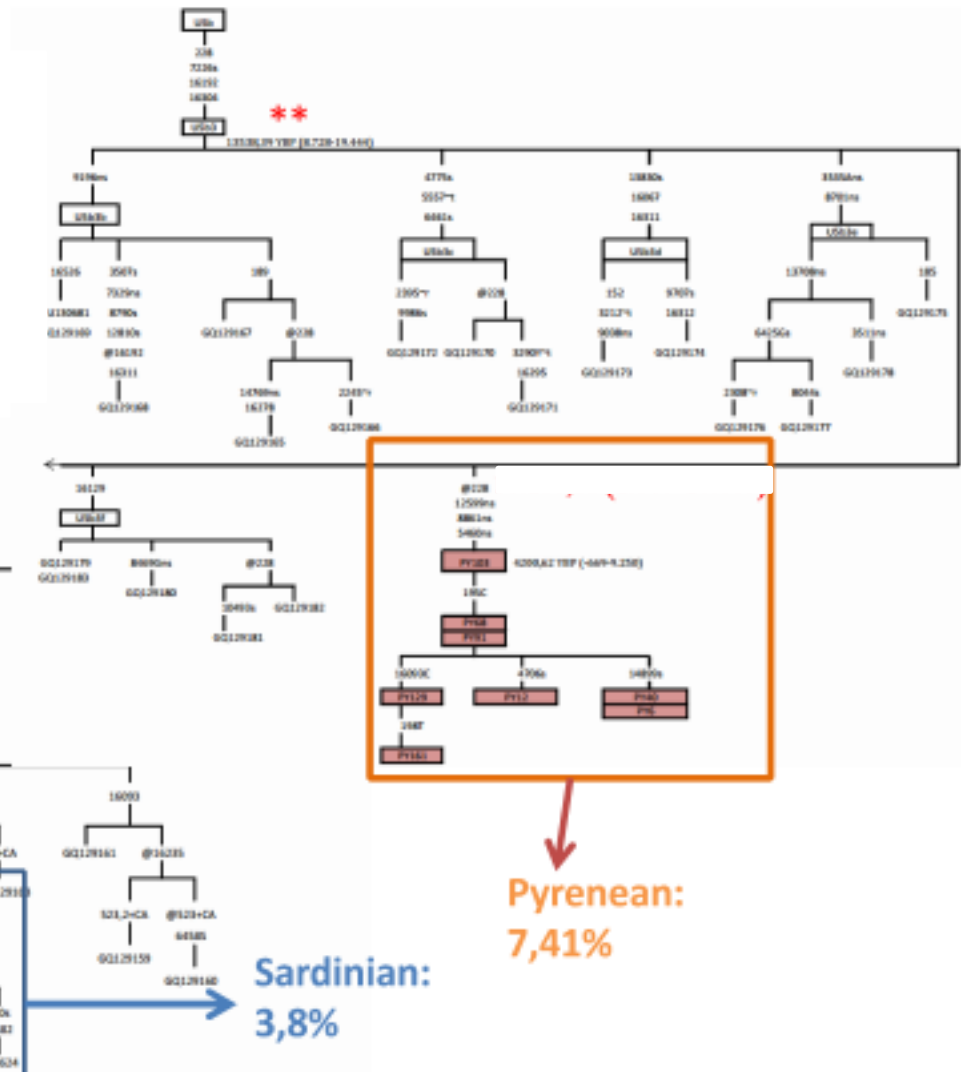
Typage

Séquençage total de l’ADN mitochondrial (partenariat GénoToul)
Chromosome Y: STR (Kit développé) + SNPs

Approche phylogéo-graphique

Avant 2018, comparaison avec les populations modernes pyrénéennes et euro-méditerranéennes

Des sous-haplogroupes « pyrénéens » aux particularismes de Vicdessos



2018-2019 Parution de nombreux articles en ADN ancien

nature

Article | Published: 21 February 2018

The Beaker phenomenon and the genomic transformation of northwest Europe

Iñigo Olalde , Selina Brace, [...] David Reich

SCIENTIFIC REPORTS

Article | Open Access | Published: 02 August 2018

Mitochondrial genomes reveal an east to west cline of steppe ancestry in Corded Ware populations

Anna Juras , Maciej Chyleński, Edvard Ehler, Helena Malmström, Danuta Żurkiewicz, Piotr Włodarczyk, Stanisław Wilk, Jarosław Peška, Pavel Fojtík, Miroslav Králík, Jerzy Libera, Jolanta Bagińska, Krzysztof Tunia, Viktor I. Klochko, Mirosława Dabert, Mattias Jakobsson & Aleksander Kosko

Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe

Rosa Fregel^{1,2}, Fernando L. Méndez³, Youssef Bokbot⁴, Dimas Martín-Socas⁵, María D. Camalich-Massieu⁶, Jonathan Santana⁷, Jacob Morales⁸, María C. Ávila-Arcoos⁹, Peter A. Underhill¹⁰, Beth Shapiro¹¹, Genevieve Wojcik¹², Morten Rasmussen¹³, André E. R. Soares¹⁴, Joshua Kapp¹⁵, Alexandra Sockell¹⁶, Francisco J. Rodríguez-Santos¹⁷, Abdelmalik Mikdad¹⁸, Aioze Trujillo-Mederos¹⁹, and Carlos D. Bustamante²⁰

OPEN Ancient DNA of Phoenician remains indicates discontinuity in the settlement history of Ibiza

Received: 9 April 2018
Accepted: 9 November 2018
Published online: 04 December 2018

Pierre Zalloua¹, Catherine J. Collins², Anna Gosling³, Simone Andrea Biagini⁴, Benjami Costa⁵, Olga Kardalsky⁶, Lorenzo Nigro⁷, Wissam Khalil⁸, Francesc Calafell⁹ & Elisabeth Mathieson-Simithy¹⁰

nature

Article | Published: 09 May 2018

137 ancient human genomes from across the Eurasian steppes

Peter de Barros Damgaard, Nina Marchi, [...] Eske Willerslev

Four millennia of Iberian biomolecular prehistory illustrate the impact of prehistoric migrations at the far end of Eurasia

Cristina Valdiosera^{1,2,3,4,5}, Torsten Günther^{6,7,8}, Juan Carlos Vera-Rodríguez⁹, Irene Ureña^{10,11}, Eneko Iriarte¹², Ricardo Rodríguez-Varela¹³, Luciana G. Simões¹⁴, Rafael M. Martínez-Sánchez¹⁵, Emma M. Svensson¹⁶, Helena Malmström¹⁷, Laura Rodríguez¹⁸, José-Maria Bermúdez de Castro¹⁹, Eudald Carbonell²⁰, Alfonso Alday²¹, José Antonio Hernández Vera²², Anders Götherström²³, José-Miguel Carretero²⁴, Juan Luis Arsuaga²⁵, Colin I. Smith²⁶, and Mattias Jakobsson^{10,27}

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A western route of prehistoric human migration from Africa into the Iberian Peninsula

Research
Check for updates
Cite this article: González-Fortes G et al. 2019 A western route of prehistoric human migration from Africa into the Iberian Peninsula. *Proc. R. Soc. B* **286**: 20182288. <http://dx.doi.org/10.1098/rspb.2018.2288>

G. González-Fortes¹, F. Tassi^{1,2}, E. Trucchi^{1,3,4}, K. Henneberger⁵, J. L. A. Pajmams⁶, D. Díez-del-Molino⁷, H. Schroeder⁸, R. R. Susca¹, C. Barroso-Ruiz⁹, F. J. Bermúdez², C. Barroso-Medina¹⁰, A. M. S. Bettencourt¹¹, H. A. Sampaio¹², A. Grandal-d'Anglade¹³, A. Salas¹⁴, A. de Lomber-Hermida¹⁵, R. Fabregas Valcarlos¹⁶, M. Vaquero^{11,12}, S. Alonso^{11,12}, M. Lozano^{11,12}, X. P. Rodríguez-Alvarez^{11,12}, C. Fernández-Rodríguez¹³, A. Manica¹⁴, M. Hofreiter⁷ and G. Barbujani¹

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Ancient Mitochondrial Genomes Reveal the Absence of Maternal Kinship in the Burials of Çatalhöyük People and Their Genetic Affinities

Open Access Article
by Maciej Chyleński^{1,2}, Edvard Ehler², Mehmet Sömel³, Reyhan Yaka³, Maja Krzewińska⁴, Mirosława Dabert⁵, Anna Juras⁶ and Arkadiusz Marciniak¹

Journal of Archaeological Science: Reports
Volume 26, August 2018, Pages 200-209

Ancient Roman mitochondrial genomes and isotopes reveal relationships and geographic origins at the local and pan-Mediterranean scales

Matthew V. Emery^{1,2,3,4}, Ana T. Duggan^{5,6}, Tyler J. Murchie^{7,8}, Robert J. Stark^{9,10}, Jessica Huder^{11,12}, Katherine Eaton¹³, Emil Karjalainen¹⁴, Henry P. Schwarz¹⁵, Hendrik Tracy L. Probst¹⁶

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The formation of human populations in South and Central Asia

Vagheesh M. Narasimhan et al.

Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands

Rosa Fregel^{1,2,3}, Alejandra C. Ordóñez⁴, Jonathan Santana-Cabrera⁵, Vicente M. Cabrera⁶, Javier Velasco-Vázquez⁷, Verónica Alberto⁸, Marco A. Moreno-Benitez⁹, Teresa Delgado-Darias¹⁰, Amelita Rodríguez-Rodríguez¹¹, Juan C. Hernández¹², Jorge Páiz¹³, Raísa González-Montelongo¹⁴, José M. Lorenzo-Salazar¹⁵, Carlos Flores^{16,17,18}, M. Carmen Cruz-de-Mercedad¹⁹, Nuria Álvarez-Rodríguez²⁰, Beth Shapiro^{21,22}, Muriel Arroyo²³, Carlos D. Bustamante²⁴

2018
2020

Extension de la base de données Intégration des données en ADN ancien et moderne

Welcome to Ancient mtDNA database!

This is the place where you can find an updated list of the published mitochondrial sequences coming from the ancient DNA samples (aDNA). The main interest of our database lies in the anatomically modern Homo sapiens samples, ranging from the late Pleistocene to roughly 10k Age-lims, focusing on an Eurasian geographical area. We provide both the mtDNA sequence (in FASTA format), and the metadata for the samples (ID, sex, production, site, culture, mtDNA haplogroup, etc.), available to download in a comma-separated CSV text file.

Quick tour

- Identify and download the database inventory.
- Display associated samples or reference map.
- Download the dataset associated to a file or a group.
- Download the dataset or other elements (FASTA, CSV, and metadata) in the list of references.
- Upload the dataset if you have any new samples or update you want your samples (via a link to a CSV file).
- View AmdDB in the browser and in a desktop app.
- Send our terms of service.

AmdDB content statistics
v1.04 (12/12/2018) (log)

Samples	104
Countries	11
Epochs	38
Sexes	11
Cultures	10
Sites	10

AmdDB in Czech media

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- aktuality.cz
- praha24.cz
- novy.cz
- aktualne.cz
- novinky.cz
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- novinky.cz

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doi: 10.1093/nar/ky843

AmdDB: a database of ancient human mitochondrial genomes

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ABSTRACT

Ancient mitochondrial DNA is used for tracing human past demographic events due to its population-level variability. The number of published ancient mitochondrial genomes has increased in recent years, alongside with the development of high-throughput sequencing and capture enrichment methods. Here, we present AmdDB, the first database of ancient human mitochondrial genomes. Release version contains 1107 hand-curated ancient samples, freely accessible for download, together with the individual descriptors, including geographic location, radiocarbon dating and archaeological culture affiliation. The database also features an interactive map for sample location visualization. AmdDB is a key platform for ancient population genetic studies and is available at <https://amddb.org>.

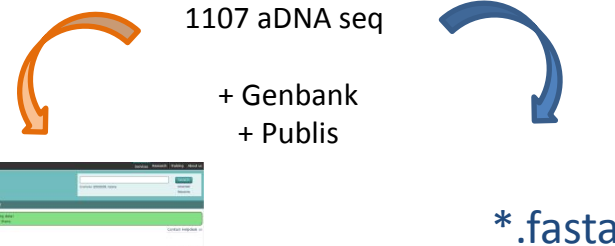
Despite the long-standing interest in ancient mtDNA, it was only in the past few years, when a high number of complete mt genomes were made available, alongside with the development of the high-throughput sequencing, often combined with the capture enrichment methods. Mitochondrial DNA, often as a part of nuclear genome studies, was used to reconstruct demographic events that took place in pre-LGM (Last Glacial Maximum) and post-LGM era in Europe (34), to trace demographic changes that shaped past and modern populations' mtDNA variation (5–13), including the influence of Neolithization process (14–23), and Steppe migrations (24–26). Moreover, mtDNA was used in several kinship studies as a molecular marker which excludes direct maternal kinship between ancient individuals (27–31).

Although there are currently available modern mtDNA databases, e.g. EMPOP (32), MITOMAP (33), HmtDB (34), and mtDB (35), there is no database that would be dedicated specifically to ancient mt genomes. A database com-

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Name	Group	Epoch	Country	Sex	Year from	Year to	Haplogroup	Sequence source	Seq. coverage	References	Download	Map
19159	NENE	Neolithic	Turkey	U	-6450	-6390	N	reconstructed	13.7	FASTA metadata	FASTA metadata	
19127	NENE	Neolithic	Turkey	M	-6450	-6390	K	reconstructed	25.5	FASTA metadata	FASTA metadata	
20106	NENE	Neolithic	Turkey	U	-6450	-6390	U	reconstructed	242.3	FASTA metadata	FASTA metadata	
20101	NENE	Neolithic	Turkey	U	-6450	-6390	U92	reconstructed	19.0	FASTA metadata	FASTA metadata	
20374	NENE	Neolithic	Turkey	U	-6450	-6390	X294	reconstructed	41.9	FASTA metadata	FASTA metadata	
20810	NENE	Neolithic	Turkey	U	-6450	-6390	W1C	reconstructed	23.1	FASTA metadata	FASTA metadata	
20832	NENE	Neolithic	Turkey	F	-6450	-6390	H+73	reconstructed	6.3	FASTA metadata	FASTA metadata	
20550	NENE	Neolithic	Turkey	M	-6450	-6390	H	reconstructed	11.3	FASTA metadata	FASTA metadata	
21981	NENE	Neolithic	Turkey	M	-6450	-6390	K1a17	reconstructed	3.8	FASTA metadata	FASTA metadata	
30900	NENE	Neolithic	Turkey	U	-6450	-6390	U	reconstructed	36.3	FASTA metadata	FASTA metadata	
Afrosync3493	HOZE	Neolithic	Russia	F	-15480	-15480	R0	fasta	<NA>	fasta	FASTA metadata	
AH1	NEME	Neolithic	Iran	F	-7500	-7750	R2	fasta	<NA>	fasta	FASTA metadata	
AH2	NEME	Neolithic	Iran	M	-7005	-7756	R2	fasta	<NA>	fasta	FASTA metadata	
AH4	NEME	Neolithic	Iran	F	-8004	-7755	T2c	fasta	<NA>	fasta	FASTA metadata	
Ampack_1	BBC	Bronze Age	Germany	M	-2476	-2310	T2b33	reconstructed	1897.4	FASTA metadata	FASTA metadata	
ANI152	CABA	Copper Age	Bulgaria	M	-4863	-4406	U2	bam	<NA>	FASTA metadata	FASTA metadata	
ANI153	CABA	Copper Age	Bulgaria	M	-4551	-4374	U4	bam	<NA>	FASTA metadata	FASTA metadata	
ANI159	CABA	Copper Age	Bulgaria	M	-4711	-4530	T2b29	bam	<NA>	FASTA metadata	FASTA metadata	
ANI160	CABA	Copper Age	Bulgaria	M	-4655	-4459	H1a9	bam	<NA>	FASTA metadata	FASTA metadata	
ANI163	CABA	Copper Age	Bulgaria	F	-4711	-4542	H7a1	bam	<NA>	FASTA metadata	FASTA metadata	
ATP16	CAB	Copper Age	Spain	F	-3261	-2916	X2c	bam	<NA>	FASTA metadata	FASTA metadata	

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ENA
European Nucleotide Archive

Sample: SAREIA122555

Accession: ENA012255

FASTA | metadata

Import, paleomix (haplogrep)

+ complement Genbank

Réalisation des arbres avec intégration de l'aDNA

Discussion mtDNA niveau de définition <

Comparaison au chromosome Y
(lignées féminines vs masculines)

Discussion des données à la lumière des autres Proxi
notamment Paléo-environnementales

Remerciements : Labex DRIIHM, GenoToul
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LabEx DRIIHM

