

PUBLICATIONS 2014 - PRESENT

Hernández CL, Dugoujon J-M, Sánchez-Martínez LJ, Novelletto A, Calderón R (2019) Paternal lineages in southern Iberia provide time frames for gene flow from mainland Europe and the Mediterranean world. *Ann Hum Biol*

Montalbano Di Filippo M, Berrilli F, Di Cave D, Novelletto A (2019) Novel data from Italian *Vermamoeba vermiformis* isolates from multiple sources add to genetic diversity within the genus. *Parasitol Res*

Benvisto A, Messina F, Finocchio A, Popa L, Stefan M, Stefanescu G, Mironeanu C, Novelletto A, Rapone C, Berti A (2018) A genetic portrait of the South-Eastern Carpathians based on autosomal STR loci used in forensics. *Am J Hum Biol*: e23139

D'Atanasio E, Trombetta B, Bonito M, Finocchio A, Di Vito G, Seghizzi M, Romano R, Russo G, Paganotti GM, Watson E, Coppa A, Anagnostou P, Dugoujon J-M, Moral P, Sellitto D, Novelletto A, Cruciani F (2018) The peopling of the last Green Sahara disclosed by high-coverage resequencing of trans-Saharan patrilineages. *Genome Biol* 19: 20

Finocchio A, Trombetta B, Messina F, D'Atanasio E, Akar N, Loutradis A, Michalodimitrakis EI, Cruciani F, Novelletto A (2018) A finely resolved phylogeny of Y chromosome Hg J illuminates the processes of Phoenician and Greek colonizations in the Mediterranean *Sci Rep*, pp 7465

Messina F, Finocchio A, Akar N, Loutradis A, Michalodimitrakis EI, Brdicka R, Jodice C, Novelletto A (2018) Enlarging the gene-geography of Europe and the Mediterranean area to STR loci used in forensics: longitudinal and latitudinal frequency gradients. *Ann Hum Biol* 45: 77-85

Tolve L, Casale P, Formia A, Garofalo L, Lazar B, Natali C, Novelletto A, Vallini C, Bužan E, Chelazzi G, Gaspari S, Fortuna C, Kocijan I, Marchiori E, Novarini N, Poppi L, Ciofi C (2018) A comprehensive mitochondrial DNA mixed stock analysis clarifies the composition of loggerhead turtle aggregates in the Adriatic Sea. *Mar Biol* 165: 68

Hernández CL, Dugoujon J-M, Novelletto A, Rodríguez JN, Cuesta P, Calderon R (2017) The distribution of mitochondrial DNA haplogroup H in southern Iberia indicates ancient human genetic exchanges along the western edge of the Mediterranean. *BMC Genetics* 18: 46

Kulichová I, Fernandes V, Deme A, Nováčková J, Stenzl V, Novelletto A, Pereira L, Černý V (2017) Internal diversification of non-sub-Saharan haplogroups in Sahelian populations and the spread of pastoralism beyond the Sahara. *Am J Phys Anthropol* 164: 424-434

- Montalbano Di Filippo M, Novelletto A, Di Cave D, Berrilli F (2017) Identification and phylogenetic position of *Naegleria* spp. from geothermal springs in Italy. *Exp Parasitol* 183: 143-149
- Doro MG, Casu G, Leoni GG, Naitana S, Pirastu M, Novelletto A, Fraticelli F (2016) The complete mitochondrial DNA sequence of the Montecristo goat. *Livestock Sci* 188: 120-123
- Messina F, Finocchio A, Akar N, Loutradis A, Michalodimitrakis EI, Brdicka R, Jodice C, Novelletto A (2016) Spatially explicit models to investigate geographic patterns in the distribution of forensic STRs: application to the North-Eastern Mediterranean. *PLoS ONE* 11: e0167065
- Novelletto A, Testa L, Iacovelli F, Blasi P, Garofalo L, Mingozi T, Falconi M (2016) Polymorphism in mitochondrial coding regions of Mediterranean loggerhead turtles: evolutionary relevance and structural effects. *Physiol Biochem Zool* 89: 473-486
- Batini C, Hallast P, Zadik D, Delser PM, Benazzo A, Ghirotto S, Arroyo-Pardo E, Cavalleri GL, de Knijff P, Dupuy BM, Eriksen HA, King TE, de Munain AL, Lopez-Parra AM, Loutradis A, Milasin J, Novelletto A, Pamjav H, Sajantila A, Tolun A, Winney B, Jobling MA (2015) Large-scale recent expansion of European patrilineages shown by population resequencing *Nat Commun*. Nature Publishing Group, a division of Macmillan Publishers Limited. All Rights Reserved., pp 7152
- Batini C, Hallast P, Zadik D, Delser PM, Benazzo A, Ghirotto S, Arroyo-Pardo E, Cavalleri GL, de Knijff P, Dupuy BM, Eriksen HA, King TE, de Munain AL, Lopez-Parra AM, Loutradis A, Milasin J, Novelletto A, Pamjav H, Sajantila A, Tolun A, Winney B, Jobling MA (2015) Large-scale recent expansion of European patrilineages shown by population resequencing. *Nature Communications* 6
- Hallast P, Batini C, Zadik D, Maisano Delser P, Wetton J, Arroyo-Pardo E, Cavalleri G, de Knijff P, Destro Bisol G, Myhre Dupuy B, Eriksen H, Jorde LB, King T, Larmuseau M, Lopez de Munain A, López-Parra AM, Loutradis A, Milasin J, Novelletto A, Pamjav H, Sajantila A, Schempp W, Sears M, Tolun A, Tyler-Smith C, Van Geystelen A, Watkins W, Winney B, Jobling M (2015) The Y-chromosome tree bursts into leaf: 13,000 high confidence SNPs covering the majority of known clades. *Mol Biol Evol* 32: 661-673
- Hernández CL, Soares P, Dugoujon JM, Novelletto A, Rodríguez JN, Rito T, Oliveira M, Melhaoui M, Baali A, Pereira L, Calderón R (2015) Early holocenic and historic mtDNA African signatures in the Iberian Peninsula: The Andalusian region as a paradigm. *PLoS ONE* 10: e0139784
- Polimanti R, Piacentini S, Iorio A, De Angelis F, Kozlov A, Novelletto A, Fuciarelli M (2015) Haplotype differences for copy number variants in the 22q11.23 region among human populations: a pigmentation-based model for selective pressure. *Eur J Hum Genet* 23: 116-123

- Trombetta B, D'Atanasio E, Massaia A, Ippoliti M, Coppa A, Candilio F, Coia V, Russo G, Dugoujon J-M, Moral P, Akar N, Sellitto D, Valesini G, Novelletto A, Scozzari R, Cruciani F (2015) Phylogeographic refinement and large scale genotyping of human Y chromosome haplogroup E provide new insights into the dispersal of early pastoralists in the African continent. *Genome Biol Evol* 24: 1940-1950
- Trombetta B, D'Atanasio E, Massaia A, Myres NM, Scozzari R, Cruciani F, Novelletto A (2015) Regional differences in the accumulation of SNPs on the male-specific portion of the human Y chromosome replicate autosomal patterns: implications for genetic dating. *PLoS ONE* 10: e0134646
- Doro MG, Piras D, Leoni GG, Casu G, Vaccargiu S, Parracciani D, Naitana S, Pirastu M, Novelletto A (2014) Phylogeny and patterns of diversity of goat mtDNA haplogroup A revealed by resequencing complete mitogenomes. *PLoS ONE* 9: e95969
- Hernández CL, Reales G, Dugoujon J-M, Novelletto A, Rodríguez JN, Cuesta P, Calderon R (2014) Human maternal heritage in Andalusia (Spain): its composition reveals high internal complexity and distinctive influences of mtDNA haplogroups U6 and L in the Western and Eastern side of region. *BMC Genet* 15: 11
- Reales G, Hernández CL, Dugoujon JM, Novelletto A, Fortes-Lima C, Rodríguez JN, Calderón R (2014) New insights into the distribution of APOE polymorphism in the Iberian Peninsula. The case of Andalusia (Spain). *Ann Hum Biol* 41: 443-452
- Scozzari R, Massaia A, Trombetta B, Bellusci G, Myres NM, Novelletto A, Cruciani F (2014) An unbiased resource of novel SNP markers provides a new chronology for the human Y chromosome and reveals a deep phylogenetic structure in Africa. *Genome Res* 24: 535-544
- Veneziano L, Mantuano E, Catalli C, Gellera C, Durr A, Romano S, Spadaro M, Frontali M, Novelletto A (2014) A shared haplotype for dentatorubropallidolusian atrophy (DRPLA) in Italian families testifies of the recent introduction of the mutation. *J Hum Genet* 59: 153-157