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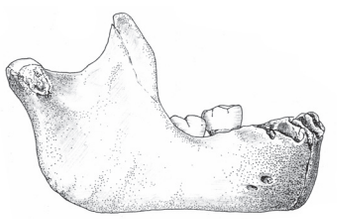

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Pecha Kucha Presentation Session 6, Friday 11:00

Palaeogenomic investigations at the Troisième caverne of Goyet, Belgium

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The main excavations at the Troisième caverne of Goyet in Belgium were conducted by Edouard Dupont in 1868 who identified Palaeolithic human occupations later attributed to the Middle and Upper Palaeolithic. These are represented by an archaeological record that spans the Mousterian, Lincombian-Ranisian-Jerzmanowician, Aurignacian, Gravettian, and Magdalenian, and then extends into the Neolithic and historic periods. Due to the lack of detailed documentation of the excavated materials, their association to a specific chronocultural context has been challenging. Morphometric and taphonomic analyses, combined with direct radiocarbon dating as well as isotopic and genetic analyses, were used to assign human remains to either late Neanderthals or ancient modern humans from different chronocultural groups. In 2016 the first palaeogenetic investigation of Neanderthal specimens from Goyet was published [1]. Taxonomic assignment was confirmed by performing hybridization capture of the mitochondrial DNA (mtDNA) and later inspecting diagnostic mutations at nucleotide positions that distinguish modern humans from Neanderthals. Moreover, a phylogenetic reconstruction placed seven nearly complete mtDNA sequences from Goyet within the diversity of late Neanderthal mtDNA. An around two-fold coverage nuclear genome was later sequenced from one of those individuals (Goyet Q56-1) [2], revealing a high genetic similarity to other late Neanderthals that is well correlated to their geographical distance. Analyzing modern human remains retrieved at Goyet, mtDNA genomes were initially reported for two specimens directly dated to the Aurignacian, five to the Gravettian, and one to the Magdalenian [3]. Aurignacian-related individuals were particularly intriguing as they were found to carry mtDNA haplogroup M, which is almost entirely absent in present-day Europeans. For Gravettian- to Magdalenian-related individuals, the shift from U2/U5 to U8 haplogroups was detected locally - as in other regions of Central Europe - likely influenced by the genetic bottleneck during the Last Glacial Maximum (LGM). Furthermore, nuclear sequences of five modern human individuals from Goyet were produced through genome-wide targeted enrichment [4] revealing local replacement between Aurignacian- and Gravettian-related populations. However, the genetic component associated with a 35,000-year-old individual (Goyet Q116-1) reappeared after the LGM, first in Spain and then in other European regions including in a Magdalenian-related individual from Goyet (Goyet Q-2). This individual was later found to be the best proxy for a genetic component that was largely displaced in Europe from around 14,000 years ago onwards while surviving in high proportion among Mesolithic individuals from Iberia [5]. Here we present new palaeogenetic data of Neanderthal and modern human individuals from this iconic site. First, we expand the molecular taxonomic identifications with three additional Neanderthal specimens and reconstruct their partial mtDNA genomes. Those confirm the general picture of a limited genetic diversity for late Neanderthals, which is also apparent among the Goyet Neanderthals. Second, working on modern human remains, we produced new mtDNA and nuclear data from four Gravettian specimens. They belong to mtDNA haplogroups U2 and U5, further extending the observation of both mtDNA types being largely present in pre-LGM Europe. Moreover, their nuclear genomes provide additional evidence for the genetic affinity between Gravettian-related groups across Europe, from the present-day regions of the Czech Republic to Belgium and Southern Italy. In conclusion, the deep temporal range covered by the human remains from the Troisième caverne of Goyet provides the unique opportunity to describe within a single archaeological site the major genetic transformations that took place in Europe throughout the Middle and Upper Palaeolithic.

References:[1] Rougier, H., Crevecoeur, I., Beauval, C., Posth, C., Flas, D., Wissing, C., Furtwangler, A., Germonpre, M., Gomez-Olivencia, A., Semal, P., van der Plicht, J., Bocherens, H., Krause, J., 2016. Neandertal cannibalism and Neandertal bones used as tools in Northern Europe. Sci Rep 6, 29005.[2] Hajdinjak, M., Fu, Q., Hubner, A., Petr, M., Mafessoni, F., Grote, S., Skoglund, P., Narasimham, V., Rougier, H., Crevecoeur, I., Semal, P., Soressi, M., Talamo, S., Hublin, J.J., Gusic, I., Kucan, Z., Rudan, P., Golovanova, L.V., Doronichev, V.B., Posth, C., Krause, J., Korlevic, P., Nagel, S., Nickel, B., Slatkin, M., Patterson, N., Reich, D., Prufer, K., Meyer, M., Paabo, S., Kelso, J., 2018. Reconstructing the genetic history of late Neanderthals. Nature 555, 652-656.[3] Posth, C., Renaud, G., Mittnik, A., Drucker, D.G., Rougier, H., Cupillard, C., Valentin, F., Thevenet, C., Furtwangler, A., Wissing, C., Francken, M., Malina, M., Bolus, M., Lari, M., Gigli, E., Capecchi, G., Crevecoeur, I., Beauval, C., Flas, D., Germonpre, M., van der Plicht, J., Cottiaux, R., Gely, B., Ronchitelli, A., Wehrberger, K., Grigorescu, D., Svoboda, J., Semal, P., Caramelli, D., Bocherens, H., Harvati, K., Conard, N.J., Haak, W., Powell, A., Krause, J., 2016. Pleistocene Mitochondrial Genomes Suggest a Single Major Dispersal of Non-Africans and a Late Glacial Population Turnover in Europe. Curr Biol 26, 827-833.[4] Fu, Q.M., Posth, C., Hajdinjak, M., Petr, M., Mallick, S., Fernandes, D., Furtwangler, A., Haak, W., Meyer, M., Mittnik, A., Nickel, B., Peltzer, A., Rohland, N., Slon, V., Talamo, S., Lazaridis, I., Lipson, M., Mathieson, I., Schiffels, S., Skoglund, P., Derevianko, A.P., Drozdov, N., Slavinsky, V., Tsybankov, A., Cremonesi, R.G., Mallegni, F., Gely, B., Vacca, E., Morales, M.R.G., Straus, L.G., Neugebauer-Maresch, C., Teschler-Nicola, M., Constantin, S., Moldovan, O.T., Benazzi, S., Peresani, M., Coppola, D., Lari, M., Ricci, S., Ronchitelli, A., Valentin, F., Thevenet, C., Wehrberger, K., Grigorescu, D., Rougier, H., Crevecoeur, I., Flas, D., Semal, P., Mannino, M.A., Cupillard, C., Bocherens, H., Conard, N.J., et al., 2016. The genetic history of Ice Age Europe. Nature 534, 200-205.[5] Villalba-Mouco, V., van de Loosdrecht, M.S., Posth, C., Mora, R., Martinez-Moreno, J., Rojo-Guerra, M., Salazar-Garcia, D.C., Royo-Guillen, J.I., Kunst, M., Rougier, H., Crevecoeur, I., Arcusa-Magallon, H., Tejedor-Rodriguez, C., Garcia-Martinez de Lagran, I., Garrido-Pena, R., Alt, K.W., Jeong, C., Schiffels, S., Utrilla, P., Krause, J., Haak, W., 2019. Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. Curr Biol 29, 1169-1177 e1167.