

The European mitochondrial lineage may protect against severe forms of COVID-19

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An international study led by Spanish research teams has identified how genetic factors can influence the severity of disease caused by SARS-CoV-2

A study published in the journal [Communications Biology](#) shows that specific genetic variants in the mitochondrial DNA of Europeans may protect them against the more severe forms of COVID-19. The results of the study provide new clues to the origin of individual differences in the response to infection. The research was led by Dr. [José Antonio Enríquez](#), head of the [GENOXPHOS](#) group at the [Centro Nacional de Investigaciones Cardiovasculares](#) (CNIC) and a member of the Spanish research network on frailty and healthy aging ([CIBERFES](#)).

The study identified patterns suggesting a possible relationship between certain mitochondrial haplogroups (genetic variants shared by individuals with a common ancestor) and susceptibility to more severe forms of COVID-19. “The study demonstrates the **importance of the mitochondrial HV lineage as a protective factor against the severe consequences of infection with SARS-CoV2**, supporting the idea that mitochondria play a key role in the response to infectious disease,” explained José Antonio Enríquez.

Dr. José Luis Cabrera, first author on the study, added that “these results **advance our understanding of the variability in the response to SARS-CoV-2 and may help to improve the personalized care of patients with COVID-19.**”

The study analyzed data from more than 14300 patients in the SCOURGE registry (Spanish Coalition to Unlock Research on Host Genetics on COVID-19) and confirmed that **individuals with genetic variants found in the HV lineage—the most common mitochondrial lineage among Europeans, accounting for 37%–58% of the European population—had a lower risk of developing severe forms of COVID-19.** Mitochondrial DNA is the only part of the human genome that is inherited exclusively through the maternal line and plays **a key role in the cellular generation of energy and the inflammatory response**

In addition to the CNIC and CIBERFES, acclaimed Spanish and international institutions participating in the study included the [University of Santiago de Compostela](#) (USC), [Marqués de Valdecilla University Hospital-IDIVAL](#), [Nuestra Señora de Candelaria University Hospital](#), [La Paz University Hospital](#), and the [Autonomous University of Nuevo León](#) (México).

The study used advanced genetic analysis models to identify data patterns, revealing how **previous pandemics may have influenced the current distribution of these genetic variants in Europe** through the process of natural selection.

Ángel Carracedo, who heads the [Spanish research network on rare diseases](#) (CIBERER) at [USC](#) and [CIMUS](#) (*Centro Singular de Investigación en Medicina Molecular y Enfermedades Crónicas*), and who also participated in the study, added, “the results not only contribute to the understanding of COVID-19, but could also have **implications for the study of other infectious diseases and their relation to mitochondrial genetics.**”

- [Cabrera-Alarcon JL, Cruz R, Rosa-Moreno M, Latorre-Pellicer A, de Almeida SD; Scourge Cohort Group; Riancho JA, Rojas-Martinez A, Flores C, Lapunzina P, Sánchez-Cabo F, Carracedo Á, Enríquez JA. Shaping current European mitochondrial haplogroup frequency in response to infection: the case of SARS-CoV-2 severity. *Commun Biol.* 2025 Jan 9;8\(1\):33. doi: 10.1038/s42003-024-07314-y. PMID: 39789223; PMCID: PMC11718132](#)

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