

Draft genome sequence of a new *Fusarium* isolate collected from hazelnut in Central Italy

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In summery 2019, during a survey on the health status of an hazelnut orchard located in the Tuscia area (province of Viterbo, Latium, Italy), symptomatic hazelnut were found and collected for further studies. The symptoms resembled the one previously described as Nut Gray Necrosis (NGN) associated to *Fusarium lateritium*, including brown-greyish spots at the bottom of the nuts progressing upwards to the apex, and of necrotic patches on the bracts and less often on the petioles.

This disease could have an economic impact on the Italian hazelnut cultivation, since its large area of 85,000 ha, covering Campania, Latium, Sicily and Piedmont, makes Italy one of the largest world hazelnut producers, together with Turkey, Spain, USA and Greece.

For this reason, we performed a whole genome sequencing of the strain isolated from hazelnut, taking advantage of the long Nanopore reads technology in combination with the higher precision of the Illumina reads, to finally reach a more complete and precise draft genome sequence. Phylogenetic and comparative genomics analysis suggest that this isolate is more related to *Fusarium tricinctum* species complex than *Fusarium lateritium* as symptoms initially suggested and thus, it could be speculated that a new species infecting *Corylus avellana* has been found.

Further studies would better clarify its biology, epidemiology, infection mechanisms and host spectrum, with the aim to define its potential risks and develop a specific control strategy in time.

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