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

## A. Grottoli<sup>1</sup>, S. Turco<sup>2\*</sup>, M. I. Drais<sup>2</sup>, L. Faino<sup>3</sup>, M. Reverberi<sup>3</sup>, V. Cristofori<sup>2</sup>, A. Mazzaglia<sup>2</sup>

<sup>1</sup>Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro di ricerca difesa e certificazione (CREA-DC), Via C.G. Bertero, 22, 00156 Roma

<sup>2</sup>Dipartimento di Scienze Agrarie e Forestali, Università degli Studi della Tuscia, Via S. Camillo de Lellis snc, 01100 Viterbo, Italy

<sup>3</sup>Dipartimento di Biologia Ambientale, Sapienza, Università di Roma, Piazzale Aldo Moro, 5, 00185, Roma *E-mail: silvia.turco@unitus.it* 

In summery 2019, during a phytosanitary monitoring of a hazelnut orchard located in the Tuscia area (province of Viterbo, Latium, Italy), diseased hazelnuts were found and collected for further studies. The symptoms resembled the previously described Nut Gray Necrosis (NGN), mainly 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 has a potentially significant 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 reads produced by Nanopore technology in combination with the higher precision of the short Illumina reads, to finally reach a completer and more precise draft genome sequence. Phylogenetic and comparative genomics analysis suggest that this strain in more related to *Fusarium tricinctum* species complex than *Fusarium lateritium*, as the symptoms initially suggested. Thus, it could be speculated that a new *Fusarium* 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 to develop a specific control strategy.

*This work has been supported by the European Commission under the Grant Agreement number 774571 (project PANTHEON – 'Precision farming of hazelnut orchards').*