

# Genome of bacteria responsible for tuberculosis of olive tree sequenced

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This is an olive tree with tumors (warts) produced by tuberculosis Credit: Public University of Navarra

Researchers at the Public University of Navarra, the Polytechnic University of Madrid (CBGP), the University of Malaga, the University of Wisconsin and the Valencian Institute of Agricultural Research have managed to sequence the genome of the bacteria responsible for tuberculosis in the olive tree.

The study, included in the June issue of *Environmental Microbiology*, represents the first sequencing of the genome of a [pathogenic bacteria](#)

undertaken in Spain, being the first genome known worldwide of a pathogenic *Pseudomonas* in woody plants.

The sequencing of the genome of this pathogen opens the doors to the identification of the genes responsible for the virulence of this bacteria and its survival on the phyllosphere (leaf surface), thus facilitating the design of specific strategies in the fight against the disease and enabling drawing up programmes for the genetic improvement of olive groves.

*Pseudomonas savastanoi* is the agent that gives rise to tuberculosis in the olive tree, a disease that causes important losses in the olive crops in Spain. Trees affected present tumours (known as verrucas) that can grow to several centimetres diameter in trunks, branches, stalks and buds. Diseased trees are less robust and have less growth, to the point of being non-productive if the attack is very intense. To date, due to the absence of effective methods of control, preventive strategies have been carried out, reducing populations of [bacteria](#) with phytosanitary treatment.

Plant diseases produced by pathogenic microorganisms not only reduce production but can also alter the quality of the food and drastically diminish the commercial value of the crops. The new strategies for disease control today involve the analysis of information contained in the genome of pathogenic organisms. Similar to what has happened with the human [genome](#), this technology is generating a great amount of valuable information for the development of innovative technologies, that will enable identifying and controlling the pathogen as well as obtaining new varieties of the host plant that have greater resistance to the disease.

Provided by Elhuyar Fundazioa

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