

Opinion

Possible bases of the resistance of Coconut palm to the phytoplasma that causes lethal yellowing disease

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Phytoplasmas belong to the parasitic group of mollicutes, which represent a phylogenetically coherent group of pathogens that colonize a wide spectrum of hosts and insects [1]. Phytoplasmas are restricted in phloem cells and are transmitted to plants by insect vectors belonging to the Cicadellidae, Fulgoridae, or Psyllidae families [2]. They are phylogenetically related to the gram-positive bacteria from which they evolved in a retrograde manner by a drastic reduction of their genome, resulting in the loss of many of their biosynthetic abilities, including the most common pathways considered essential for any living organism, as a consequence of their parasitic life [3]. We are interested in the phytoplasma that causes lethal yellowing (LY) disease on coconut palms, denominated “*Candidatus* Phytoplasma palmae,” whose only known vector is *Haplaxius crudus* Van Duzee [4]. It has been found that the different varieties of coconut palms possess different degrees of resistance. The dwarf varieties, such as the Malayan dwarf, are the most resistant, whereas the most susceptible varieties are the tall ones, such as the Atlantic Tall. The hybrids between these two ecotypes possess an intermediate level of resistance [5]. In the case of the other palm species, it has been observed that they generally have moderate resistance. There are several hypotheses on what causes this resistance or susceptibility, one of which could be the different compositions of the waxes in the leaves that act as physical barriers to pathogens and insects. Arroyo-Serralta, et al. [6], reported a different composition among the cuticular wax components in the leaves of tall and dwarf varieties of the coconut palm. Another explanation could come from the fact that the only vector known so far does not feed on dwarf varieties. However, *H. crudus* has been frequently found in all varieties studied [7].

Resistance genes—which code for proteins that can recognize structural molecules of pathogens or effectors (molecules that help colonize the pathogen), trigger a cascade of physiological processes that end in the hypersensitive response and activate the systemic acquired resistance [8]—

could play a key role in resistance in palms. In the case of phytoplasmas, we may think that they are not recognized by the host defense system since they are directly delivered into the host cell by the insect. However, it is known that these small bacteria have the information to produce effectors [9]. In the case of the Aster yellows phytoplasma, 54 effector candidates have been identified [9]. These effectors destabilize the plant cell by affecting the expression of transcription factors, such as those involved in the regulation of the biosynthesis of jasmonic acid, a phytohormone that mediates the resistance of plants to insects [10]. It is possible that resistance genes can neutralize phytoplasma effectors, as has been well-studied in phytopathogenic fungi and bacteria [11]. In our laboratory, we have characterized more than 240 resistance gene candidates (RGC), many of which recognize various plant pathogens [12]. Additionally, we have found an RGC in coconut palm that presents high homology to *Bph14*, a gene that confers resistance to brown planthopper that, in rice, activates plant defense systems, such as callose deposition and trypsin inhibitor production [13]. Therefore, such resistance could be attributed to the fact that the vector insect cannot feed on the palm.

On the other hand, it has been reported that the endophytic microbiome of plants plays certain significant roles. In plants, the endophyte microbial community has been reported to alter its composition in citrus and almond trees infected with “*Ca. Liberibacter asiaticus*” and *Xylella fastidiosa* pathogens,

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respectively, which are obligate parasites of plants, such as phytoplasmas [14,15]. In the grapevine, a greater diversity of the microbial community was observed in healthy plants compared to plants infected with phytoplasmas [16]. In these studies, some bacteria species showed a negative interaction with the pathogen. Moreover, the inoculation of some endophytic bacteria, such as *Dyella*-like bacterium [17] and *Pseudomonas migulae* 8R6 [18], reduced the disease symptoms of *Vitis vinifera* and *Catharanthus roseus* infected with phytoplasmas. In coconut palm, Morales-Lizcano, et al. [19] and our preliminary results indicate that the endophytic bacteria composition of the coconut is altered when the palm is infected with Côte d'Ivoire lethal yellowing and LY-phytoplasma, respectively. The vector endophytic microbiome could also have relevance for phytoplasma multiplication and transmission, as highlighted by Gonella, et al. [20]. This evidence could indicate that the endophytic microbial community has a relevant role in the resistance of plants against pathogens.

Finally, it is important not to forget that other factors could affect the resistance of coconut palms against LY-phytoplasma, such as field conditions (temperature, wind, etc.), suboptimal growing conditions of coconut palms, weeds (that can favor vector populations), vector preference, or different phytoplasma strains [4].

In summary, there may be many resistance strategies used by the palms to overcome phytoplasmas, starting with the structural factors that prevent vectors from feeding. The presence of resistance genes, which recognize the structural molecules or effectors of both phytoplasma and insect vectors, and the endophyte microbiome could be determining factors in affecting the abundance of the pathogen in the host and may help some palm varieties resist this deadly pathogen [21].

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