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AN INTEGRATED MODEL SYSTEM TO INVESTIGATE THE EFFECT OF COPPER ON PLANT PATHOGEN INTERACTION

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Copper is an essential trace element for any living organism and microorganism. However, copper is highly toxic when in excess, affecting several physiological and biochemical processes. Copper accumulates in the soil and the environment, so that a dramatic increase of free Cu^{2+} occurs in the agrosystems due to intensive copper applications as fungicides and bactericides. Additionally, its extensive use leads to the selection of copper-resistant bacteria, reducing the efficacy of copper treatments. Actually, copper tolerance was recently associated to the ability of several pathogenic bacteria for humans to survive the innate immune response during infection (Hodgkinson & Petris, 2012). Moreover, mutations in genes determining copper-resistance in the phytopathogenic bacterium *Xanthomonas campestris* pv. *campestris* resulted in the attenuation of its virulence (Hsiao *et al.*, 2011). According to this unexpected role for copper in pathogenic bacteria – host interactions, the aim of our work was to develop an *in vitro* model to contribute to this new field of biometals research, based on *Nicotiana benthamiana* and *N. tabacum* challenged by *Pseudomonas syringae* pv. *tabaci* ATCC11528. By an integrated approach involving plant tissue culture, plant pathology, chemistry and electrochemistry, we provided evidences concerning the differential thresholds of copper toxicity on whole plant, plant pathogenic bacteria and even at subcellular level. On bacteria, copper toxicity was inversely correlated with the presence/availability of organic substances in the medium, suggesting a similar phenomenon occurring in soil. Moreover, copper damages were more pronounced on the host than on phytopathogenic bacteria, even at concentrations traditionally used in plant protection.

References

Hodgkinson & Petris (2012) *J. Biol. Chem.* 287:13549-13555
Hsiao *et al.*, (2011) *J. Agric. Food Chem.* 59: 9290–9302

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