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UNLOCKING THE POTENTIAL OF THE HOLOGENOME: DEVELOPMENT OF MICROBIAL BREEDING APPROACHES TO FACE THE DOMESTICATION SYNDROME AND IMPROVE RESILIENCE AGAINST CLIMATE CHANGE

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Domesticated plants, and even more genetic improved ones, are much more pampered than their wild parents through fertilization, irrigation, and other defence measures, consequently lowering their ability to interact with or adapt to environmental stressors. Commercial genotypes in fact are often characterized by an unbalanced allocation of energy resources, which are spent for growth and reproduction. This phenomenon leads to limited ability of interaction with the surrounding environment, including a reduced ability in recruitment of beneficial microbes. Indeed, microbiomes represent a promising tool to restore the growth–defense trade-off balance in plants, allowing to develop an agricultural system able to survive with limited external inputs. Thus, application of novel approaches such as the selection and characterization of specific microorganisms able to restore growth–defense trade-off features, the exploitation of complementary -omics tools, and the synthetic microbial communities (SynComs) application is a mandatory way to uncover fundamental processes. In this fashion, we built a publicly available repository for plant-associated microbes with the aim of

preserving the microbial biodiversity associated to grapevine and exploit such arsenal to improve the viticulture sustainability and resilience. To reach this objective, we attempted the manipulation of the holobiont/hologenome through the development of tailored synthetic microbial communities (SynComs). Specifically, we exploited a collection of endophytic bacterial isolates isolated directly from grapevine woody tissues for producing an ad-hoc inoculum encompassing potential biological control agents to counteract the esca syndrome. Thanks to a holistic approach that considered molecular (targeted microbial community analysis and RNAseq), biochemical and physiological responses, we showed that SynCom treatment shaped the plant growth-defence trade-off. In specific, we observed that the SynCom inoculated plants moved the energy allocation through the defence pathways by affecting the efficiency of physiological performances. Our results suggest that, in contrast to what done in previous studies, an approach considering both the bacterial features as well as their impacts on plant growth and defence could shade light on the complex responses occurring among interacting plant and microbes. Indeed, despite the enormous potential of SynCom, we still miss important information, and we need to verify the “dark-side effects” of the application of SyComs, to allow their exploitation with a refined awareness.