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SYNERGISTIC MECHANISM BETWEEN INFLUENZA A VIRUS AND *Streptococcus pneumoniae* IN PNEUMOCYTES

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Influenza A Virus (IAV) and *Streptococcus pneumoniae* (Spn) are considered as two of the most important human pathogens. Co-infections with both microorganisms usually lead to severe respiratory disease, and occasionally, death. Although it has been described a clear synergism between these two pathogens, the mechanism of how they interact during infection of eukaryotic cells is poorly understood. We set up a co-infection model using A549 pneumocyte cells, and we observed that when cells were previously infected with IAV, the intracellular survival of Spn duplicated in comparison with non-IAV-infected cells. It has been reported that Spn can be eliminated by the autophagic pathway in pneumocytes. Our hypothesis was that the increased Spn survival in IAV-infected cells is due to a blockage of the autophagosome/lysosome fusion caused by the viral M2 protein. This was confirmed by over-expression of M2 in A549 cells, where we observed an increased Spn survival. In addition to this host factor, we also proposed that Spn should sense IAV-induced changes at intracellular level in pneumocytes to increase its survival, and these changes should be sensed by a two-component system (TCS) to induce a bacterial response to these stress conditions. We screened TCS mutants and we found that the ΔvisRH did not increase its survival as wt cells. An RNAseq analysis revealed that VisRH regulates the expression of many genes that are involved in the acidic/oxidative stress response. Taken together, these results contribute to elucidate the Spn survival mechanism in IAV-infected pneumocytes.

MI-C16
DIFFERENTIAL YEAST POPULATIONS IN GRAPE MUSTS FROM DIFFERENT *Vitis* SPECIES IN A SHARED TERROIR

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The study of indigenous microbial communities in *V. vinifera L.* ecosystems constitutes a major research area in oenology. Few studies, however, consider the yeast communities present in non-vinifera Vitis ecosystems. Moreover, there are no comparative studies concerning yeast communities in V. vinifera L. and non-vinifera Vitis ecosystems in a shared terroir. In this work, we report the identification and characterization of the main indigenous yeast species present during spontaneous fermentation of Malbec (*V. vinifera L.*) and Isabella (*V. labrusca L.*) grapes harvested from neighboring vineyards. Our studies showed that *Hanseniasporauvarum* was the predominant non-*Saccharomyces* species in both Malbec and Isabella ecosystems. *Hanseniasporavineae*, *Metschnikowiapulcherrima* and *Torulasporadelbrueckii*, yeast species commonly found in *V. viniferaL*. grape musts, were isolated only from the Malbec ecosystem. Candida californica, on the other hand, was only isolated from the Isabella ecosystem. Phenotypic analyses of four randomly selected *H. uvarum*, *Starmerellabacillaris* and *Saccharomyces cerevisiae* isolates, as well as microsatellite genotyping of *S. cerevisiae* isolates from each Malbec and Isabella grape musts, suggest that *V. vinifera L.* and *V. labrusca L.* ecosystems could potentially harbor yeast strain populations that are specific to each *Vitis*species. Non-conventional *Vitis*ecosystems could constitute a relevant research system for the ecological and evolutionary study of wine yeast species.

PLANT

PL-C01
ROLE OF THE MIR394 PATHWAY IN THE REGULATION OF FLOWERING TIME IN *Arabidopsis* AND MAIZE

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The microRNA miR394 regulates the accumulation of a transcript coding for LCR, a member of the F-BOX family. These proteins are part of SCF complexes responsible for the addition of ubiquitin residues to a target protein, marking it for degradation by the proteasome. The miR394 pathway participates in the regulation of leaf morphology, in the development of the shoot apical meristem and in the response to abiotic stress produced by drought and salinity in *Arabidopsis thaliana*. We generated Arabidopsis mutant plants in the two endogenous *MIR394* genes (*mir394a/mir394b*) and maize mutant plants in the two *ZmLCR*genes regulated by miR394 (*zmlcr1/zmlcr2*) and determined that this pathway is also involved in the regulation of flowering time in both species. In this work, we present the characterization of *mir394a/mir394b* mutant plants, which show an early flowering phenotype which correlates with a higher expression of the floral integrators *FT* and *SOC1* during plant development, compared to wild-type Col-0 plants. Conversely, a late flowering phenotype was observed for *zmlcr1/zmlcr2* mutants. Moreover, we used a phylogenetic approach to identify the maize orthologue of the MLP proteins shown to be marked for degradation by the mR394 pathway in Arabidopsis and characterized their expression in maize mutants in the components of this pathway

PL-C02