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horizontal transfer on the other hand is also important in shaping LAB gene pools. Horizontally acquired genes have been shown to be essential in technological properties of starters and in probiosis or virulence of commensals. Progress in bioinformatics tools has allowed rapid annotation of LAB genomes and the direct assignment of genetic traits among species strains through comparative genomics. In this way the molecular basis of many important traits of LAB has been elucidated including aspects of sugar fermentation, flavor and odor formation, production of textural substances, stress responses, colonization of and survival in the host cell, cell interactions and pathogenicity. Functional genomics and proteomics have been employed in a number of instances to support *in silico* predictions. Given that the costs of advanced next generation methodologies like RNA seq are dropping fast, bottlenecks in the *in silico* characterization of LAB genomes will be rapidly overcome. Another crucial advancement in LAB research is the application of systems biology approaches by which the properties and interactions of components or parts of a biological system are investigated to accurately understand or predict LAB behavior. Practically, systems biology involves the mathematical modeling of complex biological systems that can be refined iteratively with wet lab experiments. High throughput experimentation generating huge amounts of data on the properties and quantities of many components such as transcripts, enzymes and metabolites has resulted in several systems models of LAB. Novel techniques allow modelling of additional levels of complexity including the function of small RNAs, structural features of RNA molecules and post translational modifications. In addition, researchers have started to apply systems approaches in the framework of LAB multispecies ecosystems in which each species or strain is considered as a part of the system. Metatranscriptomics, metaproteomics and metametabolomics offer the means to combine cellular behavior with population dynamics in microbial consortia.

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