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Modification of membrane fluidity in response to variable contents of cholesterol and PUFA: Role in beta-amyloid aggregation

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Abstract
Cholesterol and polyunsaturated fatty acids (PUFAs), normal constituents of dietary food, play a crucial role in the modulation of cell membrane fluidity. Specifically they are proved responsible for the increase and the reduction of membrane fluidity[1]. Modification of cell membrane fluidity is related to the etiopathogenesis of important pathologies such as neurodegenerative diseases. A large amount of evidences show that the deposition of amyloid fibrils as consequence of -amyloid peptide aggregation, is related to membrane fluidity modification in Alzheimer disease. Here we present a biophysical characterization based on electronic paramagnetic resonance (EPR) and atomic force microscopy (AFM) of amyloid peptide in membrane models containing variable quantities of cholesterol and PUFAs. Our data puts in evidence the tendency of beta amyloid peptide to follow distinct aggregation pathways in response to qualitatively and quantitatively different content of lipids.

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Application of DNA-based methods for the cultivar identification of wines of *Vitis vinifera*

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Abstract
The quality of wines is highly dependent on different factors among which the grapevine variety is of primary importance. The cultivar used is essential in the case of monovarietal wines or in wines identified by an appellation of origin (DOC) that include more than one variety in a specific ratio. Sometimes, the irregular addition of wines derived from other grapevine varieties is used with the aim of enhancing the sensory characteristics of the final product and/or to decrease the production cost. Therefore technical approaches and legislative guidelines have been developed for grape, must, and wine traceability in order to guarantee product origin and detect fraud. DNA-based methodologies are expected to became the gold standard for the characterization of varieties in grape musts and wines; other methods such as must profiling of proteins, anthocyanins, amino acids, aromatic compounds, and chemical elements, are indeed more time-consuming and can be affected by various parameters such as soil composition, weather conditions, winemaking methodologies, and wine aging. DNA extraction from commercial wines was reported in few papers while PCR based molecular markers were successfully applied to the analysis of grape juice, must, fermenting must and unprocessed wines. Nevertheless, efficient DNA extraction and amplification from must and wine samples remains difficult. The aim of our project is the improvement of molecular tools for wine traceability through the optimization of DNA isolation protocols and the development of molecular probes useful not only to identify the grapevine cultivar, but also potentially applicable to the quantification of the relative amount of different varieties that may be present in a wine.