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Título	Mass-Spectrometry-Based Lipidomics Discriminates Specific Changes in Lipid Classes in Healthy and Dyslipidemic Adults
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Resumo	Triacylglycerols (TAGs) and cholesterol lipoprotein levels are widely used to predict cardiovascular risk and metabolic disorders. The aim of this study is to determine how the comprehensive lipidome (individual molecular lipid species) determined by mass spectrometry is correlated to the serum whole-lipidic profile of adults with different lipidemic conditions. The study included samples from 128 adults of both sexes, and they were separated into four groups according to their lipid profile: Group I—normolipidemic (TAG < 150 mg/dL, LDL-C < 160 mg/dL and HDL-c > 40 mg/dL); Group II—isolated hypertriglyceridemia (TAG ≥ 150 mg/dL); Group III—isolated hypercholesterolemia (LDL-C ≥ 160 mg/dL) and Group IV—mixed dyslipidemia. An untargeted mass spectrometry (MS)-based approach was applied to determine the lipidomic signature of 32 healthy and 96 dyslipidemic adults. Limma linear regression was used to predict the correlation of serum TAGs and cholesterol lipoprotein levels with the abundance of the identified MS-annotated lipids found in the subgroups of subjects. Serum TAG levels of dyslipidemic adults have a positive correlation with some of the MS-annotated specific TAGs and ceramides (Cer) and a negative correlation with sphingomyelins (SMs). High-density lipoprotein-cholesterol (HDL-C) levels are positively correlated with some groups of glycerophosphocholine, while low-density lipoprotein-cholesterol (LDL-C) has a positive correlation with SMs.
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