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Sommario/riassunto	The aim of the present Special Issue is to address the state-of-art of mitochondrial genomics and phylogenomics. Mitochondrial markers are widespread in phylogenetics; however, it is becoming increasingly clear that (i) many discordance issues arise with respect to nuclear markers and (ii) many features that are normally considered 'typical' for the mitochondrial genome are indeed highly unstable and unconserved.