

Update of the human mitBASE database

M. Attimonelli^{1*}, J.M. Cooper², D. D'Elia³, A. de Montalvo⁴, M. De Robertis⁵, H. Lehtinen⁵, S.B. Malladi⁵, F. Memeo¹, K. Stevens^{2,6}, A.H.V. Schapira^{2,6} and C. Saccone¹

¹Dipartimento di Biochimica e Biologia Molecolare, Università degli Studi di Bari, 70126 Bari, IT
²University Department of Clinical Neurosciences, Royal Free and University College Medical School, UCL, London, UK

³Area di Ricerca di Bari, CNR, 70126 Bari, IT

⁴Departamento de Biología Molecular, Hospital Universitario "Marqués de Valdecilla", Universidad de Cantabria, 39011 Santander, SP

⁵Centro di Studio sui Mitocondri e Metabolismo Energetico, CNR, 70126 Bari, IT

⁵EMBL Outstation, European Bioinformatics Institute, Wellcome Trust genome Campus, Hinxton Hall - Hinxton Cambridge, UK

⁶University Department of Clinical Neurology, Institute of Neurology, London, UK

Human MitBASE is a database collecting human mtDNA variants. This database is part of a greater mitochondrial genome database (MitBASE) funded within the EU Biotech Program (1). The present paper reports the recent improvements in data structure, data quality and data quantity. As far as the database structure is concerned it is now fully designed and implemented. Based on the previously described structure (2) some changes have been made to optimise both data input and data quality. Cross-referencings with other bio-databases (EMBL, OMIM, MEDLINE) have been implemented. Human MitBASE data can be queried with the MitBASE Simple Query System (<http://www.ebi.ac.uk/htbin/Mitbase/mitbase.pl>) and with SRS at the EBI under the 'Mutation' section (<http://srs.ebi.ac.uk/srs5/>). At present the Human MitBASE node contains about 5000 variants related to studies investigating population polymorphisms and pathologies.