Multiple Endocrine Neoplasia Type 2 RET Proto-oncogene Sequence Variation Database

Rebecca L Margraf *, David K Crockett*, Ryan Seamos*, Patti Franckowiak*, Fernanda Calderon*, Rong Mao *†

* ARUP Institute for Clinical and Experimental Pathology, Salt Lake City, UT, USA.
† Department of Pathology, University of Utah Medical School, Salt Lake City, UT, USA.

Abstract

Introduction: Multiple endocrine neoplasia type 2 (MEN2) is an inherited, autosomal dominant disorder which is caused by deleterious mutations within the RET proto-oncogene. MEN2 RET mutations are heterogeneous; thousands of sequence changes found within exons 8, 10, and 11 have been publicly available MEN2 mutations database in RET gene of MEN2 phenotypes classification.

Aim: The aim of this MEN2 RET database is to record all sequence variations within the RET proto-oncogene relevant to the MEN2 syndromes, as well as any associated clinical information and the most informative literature references. The database was created using the Human Genome Variation Society (HGVS) and HUGO recommendations for sequence variation nomenclature and database content. Information sources for the current MEN2 RET database entries were public reports on MEN2 or RET sequence variation found in 2009 and on the World Wide Web. The database’s MEN2 phenotype definitions were derived from the International RET Mutation Consortium (IRMCl) MEN2 classification guidelines.

Methods: The MEN2 RET database was created using the Human Genome Variation Society (HGVS) and HUGO recommendations for sequence variation nomenclature and database content. Information sources for the current MEN2 RET database entries were public reports on MEN2 or RET sequence variation found in 2009 and on the World Wide Web. The database’s MEN2 phenotype definitions were derived from the International RET Mutation Consortium (IRMCl) MEN2 classification guidelines.

Results: The searchable database contains 132 RET sequence variation entries as of April 2009. Each database entry contains these descriptive fields: location within the RET gene, codon number, change, protein change, genotype, pathogenicity, classification, MEN2 phenotype, youngest of MTC onset, first litterature reference, and comments. The comments for each entry may contain more information on MEN2 clinical features, describe phenotype for unusual genotypes (such as homozigosity or multiple RET changes), as well as additional literature references listed as PMID numbers. Search-Processed (http://www.ncbi.nlm.nih.gov/sites/entrez) with the PMID #. These additional references were the most relevant for determining pathogenicity.

Conclusions: The MEN2 RET database is a unique and useful reference for the MEN2 syndromes result in a high lifetime risk of developing medullary thyroid carcinoma, and pheo), or if MTC is diagnosed in at least three unrelated individuals with the same germline sequence change.

Significance

The database is found under Disease Databases on the ARUP Online Scientific Resource at http://www.arup.utah.edu/database/MEN2/ or directly accessed at http://www.arup.utah.edu/database/MEN2/MEN2_welcome.php

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