



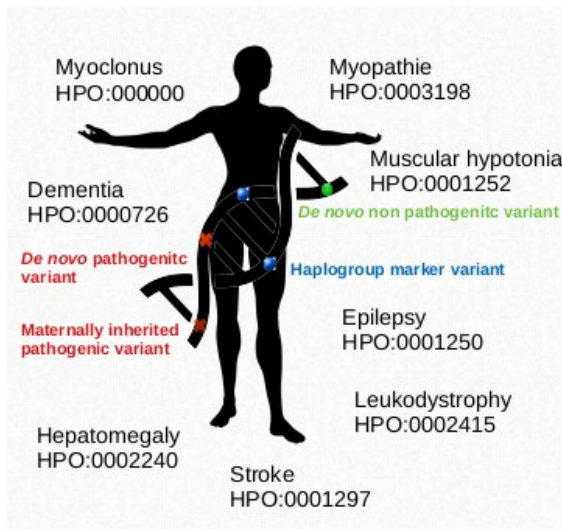
MITOMATCHER DB, a French clinical-biological national database to aid in mitochondrial variant prioritization

BODRUG Alexandrina¹, CHOURY A¹, MEHTARIZADEH M², COLIN V², BRIS C¹, BANNWARTH S³, GOUDENEGE D¹, AMATI-BONNEAU P¹, DESQUIRET-DUMAS V¹, ROUZIER C⁻, AIT-EL-MKADEM SAADI S³, MARTIN-NEGRIER ML⁴, TRIMOUILLE A⁴, ALLOUCHE S⁵, HARDY G⁶, DEVOS A⁷, ACQUAVIVA-BOURDAIN C⁸, PAGAN C⁸, VASSEUR S⁸, GAIGNARD P⁹, JARDEL C¹⁰, RUCHETON B¹⁰, BARCIA G¹¹, BONNEFONT JP¹¹, LEBRE AS¹², REYNIER P¹, COSSEE M¹², PION E¹³, SHAHRAM A¹³, BROOKES A², PAQUIS-FLUCKINGER V³, PROCACCIO V¹

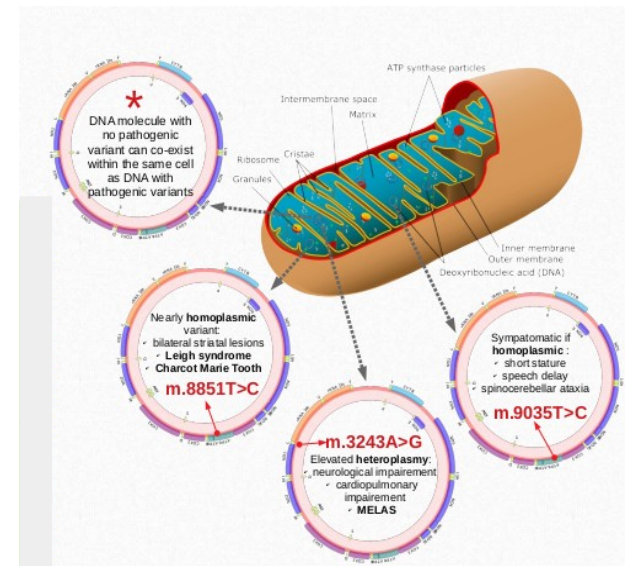
1 : CHU d'Angers - 2 : Université de Leicester - 3 : CHU Nice - 4 : CHU Bordeaux - 5 : CHU de Caen - 6 : CHU Grenoble - 7 : CHU Grenoble - 8 : CHU Lyon - 9 : Kremlin-Bicêtre - 10 : La Pitié Salpêtrière - 11 : Hôpital Necker-Enfants Malades - 12 : CHU Montpellier - 13 : Filnemus

CONTEXT & GOALS

Mitochondrial diseases affect 1 in 4,300 live births. Mitomatcher DB aims at gathering phenotypic and genetic data to improve diagnostics and permit the search for co-occurring variation, interpretation of Variants of Unknown Significance and impact of mitochondrial haplogroup and heteroplasmy on pathogenicity.



Urgent need for a national database joining **genetical** and **phenotypical** data in a comprehensive manner.



- Clinical data
 - Age, age of onset
 - Cosanguinity
 - **HPO terms**
- Sampling
 - tissue
 - Sequencing technique
 - analysis metadata
- Reference center
 - laboratory
 - medical staff (user)

- Mitochondrial DNA
 - 16,5 kbp
 - 37 genes, 15 proteins
 - **heteroplasmy ***
- Nuclear DNA
 - 1500 proteins involved in mitochondrial functions
- Annotations
 - Pathogenicity scores
 - Frequencies
 - Conservation scores

Setting a secure environment and enabling complex querying through an user friendly interface.

Genetic data

Phenotypic data

DATABASE & QUERYING

- Samples
 - 3k patients
 - 51k genbank
- Secure hosting environment
 - Dynamic Virtual Machine
 - Double authentication
 - Indirect querying (elasticsearch)
- Complex querying
 - Variant co-occurrence
 - Similar phenotypes
- User friendly interface
 - Cafe Variome

Mitomatcher DB

TABLE_NAME	TABLE_ROWS
Analysis	56041
Annotation	14505
Clinical	548
Clinical_Sample	548
Gene	37
Gene_Variant	12355
Laboratory	13
Ontology	63
Ontology_Sample	10013
Sample	50051
Technique	5
User	18
Variant	14438
Variant_Call	1757403

Data is gathered from mitochondrial rare disease reference centers.

Visit → mitodiag.fr/network

MySQL, python
PHP, CodeIgniter

display

The web app permits complex queries.

- (1) Heteroplasmy filtering
- (2) Co-occurring variants (mt/mt or mt/nucl.)
- (3) Human Phenotype Ontology search
- (4) HPO similarity
- (5) Extracting query results in .csv or .xls format

Cafe Variome web app

The screenshot shows the Cafe Variome web app interface. It includes a search bar, a 'VARIANT' section with filters for heteroplasmy and co-occurring variants, an 'HPO' section for phenotype search, and a 'Build Query' button. Red annotations highlight specific features: (1) Heteroplasmy filtering, (2) Co-occurring variants, (3) HPO search, (4) HPO similarity, and (5) Exporting results.

Video DEMO:

<https://drive.google.com/file/d/1yyN0a-Qp87XWdw9igf3wYyboIPR7PGgM/view?usp=sharing>

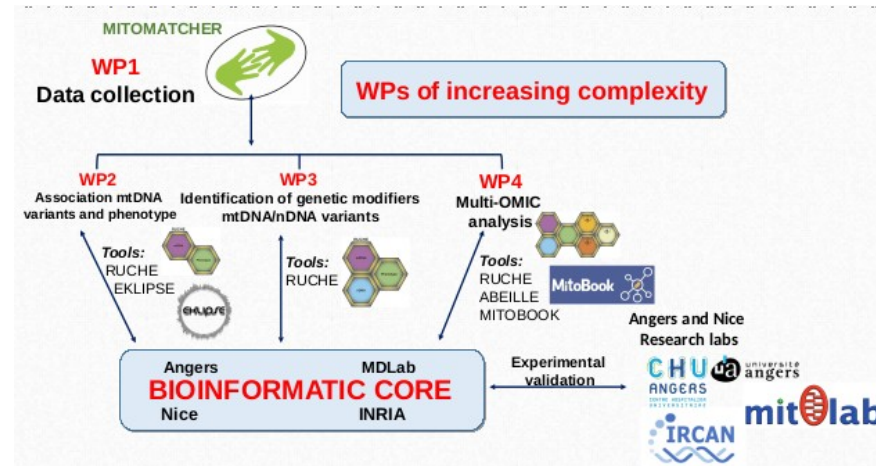
PROSPECTS

Better understanding of the molecular mechanisms responsible for the **clinical-genetic heterogeneity of mitochondrial diseases** by building Work Packages of increasing complexity.

Societal and ethical implications → *Social Science Humanities, Nantes University, Pr Tirard*

Mitomics – Mitomatcher project received national **PIA4 funding**.

Pending data sharing authorization (CNIL).



- Pathologies liées à des mutations de l'ADN (Bris et al. 2018)
- Prevalence of rare mitochondrial DNA mutations in mitochondrial disorders (Bannwarth et al. 2013)
- Peculiar combinations of individually non-pathogenic missense mitochondrial DNA variants cause low penetrance Leber's hereditary optic neuropathy. (Caporali et al. 2018)