

# MID: a specific database and online platform for male infertility

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## Abstract

In developing countries, especially like India and China, people have a strong mindset and fully emphasis on child-bearing. Currently, human male infertility percentage is increasing drastically. Infertility is not a disease and it is treated as a condition with physiological, medical implications. Diagnosis of idiopathic males is difficult than any other category and it is very hard to find out the reasons for infertility. There are no existing databases to study easily about the various genes associated with male infertility. To elucidate the basic knowledge about semen and its composition, various causes, microelements and its role, treatments and genetic causes, as well as to retrieve the basics about the genes and proteins involved with male infertility. MID (Male Infertility Database) was implemented as a web interface using PHP scripting language at backend and HTML, CSS & JavaScript (jQuery Framework) were used at the frontend/client side. The data were collected from the bioinformatics common database like PDB, UniProt and Entrez databases. These data were appropriately filtered using specialized systematic literature and our previous knowledge on male infertility. The current information about male infertility and updated literature were retrieved from Science direct, Science alert, Goggle Scholar, PubMed and PubMed central. MID provides three modules (“Search”, “Browse” and “Statistics”) that enable searches, acquisition of contents and access to all updated statistical data. The direct links to matching external databases are also available. The database will be updated at interval corresponding to genes and protein related to male infertility. The compilation of all general information, sequence and structural data of all genes and protein in one platform is highly useful for current experts and budding researchers in human reproduction and male infertility area.

**Key words:** Male Infertility Database (MID), Semen Quality, Fertility Associated Proteins, Semen Parameters.

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## INTRODUCTION

Human male infertility becomes a major problem in the evaluation of infertile couple and it is not done an impact before 50 years (Kumar and Singh, 2015). But now the male infertility is treated as a predominant problem and it affects the life quality of the married couple in the developing countries (Agarwal et al., 2015). There are reports that, the quality of the semen measured by number of sperm cells, active motile cells, morphologically good motile cells has been declined by almost 50% between the years 1950 to 2010 (Johnson et al., 2015). Even the World health organization has reduced its own standard parameter values to access the semen quality in their new editions (Esteves, 2014). This shows that overall there is a decline the semen quality throughout the world and especially in Western countries it is high (Virtanen et al., 2017). The increase in prevalence is due exposure by number of environmental factors such as exposure to heavy metals (Zafar et al., 2015), drugs (Calogero et al., 2017), adulterated foods (Wahab and Sultana, 2017), testicles heat exposure (Durairajanayagam et al., 2015) and lifestyle modifications (Wright et al., 2014). These environmental factors also disturbs the genetic material present in sperm cells and causes the alterations and modifications in DNA structure and leads to alter the function of the specific protein encoded by the specific gene (Carrell et al., 2016). Genomics and proteomics studies on human male infertility are the most advanced study that enables some proper idea for the diagnosis of

human male infertility (Ayaz et al., 2018). With the advance in genomic, proteomic, immunomic techniques, it is now very easy for the diagnosis and prognosis of human male infertility. As spermatogenesis is a complex process, as expected 2300 genes were involved in regulating the spermatogenesis from the initial step until the intermediate step of maturation of sperm cells to the final step in reaching female reproductive tract for fusion (Miyamoto et al., 2015).

Integrative omics approach like epigenomics, genomics, and proteomics; it is very easier now to elucidate the important genes associated with human male infertility. Idiopathic type of human male infertility cannot be diagnosed by using the standard semen parameters, because idiopathic males were found with normal values for all the parameters, and some unknown factors could be the reason for that category (Jodar et al., 2015). In those cases, the integrative omics approach with big data enumerates some substantial reasons for the cause. Measure of spermatozoa RNA may lead to know the paternal contribution towards giving live birth in a timed intercourse. RNA's in spermatozoa sometimes lack in their number and it could be the reasons for the male infertility in idiopathic males (Pereira et al., 2016). There are many number of assumptions, important genes involved in male infertility, but there exist no database for human male infertility. So, we decided to create a male infertility database (MID) that could have very basics about the semen quality (Gaskins et al., 2015), semen composition (Byrne et al., 2017), the role of Zn towards male infertility (Fallah et al., 2018), glucosidase and fructose in seminal fluid (Huyen et al., 2018), the cause of human male infertility by environmental factors, smoking (Sharma et al., 2016), and consumption of heavy metals, as a genetic cause about robertsonian translocations (Kirkpatrick et al., 2015) were discussed in this database.

More over important genes associated with human male infertility were retrieved from Uniprot and made to table to represent the same in the database. By this, one can easily retrieve the basic data about the protein that might involve with human male infertility by simply browsing the Uniprot ID of the protein. This database will be helpful for the researchers working with reproduction, male fertility and infertility and it will provide the basic data. The gene and protein sequences related to male infertility were retrieved from Uniprot database (Table 1).

### Materials and Methods

The current database has been developed and configured using X/WAMP server. WampServer is a Windows based web development environment. It allows us to create web applications with Apache2, PHP and a MySQL database. PhpMyAdmin, is web portal that is easy way for the admin/users to manage the database as well as the backend server settings. Most of the separation logic is written at the UI side using jQuery framework. Since our application is mostly a Content management site so keeping the logic at UI helps run our code seamless without much server-side rendering which makes application loading incredibly fast. We have separate pages for each of the type Gene Name/Protein type that gets loaded based on the search field. Searching is done using jQuery based on keypress event in input search field.

### Results and Discussion

Bioinformatics, an advance field using Information technology and programming to create public available database by store, organize and analyze the vast and critical biological data in the form of information, features, sequences and structures of DNA, RNA and proteins (Ragunath et al., 2009). Mainly, biological database is actively used in two ways i) collection of biological data in a form that can be easily accessed by user ii) available to multi user (Nishant et al., 2011). The overall database scheme was shown in Figure 1. The homepage of MID contains introduction about male infertility and various icons for the sublink of the database shown in Figure 2. The general introduction of male fertility further explained in various sub links like human semen, HSP proteins, Seminal functions, Zinc and its importance, etc shown in Figure 3. The critical feature of the database was gene and protein involved in male infertility was browse and search option that can gene key information for the user shown in Figure 4. Future research on critical proteins and genes may lead to annotation of various mechanism and treatment of male infertility worldwide. The result page of protein search results in FASTA format that can leads to bioinformatics research in male infertility shown in Figure 5 .

### Conclusion and future update

To best of our knowledge, MID is the first comprehensive database and online platform for the genes and proteins involved in male infertility. The main goal of the database was the researchers should able to access a free web interface with highly curated information and represented in coherent manner. We assure this platform will help researchers in understanding the genes and proteins directly and indirectly involved in cause of male infertility. In future, we will update with structural information and further novel information.

### Disclosure statement

The authors declare no conflict of interest.

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**Table 1:** Important proteins involved as a cause of human male infertility

Sl. No.	Uniprot ID	Gene Name	Protein Name
1	Q99497	PARK7	Protein deglycase DJ-1
2	Q96RN1	SLC26A8	Testis anion transporter 1
3	P31213	SRD5A2	3-oxo-5-alpha-steroid 4-dehydrogenase 2
4	P07333	CSF1R	Macrophage colony-stimulating factor 1 receptor
5	P09603	CSF1	Macrophage colony-stimulating factor 1
6	O60266	ADCY3	Adenylate cyclase type 3
7	Q8NEC5	CATSPER1	Cation channel sperm-associated protein 1

8	Q95925	EPPIN	Eppin
9	Q8NEP3	DNAAF1	Dynein assembly factor 1, axonemal
10	Q8IWB6	TEX14	Inactive serine/threonine-protein kinase TEX14
11	Q8TE73	DNAH5	Dynein heavy chain 5, axonemal
12	P36969	GPX4	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial
13	Q4G0P3	HYDIN	Hydrocephalus-inducing protein homolog
14	Q8IZP9	ADGRG2	Adhesion G-protein coupled receptor G2
15	Q86X45	LRRC6	Protein tilB homolog
16	O14556	GAPDHS	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific
17	Q96DT5	DNAH11	Dynein heavy chain 11, axonemal
18	Q4G0X9	CCDC40	Coiled-coil domain-containing protein 40
19	O75344	FKBP6	Inactive peptidyl-prolyl cis-trans isomerase FKBP6
20	Q9UFE4	CCDC39	Coiled-coil domain-containing protein 39
21	Q9BXA6	TSSK6	Testis-specific serine/threonine-protein kinase 6
22	A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6
23	Q9NR20	DYRK4	Dual specificity tyrosine-phosphorylation-regulated kinase 4
24	Q8N427	NME8	Thioredoxin domain-containing protein 3
25	Q9UI46	DNAI1	Dynein intermediate chain 1, axonemal
26	Q8IW40	CCDC103	Coiled-coil domain-containing protein 103
27	Q9GZS0	DNAI2	Dynein intermediate chain 2, axonemal
28	Q86Y56	DNAAF5	Dynein assembly factor 5, axonemal
29	Q5TD94	RSPH4A	Radial spoke head protein 4 homolog A
30	O14967	CLGN	Calmegin
31	Q9BW62	KATNAL1	Katanin p60 ATPase-containing subunit A-like 1
32	Q9NVR5	DNAAF2	Protein kintoun
33	Q75WM6	H1FNT	Testis-specific H1 histone
34	Q9H1X1	RSPH9	Radial spoke head protein 9 homolog
35	Q8N9W5	DNAAF3	Dynein assembly factor 3, axonemal

36	Q9UBK7	RABL2A	Rab-like protein 2A
37	Q4LDG9	DNAL1	Dynein light chain 1, axonemal
38	Q6JVE9	LCN8	Epididymal-specific lipocalin-8
39	Q5GAN6	RNASE10	Inactive ribonuclease-like protein 10
40	Q6JVE6	LCN10	Epididymal-specific lipocalin-10
41	Q6JVE5	LCN12	Epididymal-specific lipocalin-12
42	Q9UNT1	RABL2B	Rab-like protein 2B
43	P62502	LCN6	Epididymal-specific lipocalin-6

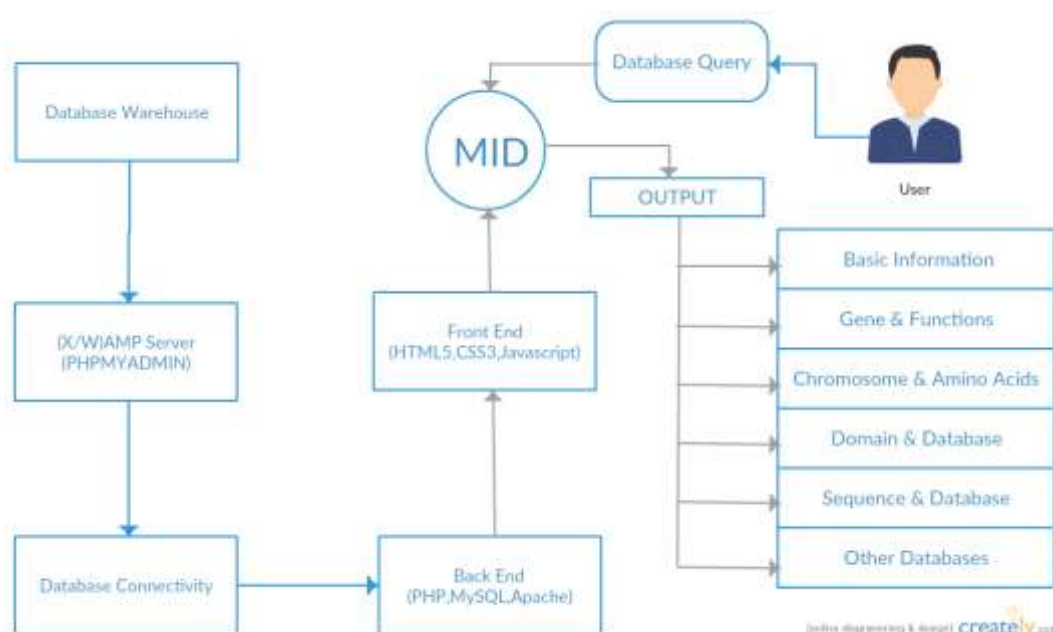


Figure 1: Flow chart of MID scheme.



Figure 2: Home page of MID.



Figure 3: Result page of general introduction on male infertility in MID.

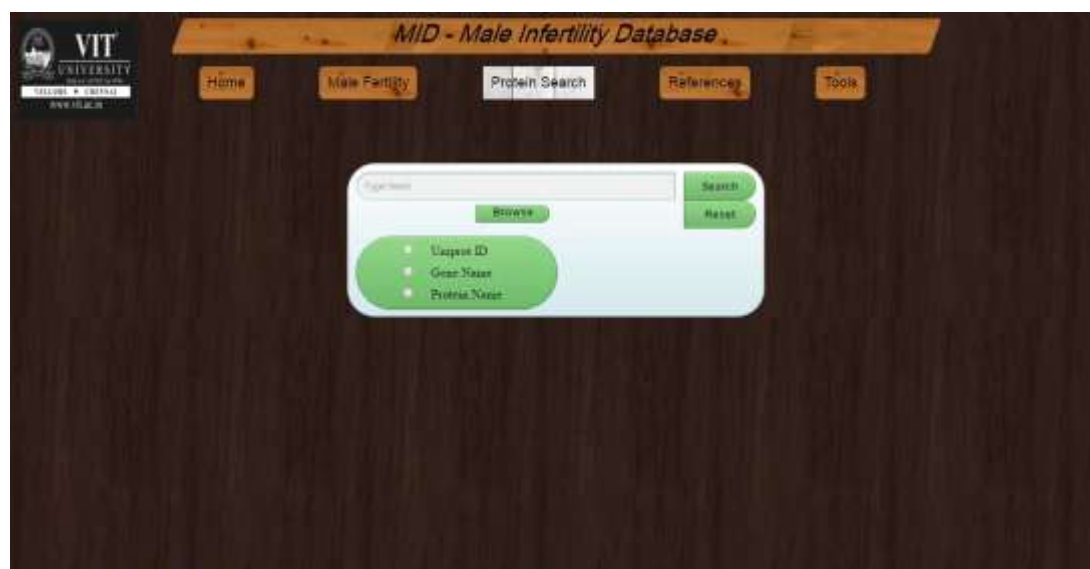


Figure 4: Home page of protein search option in MID.

The screenshot displays the MID - Male Infertility Database interface. At the top, there is a navigation bar with tabs for Home, Male Fertility, Protein Pages, Genes, and Tools. A search bar is prominently featured, with the query 'Q99497 - PARK7' entered. Below the search bar, the results are organized into sections:

- Basic Information:**
  - Uniprot ID: Q99497
  - Protein Name: Protein deglycase DJ-1
  - Gene Name: PARK7
  - Molecular Weight(kDa): 16.84
  - Integration Date: 07-Dec-04
  - Last Modified: 20-Jan-07
- Gene & Functions:**
  - Gene & Functions:**
    - Function:**

Protein deglycase that repairs methylglyoxal- and glyoxal-glycated amino acids and proteins, and releases repaired proteins and lactate or glycolate, respectively. Deglycases cysteines, serines and tyrosine residues in proteins, and thus reactivates these proteins by reversing glycation by glyoxals. Acts on early glycation intermediates (hexosylamines and aminoimidazole), preventing the formation of advanced glycation endproducts (AGE) (PubMed:2548795). Plays an important role in cell protection against oxidative stress and cell death acting as oxidative stress sensor and redox-sensitive chaperone and protease; functions probably related to its primary function (PubMed:1995934, PubMed:2095498, PubMed:1871036, PubMed:1789442, PubMed:1822308, PubMed:2048763). It is involved in neuroprotective mechanisms like the stabilization of NF- $\kappa$ B and RAGE proteins, male fertility as a positive regulator of embryonic signaling pathway as well as cell growth and transformation through, for instance, the modulation of NF- $\kappa$ B-p300 signaling pathway (PubMed:2010093, PubMed:1992204, PubMed:1448723, PubMed:1935934, PubMed:2087936, PubMed:1871945). Its involvement in protein repair could also explain other unrelated functions. Eliminates hydrogen peroxide and protects cells against hydrogen peroxide-induced cell death (PubMed:1930002). Required for correct mitochondrial morphology and function as well as for autophagy of dysfunctional mitochondria (PubMed:222940, PubMed:1992349). Plays a role in regulating expression or stability of the mitochondrial uncoupling proteins UCP2/4 and SLC25A7 in dopaminergic neurons of the substantia nigra pars compacta and attenuates the oxidative stress induced by calcium entry into the neurons via L-type channels during increasing (PubMed:1871148). Regulates estradiol inflammatory responses, may modulate lipid self-dependent endocytosis in astrocytes and neuronal cells (PubMed:23847945). Binds to a number of miRNAs containing multiple copies of GG or GC motifs and partially inhibits their translation but dissociates following oxidative stress (PubMed:3002006). Metal-binding protein able to bind copper as well as toxic mercury ions, enhances the cell protection mechanism against induced metal toxicity (PubMed:2970957).
    - Chromosome and Gene Set:**
      - Chromosome Information: /LPO0000043 Component: Chromosome 1
      - Length of Amino Acid: 198
      - Domain and Database
      - Phm ID: P10365 (1,7,26,76)
      - Protein ID:
      - No protein info
      - Sequence and Database

Figure 5: Results of the protein search for the query input in MID.