

Study of Genetic Disorders, Inheritance and Databases Development for Family Pedigree

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Abstract— Genetic disorders are the abnormalities cause due to defect in one or more genes . The defect in genes can be cause due mutations and this disorders can be inherited from one generation to another .to examine those inheritances predigree are constructed on the bases of which genesist can determine the pattern of inheritance ,diagnostic testing, with the goal of disease prevention or early diagnosis and management of the disease . We also have certian databases which can trace our ancestors . This paper contain the study of genetic disorders , inheritance , pedigree , genetic databases and a hypothesis for a database which can predict weather the next generation will be affected by a disease or not.

Keywords— NanoDB; nanophase; nanomaterials; nanostructures

I. INTRODUCTION

The defect in gene can lead to sever genetic diseases or even death in many cases, and it can be inherit from one generation to the next. Many people live very healthy life

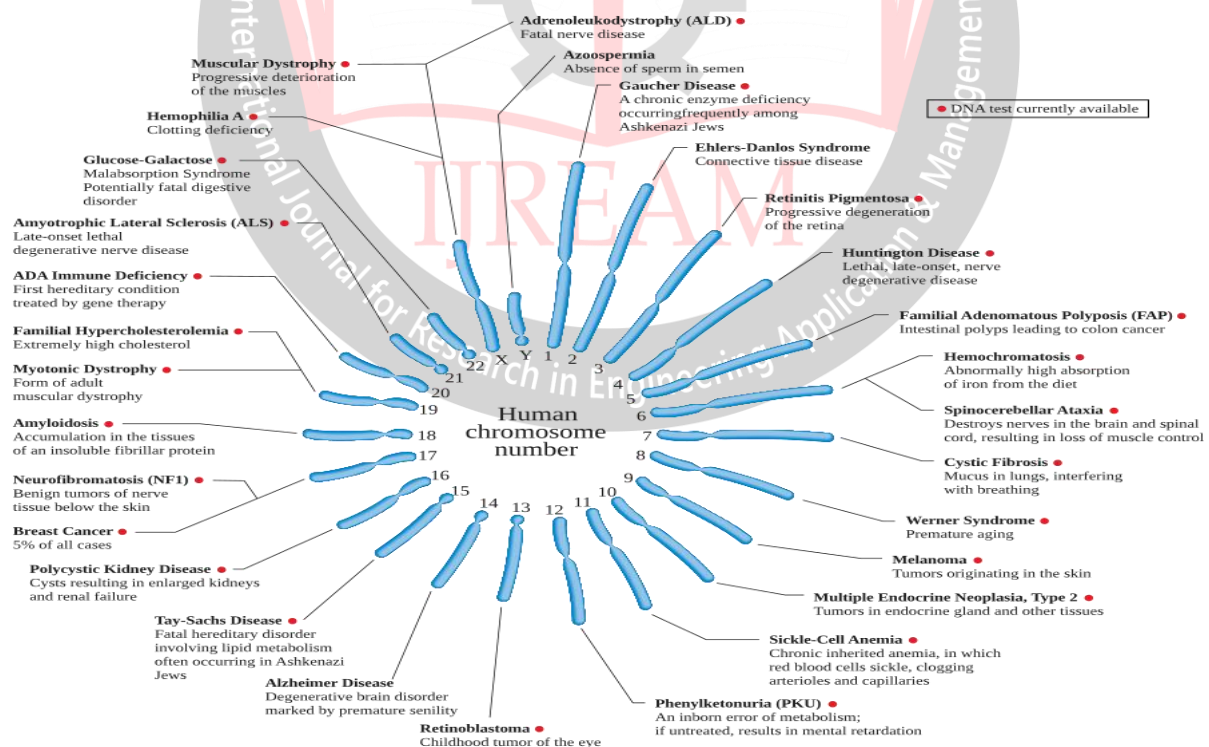


Fig. 1: Chromosomal number and disease associated [6]

Style but still suffer from diseases the reason behind this is genetics, century back Mendel put fort his famous experiment

on pea plant where he showed the inheritance (transfer on characters from one generation to another) same is applicable

for all the sexually reproducing organisms. Presented research work study the genetic disorders and their inheritance from one generation to another and databases related to genetics. Based on that we made a hypothesis whether a database is possible which will predict the inheritance like we study pedigree. This database will also create awareness about genetic diseases. In short this databases will contain information of all genetic diseases, causes, mutation, inheritance pattern in particular family, chance of progeny to born with disease.

II. LITERATURE SURVEY

2.1. Genetic disorder and inheritance

Genetic disorders occur in families with a pattern that reflects the inheritance of a single causative gene. In 1985 Gregor Mendel published his observations of a pea plants. By describing the principles governing transmission of characters he laid the foundation for study of inheritance human disease.

These early genetic experiments, confirmed and rediscovered independently in 1900 by Carl Correns, Hugo de Varies and Erich Tschermak demonstrated that the units of inheritance are independent of one another and each is transmitted separately from parent to offspring

2.2 The chromosomal basis of inheritance

Chromosomes are the thread like structure of nucleic acids found in the nucleus of most living cells, carrying genetic information in the form of genes. The chromosomes are the vehicle for transmission of genetic information. By 1902 Walter Sutton and Theodor Boveri had independently put forth the chromosomal theory of inheritance, providing a mechanistic basis for the concepts of inheritance and setting the scene for development of cytogenetics. By the late 1980s, a proposal to establish the entire DNA sequence of human genome was put forth and gaining favour, and the entire sequence of 3×10^9 bp was established in the year 2000.

2.3 Principles of Mendelian analysis

Genes are encoded in DNA molecules that are packed into chromosome which are diploid and these separate during meiosis such that gametes contain only a single chromosome. This process, and the occurrence of genetic recombination during meiosis, is the mechanism of inheritance encapsulated in Mendel's law of segregation and the law of independent assortment. According to Mendel behavior of characters is either dominant or recessive. Dominant character is one that is expressed in the heterozygote and the recessive character is one that only expressed when an individual is homozygous. Many trait can show partial dominance or even co dominance contributing equally to the phenotype.

Only a small portion of human traits and diseases have clear inheritance pattern. In human genetics analysis we often dealing with information about likely inheritance patterns that is incomplete, disease and traits that may exhibit at greater or lesser severity in different family members and a range of

potentially sensitive ethical, cultural and social issues that impact on the study of inherited disease

The occurrence of a disease in a family may occur in several main patterns or models. These are grouped according

- i. Sex specific(X- linked or Y-linked)
- ii. Autosomal

X-linked recessive conditions generally occur only in males. Females are carriers, because their second X-chromosome provides a normal allele, but males who inherit the recessive gene on their sole X-chromosome will be affected. Occasionally females will show a degree of affectedness. Female carriers will transmit the gene to all of their sons (because they inherit only their mother's X- chromosome) and to half their daughters. Affected males will transmit the gene to all their daughters, all of whom will therefore be carriers.

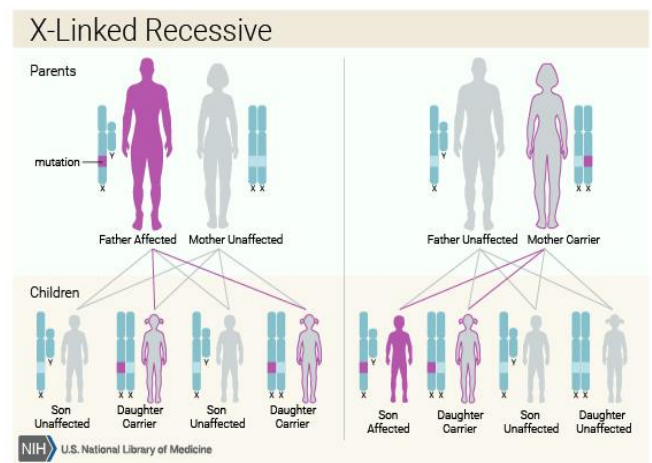


Fig 2.3.1: inheritance of X- linked Recessive

Autosomal Dominant disease occurs in both males and females, other affecting many individuals throughout pedigree. Affected individuals are heterozygous. The risk of transmission of such condition from affected individual is 50%. This is the most common pattern of inheritance observed for Mendelian disorder.

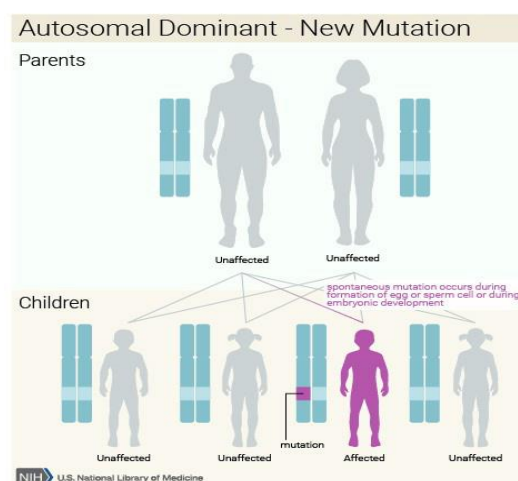


Fig. 2.3.2: Inheritance of autosomal dominant

Autosomal recessive, which occur when two healthy individuals are carried usually will have no family history. The conditions often only occur within the children from one relationship. The risk of transmission of the disorder is 25% and half of the unaffected offspring will be carriers for the gene [1].

Autosomal Recessive Genetic Disease

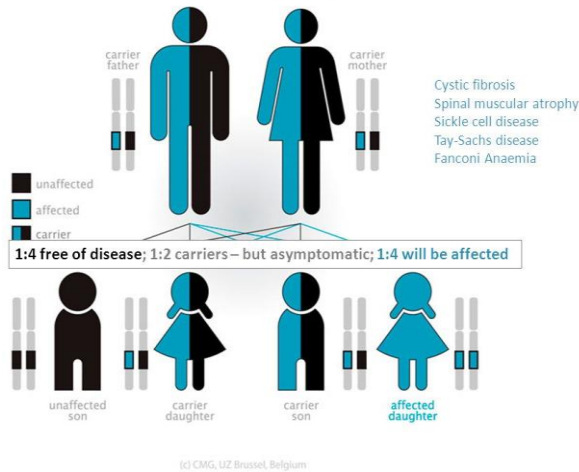


Fig 2.3.3 : Inheritance of autosomal recessive

2.4. Family pedigree

Family histories are reported, pedigree construction and disease are the mean by which translated into verified clinical tool information risk assessment and management decisions by clinical Genetics staff. The following table illustrates the evaluation of generation of pedigree [2]

Table 2.4.1 some diseases or conditions which may be evaluated by generation of a pedigree [2]

Broad categories	Examples
Congenital birth defects	Cleft lip and/or palate Congenital heart defect Spine bifida or other neural tube defect Hydrocephalus Pyloric stenosis Club foot
Chromosome anomaly	Trisomy 21 (Down syndrome) Trisomy 13 or 18 Microdeletion Complex chromosome rearrangements
Developmental delay/ mental retardation	Fragile X syndrome Other metabolic disorders Unexplained
Metabolic disorders	Phenylketonuria Tay-Sachs disease Canaan disease
Neuromuscular/ neurodegenerative	Duchene muscular dystrophy Miltonic dystrophy Spinal muscular atrophy Spinocerebellar ataxia Charcot-Marie-Tooth Neurofibromatosis Huntington's disease

Hematologic hemoglobinopathies and thalassemia	Sickle cell disease Alpha thalassemia Beta thalassemia
Bleeding disorder/ coagulopathies	Hemophilia von Willebrand disease Factor V Leiden mutationAntithrombin utation
Other gene disorders	Cystic fibrosis Hemochromatosis
Adult onset/multi factorial	Diabetes Cardiovascular disease Hypertension
Malignancy	Breast Colorectal Ovarian Sarcoma Melanoma

Table 2.4.2 Common symbols used to generate pedigree

	Male	Female	Sex unknown
Individual	□	○	◇
Affected individual	■	●	◆
Affected (more than one condition)	▨	◐	◑
Multiple individuals	4	3	5
Multiple individuals, number unknown	n	n	n
Deceased or stillbirth	⊘	⊙	⊠
Pregnancy	P	P	P
Spontaneous abortion (SAB)	△	△	△
Affected SAB	▲	▲	▲
Termination of pregnancy (TOP)	⊗	⊗	⊗
Affected TOP	⊗	⊗	⊗

Adapted with permission from Bennett RL, Steinhaus KA, Uhrich SB, Sullivan CK, Resta RG, Lochner-Doyle D, et al. Recommendations for standardized human pedigree nomenclature. Am J Human Ge net 1995;56:745-52.

2.5. Genetic databases

Gene sequence and protein databases are the most common databases used in genetics Gene sequence database are divided into two types:

- Primary databases -contain experimental result without addition information
- Secondary database – contain experimental result with additional information such as sequence information , gene variants etc.

2.5.1 OMIM

Online Mendelian Inheritance in Man is a database of human genes and genetic disorders establish to support research and

education in human genomics and the practice of clinical genetics. It was started by Dr. Victor A. McKusick. Mendelian Inheritance in Man, OMIM (www.ncbi.nlm.nih.gov/omim) is now distributed electronically by the National Centre for Biotechnology Information (NCBI). Each OMIM entry has a full-text summary of a genetically determined phenotype and/or gene and has numerous links to other genetic databases such as DNA and protein sequence, PubMed references, general and locus-specific mutation databases, approved gene nomenclature, and the highly detailed map viewer, as well as patient support groups and many others. [3] it contain information about linkage data phenotype and reference on all inherited human known disorder [4].

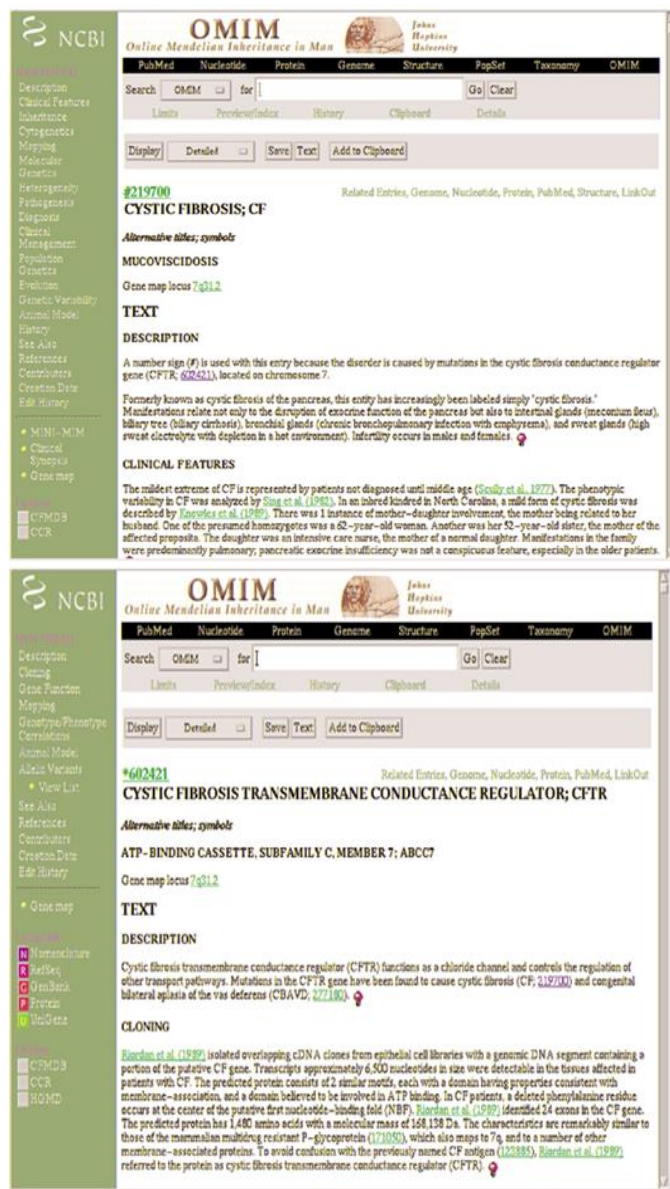


Figure 2.5.1 OMIM Database [3]

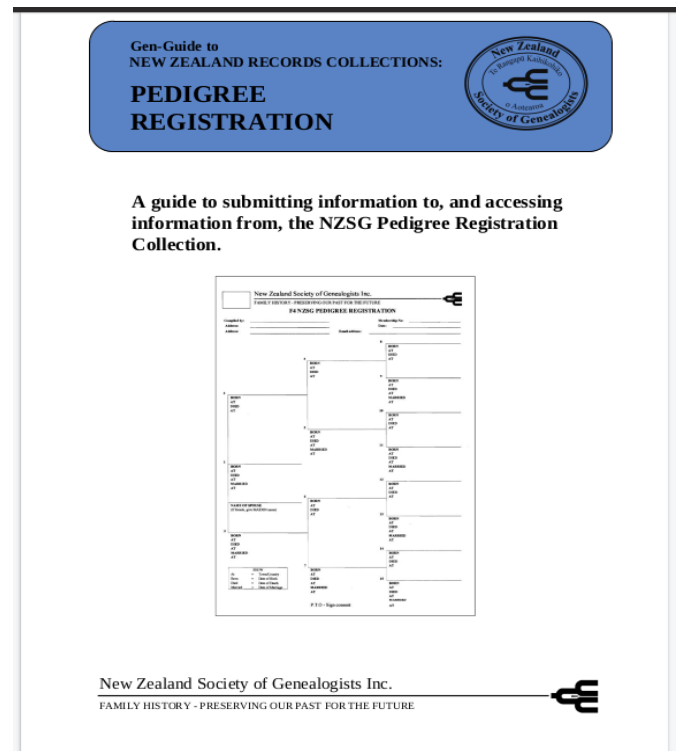


Figure 2.5.2: Pedigree Registration for Newzealand Society Genealogists [7].

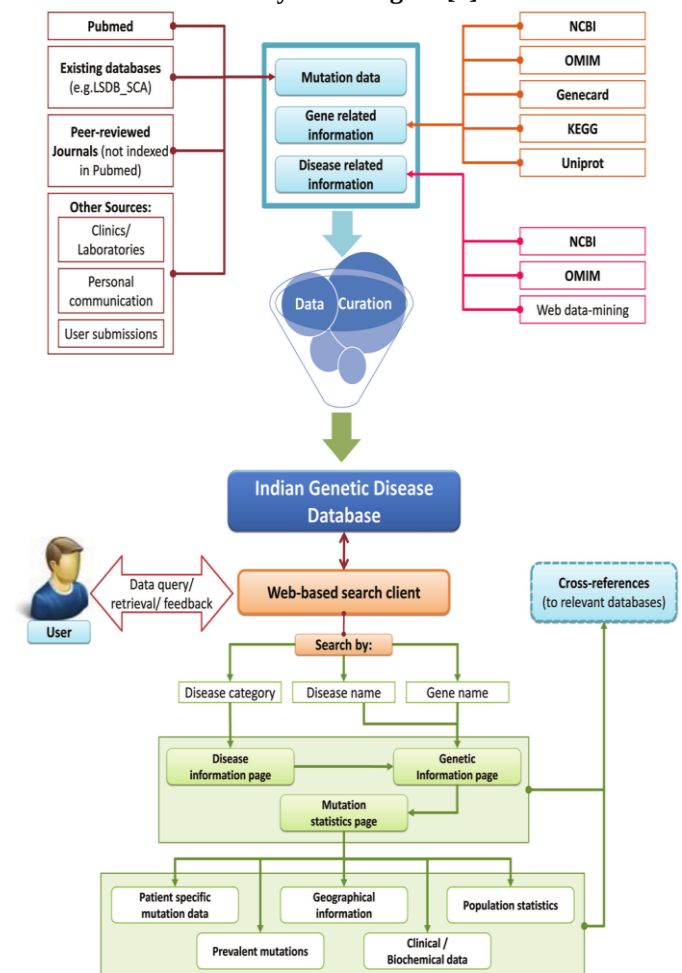


Figure 2.5.3: The Schematic representation of Indian Genetic Disease Database [5]

Above mention two figures shows that in many countries database for pedigree have been developed. In India Indian Genetic Disease Database is developing which contain the information about 52 diseases with information of 5760 individuals carrying multination alleles. Information on locus heterogeneity, type of mutation, clinical and biochemical data, geographical location and common mutations are recorded on the bases of published literature. [5]

in other countries the Gemological databases are developed where the ancestors can be traced, inspired by this can we do something by which we can predict the genotype, phenotype and inheritance of disease.

III. FURTHER DEVELOPMENT

As per the literature survey it is possible to design a database, which we will predict the inheritance of disease from one generation to another, we have pedigree chart to do so but for that we have to go to genesist and if we particularly talk about Indian population awareness about genetic diseases and its inheritance is less as compare to another.

The conceptual diagram of the Database is given below,

user will first register in the database that is he will create his account. After that user information will hit the genetic database. When user will login to the database and will submit the genetic information of his family (mother, father, wife, mother-in-law, father-in-law), the strategy of the database is to be build such that it will predict the possibilities of inheritance of disease.

The database will also provide the information about that disease, treatment available nearby, etc.

The information about genetic linkage, mutation is available through OMIM.

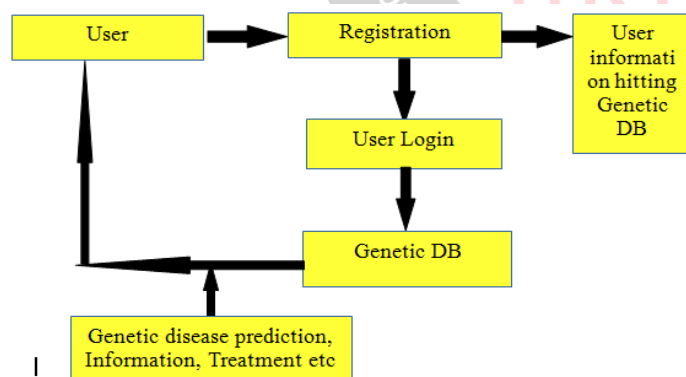


Figure 3.1 Conceptual Diagram For Database

3.1. Development of Database

A. Collection of Data:

Data collection is the systematic approach to gather and measure information from variety of sources to get a complete of an area of interest.

This database is collection of data for predition of genetic disease which can occur in next generation.

The collection of data includes genetic information of individuals, types of genetic diseases, cause of genetic disease, treatment for genetic disease etc.

B. Distribution of Data:

1. User login
2. Genetic information of user
3. Inheritance in next generation
4. Linkage analysis
5. Genetic disease information

C. E-R Model for user login

The user login will contain the name of user, father name, mother name, last name, user-Id also, genetic information will contain the user id and the genetic reports (information) of that user. With the help of this genetic information the database will predict the inheritance of disease to the next generation. After knowing the inheritance the database will provide the name, cause , treatment and type of that genetic disease.

D. Database Creation

This can be done by using MySQL

IV. RESULTS AND CONCLUSIONS

On the bases of literature study we have concluded here there is very less awareness on genetic diseases. The need for the awareness is more as many people live healthy life style but still suffer from diseases the reason behind this is inheritance of defective gene, if one get to know that what disease he or she have or whether he or she is carrier or not it will not only helpful for them but also for their next generation. This database will provide the information about disease the person suffering from, the cause of that disease, treatment available for that and very important the chances of inheritance of disease to the next generation.

ACKNOWLEDGMENT

We would like to acknowledge Director and Research director of MGM's Institute of Biosciences and Technology and also Head of Department Ms. Archana Harke madam, for giving us such fruitful environment and all the technical support time to time for our project work.

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