ANALYSIS RAT MODEL FOR DETECTING HUMAN DISEASE USING GENE EXPRESSION

[1]K.Vimala, [2]Dr.D.Usha
[1]Research Scholar, [2]Assistant Professor
Department of Computer Science
Mother Teresa Women's University, Kodaikanal, Tamilnadu, India

Abstract: The rat is the leading organism for genetic disease research. A rich resource of genetic variation occurs naturally in inbred and a special strain provides spontaneous mutations. Nevertheless, one can also obtain desired gene mutations by using the following processes: targeted mutations that eliminate function in the whole organism or in a specific tissue; forward genetic screens using chemicals or transposons; or the introduction of exogenous transgenes as DNAs, bacterial artificial chromosomes (BACs) or reporter constructs. The rat is the only mammal that provides such a rich resource of genetic diversity coupled with the potential for extensive genome manipulation, and is therefore a powerful application for modeling human disease.

Keyword: Lassa Fever, Murinetypus, Cartinoma, Hemorrhagic fever.

I. INTRODUCTION

The rat is the primary mammalian model for studying human disease and human health. The rat is small, making it an economical choice, and it also breeds very well. Researchers have amassed incredible knowledge about rat physiology, anatomy, and its genes, stemming from more than 100 years of working with them. More importantly, the rat is among the first mammalian species to have its genes modified with molecular tools.

Fig: Rat

The ability to manipulate the rat genome is what makes the rat so relevant today. It helps to sequence both the human and rat genomes, it is known that, their molecular constitutions and how the sequences vary between individuals and between the two species. Even between two healthy people, there can be millions of small sequence and structure differences that help define who those people are as individuals.

Therefore, the remaining challenges in genomics remain difficult. Researchers are hard at work investigating what effects the millions of variations present in each genome have for health and disease. Making small tweaks to individual rat genes or even sequences within a specific gene, allows many researchers to perform many research activities on disease.

II RAT MODEL FOR STUDYING HUMAN DISEASE

- Rats are biologically very similar to humans and get many of the same diseases, for the same genetic reasons.
- Rat can be genetically manipulated to mimic virtually any human disease or condition. With modern sequencing and genomic engineering technologies, the precise mutation underlying human disease can be introduced into rat, yielding more accurate and useful disease research data.
- Rat can be inbred to yield genetically identical strains. This uniformity allows for more accurate and repeatable experiments.
- Rats have an accelerated lifespan, with one rat year equaling about 30 human years. Therefore, their entire life cycle can be studied within only two or three years.
- Rats are well understood because they have been used in biomedical research for nearly a century.
- Rat sare a cost-effective and efficient research tool. They are small, they reproduce quickly, and they are relatively easy to handle and transport.

III GENETIC OF RAT

In the 1960s and 1970s, biochemical (isoenzyme) genetic marker systems were developed. In the 1980s and 1990s, DNA markers revolutionized genetic mapping: restriction fragment polymorphisms (RFLPs), simple sequence length polymorphisms (SSLPs) detected by polymerase chain reaction (PCR) amplification (e.g. MIT markers), and single nucleotide polymorphisms (SNPs). All, especially SNPs, are widespread throughout the genome. With DNA markers, newly discovered genes or mutations can be tested for linkage with many DNA markers on all chromosomes in a single cross. Also, stored DNAs from linkage crosses,

mapping panels, or recombinant inbred strains can be typed repeatedly for new markers. These advances enable the rapid identification of potential human disease-causing genes through comparative mapping.

IV MANIPULATION OF THE RAT GENOME

The choice of strain may have significant impact on the phenotype as unlinked genes contained in the strain background can have a dramatic effect on the disease phenotype. Although gene driven approaches, such as transgenics and targeted mutations, are useful for understanding gene function, it is likely that phenotype driven schemes will be necessary to fully understand the functional complexities of the rat genome.

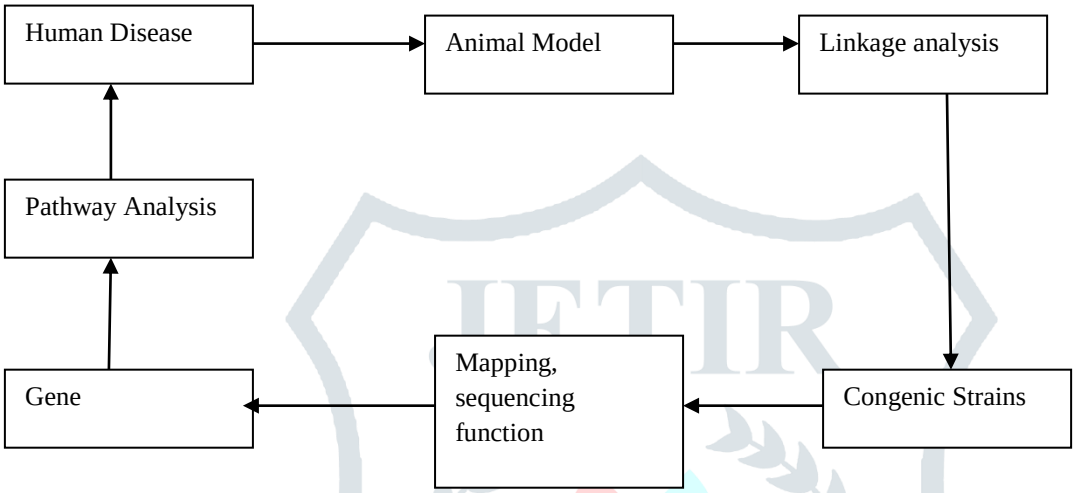

Fig 1. Analysis of animal model to detect human disease

V DISEASE DETECTED IN RAT

Three main diseases are detected in the rat model, which may provide pathway for diagnosis and prevention toward human disease

1. Lassa Fever
2. Murinetypus
3. Cartinoma

5.1. VIRAL HEMORRHAGIC FEVER

5.1.1. LASSA FEVER

Lassa fever, also known as Lassa hemorrhagic fever (LHF), is a type of viral hemorrhagic fever caused by the Lassa virus. Many of those infected by the virus do not develop symptoms. When symptoms occur they typically include fever, weakness, headaches, vomiting, and muscle pains. Less commonly there may be bleeding from the mouth or gastrointestinal tract. The risk of death once infected is about one percent and frequently occurs within two weeks of the onset of symptoms. Among those who survive about a quarter have hearing loss, which improves over time in about half.

The disease is usually initially spread to people via contact with the urine or feces of an infected multimammate rat. Spread can then occur via direct contact between people. Diagnosis based on symptoms is difficult. Confirmation is by laboratory testing to detect the virus's RNA, antibodies for the virus, or the virus itself in cell culture.

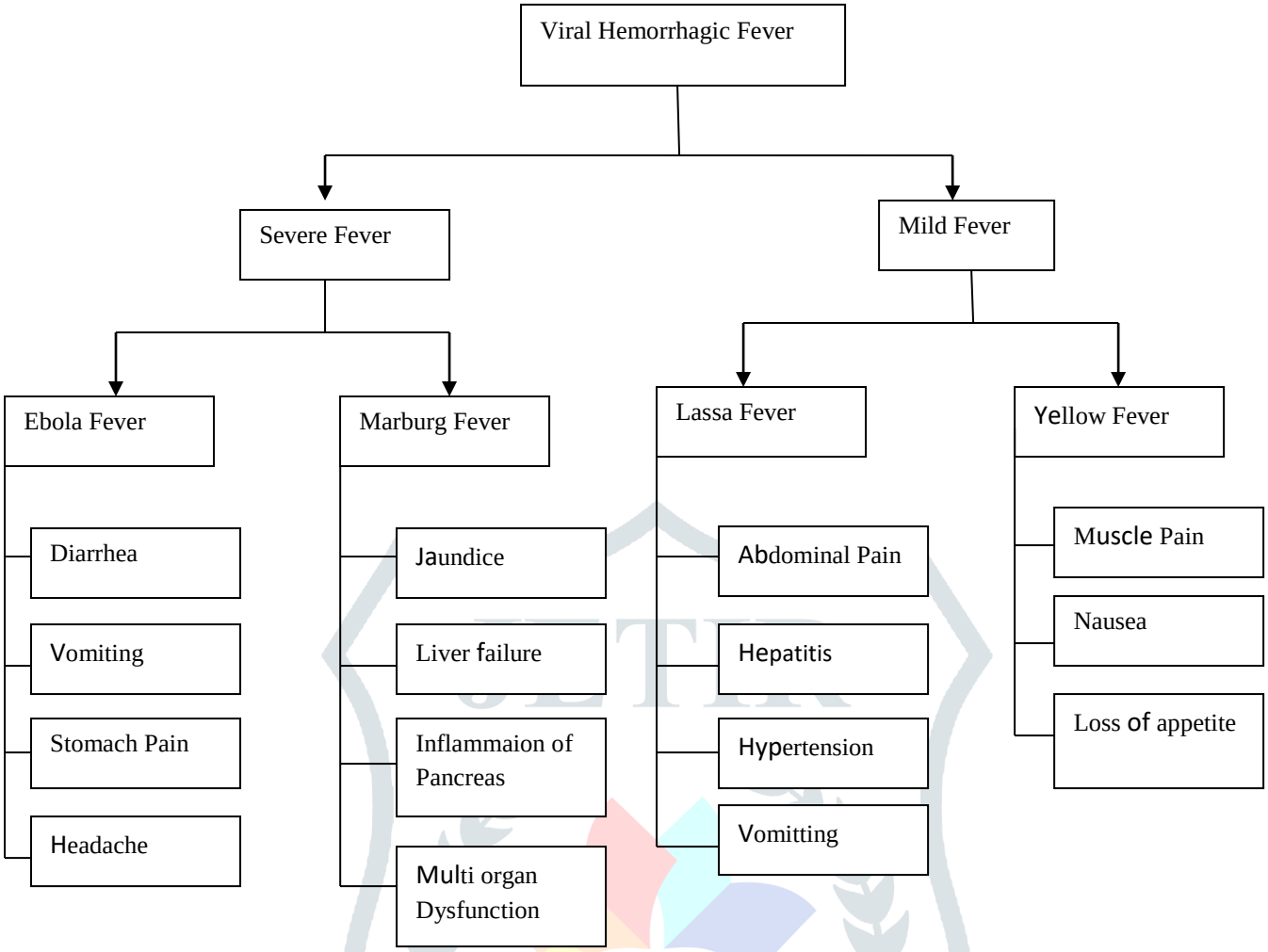

Fig 2. Viral hemorrhagic fever

Symptoms Caused using Lassa Fever

- Gastrointestinal tract
  - Nausea
  - Vomiting
  - Diarrhea
  - Abdominal pain
  - Constipation
  - difficulty swallowing
  - Hepatitis
- Cardiovascular system
  - Pericarditis
  - Hypertension
  - Low blood pressure
  - Fast heart rate
- Respiratory tract
  - Cough
  - Chest pain
  - Shortness of breath
  - Pharyngitis
  - Pleurisy
- Nervous system
  - Encephalitis
  - Meningitis

- Unilateral or bilateral hearing loss,.
- Epileptic seizures

5.2. MURINE TYPHUS

Murine typhus is a disease transmitted by fleas. Endemic typhus, flea-borne typhus, and shopfever are other names used for this disease. It is caused by the bacterium, Rickettsia typhi, and possibly Rickettsia felis, found in infected fleas and their feces. Murine typhus differs from epidemic or louse-borne typhus.

5.2.1. TRANSMISSION OF MURINE TYPHUS

Fleas defecate as they feed. Infection occurs when flea feces containing the disease agent are scratched into the bite site or other skin opening, are transferred to the eye (conjunctiva), or enter the airway.

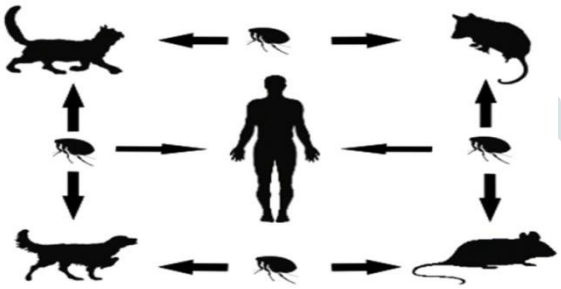

Fig 3. Transmission of Murine Typhus

5.2.2. SYMPTOMS OF MURINE TYPHUS

Symptoms may begin from 6 to 14 days after exposure. All infected persons have fever and most have headache, chills, body aches and pains. A rash on the chest, back, arms and/or legs can sometimes occur. Murine typhus shares symptoms with many other diseases and can being correctly diagnosed if a specific blood test is not performed.

5.3. CARCINOMA

Carcinoma is a type of cancer that starts in cells that make up the skin or the tissue lining organs, such as the liver or kidneys. Like other types of cancer, carcinomas are abnormal cells that divide without control.

5.3.1. TYPES OF CARCINOMA

Although carcinomas can occur in many parts of the body, the common types of carcinoma are:

- Basal cell carcinoma
- Squamous cell carcinoma
- Renal cell carcinoma
- Ductal carcinoma in situ (DCIS)
- Invasive ductal carcinoma
- Adenocarcinoma

VI CONCLUSION

The rat model is used to diagnosis diseases such as Lassa Fever, Murinetypus, Cartinoma, Hemorrhagic fever. The protein sequence analysis is detected inorder to verify the gene expression changes and help to identify diseases. This provides the pathway analysis to detect human disease.

VII REFERENCE

[1] Joseph Oluchukwu Wogu, Christiana Ogeri Chukwu, "Mass media reportage of Lassa fever in Nigeria: a viewpoint" ,Journal of International Medical Research 2019 January 18,

[2] Dylan M Johnson, Jenny D Jokinen, Igor S Lukashevich,"Attenuated Replication of Lassa Virus Vaccine Candidate ML29 in STAT-1 Mice", Pathogens 2019 January 15, 8 (1)

[3] Giulia Torriani, Evgeniya Trofimenko, Jennifer Mayor," Identification of clotrimazole-derivatives as specific inhibitors of Arenavirus fusion",Journal of Virology 2019 January 9

[4] Athanase Badolo, Felicity Burt, Susan Daniel, Rachel Fearns, "Third Tofo Advanced Study Week on Emerging and Re-emerging Viruses, 2018", Antiviral Research 2018 December 28

[5] Fabian D Mairinger, Robert F H Walter, "Activation of angiogenesis differs strongly between pulmonary carcinoids and neuroendocrine carinomas and is crucial for carcinoid tumourgenesis",Journal of Cancer 2014, 5 (6): 465-71

[6] Svetlana A Maslakova, Mark Q Martindale, Jon L Norenburg," Fundamental properties of the spiralian developmental program are displayed by the basal nemertean Carinoma tremaphoros (Palaeonemertea, Nemertea)",Developmental Biology 2004 March 15, 267 (2): 342-60

[7] S A Maslakova, M Q Martindale, J L Norenburg,"Vestigial prototroch in a basal nemertean, Carinoma tremaphoros (Nemertea; Palaeonemertea),Evolution & Development 2004, 6 (4): 219-26

[8] Anthony M Brade, Sylvia Ng, James Brierley, "Phase 1 Trial of Sorafenib and Stereotactic Body Radiation Therapy for Hepatocellular Carcinoma",International Journal of Radiation Oncology, Biology, Physics 2016 March 1, 94 (3): 580-7

[9] Suleyman Bayram, Hikmet Akkız, Aynur Bekar," The association between the survivin -31G/C promoter polymorphism and hepatocellular carcinoma risk in a Turkish population",Cancer Epidemiology 2011, 35 (6): 555-9

[10] Boostrom A, Beier MS, Macaluso JA, Macaluso KR, Sprenger D, Hayes J, et al." Geographic association of Rickettsia felis-infected opossums with human murine typhus, Texas". Emerging Infectious Disease journal. 2002;8(6):549–554

[11] Gikas A, Kokkini S, Tsioutis C, Athenessopoulos D, Balomenaki E, Blasak S, et al. Murine typhus in childrenclinical and laboratory features from 41 cases in Crete, Greece. Clinical Microbiology Infection journal. 2009;15(2):211–212.

[12] Renesto P, Samson L, Ogata H, Azza S, Fourguet P, Gorvel JP, et al. Identification of two putative Rickettsial adhesins by proteomic analysis. Research in Microbiology journal. 2006;157:605–612.