Multi-Knowledge Electronic Comprehensive Journal For Education And Science Publications (MECSJ)
ISSUE (27), December (2019)
ISSN: **2616-9185**

www.mecsj.com

The Design of Immunity Based on Genetics

Roua Alsubki
Department of clinical laboratory sciences, College of Applied Medical Sciences
King Saud University, Riyadh, KSA
r.subki@gmail.com

Abstract

This study mainly aims to evaluate the design of immunity based on genetics, this includes the following sub- objectives; first: to identify the complex regulation of immunity, and the cause of complexity in immunity. Second: to determine how the immune response and sensitivity to infectious diseases are genetically controlled. Third: to identify systems related to agriculture and ecology in immunity.

A descriptive approach was adopted in the preparation of this study to extrapolate the literature of the design of immunity based on genetics.

The discussion showed that: different components of the immune response have different timing of expression, suggesting a complex and specific regulatory control; immunological efficiency is a dynamic feature that changes over the lifetime of the host, while there is a tendency to treat immunogenicity as a static property of the host; the immune capacity decline with age; immune genes increase with age, even in the absence of infection; the genetic engineering of immune power varies between the two ages, with a stronger correlation between energy metabolism and immune power in older flies; there is strong evidence of a relationship with controlling or reducing exposure to infectious agents or disease progression for some host genetic variants; and finally agricultural systems can sometimes be designed to resist diseases.

Accordingly, this study emphasized the need to; improve the classical human immunological approach with both evolutionary biology and with data sets produced by human genome projects; intensify genome-wide correlation studies, build a close collaboration between researches developed on wild reservoirs and humans that would ultimately improve the knowledge of the dangers of the Hantavirus epidemic, and to intensify the work in understanding the pathogenesis of the disease.

Keywords: Immunity, Genetics, Pathology, immunogenetics, Agriculture, Ecology.

1. Introduction

It has now been shown that host genetic change affects an individual's susceptibility to infectious diseases as well as autoimmunity (Chapman & Hill, 2012). The immunogenetics field is at the research core aimed at understanding and identifying the association between immunity-related diseases or immune phenotypes and genetic factors (Geraghty, Daza, Williams, Vu, & Ishitani, 2002).

Based on approaches of candidate gene, immunology has moved to genomics with the advent of new techniques including next-generation sequences and microarrays of DNA. The complete genome sequencing of individuals with severe phenotypes and subsequent genome-related studies now contributes to the detection of genetic underpinnings of human vulnerability to certain infectious diseases and the decoding of the immune mechanisms underlying their pathogenesis (Trowsdale & Knight, 2013). The study of spatial and temporal variations of SNP polymorphisms in these genes / geographic location further highlighted the potential role of exposure to infectious diseases, the epidemiological consequences of this variation and the evolutionary mechanisms (drift, migration, selection). Maintain immune genetic diversity. Surprisingly, only recently has this evolutionary perspective been explored in human studies (Charbonnel, et al., 2014).

The scientific community now possesses the information and tools needed to address the complex genetics of diseases. Significant advances in genetics will allow us to apply reverse logic to our endeavors as we use genes to identify pathways for analysis rather than pathways that lead us to genes. Comprehensive detection of polymorphism in biological pathways highlights the key elements in the pathogenesis of the disease, and many are involved in more than one disease (Donaldson, 2019).

Immunogenetics is a branch of medical research that examines the relationship between the immune system and genetic genes and is a section of microorganisms. Immunology is an important and fundamental science to be learned in the study of medical sciences (Cooke & Hill, 2001). Significant advances in immunology occurred in the early and mid-20th century. Recent advances in immunology include the identification of genes responsible for certain immune functions and the detection of T cell receptors and cytokines. For example, geneticists were able to identify the genes responsible for the production of immunoglobulins (Charbonnel, et al., 2014).

1.1 Problem statement

Because genetic factors can affect immune responses, and the immune associations act as an indicator of disease progression and as a biological indicator of disease progression, the study of immunology is important for basic genetics and immunology, as well as in translational and individual medicine. Therefore, the problem of the study lies in the lack of topics related to the design of immunity based in genetics, for these reasons, it is extremely important to increase the volume of studies on his topic.

1.2 Research Questions

The main question of this study is: **"What is the design of immunity based in genetics?"**

This main question is subdivided into the following sub-questions:

1. How is genetic control of the immune response and sensitivity to infectious diseases?
2. What are the complex regulation of immunity, and the cause of complexity in immunity?
3. What are the agriculturally and Ecologically Relevant Systems in immune?

1.3 Research Objectives

The main objective of this study is: **"To evaluate the design of immunity based in genetics."** This main objective is subdivided into the following sub-objectives:

1. To identify the complex regulation of immunity, and the cause of complexity in immunity.
2. To determine how the immune response and sensitivity to infectious diseases are genetically controlled.
3. To identify systems related to agriculture and ecology in immunity.

1.4 Research Significance

The importance of this study comes from the significance of genetics which represent a worldwide issue and an important area of research. Studies of genetics and immunity are scarce; therefore, conducting such a research regarding this topic is expected to have a high positive reflections and significance that can be summarized as in the following:

1) This study will be fruitful source of information on the genetics and immunity topic, over time, more consideration will be given to this topic.
2) This study would represent a good reference for the future studies as long as it would provide the subsequent researchers and interested scholars in the field of immunity with valued literature, recommendations and suggestions that are important for their proposed studies in the light of contemporary.

1.5 Research Method

A descriptive approach was adopted in the preparation of research through reference to these, theses, scientific research and foreign books, where it is it requires extrapolation of literature of the design of immunity based in genetics

2. Background & Literature Review

2.1 Immunity

Immunity is the body's ability to resist certain harmful substances such as bacteria and viruses that cause diseases. The body defends itself against diseases and harmful organisms through a complex structure, consisting of a group of cells, molecules and tissues, called the immune system, where this device provides protection against a variety of harmful substances that invade the body (Pradeu., 2012)

An essential feature of the immune system is its ability to destroy alien organisms without affecting the rest of the body's healthy cells. But the immune system sometimes attacks and destroys these cells. This response is called an autoimmune or autoimmune response (Holt, Macaubas, & Cooper, 1997).

The immune system cannot protect the body from all diseases on its own, but sometimes it needs help. Doctors give patients vaccines to prevent some acute life-threatening infections. Vaccines and serums enhance the body's ability to defend itself against certain types of viruses or bacteria. Vaccination and vaccination for prevention is called immunization. The scientific study of the immune system is called immunology, and the history of immunology dates back to the late 19th century. Until then, scientists had little information on how the immune system worked. Today, there has been considerable progress in the information available to immunologists, i.e. doctors and scientists studying the immune system, on how this system works (Christiansen, 2012).

Immunity is the force that the body acquires to resist and overcome infections, that is, the means of defending the human body against invading the pathogens that cause the disease. It can be defined as the body's ability to resist microorganisms and toxins and some exotic compounds from the body, which can harm him and hurt him, as more comprehensive can be immune defined as the various ways in which Etjaoppea the body towards vehicles and exotic elements and sometimes the body's own components, which are Contact with tissues in an attempt by the body to dispose of these compounds and elements and invalidate their harmful effect (BOWERS, 2003).

The body itself forms an active immunity during its conflict with the attacking germs, and consists of an antibody reaction that usually lasts longer than the passive immune state (transmitted antibodies). Humans have learned to mimic the invasion of germs by injecting the body with a vaccine after they have been neutralized or diluted, or by microbial products subject to controlled and vaccine-made cases. Here, the human body responds to this vaccine and produces antibodies that gain effective immunity that protects against subsequent invasions by similar or nearby germs. Therefore, the purpose of vaccines is to build immunity (i.e., antibody formation) against infectious diseases (ABDUL-GHAFFAR, 2003).

The immune system consists of special cells and organs that deal with foreign factors and allergens. These cells produce antibodies to fight infection and extraneous alien agents.

In order for the immune system to defend the body it must recognize both the factors that belong to the body (Subjective factors) and those alien to it. Autoimmune diseases occur when the body fails to distinguish between autoimmune and non-autoimmune factors.

When this happens, the body produces antibodies directed against the body's own tissues called self-antibodies, which mistakenly attack the body's normal cells.

Immunogenetics is a study of the immune system and is a very important branch of medical and biological sciences. The immune system protects us from infection through various defense lines. If the immune system does not function properly, it can lead to various diseases, such as autoimmune diseases, allergies and cancer. It is now clear that immune responses contribute to the development of many common disorders that are not traditionally seen as immune, including some metabolic, cardiovascular, and neurodegenerative disorders such as Alzheimer's (Lazzaro, 2014).

Developing our understanding of essential immunity is essential for clinical and commercial application. It has facilitated the discovery of new diagnoses and treatments for a wide range of diseases. In addition to technological advances, immunological research has provided very important research techniques and tools, such as flow cytometry and antibody technology (Charbonnel, et al., 2014).

The immune system is a complex system of structures and processes that have evolved to protect us from disease. Molecular and cellular components make up the immune system. The function of these components is divided into two parts: The first have non-specialized and innate mechanisms of the organism called innate immunity. The second has specialized mechanisms called specialized immunity, dealing with pathogens and acquired during the life of the organism after exposure to microbes and bacteria causing disease. Their compounds are selective and specialized, as each cell or its particle can act against a single pathogen (Christiansen, 2012).

It is increasingly recognized that defense against infection has a complex design, shaped by the contributions of multiple genes and many environmental factors. While we might traditionally imagine that defense against infection is determined primarily by the activity of the host immune system, recent studies have established various biological mechanisms to regulate defense.

Immunogenetics is studied using a wide range of methods and organisms from agriculture-related plants to genetic models such as Drosophila for humans (Lazzaro, 2014).

Immune responses to vaccines vary among individuals. The main goal of vaccines is to deal with genes that may explain a large part of this difference.

For example, studies show that the variation in antibody response to hepatitis B surface antigen (HBsAg), measles virus, mumps virus and rubella virus is about 60, 88, 38 and 45% on a genetic basis. In general, HLA and non-HLA genes that encode cytokines, cell surface receptors and TLRs affect immune responses to vaccines, for example, HBV, smallpox, MMR, and seasonal influenza. Furthermore, there is evidence that genetic factors play a role in determining the safety of vaccines and adverse events, and therefore, have led to adventures. In general, vaccines and adventures facilitate the prediction of the effectiveness and safety of the vaccine using immunological knowledge, which in itself helps to develop more effective vaccines (Pradeu., 2012).

2.2 Genetics

Genetics is the scientific study of inherited variation. Human genetics is the scientific study of inherited human diversity. This field has been activated in recent years by the Human Genome Project. Scientists expect the project to lead to the development of new drugs aimed primarily at specific genetic disorders.

Modern genetics increasingly comprises genetic engineering; a technique used to manipulate genes and has produced several advances in medicine. There are several principles of genetics (Kapiel, 2005):

- The function of each cell within the organism is determined by genetic information encoded in DNA.
- The location where genes work is the cell.
- In prokaryotes (single-celled organisms lacking membrane-bound internal structures), DNA floats freely within the cell body.
- In eukaryotes (living organisms whose cells contain a nucleus), DNA is found within the membrane-linked structures in the cell (nucleus, mitochondria and chloroplasts in plants).
- Each chromosome in a cell contains many genes, and each gene is located at a specific location, or locus, on the chromosome.
- DNA is packaged in structures called chromosomes within the cell.
- The number of identical chromosomes in the human body contains 23 pairs of chromosomes.
- Chromosomes usually occur in identical pairs called congeners.

2.3 Immunogenetics: Methods and Applications in Clinical Practice

Methods and applications in clinical practice focus on human clinical practice methods. The focus is on those assays of fixed or potential clinical benefit that are likely to be included in the testing package provided by the routine diagnostic and service laboratory (Christiansen, 2012). HLA molecules are important regulators of the immune response by mediating antigen presentation and interaction between the main immune mesenchymal cells. They are also the main histological barriers to transplantation, which are the clinical model of self versus self-concept. It is now recognized that this variety of gene systems involved in immune response control has proven to be important in many aspects of clinical practice.

As a result, many new molecular and cellular methods have been developed to identify these genes and polymorphisms, and immune laboratories specializing in these methods have been developed to support organ transplants and other clinical programs Immunology (Christiansen, 2012).

2.4 Complex Regulation of Immunity

Many of the articles refer to studies on immune regulation in new contexts. Anjum et al examined the modification of the Toll pathway, known in Drosophila for its role in activating the synthesis of antimicrobial peptides in response to bacterial infections and in vertebrates to induce inflammatory responses to microbial and viral triggers (Anjum SG, 2013). Anjum focused on the activity of the Toll pathway in Drosophila, and concluded that poor activation leads to the appearance of inflammatory-like patterns to increase cell proliferation (immune cells), the appearance of melanocytes, and the induction of antimicrobial peptides (Medina-Acosta, Takashi, Nakaya, & Pontillo, 2014).

They found that the activity of Toll in Drosophila larvae is negatively regulated by sumoylation controlled by the β-arrestin gene Kurtz. Loss of Kurtz or SUMO protease Ulp1 leads to ectopic immune activity and inappropriate inflammatory-like responses. However, distinct immune reactions differ in their relative sizes in mutants, suggesting that inoculation may interact with other elements of the cellular mechanism to balance the multiple activities of the Tolls pathway with multiple influences. In addition, since the mutations of Kurtz and Ulp1 lead to a global disruption of SUMO activity, there is likely to be an imbalance in the organization of other pathways that contribute to the control of inflammation and immunity (Medina-Acosta, Takashi, Nakaya, & Pontillo, 2014).

De Arras et al. (2014) A smart metamorphic screen for intersecting species was used to identify a regulator that controls the messenger RNA binding (mRNA) that encodes the Toll MyD88 transducer pathway, and hence immune activity. They have taken advantage of the high-throughput RNA (Caenorhabditis elegans) interference scan to scan the entire genome for genes that inhibit immunosuppression (De Arras L., 2014).

In another dissection of the organization of the path, Stronach et al. (2014) addressed the role of myogen-activated protein kinase (MAPKs) in developmental versus immunological cellular contexts.

MAPKs activate the Jun Kinase (JNK) pathway in response to infection and stress and are organized by themselves by kinases (MAPKKs, MAPKKKs, or MAP3Ks).

Stronach et al. (2014) hypothesized that MAP3Ks are divided into functional domains - some receive catalyst or determine subcellular localization, in addition to a distinct protein kinase domain (Stronach B, 2014).

2.5 Agriculturally and Ecologically Relevant Systems

Infection and immunity are essential in agriculture. In an instance of agricultural diseases, Connell and other (2013) conducted a case-control study in order to define why birds in chicken herds are genetically resistant to infection of Camplyobacter jejuni (Connell S., 2013).

In contrast, agricultural systems can sometimes be designed to resist diseases, for example Subbaiah and other were demonstrated by the creation of a statically converted silkworm that resists the Bombyx mori nucleopolyhedrovirus (BmNPV) virus (Subbaiah E. V., 2013).

Ellison and other suggests that Panama Golden Frog tries to resist Bd infection, but immune defense is at risk and may be a disease, leading to a reduced tolerance to infection. The effective defense observed in some other amphibian species may be the result of more immune activation and avoidance of pathogenic mechanisms in order to suppress immunity (Ellison A. R., 2014).

2.6 Complexity in Immunity

The most interesting limits in immunogenetics may arise in the interaction between immune activity and other physiological or developmental processes.

Such interactions should form a balance of traits in the organism, and determine public health in the context of infection. Evolutionary and functional studies in this field are particularly important in focusing on genetic genetics / G3 on immunogenetics, and a few of these articles are highlighted below (Medina-Acosta, Takashi, Nakaya, & Pontillo, 2014).

Johnston and other applied transcriptional profiling in a time series following the immunological challenge of Tenebrio molitor beetle. They establish that different components of the immune response have different timing of expression, suggesting a complex and specific regulatory control (Johnston P. R., 2014).

Immunological efficiency is a dynamic feature that changes over the lifetime of the host, while there is a tendency to treat immunogenicity as a static property of the host. Intuitively, we might expect the immune capacity to decline with age, a process known as immunization, and this has already been observed in advanced times. In line with previously published articles, Felix and other noted a tendency to express immune genes to increase with age, even in the absence of infection, and again found a repressed expression of genes involved in lipid metabolism after injury to flies of both ages.

Nevertheless, unexpectedly, they found that the genetic engineering of immune power (the structure of the association between genome-wide decontamination and transcription) varies between the two ages, with a stronger correlation between energy metabolism and immune power in older flies (Felix T. M., 2012).

2.7 Genetic Control of Immune Response and Susceptibility to Infectious Diseases

It is known that both genetic and nongenetic variables affect immune responses to infectious disease agents, in amplitude and size. Validation and Detection of genetic determinants in the host and pathogens is essential to better understand the basis of exposure to and control of infectious diseases. The interaction between these multiple converging and contradictory factors leads to an impressive dynamic virtual diversity in the hosts.

There is strong evidence of a relationship with controlling or reducing exposure to infectious agents or disease progression for some host genetic variants.

The perspective is that the field will benefit from both small-scale replica studies and genomide correlation studies (GWAS) (Medina-Acosta, Takashi, Nakaya, & Pontillo, 2014).

Jarduli and other contributed a prudent review of the roles of the HLA, KIR, and MICA genes as well as the common polymorphisms in pro- and anti-inflammatory cytokines (IFNG, IL1B, IL12B, IL4, IL4, IL6, IL6, TN10, LTA) and cytokine receptors (IFNGR1, IL12RB1, and IL12RB2) BAT1 and BTNL2 (associated with Class II HLA such as HYA of butyrophyllin) in resistance or susceptibility to infection by Mycobacterium leprosy and of course clinical and various manifestations of leprosy (Medina-Acosta, Takashi, Nakaya, & Pontillo, 2014).

Celsi and other bestowed an informed account of the regulatory schemes for gene expression invented by type 1 of HIV-1 to escape the immune response against infected cells,

focusing on the interaction of class I I HLA-C and class I class I HLA-G associated alleles and genotypes Effective control of viral reproduction and slow progress of AIDS. Recognizing that differences in genetic (ie, ethnic) background in the distribution of the HLAG allele (ie, HLA-G 0 0105N) may affect the results (protection / susceptibility) of the association studies urgently.

Vieira and Soares gave a new assessment of DNA circulation and / or RNA sequencing or independent or independent roles of the human APOBEC family of cytidine deaminases in immunosuppression of viral infections (including EBV, HBV, HCV, HIV-1, HPV, HSV-1 and HTLV) as well as anti-virus strategies (Medina-Acosta, Takashi, Nakaya, & Pontillo, 2014).

3. Conclusion

Immunogenetics is an area of great research opportunity, especially when traditional immune pathways intersect with other aspects of host physiology. Many authors emphasized that there is a significant slowdown between the discovery of functional genotypes and the effective introduction of practical applications, suggesting fertile research foundations in the fields of pharmacogenetics and personal medicine. In fact, there is currently no market-ready application that includes genetic / genetic testing for diseases caused by these infectious agents.

Prospects for the introduction of routine detection tests for epigenetic markers (methylation DNA), known to be highly associated with intracervical tumors and cervical cancer, meet expectations significantly reducing the number of unnecessary referrals to gynecologists.

Similarly, the introduction of TLR4 SNP and TLR2 stereotypes to identify variants or paradigm patterns associated with either an increased risk of tubal disease or protection against tubal disease, respectively, are expected to lead to a more accurate diagnosis of chlamydia chlamydia that causes infertility.

We expect the papers in this special issue to accelerate the realization of the discovery and application of genetic variables in biotechnology, diagnosis and treatment of infectious diseases of both human and anemia. J. Malogajski et al. The evidence summarized the high editorial potential of basic genomic and genetic studies of three sexually transmitted agents (HIV-1, Chlamydia trachomatis and HPV) in public health and care applications including diagnosis, treatment and disease prevention.

Understanding the genetic basis of complex diseases is a major challenge that will offer new ways to diagnose and manage patients, but it will often help us understand disease pathology. Immunology is concerned with the diversity of genes that control the immune response. Most studies to date have been concerned with human MHC syndrome, but an increasing number of researchers are now focusing on other antigens that affect innate and acquired immunity against autoimmune and foreign antigens. Immunological studies have detailed susceptibility to encoding MHC for a number of different autoimmune and viral liver diseases. Numerous studies highlight important differences and similarities between diseases and indicate different pathways in disease origin.

In type 1 autoimmune hepatitis, a model has been created whereby HLA DRB1 alleles that symbolize specific amino acid motifs can be better illustrated to demonstrate the ability and resistance of MHC encoding. This model is consistent with type I AIH as a T cell-free disease. Moreover, there is clear genetic evidence of the potential for overlap between susceptibility to viral hepatitis and exposure to type 1 health (AIH) in some populations. HLA associations may tell us more about susceptibility to potential infectious stimuli than self-antigens. In contrast, recent studies on primary sclerosing cholangitis may suggest that other pathways work. In particular, association with MHC-encoded MICA alleles may indicate the role of unconventional T cells or NK cells.

MHC appears to have a lesser role in PBC where the major correlations are associated with disease progression rather than vulnerability per se. There is clear evidence that host MHC genes affect the outcome after exposure to hepatitis A, B and C.

These observations may have implications for vaccine design, as well as help us understand the mechanisms involved in virus removal.

General studies of non-MHC genes were disappointing. The problem lies in the study design. Many lessons have been learned and new and interesting associations have emerged, particularly with regard to antiviral therapy in viral hepatitis. Through the application of new techniques, for example array analysis and high-throughput genotyping, rapid progress will be made in understanding the genetics of complex liver disease. Although genetics will provide only one part of the panorama in understanding disease pathogenesis, this knowledge is expected to help us find and assemble the remaining parts.

4. Recommendations

Depending on the results, the researchers recommend:

1. Emphasize the need to improve the classical human immunological approach with both evolutionary biology and with data sets produced by human genome projects.
2. The need to intensify genome-wide correlation studies
3. Close collaboration between research developed on wild reservoirs and humans should ultimately improve our knowledge of the dangers of the Hantavirus epidemic.
4. More work is needed in understanding the pathogenesis of the disease

5. Future Research

Genetics and immunology continue to seek an introduction to manuscripts on immunogenetics, and both journals will continue to highlight articles published in this field. Topics of particular interest for future publication include:

1. Genetic networks or signal that affect the function of the immune system.
2. Clarify the genetic mechanisms that lead to infection tolerance or resistance.
3. Defense responses are stimulated by damage to host tissues.
4. Genetic interactions between hosts, pathogens and coexistence that make up the results of infection.
5. Genetic responses to environmental factors that modify resistance and tolerance.
6. Identification mechanisms or memory specified in invertebrates.
7. Neurophysiology and behavioral immunity.

Reference

1. ABDUL-GHAFFAR, M. (2003). Immunodeficiency, COURSE: Medical Microbiology. Lectures #22-23. e-mail: ghaffar@med.sc.edu.
2. Anjum SG, X. W. (2013). Regulation of Toll signaling and inflammation by β-arrestin and the SUMO protease Ulp1. 2013 Dec; 195(4):1307-17.
3. BOWERS, W. (2003). Cell Interactions in Specific Immune Response, COURSE: Medical Microbiology. Lecture #13. e-mail: wbowers@med.sc.edu .
4. Chapman, S., & Hill, A. (2012). Human genetic susceptibility to infectious disease. Nat. Rev. Genet. 13, 175–188.
5. Charbonnel, N., Pagès, M., Sironen, T., Henttonen, H., Vapalahti, O., Mustonen, J., et al. (2014). Immunogenetic Factors Affecting Susceptibility of Humans and Rodents to Hantaviruses and the Clinical Course of Hantaviral Disease in Humans.
6. Christiansen, F. a. (2012). Immunogenetics: Methods and Applications in Clinical Practice.
7. Connell S., M. K. (2013). Genome-wide association analysis of avian resistance to Campylobacter jejuni colonization identifies risk locus spanning the CDH13 gene. G3 (Bethesda) 3: 881–890.
8. Cooke, G., & Hill, A. (2001). Genetics of susceptibility to human infectious disease. Nat. Rev. Genet. 2, 967–977.
9. De Arras L., L. R. (2014). Comparative genomics RNAi screen identifies Eftud2 as a novel regulator of innate immunity. Genetics 197: 485–496.
10. Donaldson, P. T. (2019). GENETICS OF LIVER DISEASE: IMMUNOGENETICS AND DISEASE PATHOGENESIS.
11. Ellison A. R., S. A. (2014). Fighting a losing battle: vigorous immune response countered by pathogen suppression of host defenses in the chytridiomycosis-susceptible frog Atelopus zeteki. G3 DOI: 10.
12. Felix T. M., H. K. (2012). Age-specific variation in immune response in Drosophila melanogaster has a genetic basis. Genetics 191: 989–1002 .
13. Geraghty, D., Daza, R., Williams, L., Vu, Q., & Ishitani, A. (2002). Genetics of the immune response: Identifying immune variation within the mhc and throughout the

genome. Immunol. Rev. 190, 69–85.

14. Holt, P., Macaubas, C., & Cooper, D. a. (1997). "Th-1/Th-2 switch regulation in immune responses to inhaled antigens. Role of dendritic cells in the aetiology of allergic respiratory disease". Adv. Exp. Med. Biol. Advances in Experimental Medicine and Biology.
15. Johnston P. R., M. O. (2014). Inducible defenses stay up late: temporal patterns of immune gene expression in Tenebrio molitor. G3 4: pii: g3.113.008516v1.
16. Kapiel, T. Y. (2005). Lecture notes: Principles of Genetics.
17. Lazzaro, B. P. (2014). The Genetics of Immunity. Available on https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4063907/.
18. Medina-Acosta, E., Takashi, T., Nakaya, I., & Pontillo, A. a. (2014). Genetic Control of Immune Response and Susceptibility to Infectious Diseases.
19. Pradeu. (2012). The Limits of the Self: Immunology and Biological Identity. New York: Oxford University Press.
20. Stronach B, L. A. (2014). Domain specificity of MAP3K family members, MLK and Tak1, for JNK signaling in Drosophila.
21. Subbaiah E. V., R. C. (2013). Engineering silkworms for resistance to baculovirus through multigene RNA interference. Genetics 193: 63–75.
22. Trowsdale, J., & Knight, J. (2013). Major histocompatibility complex genomics and human disease. Genom. Hum. Genet. 14, 301–323.