**ODOMENE JUSTICE**

**17/SCI03/006**

**BCH314 IMMUNOLOGY & IMMUNOCHEMISTRY**

1. **Discuss the genetic basis of antibody diversirty.**
2. **Discuss the immune response with respect to tumor & organ transplantation.**

**1.** Three theories have been put forth to explain antibody diversity, which allows B cells to generate an antibody repertoire capable of reacting with a wide range of antigens: (1) The *germ-line theory*postulates that separate genes exist for each antibody molecule and that the antibody repertoire is largely inherited. (2) The *deoxyribonucleic acid (DNA) rearrangement theory* proposes that a limited number of genes undergo genetic rearrangements to create antibody populations. (3) Finally, the *somatic mutation theory*proposes that a limited number of inherited genes undergo mutations to general antibody repertoires. In vivo and in vitro studies have demonstrated that both the DNA rearrangement theory and the somatic mutation theory provide the most plausible explanations for antibody diversity.

Antibodies are encoded by different germ-line genetic loci. Variable (V) region, joining (J) region, and constant (C) region gene products are assembled into a functional antibody. Variable portion genes (V) code for amino acids that constitute the framework regions of the variable region, and three hypervariable complementarity-determining regions (CDR1, CDR2, and CDR3). The hypervariable regions form the three-dimensional antigen-binding pocket. Antibody specificity is determined by the specific amino acid sequences in CDR3. The joining (J) segment is, in reality, part of the V region and provides some of the framework for the antigen-binding pocket. Only heavy chains have an additional diversity (D) gene.

 The human immune system is capable of producing a vast number of different antibody molecules, each with its own antigenic specificityThis vast diversity is possible because immunoglobulins genes undergo an unusual type of interaction

a. Embryonic DNA contains a great many genes for the variable regions of the H and L chains

b. A process of somatic recombination (DNA rearrangement and deletion), followed by RNA splicing, results in a large variety of B cell lines that encode different H chains and L chains

c. A fairly high rate of somatic mutation in k , l , and H chains further adds to the diversity.

**2.**