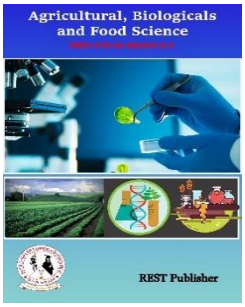
Agricultural, Biologicals and Food Science

Vol: 2(1), 2023

REST Publisher; ISBN: 978-81-956353-8-2

Website: http://restpublisher.com/Book-Series /abfs/

DOI: https://doi.org/10.46632/abfs/2/1/1



Evaluation of Cell Biology and Genetics using VIKOR Method

***Sri Ranjani Tallam, Ch. Ramadevi**

D.K.Govt College for Women (A), Nellore, Andhra Pradesh, India.

*Corresponding Author Email: tallamsriranjani@gmail.com

Abstract: *Cell biology and genetics are fields of heredity research. They enable experts to examine indigenous people's genetic data to identify their current state of health. By taking necessary precautions, one can protect their health using this technology. Cell biology has quickly expanded in the medical field and has emerged as the only treatment for issues with human reproduction. Genetics, or the science of genes and heredity, is all about the study of features that are passed down from one generation to the next. The subject of cell biology is the smallest units of life, cells, and their structures and functions. Understanding the structure and physiological functioning of single cells, and how cells interact and work together in great numbers to generate tissues and organisms, is a goal of cell biology. Cell biology is based on the notion that a cell is the basic unit of all life. Understanding the tissues and organisms that make up cells in great detail is made possible by concentrating on the cell. If you want to teach in a classroom, you can look into botany or zoology. If you're interested in biological or industrial sciences or medical research, you can choose from genetics, microbiology, or biotechnology. Cell biology encompasses both eukaryotic and prokaryotic cells and has a wide range of subtopics, including the research of cellular metabolism, cell communication, cell cycle, chemistry, and cell composition. Cells can be examined using a variety of microscopy techniques, cell culturing, and cell fractionation. There are two different cell types: prokaryotic and eukaryotic ones. Despite having differing morphologies (see Prokaryote, Eukaryote), eukaryotic organisms are remarkably comparable in terms of underlying molecular make-up and functions. Over the past 50 years, cell biology has seen remarkable expansion as a key area of basic science (1). Medicine makes use of information from basic science domains such as cell biology for the benefit of patients (2-4). A subfield of biology known as cell biology focuses on the cell, including its different types, structures, functions, and interactions with other cells. The subfields of cell biology include cell composition, cell cycle, cell communication, and cell metabolism. Research in several domains, including genetics, biochemistry, neuroscience, plant biology, molecular biology, microbiology, and immunology, is tied to those in cell biology. The VIKOR (VIšekriterijumsko Compromising Rangiranje) Optimal Replacement Select method is used in the evaluation of Epidermal Growth Factor Receptor, Fibroblast Growth Factor Receptors, Discoidin Domain Receptor, Mitogen-Activated Protein Kinase, and Nuclear Receptor-Binding SET Domain Protein alternatives for skin, lung, head/neck, and cervical cancer. Fibroblast Growth Factor Receptors have the highest rank, whereas Nuclear Receptor-Binding SET Domain Protein has the lowest rank.*

Keywords: *TPR proteins, PDZ proteins, Expanding the genetic code, VIKOR Method.*

1. INTRODUCTION

It seems like there are three main topics discussed in this passage: genetics underlying hearing loss, flavonoids and their classification, and the cellular and molecular underpinnings of Wolbachia-host interactions. In the first part of the passage, the author discusses the complex mechanisms involved in the cochlea's sensory transduction and the genetic basis of hearing loss. The author mentions that numerous genes crucial for hearing have been identified through investigations on the genetics underlying hearing problems. However, cloning these genes has not been sufficient, and extensive research in animal studies is required to clarify their function. In the second part of the passage, the author discusses flavonoids and their classification. Flavonoids are a group of rather different aromatic compounds that are generated from iron and malonyl-coenzyme A. These molecules, which are present in the majority of higher plants, fall into six major subgroups: chalcones, flavones, flavonols, anthocyanins, and condensed tannins. In the final part of the passage, the author discusses the cellular and molecular underpinnings of Wolbachia-host interactions. The author mentions that despite great improvements in understanding the ecosystem and population genetic elements of Wolbachia, the cellular and molecular underpinnings of these interactions are still poorly known. The author discusses specific subfields related to Wolbachia transmissions, the elements influencing Wolbachia reproduction, and recent mechanistic insights into CI. Flavonoids are a diverse group of chemicals found in higher plants, and they have been studied for their various biological activities, including antioxidant, anti-inflammatory, and anticancer properties. They are synthesized through the shikimate and

acetate-malonate pathways, and their biosynthesis is regulated by various transcription factors and other regulatory elements. The different subgroups of flavonoids have distinct chemical structures, and their biological activities may vary based on their chemical structure. Wolbachia is an intracellular bacterium that infects a wide range of arthropods, including insects and spiders. It has been studied for its various interactions with its host, including the induction of cytoplasmic incompatibility (CI), which is a reproductive manipulation that ensures the spread of Wolbachia through the population. The molecular mechanisms underlying these interactions are still not well understood, but recent studies have shed light on some of the key players involved in Wolbachia-host interactions, including genes involved in transcriptional regulation, germline transmission, and CI induction.

2. MATERIALS AND METHOD

2.1. TPR proteins:

It seems that Mam A is a protein found in magnetic spirilla, specifically M. gryphiswaldense and M. magnetite, and is the most prevalent protein of the magnetosome membrane (MM). Mam A contains TPR motifs, which mediate protein-protein interactions, and is involved in the formation of multiprotein complexes. It acts as a receptor that interacts with cytoplasmic proteins and plays a crucial role in the biomineralization of magnetosomes. However, it also serves an unidentified function that may involve the "activation" of magnetosome vesicles. A Mam A deficient mutant of M. magnetite produced fewer magnetite crystals with the same shape and alignment as the wild type, indicating its importance in magnetite formation.

2.2. PDZ proteins:

In MTB, it is believed that the Htr A-like serine proteases, including Mam E and Mam O, may be involved in the regulation of magnetosome formation and biomineralization. Mam E, for example, has been shown to be required for the efficient formation of magnetite crystals in M. magneticum, and it has been suggested that it may play a role in the formation or stabilization of a protein scaffold that directs the mineralization process. Mam O, on the other hand, has been implicated in the regulation of the size and shape of magnetite crystals. The PDZ domains found in Htr A-like proteins have been shown to play a role in protein-protein interactions, suggesting that these proteins may interact with other magnetosome-associated proteins to regulate magnetosome formation and biomineralization. Overall, the Htr A-like serine proteases and other magnetosome-associated proteins are important components of the magnetosome biogenesis pathway, and further research is needed to fully understand their roles in this process.

2.3. Expanding the genetic code:

The second step in creating an orthogonal synthetase-tRNA pair involves evolving a tRNA to be a substrate for the chosen synthetase. This can be done through several rounds of selection using a positive selection pressure, such as antibiotic resistance, and a negative selection pressure, such as toxicity from an unnatural amino acid that is not incorporated properly into the protein. This process results in a tRNA that is specifically charged with the chosen unnatural amino acid by the orthogonal synthetase, allowing for incorporation of the unnatural amino acid into the protein of interest at the site of the amber stop codon. Orthogonal synthetase-tRNA pairs have been used in a variety of applications, including the study of protein structure and function, the creation of novel enzymes with altered properties, and the development of new therapeutics.

3. VIKOR METHOD

The VIKOR approach is a multi-criteria decision-making (MCDM) technique used to solve complex problems with multiple criteria and conflicting objectives. It is an adaptive approach that is implemented within the MCDM problem and is used for attribute selection as a standard technique. The VIKOR method is designed to help decision-makers arrive at a final answer and uses a compromise ranking metric called the multi-criteria compromise solution (MCCS) to aggregate features within the compromise programming method. The VIKOR method is based on the concept of compromise solutions and is used to assess the quality of service in a hospital or other similar environments where there is ambiguity and uncertainty. The main purpose of this approach is to propose a set of fuzzy-based compromise VIKOR methods with parameters using triangular fuzzy numbers (TFNs). This approach considers the set theory and the VIKOR method to provide more accurate solutions to complex problems. The VIKOR Index is used simultaneously with Taguchi's SN ratio as an excellent feature for multi-response methods. The VIKOR method is introduced as an MCDM technique and makes decisions to provide more accurate solutions to complex problems. The VIKOR method is based on integrative fuzzy qualification Qi, which represents the exchange distance for a quality solution. In the presence of contradictions, limited options ranking from the set, and choosing incompatible standards with specific units, the VIKOR technique defines positive and negative perfect points within the solution area. The VIKOR method is used in various fields, including water resource planning and land use techniques to reduce economic and social costs with the potential for natural hazards. Overall, the VIKOR method is a powerful approach to solve complex problems with multiple criteria and conflicting objectives. It offers a compromise ranking metric that aggregates features within the compromise programming method and can be used in various fields to provide accurate solutions to complex problems.

4. ANALYSIS AND DISCUSSION

TABLE 1. Cell Biology and Genetics

	Skin	Lung	Head/neck	Cervical
Epidermal Growth Factor Receptor	0.34	0.85	0.75	0.13
Fibroblast Growth Factor Receptors	0.22	0.71	0.67	0.21
Discoidin Domain Receptor	0.39	0.89	0.93	0.37
Mitogen-Activated Protein Kinase	0.15	0.93	0.72	0.14
Nuclear Receptor-Binding SET Domain Protein	0.27	0.86	0.86	0.26
Best	**0.15**	**0.93**	**0.93**	**0.13**
worst	**0.39**	**0.71**	**0.67**	**0.37**

Table 1 shows the Cell Biology and Genetics for the VIKOR method. Epidermal Growth Factor Receptor, Fibroblast Growth Factor Receptors, Discoidin Domain Receptor, Mitogen-Activated Protein Kinase, Nuclear Receptor-Binding SET Domain Protein Alternatives Skin, Lung, Head/neck, and Cervical Evaluation is the Best and Worst Value.

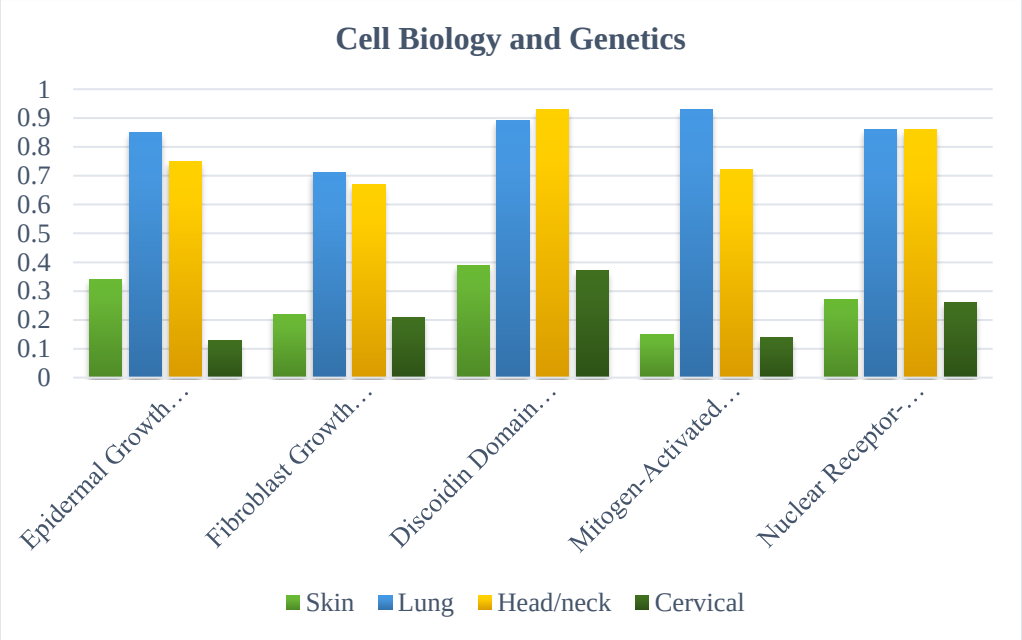


FIGURE 1. Cell Biology and Genetics

Figure 1 shows the Cell Biology and Genetics for the VIKOR method. Epidermal Growth Factor Receptor, Fibroblast Growth Factor Receptors, Discoid in Domain Receptor, Mitogen-Activated Protein Kinase, Nuclear Receptor-Binding SET Domain Protein Alternatives Skin, Lung, Head/neck, and Cervical Evaluation is the Best and Worst Value.

TABLE 2. Calculation Sj and Rj

Skin	Lung	Head/neck	Cervical	Sj	Rj
0.197917	0.090909	0.173077	0	0.461903	0.197917
0.072917	0.25	0.25	0.083333	0.65625	0.25
0.25	0.045455	0	0.25	0.545455	0.25
0	0	0.201923	0.010417	0.21234	0.201923
0.125	0.079545	0.067308	0.135417	0.40727	0.135417

Table 2 shows the calculation Sj and Rj is the sum of Normalization of tabulation 1 which is calculated from the determination of best and worst values.

TABLE 3. Final Result of Calculation Qj

	Sj	Rj	Qj	Rank
Epidermal Growth Factor Receptor	0.461903	0.197917	0.553823	3
Fibroblast Growth Factor Receptors	0.65625	0.25	1	1
Discoidin Domain Receptor	0.545455	0.25	0.875205	2
Mitogen-Activated Protein Kinase	0.21234	0.201923	0.29021	4
Nuclear Receptor-Binding SET Domain Protein	0.40727	0.135417	0.21956	5

Table 3 shows the Final Result of the Calculation Qj calculated from the sum of the calculation from the Sj and Rj from the Qj value, the rank is taken.

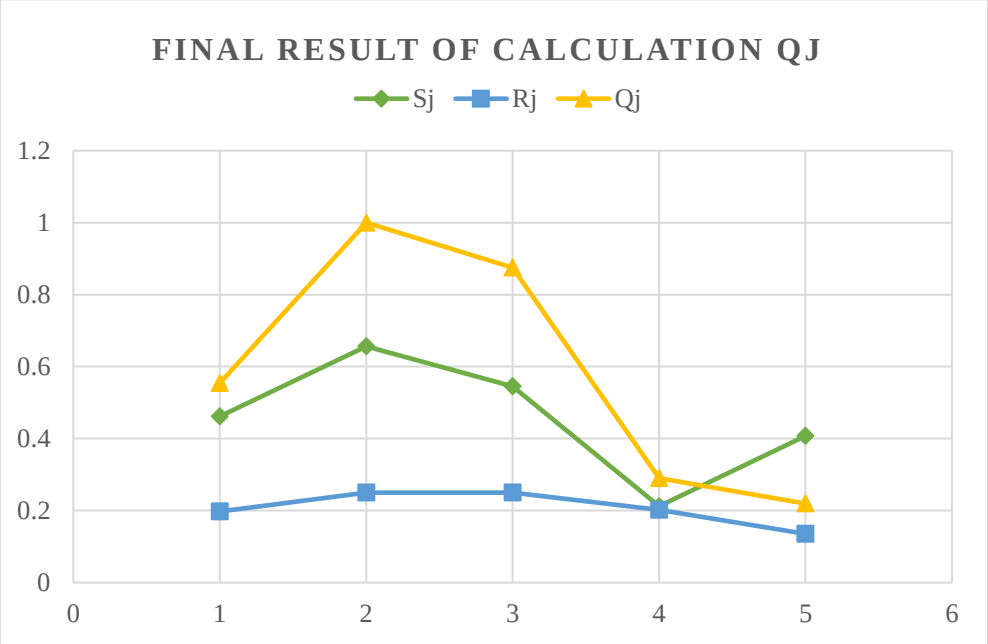


FIGURE 2. Final Result of Calculation Qj

Figure 2 Shows the Calculation Sj, Rj, and Qj data set using the VIKOR method. Qj for Fibroblast Growth Factor Receptor is showing the highest value and Nuclear Receptor -Binding SET Domain Protein is showing the lowest value.

5. CONCLUSIONS

The embryo of the Drosophila has dorsal closure. The movement paradigm morphogenetic ideal model of development is tractable genetically and suitable for cell biological investigation. Although there are still many unsolved mysteries regarding all aspects of dorsal closure, we have made progress in our understanding of its fundamental processes. This bodes well for future research into the underlying mechanisms other morphological fusion occurrences in the embryo as well as the ability of tissues to repair damage. Two significant facets of the synaptogenesis-related molecular programmers are revealed by the considerable literature mentioned in this review. The complexity of the brain is first demonstrated by the various molecular basis that preserve the uniqueness of synaptic connections. These mechanisms also give every individual neural circuit the flexibility to create precise synaptic connections. None of the methods are mutually exclusive, and specificity can be attained incrementally by sequentially recruiting positive and negative selection. Second, there are numerous redundant routes that can be taken to finish the synchronization process. No genetic modification of a single particle or group of chemicals can delete synapses, despite the widespread quest for just an again-like protein to destroy synapses. It's interesting to note that strong proof demonstrates that a few synaptic integrins are adequate to promote synapse development in vitro. Together, our results point to the likelihood that numerous redundant trans-synaptic routes interact in vivo while each has the capacity to support a complex synapse-formation program. By encrypting amino acids, which could then undergo subsequent, precise chemical reactions, proteins can perform more tasks. Protein interactions can now be defined in vivo thanks to genetically predetermined unnatural amino acids; post-translational modifications' function is still unknown; protein activity within cells needs to be activated in milliseconds to distinguish between biological roles; and protein conformational changes need to be monitored in real-time. Incorporating several distinctive, non-natural amino acid residues into proteins using emerging techniques enables the creation of whole new solutions for biological issues, such as the encoding of Worry about a thing pairing for imaging applications. Animals will also be given unusual amino acids to enable in vivo real-time analysis of molecular processes such as neural processing and development. Once contemplating EF created in the ovum and subsequent cell divisions, the quantum field method also comes to mind because, as is well known, quantum physics has spatially extended people as theoretical objects and essentials are lost or altered during cell division. Therefore, "this theory can be used to understand the fundamental properties of biological entities or persons." In order to re-discover these events in the humid climate of cells, cell ecology still remains a lot so learn from other different disciplines, such as quantum physics. To do this, it must first hunt for analogs of the relevant phenomena. Of certainly, the quickly evolving nanotechnology technologies will be beneficial to us.

REFERENCES

[1]. Dzau, Victor J. "Cell biology and genetics of angiotensin in cardiovascular disease." *Journal of Hypertension* 12 (1994): S3-S10.

[2]. Berry, D. P., and J. J. Crowley. "Cell biology symposium: genetics of feed efficiency in dairy and beef cattle." *Journal of animal science* 91, no. 4 (2013): 1594-1613.

[3]. Dror, Amiel A., and Karen B. Avraham. "Hearing loss: mechanisms revealed by genetics and cell biology." *Annual review of genetics* 43 (2009): 411-437.

[4]. Kumar, Nalin M., and Norton B. Gilula. "Molecular biology and genetics of gap junction channels." In *Seminars in cell biology*, vol. 3, no. 1, pp. 3-16. Academic Press, 1992.

[5]. Winkel-Shirley, Brenda. "Flavonoid biosynthesis. A colorful model for genetics, biochemistry, cell biology, and biotechnology." *Plant physiology* 126, no. 2 (2001): 485-493.

[6]. Jacinto, Antonio, Sarah Woolner, and Paul Martin. "Dynamic analysis of dorsal closure in Drosophila: from genetics to cell biology." *Developmental cell* 3, no. 1 (2002): 9-19.

[7]. Serbus, Laura R., Catharina Casper-Lindley, Frédéric Landmann, and William Sullivan. "The genetics and cell biology of Wolbachia-host interactions." *Annual review of genetics* 42 (2008): 683-707.

[8]. Shen, Kang, and Peter Scheiffele. "Genetics and cell biology of building specific synaptic connectivity." *Annual review of neuroscience* 33 (2010): 473-507.

[9]. Jogler, Christian, and Dirk Schüler. "Genomics, genetics, and cell biology of magnetosome formation." *Annual review of microbiology* 63 (2009): 501-521.

[10]. Berk, Arnold J. "Recent lessons in gene expression, cell cycle control, and cell biology from adenovirus." *Oncogene* 24, no. 52 (2005): 7673-7685.

[11]. Schüler, Dirk. "Genetics and cell biology of magnetosome formation in magnetotactic bacteria." *FEMS microbiology reviews* 32, no. 4 (2008): 654-672.

[12]. Williams, Terence M., and Michael P. Lisanti. "The Caveolin genes: from cell biology to medicine." *Annals of medicine* 36, no. 8 (2004): 584-595.

[13]. Liscovitch, Mordechai, Malgorzata Czarny, Giusy Fiucci, and Xiaoqing TANG. "Phospholipase D: molecular and cell biology of a novel gene family." *Biochemical Journal* 345, no. 3 (2000): 401-415.

[14]. Davis, Lloyd, and Jason W. Chin. "Designer proteins: applications of genetic code expansion in cell biology." *Nature reviews Molecular cell biology* 13, no. 3 (2012): 168-182.

[15]. Dotto, G. Paolo, and Anil K. Rustgi. "Squamous cell cancers: a unified perspective on biology and genetics." *Cancer cell* 29, no. 5 (2016): 622-637.

[16]. Pérez de Castro, Ignacio, Guillermo de Cárcer, and Marcos Malumbres. "A census of mitotic cancer genes: new insights into tumor cell biology and cancer therapy." *Carcinogenesis* 28, no. 5 (2007): 899-912.

[17]. Sato, Mitsuru, Shinsuke Suzuki, and Haruki Senoo. "Hepatic stellate cells: unique characteristics in cell biology and phenotype." *Cell structure and function* 28, no. 2 (2003): 105-112.

[18]. Emerman, Michael, and Michael H. Malim. "HIV-1 regulatory/accessory genes: keys to unraveling viral and host cell biology." *Science* 280, no. 5371 (1998): 1880-1884.

[19]. McClean, Phillip, Christina Johnson, Roxanne Rogers, Lisa Daniels, John Reber, Brian M. Slator, Jeff Terpstra, and Alan White. "Molecular and cellular biology animations: development and impact on student learning." *Cell Biology Education* 4, no. 2 (2005): 169-179.

[20]. Funk, Richard HW, Thomas Monsees, and Nurdan Özkucur. "Electromagnetic effects–From cell biology to medicine." *Progress in histochemistry and cytochemistry* 43, no. 4 (2009): 177-264.

[21]. Kamburov, Atanas, Konstantin Pentchev, Hanna Galicka, Christoph Wierling, Hans Lehrach, and Ralf Herwig. "ConsensusPathDB: toward a more complete picture of cell biology." *Nucleic acids research* 39, no. suppl_1 (2011): D712-D717.

[22]. Mahley, Robert W. "Apolipoprotein E: cholesterol transport protein with expanding role in cell biology." *Science* 240, no. 4852 (1988): 622-630.

[23]. Callier, Sophie, Marina Snapyan, Stéphane Le Crom, Delphine Prou, Jean-Didier Vincent, and Philippe Vernier. "Evolution and cell biology of dopamine receptors in vertebrates." *Biology of the Cell* 95, no. 7 (2003): 489-502.

[24]. West-Eberhard, Mary Jane. "Evolution in the light of developmental and cell biology, and vice versa." *Proceedings of the National Academy of Sciences* 95, no. 15 (1998): 8417-8419.

[25]. Elwell, Cherilyn, Kathleen Mirrashidi, and Joanne Engel. "Chlamydia cell biology and pathogenesis." *Nature Reviews Microbiology* 14, no. 6 (2016): 385-400.