Original Article

EVALUATION OF CURRENT KNOWLEDGE OF TYPE OF MUTATION IN GENETICS AMONG 2ND & 3RD YEAR BDS STUDENTS- A SURVEY

[1]Saivarshine S, [2]Dr.Priyadharshini R*, [3]Dr.Palati Sindhuja,
[1]Graduate, Department of Pathology, Saveetha Dental College and Hospitals, Saveetha Institute of Medical and Technical Sciences(SIMATS), Saveetha University, Chennai, Tamilnadu, India.
[2]*Assistant Professor, Department of Pathology, Saveetha Dental College, Saveetha Institute of Medical and Technical Sciences (SIMATS), Saveetha University, Chennai 77, TamilNadu,
[3]Assistant Professor, Department of Pathology, Saveetha Dental College, Saveetha Institute of Medical and Technical Sciences (SIMATS), Saveetha University, Chennai 77, TamilNadu,

ABSTRACT
Introduction: Mutation can affect the phenotype of an organism, especially if they occur within the protein-coding sequence of a gene. The process in which there is an increase in the rate of changes in DNA is called mutagenic. Mutagens create replication errors in DNA for instance with interference in DNA pairing and resulting in defective DNA structure.
Aim:
To assess the knowledge about the type of mutation in genetics.
Materials and methods: A self-structured - questionnaire survey based on the evaluation of current knowledge of the type of mutation in genetics, comprising about 100 people (sample size) belonging to different age groups, both Male and Female were circulated on an online survey platform (link) using Google forms, and they were asked to take up the survey by the students. The sampling method involved random sampling. The questionnaire was tested for validation at the Saveetha Dental College, Chennai. The results were collected and the data was analyzed.The data was analyzed, and it is represented as pie charts and bar charts.
Results: People of different age groups largely had a good idea about mutation in genetics. This study analyzed the statistics on the current knowledge among the 2nd and 3rd dental students about mutation in genetics and a majority of the population were aware of the various types of mutation.
Conclusion: The mutation rate differs among the gene and the genome. The mutation is one of the fundamental forces of advancement, this work will continue to be of paramount importance.

Keywords: Knowledge, Mutation, Innovative technique, Genetics, DNA
DOI: 10.47750/pnr.2022.13.S03.225

INTRODUCTION

Errors in the polymerization of the second strand of DNA may happen during the replication process. The errors occurring during DNA replication are called mutations. Mutation can affect the phenotype of an organism, especially if they occur within the protein-coding sequence of a gene. The process in which there is an increase in the rate of changes in DNA is called mutagenic. Mutagens promote DNA error in replication, for instance with interference in DNA pairing and resulting in defective DNA structure.

Any damage chemically or naturally the cells itself acquires the repair mechanism of DNA(Perry, 1980). However, the original genome sequence of the DNA doesnot always restore after repair. The particular source for DNA damage includes free oxygen radicals from aerobic cellular respiration and mutations (Song *et al.*, 2020)

Chromosomal crossover in some organisms results in exchange of DNA, recombinant genes, in meiosis resulting in mutations. Crossover errors are distinctly possible when alignment errors are adopted by the chromosomes of the partner taking up the alike chromosomal sequence which will be widely prone for mutations in a similar way (Miller, Vandome and McBrewster, 2009). Structural modifications in DNA sequence result from these errors, such as duplications, inversions, and deletions of entire regions, or the unintended exchange of entire sequences between chromosomes.

Permanent change or heritable change within the sequence of DNA nucleotides is called Mutation. within the DNA. Mutations that affect germs cells are transmitted to the progeny and may lead to inherited diseases (Kumar, Abbas and Aster, 2020), (Krishna, 2004) of several genes causing autoimmunity. Mutation of immunoregulatory protein genes, Mutation of FAS gene, Mutation of CTLA-4, Mutation of Foxp3 gene (Mandal, 2016). Mutations are of two

major classes, large mutations, and point mutations. In large mutations, many bases, sometimes many millions of bases are mutated. deleted, inserted, or translocated. If the mutations involve one or more bases, they are called as point mutations. (Krishna, 2004; Harsha and Brundha, 2017; Timothy, Samyuktha and Brundha, 2019) The mutation may involve a nucleotide of the DNA. (McMahon and Sloan, 2000).

TYPES OF MUTATION

There are three various DNA Mutations: base substitutions, deletions, and insertions.

1. Base substitution:

Single base substitutions are called point mutations, Glu → Val which causes sickle-cell disease. This foremost common form of mutation are of two types(Rosche and Foster, 2001). ('Transition (transition mutation, transitional mutation, base pair substitution)', 2015)

Figure 1: Representation of Transition & Transversion

a) **Transition**: This takes place when a purine is substituted with another purine or when pyrimidine is substituted with another pyrimidine.
b) **Transversion**: A single purine (adenine or guanine) is replaced with pyrimidine (Thiamine or Cytosine) and vice versa.
c) Ionizing radiation or alkylating agents may induce a transversion, which can be spontaneous or induced by ionizing radiation.

Sequencing of DNA is through missense, silent and nonsense mutations of proteins.

a) **Silent**: Amino acid substitution at the base of the codon where the encoded sequence is not altered and is alleged as silent coding. (Rosche and Foster, 2002)
b) **Missense**: Codon generation with the substitution of base with perceptible aminoacid lead to dissimilar sequence of polypeptide. It can be nonconservative or conservative mutations based on the substitution. Conservative mutation with minute defect on the protein structure / function. When the resutant substitution at the aminoacid ends up as with very unique properties / structure of aminoacid results in nonconservative mutation. With a deleterious effects to the proteins. (Gooch, 2011)
c) **Nonsense**: Substitution of base ends up as nonfunctional protein with a stop codon translation resulting with a malfunctioning protein. (Guttman, 2013).

Figure 2: Representation of silent, nonsense, missense, frameshift mutation, insertion and deletion.

2. Deletions:

A deletion, leads to frameshift, results when one or more base pairs are lost from the DNA (Figure 2). The translational frame is modified with a distended message and a non-functional product when one or two bases are deleted. The resultant frame will be unaffected by the deletion of three or more bases. A deletion of one or more codon proteins with missing one or more amino acids. This could be deleterious or not.

3. Insertions:

The insertion of additional base pairs may result in frameshifts based on whether multiples of three base pairs are inserted. Combinations of deletions and insertions resulting in a spread of outcomes also are possible.

CAUSES OF MUTATION

a) DNA Replication errors

A non-complementary base is sometimes incorporated into the daughter strand by DNA polymerase. During the following round of replication, the incorporated base would result in a mutation. This, however, is extremely rare because the exonuclease functions as a proofreading mechanism recognizing mismatched base pairs and excising them. (Marian, 2013)

b) DNA Recombination errors

Recombination is a process in which DNA rearranges itself resulting in a mutation (Gotoh, 2011; Brundha, Pathmashri and Sundari, 2019).

c) DNA damage by chemicals

Chemical mutagens which are exogenous and are influenced by man-made and environmental factors are capable of damaging DNA. Numerous chemotherapeutic medications and intercalating drugs act by destroying DNA (Dreval and Pogribny, 2018)**.**

d) Radiation

Free radicals are formed when X-rays, UV light and gamma rays interact within the cell, causing DNAdamage . (Becker and Sevilla, 1993)

GENERAL FEATURES OF MUTATION

Mutations in somatic cells affect only those cells and their progeny, and these are important in cancer, aging, etc. They won't usually have any phenotypic significance for the offspring. Mutation dont affects somatic cell when it comes to germ cell. Mutations usually are stable alterations. These are some mutationtional types, however, that get amplified during subsequent cell divisions and may present as disease several generations after the primary mutation. The best examples of this are fragile X syndrome and Huntington's disease. From the perspective of development, mutations have an adequate genetic variation to enable organisms to respond to changes in the environment through a natural selection process. The person with somatic cell mutation can also have several regular cells; this person is considered to be a mosaic, and this characteristic is known as mosaicism. The condition where such mosaicism could be seen in germ cells, called gonadal mosaicism, describes this variation amongst those offspring of people with the osteogenesis imperfecta gene. (Krishna, 2004). Our team has extensive knowledge and research experience that has translate into high quality publications (Kumar *et al.*, 2006; Sathivel *et al.*, 2008; Govindaraju, Neelakantan and Gutmann, 2017; Jain, 2017; Kumar, 2017; Mp, 2017; Muthukrishnan and Warnakulasuriya, 2018; Nair, Jeevanandan and Vignesh, 2018; Anbu *et al.*, 2019; Sekar *et al.*, 2019)

There are three basic types of point mutation:

Synonymous or silent mutations: Base replacement does not replace the proteins, but only shows a different codon for the similar proteins (beneficial feature of a degenerate genetic code)

Missense mutation: Base replacement changes the codon from one protein aminoacid to another.

Nonsense mutation: Base replacement changes the codon to termination codons.

The present study aims to evaluate the knowledge about the type of mutation in genetics.

MATERIALS & METHODS:

A self-structured questionnaire survey for the evaluation of current knowledge of the mutation types in genetics amongst 2nd & 3rd year BDS students, a prospective study (observational) comprising about 100 people (sample size) both male and female participants were circulated with google forms on an online survey platform (link) and were asked to take up the survey by the students. The approval of the study was given by Saveetha Review Board. The sampling method involved random sampling. The validation of the quiessionaire was given by Senior guides. Gender

and age are the independant variables. Second and third year dental students are included under the study. Exclusion includes Incomplete forms and forms which are filled twice The collected results and the data were analyzed by Pearson chi-square test through SPSS version 23.

RESULTS

Figure 3: Pie chart representing the percentage age distribution of the dental students who responded to the survey. A majority of participants, 63%, were between 18-20 (Blue), 35% were between 20-25 (Green) and 2% were between 25 & above (Beige)**.**

Figure 4: Pie chart representing the percentage gender distribution of the dental students who responded to the survey. A majority of participants, 71% were Females (Violet), 29% were Males (Ink Blue)**.**

Figure 5: Pie chart representing the percentage year of study distribution of the dental students who responded to the survey. Of the majority of participants, 77% were among the 2nd year (Purple), 23% were among the 3rd year (Azure)**.**

Figure 6: Pie chart representing the percentage distribution of responses on the knowledge about genotype. The respondents of about 55% responded genotype is an organism's morphology, development/behavior (Red), 37% responded genotype is an organism's full hereditary information (Mustard) and 8% responded to genotype is the environmental influence of an organism (Pale turquoise)**.**

Figure 7: Pie chart representing the percentage distribution of responses on the knowledge about phenotype. About 48% responded phenotype is an organism's morphology, development/behavior (Black), 41% responded phenotype is an organism's full hereditary information (DarkGreen) and 11% responded phenotype is the environmental influence of an organism(Beige)**.**

Figure 8: Pie chart with the distribution of responses on the genetic difference-single set of chromosomes. About 43% responded haploid (Dark Grey), 40% responded diploid (Cerulean) and 17% responded aneuploid (Sky Blue)**.**

Figure 9: Pie chart representing the percentage distribution of responses on the genetic difference — two sets of chromosomes. About 54% responded haploid (Dark Green), 39% responded diploid (Light Green) and 5% responded aneuploid (Light Violet) and 2% responded none of the above.

Figure 10: Pie chart representing the percentage distribution of responses on the knowledge about missense mutation. A vast majority of respondents to about 52% responded stop codon replaces an amino acid codon, leading to premature termination of translation (Yellow), 27% responded to change in reading frame followed by a stop codon (Teal) and 21% responded in a protein in which one amino acid is substituted for another amino acid (Light Beige**).**

Figure 11: Pie chart representing the percentage distribution of responses on the knowledge about nonsense mutation. About 54% responded that stop codon replaces protein codon, leading to premature termination of translation (Red), 14% responded to change in reading frame by stop codon (Light Violet) and 32% responded that one protein amino acid is substituted by another amino acid (Sapphire**).**

Figure 12: Pie chart representing the percentage distribution of responses about frameshift mutation. About 45% responded stop codon replaces an amino acid codon, leading to premature termination of translation (Grey), 35% responded to change in reading frame followed by a stop codon (Arctic) and 20% responded that one protein amino acid is substituted by another amino acid (Violet**).**

Figure 13: Association between gender and knowledge on the genetic difference between organisms with cells carrying a single set of chromosomes. The X-axis represents Gender and Y-axis represents the number of participants who answered Haploid (Blue), Diploid (Green), Aneuploid (Beige). Out of 43% who had answered haploid, 33% constituted females and 10% constituted males. Out of 40% who answered diploid, 26% of participants were female and 14% of participants were male. Out of 17% who had answered aneuploid, 12% constituted females and 5% constituent males. An association to gender and knowledge under discussion was found to be not significant by the Pearson chi-square test (chi-square value: 1.390, df-2, P-value = 0.499). Thus, statistically, the males and females have the same opinion and knowledge on the type of light preferred.

Figure 14: Association between gender and knowledge on frameshift mutation. The X-axis represents Gender and Y-axis represents the number of participants who answered 'In a protein in which one amino acid is substituted for another (Blue), leading to premature termination of translation (Green), Change in reading frame followed termination codon (Beige). Out of 20% who had answered 'In a protein in which one substituted by another, 13% constituted females and 7% constituted males. Out of 45% who answered termination codon replaced amino acid, leading to premature termination of translation, 35% of participants were female and 10% participants were male. Out of 35% who had answered 'Change in reading frame followed by stop codon',23% constituted females and 12% constituted males. An association between gender and knowledge under discussion was found to be not significant by the Pearson chi-square test (chi-square value: 1.829, df-2, P-value = 0.401). Thus, statistically, the males and females have the same opinion and knowledge on the type of light preferred.

DISCUSSION

The results and statistics analysed by SPSS. The majority of the respondents were assessed to have good knowledge about the type of mutation in genetics.

The age group (Figure 3) of the dental students responded as majority of participants, 63%, were between 18-20, 35% were between 20-25 and 2% were between 25 & above. The gender (Figure 4) of the dental students involved 71% Females, 29% were Males. The year of study (Figure 5) of the dental students who responded involved 77% of 2nd year, 23% of 3rd year. When asked about genotype (Figure 6), 100% of respondents - 55% responded genotype is an organism's morphology, development/behavior, 37% responded genotype provides complete hereditary information of the organism and 8% as genotype is influenced by environmental factors. When asked about phenotype (Figure 7), 100% of respondents - 48% responded phenotype is an organism's morphology, development/behavior, 41% responded organism's full hereditary information is phenoype and 11% responded phenotype is the environmental influence of the organism (Malcolm, 2003).

The responses about the genetic difference-single set of chromosomes included(Figure 8), 100% of respondents - 43% responded haploid, 40% responded diploid and 17% responded aneuploid (Figure 8). When asked about the genetic difference - two sets of chromosomes (Figure 9), 100% respondents - 54% responded haploid, 39% responded diploid and 5% responded aneuploid and 2% responded none of the above (Firth, Hurst and Hall, 2005). When asked about

missense mutation (Figure 10), 100% respondents - 52% responded stop codon replaces an amino acid codon, leading to premature termination of translation, 27% responded to change in reading frame followed by a stop codon and 21% responded in a protein in which one protein is substituted by another(Gooch, 2011).

Accordingly, when asked about nonsense mutation (Figure 11), 100% respondents - 54% responded stop codon replaces an amino acid codon, leading to premature termination of translation, 14% responded to change in reading frame followed by a stop codon and 32% responded that aminoacid of one protein is replaced by another (Guttman, 2013). When asked about frameshift mutation (Figure 12), 100% respondents - 45% responded stop codon replaces an amino acid, leading to premature termination of translation, 35% responded to change in reading frame followed by a stop codon and 20% responded were one protein tripeptide is replaced by anaother(Strauss, 1999)

On comparing Gender and the knowledge about the genetic difference between organisms with cells carrying a single set of chromosomes, the number of participants who answered Haploid, Diploid, Aneuploid. Out of 43% who had answered haploid, 33% constituted females and 10% constituted males. Out of 40% who answered diploid, 26% of participants were female and 14% of participants were male. Out of 17% who had answered aneuploid, 12% constituted females and 5% constituted males. An association between gender and knowledge under discussion was not significant by the Pearson chi-square test (chi-square value: 1.390, df-2, P-value = 0.499). Thus statistically the males and females have the same opinion and knowledge on the type of light preferred.

On comparing Gender and the knowledge about frameshift mutation, the number of participants who answered 'In a protein in which one amino acid is substituted for another (Blue), Stop codon replaces an amino acid codon, leading to premature termination of translation (Green), Change in reading frame followed by a stop codon (Beige). Out of 20% who had answered 'In a protein in which one amino acid is substituted for another, 13% constituted females and 7% constituted males. Out of 45% who answered 'Stop codon replaces an amino acid codon', leading to premature termination of translation, 35% of participants were female and 10% participants were male. Out of 35% who had answered 'Change in reading frame followed by stop codon',23% constituted females and 12% constituted males. An association to gender and knowledge under discussion was found to be not significant by the Pearson chi-square test (chi-square value: 1.829, df-2, P-value = 0.401). Thus statistically both genders had same opinion and knowledge on the type of light preferred.

The limitations, include minimum articles referred and minimal sample size. The future scope, includes enabling one to create and analyze the apprehension of the type of mutation in genetics with a larger population.

CONCLUSION

The type of mutation in genetics is very important to understand various diseases. By this survey, we found that many of them knew about mutation and its types. By extending this survey three is a hope that we will be able to cultivate a more detailed and accurate understanding of mutation rates. But the fundamental mutational role and understanding is important for the future intervention of the diseases.

ACKNOWLEDGMENTS

We would like to thank Saveetha Institute of Medical and Technical Sciences, SaveethaDental College and Hospitals, Saveetha University for providing us support to conduct the study.

CONFLICT OF INTEREST

The author declares that there were no conflicts of interests in the present study.

SOURCE OF FUNDING

The present project is supported by

- Saveetha Institute of Medical and Technical Sciences
- SaveethaDental College and Hospitals, Saveetha University
- ZAK Exports, Krishnagiri, Tamilnadu

REFERENCES:

1. Anbu, R.T. *et al.* (2019) 'Comparison of the Efficacy of Three Different Bone Regeneration Materials: An Animal Study', *European journal of dentistry*, 13(1), pp. 22–28.
2. Becker, D. and Sevilla, M.D. (1993) 'The Chemical Consequences of Radiation Damage to DNA', *Advances in Radiation Biology*, pp. 121–180. doi:10.1016/b978-0-12-035417-7.50006-4.
3. Brundha, M.P., Pathmashri, V.P. and Sundari, S. (2019) 'Quantitative Changes of Red Blood cells in Cancer Patients under Palliative

Radiotherapy-A Retrospective Study', *Research Journal of Pharmacy and Technology*, 12(2), pp. 687–692.
4. Dreval, K. and Pogribny, I.P. (2018) 'Chemical Carcinogen Exposure, DNA Damage, and Epigenetic Alterations', *Carcinogens, DNA Damage and Cancer Risk*, pp. 309–340. doi:10.1142/9789813237209_0011.
5. Firth, H.V., Hurst, J.A. and Hall, J.G. (2005) 'Haploid autosomal lengths of human chromosomes', *Oxford Desk Reference - Clinical Genetics* [Preprint]. doi:10.1093/med/1.1.med-9780192628961-div1-007015.
6. Gooch, J.W. (2011) 'Missense Mutation', *Encyclopedic Dictionary of Polymers*, pp. 908–908. doi:10.1007/978-1-4419-6247-8_14238.
7. Gotoh, E. (2011) 'Visualize Dynamics of Chromosome Structure Formation and DNA Repair/Recombination Coupled With DNA Replication: Tight Coupled Role of DNA Replication in Chromosome Compaction and DNA Recombination', *Fundamental Aspects of DNA Replication* [Preprint]. doi:10.5772/19131.
8. Govindaraju, L., Neelakantan, P. and Gutmann, J.L. (2017) 'Effect of root canal irrigating solutions on the compressive strength of tricalcium silicate cements', *Clinical oral investigations*, 21(2), pp. 567–571.
9. Guttman, B. (2013) 'Mutation, Nonsense', *Brenner's Encyclopedia of Genetics*, p. 548. doi:10.1016/b978-0-12-374984-0.01005-6.
10. Harsha, L. and Brundha, M.P. (2017) 'Prevalence of Dental Developmental Anomalies among Men and Women and its Psychological Effect in a Given Population', *Journal of Pharmaceutical Sciences and Research; Cuddalore*, 9(6), pp. 869–873.
11. Jain, A.R. (2017) 'Prevalence of Partial Edentulousness and treatment needs in Rural Population of South India', *World journal of dentistry*, 8(3), pp. 213–217.
12. Krishna, V. (2004) *Textbook of Pathology*. Orient Blackswan.
13. Kumar, M.S. *et al.* (2006) 'Expression of matrix metalloproteinases (MMP-8 and -9) in chronic periodontitis patients with and without diabetes mellitus', *Journal of periodontology*, 77(11), pp. 1803–1808.
14. Kumar, S. (2017) 'The emerging role of botulinum toxin in the treatment of orofacial disorders: Literature update', *Asian journal of pharmaceutical and clinical research*, 10(9), p. 21.
15. Kumar, V., Abbas, A.K. and Aster, J.C. (2020) *Robbins & Cotran Pathologic Basis of Disease E-Book*. Elsevier Health Sciences.
16. Malcolm, S. (2003) 'Genotype to phenotype: interpretation of the Human Genome Project', *Genotype to Phenotype*, pp. 1–12. doi:10.4324/9780203450420-1.
17. Mandal, A.K. (2016) *Comprehensive Textbook of Pathology for Nursing: Pathology, Clinical Pathology, Genetics*.
18. Marian, A.J. (2013) 'Errors in DNA replication and genetic diseases', *Current Opinion in Cardiology*, pp. 269–271. doi:10.1097/hco.0b013e328360426c.
19. McMahon, R.F.T. and Sloan, P. (2000) *Essentials of Pathology for Dentistry*.
20. Miller, F.P., Vandome, A.F. and McBrewster, J. (2009) *Chromosomal Crossover: Genetic Recombination, Prophase, Meiosis, Synapsis, Synaptonemal Complex, Chromosome, Thomas Hunt Morgan, Catholic University of Leuven, Chiasma (genetics), Drosophila, Harriet Creighton*. Alphascript Publishing.
21. Mp, S.K. (2017) 'Relationship between dental anxiety and pain experience during dental extractions', *Asian Journal of Pharmaceutical and Clinical Research*, pp. 458–461.
22. Muthukrishnan, A. and Warnakulasuriya, S. (2018) 'Oral health consequences of smokeless tobacco use', *The Indian journal of medical research*, 148(1), pp. 35–40.
23. *Nair, M., Jeevanandan, G. and Vignesh, R. (2018) 'Comparative evaluation of post-operative pain after pulpectomy with k-files, kedo-s files and mtwo files in deciduous molars-a randomized clinical trial', Brazilian dental journal [Preprint]. Available at: https://bds.ict.unesp.br/index.php/cob/article/view/1617.*
24. *Perry, P.E. (1980) 'Chemical Mutagens and Sister-Chromatid Exchange', Chemical Mutagens, pp. 1–39. doi:10.1007/978-1-4613-3072-1_1.*
25. *Rosche, W.A. and Foster, P.L. (2001) 'Base Substitution Mutations', Encyclopedia of Genetics, pp. 197–198. doi:10.1006/rwgn.2001.0118.*
26. *Rosche, W.A. and Foster, P.L. (2002) 'Silent Mutation', Encyclopedia of Molecular Biology [Preprint]. doi:10.1002/047120918x.emb1427.*
27. *Sathivel, A. et al. (2008) 'Anti-peroxidative and anti-hyperlipidemic nature of Ulva lactuca crude polysaccharide on D-galactosamine induced hepatitis in rats', Food and chemical toxicology: an international journal published for the British Industrial Biological Research Association, 46(10), pp. 3262–3267.*
28. *Sekar, D. et al. (2019) 'Methylation-dependent circulating microRNA 510 in preeclampsia patients', Hypertension research: official journal of the Japanese Society of Hypertension, 42(10), pp. 1647–1648.*
29. *Song, Y. et al. (2020) 'DNA Damage Repair Gene Mutations Are Indicative of a Favorable Prognosis in Colorectal Cancer Treated With Immune Checkpoint Inhibitors', Frontiers in oncology, 10, p. 549777.*
30. *Strauss, B.S. (1999) 'Frameshift mutation, microsatellites and mismatch repair', Mutation Research/Reviews in Mutation Research, pp. 195–203. doi:10.1016/s1383-5742(99)00066-6.*
31. *Timothy, C.N., Samyuktha, P.S. and Brundha, M.P. (2019) 'Dental pulp Stem Cells in Regenerative Medicine--A Literature Review', Research Journal of Pharmacy and Technology, 12(8), pp. 4052–4056.*
32. *Tafa, H., Mema, D., Mezini, A., Nikolla, J., Teferici, A., Todri, D., . . . Hafizi, H. (2020). Prevalence of chronic obstructive pulmonary disease (COPD) in albania. South Eastern European Journal of Public Health, 15, 1-12. doi:10.11576/seejph-4164*
33. *Taryam, M., Alawadhi, D., Aburayya, A., Mubarak, S., Aljasmi, M., Salloum, S. A., & Mouzaek, T. (2021). Factors affecting the uptake of COVID-19 vaccine among dubai airport's professionals. South Eastern European Journal of Public Health, 17 doi:10.11576/seejph-5091*
34. *'Transition (transition mutation, transitional mutation, base pair substitution)' (2015) The Dictionary of Genomics, Transcriptomics and Proteomics, pp. 1–1. doi:10.1002/9783527678679.dg13646.*