Dijlah Journal of Medical Sciences (DJMS) Vol. 2, No. 1, September, 2025, pp. 23-29
P-ISSN: 3078-3178, E-ISSN: 3078-8625, paper ID: 03

Detection of Some Common Genes in Different Genetic Model Organisms

Mohammad Ibrahim Khalil* and Noor Myasar Sadeq

College of Environmental Sciences/ University of Mosul

Article Info

Article history:

Received April, 12, 2025
Revised May, 25, 2025
Accepted June, 28, 2025

Keywords:

Genes
Genetics Model
Homologous
PCR
Primer

ABSTRACT

Four genetic model organisms; Zebrafish, *Arabidopsis thalina*, *Neurospora crassa* and *Homo sapiens* used to detection and comparison of some important homologous genes; *TP53*, *WC-1*, *Clock* and *TNF*. PCR primers for each gene were designed and amplify against the four organisms. Three primes to amplify of *TP53* and one primer for the *WC-1* and *Clock* gene to all organisms and two primers for the *TNF*. The results showed there are a strong relation and homologous among the genes amplified by the primers, for these genes all organisms have a different genes name but have similar function in effective, the result also showed the possibility to use may organisms as a model to study some important genes and simulation the human genes for drug designed and genetics therapy.

Corresponding Author:

* Mohammad Ibrahim Khalil
College of Environmental Sciences/ University of Mosul, Mosul, Iraq
Email: mohammadibrahim@uomosul.edu.iq

1- INTRODUCTION

For an organism used to investigate a particular phenomenon, many reasons and conditions must be available such as trait, or disease; or because of its close resemblance to humans, rapid generation, and well-characterized genome. Many samples of these organisms were used in these studies such as Drosophila, Fish, Rodents, or Mice, their genetic material is well-known and available for laboratory experiments [1]. Using different organisms in genetics studies enabled scientist to study different characteristics and development of many diseases that infect human, especially the homologous genes which are similar in function and expression, these organisms have specifications that made them a good tool in many cases in pathology, genetics, and molecular biology [2]. This specification represented with discovering whole genome and all genes in DNA as well as the easy to deal with them and have some genetics characters such as have two types of cell nucleus diploid and haploid chromosome and the life cycle is short for rapid study results [3]. These organisms are:

Danio rerio:

Danio rerio or in common name Zebrafish is one of the organisms which is widely used in genetics studies as it is fully sequenced and easy to follow the embryo development and rapidly grow, the Zebrafish live in fresh water in South Asia, the researcher has used Zebrafish to understand many diseases in human, especially in brain disorder such as Alzheimer`s disease and another dystrophy of muscle (Muscle Dystrophy) [4].

Neurospora crassa:

N. crassa is a fungus that widely used as a model in genetics studies, it has a haploid chromosome in his life cycle and none pathogenic make it easy to grow in laboratory condition. These fungi have completely sequenced and have more than 10k genes as well as have several specifications such as circadian rhythms, cell fusion, epigenetics and cell polarity [5].

Arabidopsis Thalina:

Arabidopsis thaliana is a small flowering plant widely used as a model organism in plant biology and genetics. As a winter annual with a relatively short lifecycle, A. Thaliana has become a popular choice for studying plant genetics and development. It is a multicellular eukaryote with a relatively small genome of about 135 megabase pairs. Notably, A. thaliana was the first plant to have its entire genome sequenced, making it a valuable tool for scientific research. It has been extensively used to study various plant traits, including flower development, light sensing, and the effects of environmental factors [6].

2- MATERIAL AND METHODS

Data Base:

All data were obtained from the National Center for Biotechnology Information (NCBI).

Genes types:

Four genes TP53, WC-1, Clock and TNF were investigated for homologous in four organisms; *Zebrafish*, *Arabidopsis thalina, Neurospora crassa and Homo sapiens*

Primer design:

The primer was design by using NCBI primer design tools, Primer3 and Snapgene

PCR reaction:

The amplification of all primers design were tested insilico by using snapgene software, this step is very important to ensure the efficiency of the primers.

3- RESULTS AND DISCUSSION

All gene were investigated by designed PCR primer by using specific software (Snapgene, Primer3 and NCBI primer design).

TP53 gene:

The results of TP53 gene primers obtain 10 primers, three of them were used to blast for the four genetics organisms, table (1), the primer 1 blast in Zebrafish (Danio rerio) gave tnfaip8l2a gene The TNFAIP8 gene family has been connected to the control of immune system and homeostasis as well as the emergence of several cancer types [8]. While in A. thalina the primer no. 4 blast ABCG1 gene; it's an important gene for cholesterol metabolism and transformation of lipid and conversion to HDL, and this gene has a critical role in mediating cholesterol effluent to HDL and preventing cellular lipid accumulation, the ABC gene including protein within membrane which depending the ATP translocation of lipophilic and amphiphilic molecules [9]. The ATP is very important for energy of transporting action of lipid. The primer no. 8 blast results showed in Homo sapiens the TP53, this gene coded the tumor protein which is has an important activity in suppressor any tumor or unusual divisions in the cell and could be out of control [10]. The same primer blast against N. Crassa, the result showed VPS9 gene [11], this gene is a domain protein 1 (GAPVD1) which consider a one of the components of cytoplasmic of the cell and regulated the tumor suppressor protein (TP53) fig. (1; A) [12].

The growth silencer gene TP53, like the gene Rb, works to stop the onset and spread of tumor. If a person inherits only one active copy of the TP53 gene from their parents, they are predisposed to disease and typically encourage a few uncontrolled growths in various organs throughout their early adult years. This illness, sometimes called Li-Fraumeni disorder, is interesting. However, most cancer forms have TP53 mutations or changes, which adds to the confusing grouping of atomic events causing growth formation [7].

Table (1) *TP53* gene designed primers

	Primer	organism	Blast results
Primer 1	Forward: AGTGGGGATCCAGCATGAGA Reverse: GTGTCCGAAGAGAATGGGCA	Zebrafish	tnfaip8l2a
		Homo sapiens	TP53
Primer 4	Forward: GGGATCCAGCATGAGACACTT Reverse: GAGTGCTTGGGTTGTGGTGA	*Arabidopsis thalina*	ABCG1
Primer 8	Forward: CAATATCGTCCGGGGACAGC Reverse: TCTCATGCTGGATCCCCACTT	*Homo sapiens*	TP53
		Neurospora crassa	VPS9

WC1 gene

One primer designed for WC-1 gene and able to amplify a region in DNA in four model organisms in this study, table 2. In Zebrafish the primer blast result amplify *Si:dkey-159918.1* gene which symbol of sortilin. This gene plays as protein receptor, transporter and transduction of signal, it's had an important function in neurogenesis and maintenance the nervous system specifically in Alzheimer's disease and chronic sleep disorder, fig. (1;B) [13].

In A. *thalina* the primer amplifying the *TCP12* gene, it's controlled the development the plant leaf and also expression and have a main function to regulate the circadian rhythm. In Homo sapiens the primer blast result was a Parkin coregulate (DACRG),(6) this gene gives information to cell to break down unnecessary protein and accumulate degraded protein in substance namely ubiquitin, any mutation in Parkin gene leads to cause Parkinson's disease [14, 15].

The fungi *N. crassa* gene *WC-1* amplify by the primer, this gene controlled the circadian rhythm in the fungi and play an important role in clock period of the growth and conidia formation in fungi.

These entire genes have the same function or linked in time regulation to maintain the physiological process and metabolism according to day time and light / dark succession [13].

Table (2) WC1 Gene designed primers

	Primer	Organism	Blast results
Primer 1	Forward: TCA TGC GCA AGG AAT CCA Reverse: TCG CGA TCT TGC CCT TTC TA	Zebrafish	Si:dkey-159918.1
		Arabidopsis thalina	TCP12
		Homo sapiens	Parkin
		Neurospora crassa	WC1

One of the genes in *Neurospora crassa* that codes for the WC-1 (127 kDa) protein is called white collar 1 (wc-1). WC-1 has two distinct roles in the cell. To begin with, it is the founding member of the class of rule blue light photoreceptors in all fungi and the primary photoreceptor for Neurospora. The second important function is controlling circadian rhythms in FRQ. It is an important component of a circadian circuit that controls several behavioral activities. The White-Collar Complex (WCC), which interacts with the *Neurospora* circadian clock, is found in WC-1 and WC-2, a cooperating partner of WC-1. Transcriptional enactment spaces, PAS regions, and zinc finger DNA-restricting spaces are all found in the WCC complex of atomic record factor proteins (GATA). In order to form heterodimers, WC-1 and WC-2 [1].

Clock gene:

One primer has been designed for this gene and blast against the four model organisms, in Zebrafish the product was chromosome 13, while in *A. thalina* was blast chromosome 1, while in *H. sapiens* the blast product was clock gene, fig (1; C) and no target in the fungi *N. crassa*, table 3.

Table (3) Clock gene designed primers

	Primer	organism	Blast results
Primer 1	Forward:TCCAGCAGTTTCATGAGATGC Reverse:GAGGTCATTTCATAGCTGAGC	Zebrafish	chromosome: 13
		Arabidopsis thalina	chromosome: 1
		Homo sapiens	Clock gene
		Neurospora crassa	No target templates were found

Clock genes act as the premise of an intracellular timekeeping framework, present all through the body, which produces around 24-hour rhythms in physiology and conduct. Records and protein results of these genes show almost 24-hour motions in articulation [1].

TNF gene

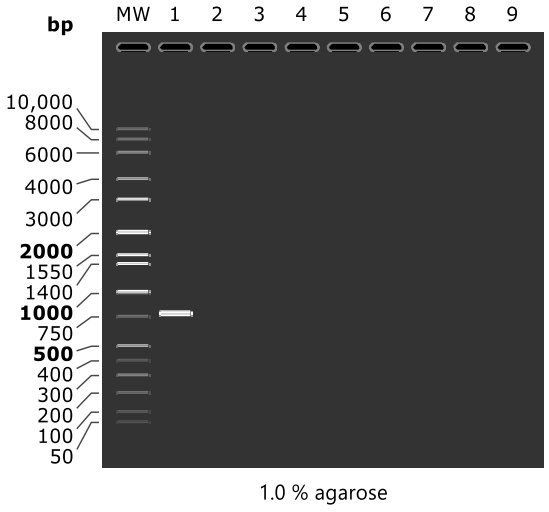
Two specific primers were designed for the organisms, except the fungi *N. crassa* no template was found, table 4.

In Zebrafish and *Homo sapiens* the *NTF* gene has been amplified, fig. (1;D), while in *A. thalina* the primer blast amplifies the *SABRE* gene which is controlled the shape of the organ and normal expansion in the cell [16] any mutation in this gene leads to abnormal growth and it inhibit promoting radial and random growth [17].

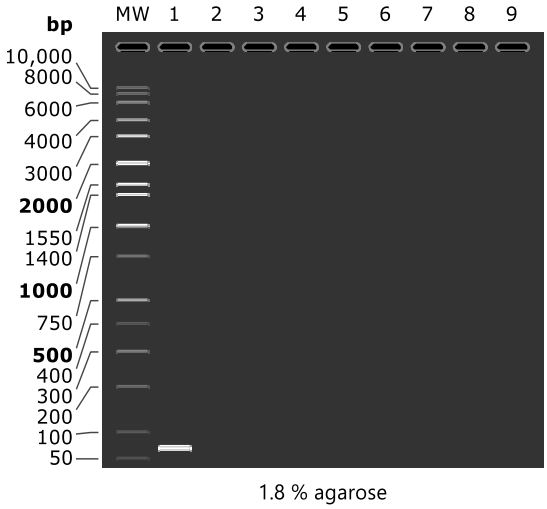
Table (4) *TNF* gene designed primers

Primer		organism	Blast results
Primer 1	Forward: AAAGGAACACAGCAAGGAGAA Reverse: AGTCGAATTTCTTGCCCTGA	Zebrafish	TNF
		Arabidopsis thalina	SABRE
None	None	*Neurospora crass*	None
Primer 2	Forward: TATGGAGACAGATGTGGGGTG Reverse: CTTAGCCCTGAGGTGTCTGG	*Homo sapiens*	TNF

Clock genes act as the premise of an intracellular timekeeping framework, present all through the body, which produces around 24-hour rhythms in physiology and conduct. Records and protein results of these genes show almost 24-hour motions in articulation [1].



1.0 % agarose



1.8 % agarose

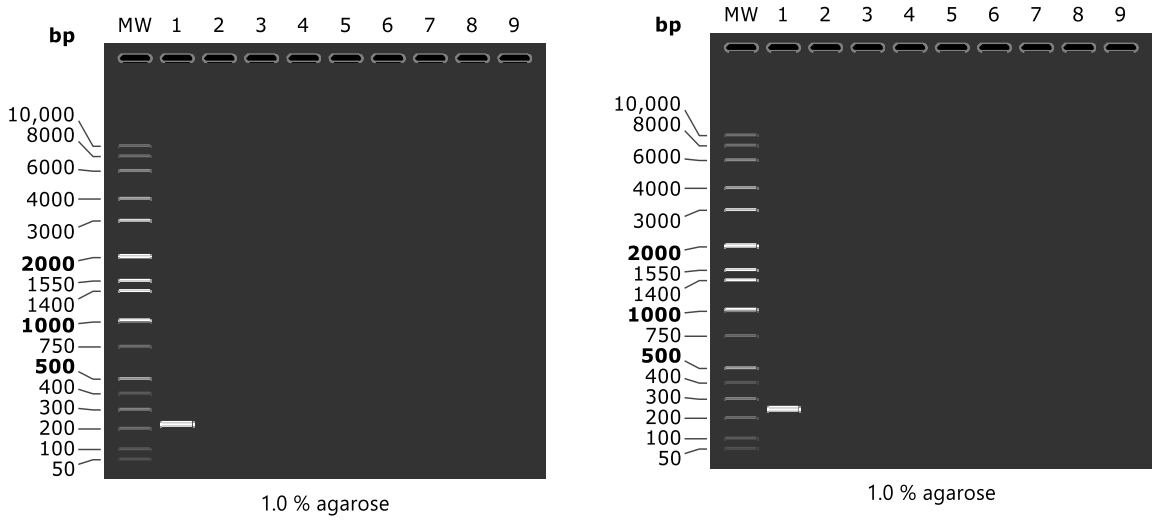


Figure (1); Agarose Gel Simulation of Human genes Primer design
A: TP53 gene B: WC1 gene C: Clock gene D: TNF gene

4- CONCLUSION

Many organisms sharing several genes differ in names and similar in function, these organisms specially those with whole genomic sequenced Zebrafish, *Arabidopsis thalina*, *Neurospora crassa* and *Homo sapiens* effort a good tool for genetic studies in gene expression experiments to serve as a model for human being therapy.

ACKNOWLEDGEMENTS

Author thanks want to thanks the University of Mosul provided equipment that the writers would like to thank for as it raises.

REFERENCES

[1] Smadi, A. A., Ajao, B. T., Johnson, B. K., Lei, H., Chakhchoukh, Y., & Al-Haija, Q. A. (2021). A comprehensive survey on cyber-physical smart grid testbed architectures: Requirements and challenges. *Electronics, 10*(1043). https://doi.org/10.3390/electronics10091043

[2] Albulayhi, K., Smadi, A. A., Sheldon, F. T., & Abercrombie, R. K. (2021). IoT intrusion detection taxonomy, reference architecture, and analyses. *Sensors, 21*(6432). https://doi.org/10.3390/s21196432

[3] Wu, Y., Chen, Y., Wang, L., Ye, Y., Liu, Z., & Liu, Y. (2019). Large scale incremental learning. In *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition* (pp. 374–382). https://doi.org/10.1109/CVPR.2019.00046

[4] Mosavi, A., Shamshirband, S., Salwana, E., Chau, K. W., & Tah, J. H. M. (2019). Prediction of multi-inputs bubble column reactor using a novel hybrid model of computational fluid dynamics and machine learning. *Engineering Applications of Computational Fluid Mechanics, 13*(1), 482–492. https://doi.org/10.1080/19942060.2019.1613448

[5] Palanisamy, V., & Thirunavukarasu, R. (2019). Implications of big data analytics in developing healthcare frameworks – A review. *Journal of King Saud University - Computer and Information Sciences, 31*(4), 415–425. https://doi.org/10.1016/j.jksuci.2017.12.007

[6] Sadowski, J. (2019). When data is capital: Datafication, accumulation, and extraction. *Big Data & Society, 6*(1), 1–12. https://doi.org/10.1177/2053951718820549

[7] Saura, J. R., Herraez, B. R., & Reyes-Menendez, A. (2019). Comparing a traditional approach for financial brand communication analysis with a big data analytics technique. *IEEE Access, 7*, 37100–37108. https://doi.org/10.1109/ACCESS.2019.2905301

[8] Nallaperuma, D., Vlahogianni, E. I., Chien, S., & Antoniou, C. (2019). Online incremental machine learning platform for big data-driven smart traffic management. *IEEE Transactions on Intelligent Transportation Systems, 20*(12), 4679–4690. https://doi.org/10.1109/TITS.2019.2924883

[9] Schulz, S., Becker, M., Groseclose, M. R., Schadt, S., & Hopf, C. (2019). Advanced MALDI mass spectrometry imaging in pharmaceutical research and drug development. *Current Opinion in Biotechnology, 55*, 51–59. https://doi.org/10.1016/j.copbio.2018.08.003

[10] Shang, C., & You, F. (2019). Data analytics and machine learning for smart process manufacturing: Recent advances and perspectives in the big data era. *Engineering, 5*(6), 1010–1016. https://doi.org/10.1016/j.eng.2019.01.019

[11] Yu, Y., Li, M., Liu, L., Li, Y., & Wang, J. (2019). Clinical big data and deep learning: Applications, challenges, and future outlooks. *Big Data Mining and Analytics, 2*(4), 288–305. https://doi.org/10.26599/BDMA.2019.9020007

[12] Huang, M., Liu, W., Wang, T., Song, H., Li, X., & Liu, A. (2019). A queuing delay utilization scheme for on-path service aggregation in services-oriented computing networks. *IEEE Access, 7*, 23816–23833. https://doi.org/10.1109/ACCESS.2019.2899402

[13] Friulla, L., & Varone, L. (2025). Artificial light at night (ALAN) as an emerging urban stressor for tree phenology and physiology: A review. *Urban Science, 9*(1), 14. https://doi.org/10.3390/urbansci9010014

[14] Son, M., Kim, D. Y., & Kim, C.-H. (2022). Disease modeling of rare neurological disorders in zebrafish. *International Journal of Molecular Sciences, 23*(7), 3946. https://doi.org/10.3390/ijms23073946

[15] Kam, M. K., Kim, B., Lee, D. G., Lee, H. J., Park, Y.-H., & Lee, D.-S. (2022). Amyloid beta oligomers-induced parkin aggravates ER stress-mediated cell death through a positive feedback loop. *Neurochemistry International, 155*, 105312. https://doi.org/10.1016/j.neuint.2022.105312

[16] Li, S. (2015). The *Arabidopsis thaliana* TCP transcription factors: A broadening horizon beyond development. *Plant Signaling & Behavior, 10*(7), e1044192. https://doi.org/10.1080/15592324.2015.1044192

[17] Susmi, T. F., Hossain, M. M., Zahan, M. R., Ahmed, M. F., Akhtar, M. T., & Acharjee, M. Z. (2021). Prognostic and clinicopathological insights of phosphodiesterase 9A gene as novel biomarker in human colorectal cancer. *BMC Cancer, 21*(1), 577. https://doi.org/10.1186/s12885-021-08289-y

[18] Nisansala, T., Wickramasinghe, N. D., Weerasekera, M. M., Munasinghe, C. A., Abeygunasekara, C. A., & Agampodi, S. B. (2021). Contributing role of TNF, IL-10, sTNFR1 and TNF gene polymorphisms in disease severity of leptospirosis. *Medical Microbiology and Immunology, 210*(4), 211–219. https://doi.org/10.1007/s00430-021-00700-w