International Journal of All Research Education and Scientific Methods (IJARESM), ISSN: 2455-6211
Volume 9, Issue 3, March -2021, Impact Factor: 7.429, Available online at: www.ijaresm.com

Genetic Traits and Disorder Analysis through Survey in Individuals of Various Families at Thalassery, Kannur District, Kerala

Seema Gupta[1], Bhramacharini Sheela[2], Nandana P[3], Nandana K[4], Sruthi M[5], Adith R[6], Akshaya P[7], Anagha P[8], Anamika BV[9], Ananya P[10], Avanthika S[11], Nihariga A M[12]

[1,2,3,4,5,6,7,8,9,10,11,12]Amrita vidyalayam, Punnol, Thalasshery, Kerala.

----------**********----------

ABSTRACT

Genetics is a topic of fine research and development in many sectors of biotechnology, molecular biology, medical biology and evolution. In the similar interest the present research work focus on to study and analyse the various traits or characteristics along with genetic disorders in individuals from 38 families of kannur dictrict. Herein, survey methodology based on phenotypic characters have generated data for further studies on the topics mentioned before. Altogether nine traits and eight disorders are included in this study. Some of the traits are found to be common character between most of the individuals of the studied families. Few traits are very rarely seen and finally one trait is found to be nilling among the population. Only one genetic disorder is traced, this may be due to insufficient data collected as a result of non-reveiling the facts by individuals.

Key words: Genetic trait, Chromosomal disorders, Mendelian disorders, phenotype, survey.

INTRODUCTION

In the era of research and developement, genetics is one of the greatest milestones that humans have discovered. Many unsolved queries and curiosity for the various characters inherited by different organisms is answered by the study of genes and DNA. It has a major role in identifying one's phenotype and genotype generation after generation including assuming the one which is yet to be born. Genetics is key to unfold mystery of human evolution from chimpanzees to today's modern man. There are many characters which are evolved and some are recently studies such as pigmentation, keratinization and high altitude adaptation [6], [4],[8]. Development of the traits and genes is highly regulated process through complex gene regulation networks [2]. Many genetic and nongenetic factors interact to determine the final phenotype, whether that phenotype is susceptibility to disease, or a quantifiable trait such as height, weight, serum cholesterol or blood pressure [10].

Work of Mendel and other geneticist have contributed enormous growth and advancement in medicine and health science. Study of these heredity characters and variations have been a boon to medical field and henceforth, a new branch of medical genetics and molecular biology is evolved. Through these techniques of DNA screening many congenital defects, mutations and disorders can be traced in a foetus before birth. Disorders which are migrated from generations can be studies through genetic traits and family history analysis and pedigree studies [7],[12],[3]. Certain single gene disorders cystic fibrosis, hemochromatosis, Tay-Sachs, and sickle cell anemia leads to foetal death and infertility in some individuals. most singlegene diseases are rare, whereas most polygenic diseases are common; population genetic arguments predict that for common diseases, some of the causal genetic variation should have a high frequency in the population, due to the demographic history of the human population [13]. Some mutations caused due to translocation of genes during cell division in embryo results in Down syndrome and Klinefelter's syndrome can be traced through population and family studies. Point mutations like Haemophilia, phynylketonuria and colour blindness are studied in present work along with other mutations noted here.

MATERIALS AND METHODS

Site of survey

The study through survey is conducted at various regions of Thalassery, Kannur, Kerala. This region lies 11°45′2.24″N 75°29′13.28″E, with total area of 23.96 km2 and nearly 92,558 of population count. Thalassery lies 11m above sea level and has significant rainfall most months. The average annual temperature in Thalassery is 27.3 °C / 81.2 °F. The annual rainfall is 3512 mm.

Data collection

The research work is completed through study of 38 families residing at kannur district. Work is conducted by survey of individuals for different genetic traits like cleft chin, widow peak, dimples, hair colour, eye colour, freckles, earlobe attachment and rolling tongue. Along with this certain genetic mutations like Down's syndrome, Klinfelter's syndrome, Turner's syndrome, Haemophilia, Sickle cell anaemia, Duchenne muscular dystrophy, Phenylketonuria and colour blindness are also traced.

RESULT AND DISCUSSION

Study of genetic traits and disorders from Kannur district enables us to understand the heredity and variation between individuals of 38 families and thereby DNA defects if any. Similar work is seen with the observations made in a study of interaction between genes, behavior and social environment of individuals at US by Institute of Medicine [9]. The data collected is segregated into tables for genetic traits with nine dominant characters i.e cleft chin, widow peak, dimples, brown/black hair colour, freckles, brown clack eye colour, wide eyes, free earlobe and rolling of tongue (table 1). [1] conducted studies on different genetic traits in students and found many dominant characters as in this research. Among which brown/ black hair, brown / black eye, free earlobes are most found dominant trait in almost all individuals from various families included in study. Nearly half of the population is observed with wide eyes and remaining few individuals with cleft chin. It is observed that mostly males are observed with cleft chin and some characters like widow peak dimples in both male and females and in both. Freckles are not observed in any individual from the studied families. With regard to genetic disorders only 3 cases of Haemophilia are recorded in individuals from different families (table 2). This study gives us a brief information about the common trait found in a region like Thalassery, kannur. It may be due to common atmospheric conditions, food and other lifestyle of the individuals [11] reported that family history study can be used to predict an individual's disease risk representing genomic and environmental interactions.

Table 1: Survey Report of Families Representing Various Genetic Traits

Family No.	Age	Gender	Blood Group	Genetical Traits Dominant Characters								
				Cleft Chin	Widow Peak	Dimples	Brown / Black Hair	Freckles	Brown/ Black Eye	Wide Eye	Free Earlobe	Rolling Tongue
1	44	F	A+VE		P		P		P		P	
	21	M	O+VE		P		P		P		P	P
	14	F	O+VE				P		P		P	P
2	85	M	B+VE				P		P		P	
	54	M	B+VE				P		P		P	P
	13	M	B+VE				P		P		P	
3	41	F	B+VE				P		P		P	P
	15	F	B+VE				P		P		P	P
	09	M	B+VE		P		P		P		P	P
4	38	F	B+VE				P		P	P	P	P
	16	F	B+VE				P		P	P	P	P
	8	M	B+VE				P		P	P		P
5	45	F	A+VE		P		P		P		P	
	27	M	O+VE		P		P		P		P	P
	18	F	O+VE				P		P		P	P
6	49	M	O+VE	P					P	P	P	P
	21	M	O+VE						P	P	P	P
	17	F	B+VE	P	P	P	P		P	P	P	P
7	65	F	A+VE				P		P		P	P
	45	M	A+VE				P		P			P
	34	F	B+VE	P	P	P	P		P	P		P
	21	F	A+VE				P		P	P		
	13	F	O+VE				P		P			P
	11	M	B+VE			P	P		P	P		P

	01	M	B+VE	P		P	P		P	P		
8	42	M	A+VE				P		P			P
	34	F	A+VE				P		P	P	P	P
	16	F	A+VE				P		P	P	P	P
	14	M	A+VE				P		P			P
9	79	M	A+VE				P		P		P	P
	69	F	B+VE				P		P		P	P
	51	M	B+VE				P		P			
	46	F	A+VE				P		P	P	P	
	48	M	B+VE				P		P			P
	40	F	A+VE				P		P	P		
	45	M	B+VE				P		P		P	P
	38	F	A+VE	P	P		P		P	P		P
	25	F	A+VE				P		P		P	P
	20	F	A+VE				P		P	P		P
	15	M	B+VE	P			P		P			
	18	F	A+VE				P		P	P		P
10	56	F	B+VE				P		P	P		P
	27	M	B+VE		P	P	P		P		P	P
	25	F	A+VE				P		P	P		P
11	75	M	A+VE	P			P		P			P
	65	F	A+VE		P		P		P			P
	47	M	B+VE	P	P		P		P	P	P	P
	39	F	A+VE		P		P		P		P	P
	18	F	B+VE	P			P		P			P
	11	F	B+VE				P		P	P	P	P
12	38	M	O+VE	P			P		P			P
	32	F	O+VE	P	P		P		P	P		P
	16	F	O+VE	P			P		P		P	P
	07	M	O+VE				P		P		P	P
13	53	F	B+VE				P		P	P		P
	48	F	B+VE				P		P	P		P
	26	F	AB+VE				P		P			P
14	41	M	A+VE	P			P		P			P
	34	F	B+VE		P		P		P	P	P	P
	18	F	B+VE		P		P		P	P	P	P
15	38	F	B+VE				P		P	P	P	P
	16	F	B+VE				P		P	P	P	P
	8	M	B+VE				P		P	P		P
16	41	F	B+VE				P		P		P	P
	15	F	B+VE				P		P		P	P
	09	M	B+VE		P		P		P		P	P
17	85	M	B+VE				P		P		P	
	54	M	B+VE		P		P		P		P	P
	13	M	B+VE		P		P		P		P	P
18	44	F	A+VE				P		P		P	
	21	M	O+VE		P		P		P		P	P
	14	F	O+VE		P		P		P		P	P
19	58	M	O+VE				P		P		P	P
	38	F	O+VE		P		P		P		P	P
	16	F	O+VE				P		P		P	P
20	52	F	B+VE	P			P		P			

	28	F	B+VE		P		P		P			P
	01	M	O+VE	P	P		P		P			P
21	49	F	O+VE		P		P		P		P	P
	21	F	A+VE	P			P		P	P	P	P
	01	M	O+VE				P		P			P
22	73	M	O+VE	P			P		P	P	P	
	45	F	O+VE		P		P		P		P	
	16	F	O+VE		P		P		P	P	P	
23	79	M	O+VE				P		P	P	P	
	40	M	O+VE	P			P		P	P	P	P
	13	M	O+VE				P		P	P	P	P
24	80	M	O+VE				P	P	P	P	P	P
	76	F	AB+VE				P	P	P	P	P	P
	55	M	A+VE				P	P	P	P	P	P
	47	F	O+VE				P		P	P	P	P
	19	M	O+VE				P		P	P	P	
	11	F	O+VE				P		P	P	P	
25	52	M	A+VE				P		P		P	P
	42	F	A+VE				P		P		P	P
	16	F	A+VE				P		P		P	P
	7	M	A+VE				P		P	P	P	P
26	49	F	O+VE				P		P	P	P	P
	62	M	B+VE				P		P		P	P
	24	M	O+VE	P			P		P		P	P
	21	F	B+VE				P		P	P	P	P
	47	F	O+VE				P		P	P	P	P
	52	M	O+VE				P		P	P	P	
	20	M	O+VE				P		P	P	P	P
	18	M	O+VE				P		P	P	P	P
27	43	M	A+VE				P		P		P	P
	34	F	A+VE				P		P		P	P
	10	M	A+VE				P		P	P	P	P
	7	F	A+VE				P		P	P	P	P
28	64	F	B+VE				P		P	P	P	
	47	M	O+VE				P		P	P	P	P
	43	F	B+VE				P		P	P	P	P
	43	M	A+VE				P		P	P	P	P
	33	F	B+VE		P		P		P	P	P	P
	9	F	B+VE				P		P		P	P
	7	M	B+VE				P		P	P	P	P
	38	F	B+VE				P		P	P	P	P
	47	M	B+VE				P		P	P	P	P
	11	F	B+VE				P		P	P	P	P
	7	F	O+VE				P		P	P	P	
29	71	F	A+VE				P		P	P	P	P
	45	F	A+VE				P		P	P	P	P
	43	F	A+VE				P		P		P	P
	43	M	A+VE						P	P	P	P
	13	F	A+VE				P		P	P	P	P
	9	F	A+VE				P		P	P	P	P
30	46	M	O^+ VE	P			P	P	P		P	P
	24	M	O^+ VE		P		P	P	P		P	P

	18	M	O^+ VE				P	P	P		P	P
31	18	F	O^+ VE					P	P	P	P	P
	54	M	O^+ VE						P	P	P	P
	84	F	O^+ VE		P		P	P	P	P		
32	35	M	AB^+ VE				P	P	P			
	7	F	A^+ VE				P	P	P	P	P	P
	65	M	A^+ VE	P			P	P	P		P	P
33	72	F	B^+ VE	P	P		P	P	P		P	P
	38	M	B^+ VE	P			P	P	P		P	
	36	M	B^+ VE	P	P		P	P	P		P	
	85	M	O^+ VE					P	P	P	P	P
	50	M	O^+ VE	P		P	P	P	P	P	P	P
	15	F	O^+ VE					P	P		P	P
34	38	M	A^+ VE	P			P	P	P	P	P	P
	75	M	A^+ VE				P	P	P	P	P	P
	7	F	A^+ VE			P	P	P	P	P	P	P
	4	M	A^+ VE				P	P	P			P
35	17	F	O^+ VE			P	P		P		P	
	11	M	A^+ VE				P		P	P	P	
	71	M	A^+ VE				P		P	P	P	P
	44	M	A^+ VE	P			P		P	P	P	P
36	46	M	A+VE				P		P		P	
	38	F	A+VE				P		P		P	
	11	F	A+VE				P	P	P		P	
	9	F	A+VE	p			P	P	P	P	P	
	46	M	A+VE				P		P	P	P	
37	51	F	O+VE				P		P	P	P	
	19	F	O+VE				P		P	P	P	
	24	M	O^-+VE				P		P	P	P	
	59	M	O+VE	p			P		P	P	P	
38	64	M	B+VE	p			P		P	P	P	
	50	F	O+VE				P		P		P	
	29	M	O+VE				P		P		P	
	32	F	O+VE				P		P		P	
	45	M	A+VE				P		P		P	
	15	M	A+VE	p			P		P		P	
	37	F	O+VE				P		P		P	
	49	M	A+VE				P		P		P	

Table 2: Survey Report for Genetical Disorders Including Chromosomal and Mendelian

Family No.	Age	Gender	Blood Group	Chromosomal Disorders			Mendelian Disorder				
				Down's Syndrome	Klinefelter's Syndrome	Turner's Syndrome	Haemophilia	Sickle-Cell Anaemia	Duchenne Muscular Dystrophy	PKU	Colour Blindness
4	38	F	B+VE				P				
	16	F	B+VE								
	8	M	B+VE								
7	65	F	A+VE								
	45	M	A+VE								
	34	F	B+VE				P				
	21	F	A+VE				P				
	13	F	O+VE								
	11	M	B+VE								
	01	M	B+VE								

ACKNOWLEDGEMENT

The author of this research paper extends gratitude towards Mata Amritanandamayi for her support and blessings for this research during this pandemic period of Corona virus. First author is thankful and appreciate the efforts of co- authors and students of Amrita vidyalayam, Punnol, Thalassery, kannur.

REFERENCES

[1]. Ashraful Kabir (2019). Dominant-Recessive Interaction and Their Probability on Human Phenotype. CPQ Medicine, 7(4), 01-07.
[2]. Davidson E H and Erwin D H (2006). Gene regulation networks and evolution of animal body plans. Science 311, 796-800.
[3]. Florez JC, Hirschhorn J, Altshuler D (2003). The inherited basis of diabetes mellitus: implications for the genetic analysis of complex traits. Annu Rev Genomics Hum Genet 4:257–291
[4]. Gautam P, Chaurasia A, Bhattacharya a, Grover R, Indian genomevariation consortium, Mukerji M and Natarajan V T (2015). Population diversity and adaptive evolution in keratization genes: impact of environment in shaping skin phenotypes. Mol. Biol. Evol. 32, 555-573.
[5]. Genomic approaches to studying human-specific developmental traits Lucía F. Franchini1,* and Katherine S. Pollard (2015). Published by The Company of Biologists Ltd | Development 142, 3100-3112 doi:10.1242/dev.120048.
[6]. Handcock, A M, Witonsky D B, Alkorta-Aranburu G, Beall C M, Gebremedhin A, Sukernik R, Utermann G, Pritchard J K, Coop G and Di Rienzo A.(2011). Adaptation to climate- mediated selective pressure in humans. PLoS Genet. &, e1001375.
[7]. Hirschhorn JN (2003). Genetic epidemiology of type 1 diabetes. Pediatr Diabetes 4:87–100 2.
[8]. Huerta-Sanchez E, Jin X, Asan X, Bianba, Z, Peter B M, Vinckenbosch N, Liang, Y, Yi, X, He, M, Somel, M (2014). Altitude adaptation in Tibetans caused by introgression of Denisovan- like DNA. Nature 512, 194-197.

[9]. Institute of Medicine (US) Committee on Assessing Interactions Among Social, Behavioral, and Genetic Factors in Health; Hernandez LM, Blazer DG, editors. Washington (DC): National Academies Press (US); 2006.
[10]. Joel N H (2005). Genetic Approaches to Studying Common Diseases and Complex Traits Vol. 57, No. 5, Pt 2, Copyright © 2005 International Pediatric Research Foundation, Inc. Printed in U.S.A.
[11]. Kardia SL, Modell SM, Peyser PA (2003). Family-centered approaches to understanding and preventing coronary heart disease. American Journal of Preventive Medicine. 24(2):143–151.
[12]. Redondo MJ, Fain PR, Eisenbarth GS (2001). Genetics of type 1A diabetes. Recent Prog Horm Res 56:69–89
[13]. Reich DE, Lander ES (2001). On the allelic spectrum of human disease. Genes, Behavior, and the Social Environment: Moving Beyond the Nature/Nurture Debate. Trends Genet 17:502–510