Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

GENOMICS RELATED TO HYPERTENSION: A REVIEW

BHASKARCHARANA KABI
Professor, Department of Biochemistry, School of Medical Sciences and Research and Sharda Hospital, Sharda University, Greater Noida, Uttar Pradesh, India.

MANOJ KUMAR NANDKEOLIAR
Professor, Department of Biochemistry, School of Medical Sciences and Research and Sharda Hospital, Sharda University, Greater Noida, Uttar Pradesh, India.

NIRUPMA GUPTA
Professor, Department of Anatomy, School of Medical Sciences and Research and Sharda Hospital, Sharda University, Greater Noida, Uttar Pradesh, India.

THURAYA ABDULLSALAM AA ALAZAZI *
PhD Scholar, Department of Biochemistry, School of Medical Sciences and Research and Sharda Hospital, Sharda University, Greater Noida, Uttar Pradesh, India.
*Corresponding Author Email**:** thoraya1020@gmail.com

Abstract

Due to the combination of hereditary and environmental risk factors, essential hypertension is a complicated illness with sociodemographic variables playing a substantial role in its development. This has been shown in several epidemiological research. Finding the underlying molecular causes of hypertension and the genetic risk factors connected with it may open the door to more clinical treatment interventions and research into the disease's prevention. To understand the intricate pathophysiology of hypertension, researchers must pinpoint the susceptibility genes involved. It is important to remember that gene variations that cause hypertension usually cause a small increase in risk and are influenced by a number of dietary habits, interactions with other genes, and socioeconomic factors. Being a complex disease influenced by both hereditary and environmental factors, hypertension cannot be fully explained by a single gene mutation.

INTRODUCTION

Hypertension (HTN) is defined as elevated blood pressure (BP), which occurs when blood vessels are under excessive pressure (140/90 mmHg or higher). It is prevalent, but if left untreated, it can be hazardous. Patients with high BP may not display any symptoms; only a blood pressure test will reveal their condition (1).

When the heart pulses, systolic blood pressure (SBP = 140 mmHg) indicates how much force the blood exerts on the walls of the arteries. Whereas diastolic blood pressure (DBP=90mmHg) designates the BP exerts against the wall of arteries between heartbeats (AHA, 2021), systolic blood pressure (SBP=120) indicates the pressure blood exerts against artery walls during a heartbeat. In general, SBP is considered as the most important impact player for cardiovascular disease (CVD) in those over 50 years old. SBP typically increases with age in the majority of people as a result of the rigidity of big arteries, the progressive deposing of plaque, the increased prevalence of cardiovascular and vascular illness. Hypertension may be identified using either an increased SBP or

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

DBP reading. According to recent studies, when systolic blood pressure increase by 20 mmHg or 10 mmHg rise in diastolic BP for persons aged 40 or more doubles their chance of dying from ischemic heart disease and stroke (2)

It has been established that 31.7% of the US population has HTN using the earlier recommendations of JNC7. Essential Hypertension (EH) is to blame for 24% of coronary heart failure fatalities and 57% of deaths from cerebral haemorrhage in India. Along with environmental influences, epigenetics affects EH (3).

Hypertension, or high blood pressure, is a non-communicable disorder marked by chronically high blood vessel pressure. The World Health Organisation (WHO) estimates that 1.13 billion people have hypertension in worldwide, a significant medical disease. Globally, 25% of people are anticipated to develop hypertension by 2025. Recently, epidemic levels of hypertension have been seen. With far-reaching consequences for the worldwide burden of disease including cardiovascular and end-stage renal disorders, etc., hypertension continues to be a major public health problem (4)

HTN is one of the most renowned and widespread disorders which is influenced by both hereditary and environmental variables, which lead to an increase in BP. By defining the mechanism which generates blood pressure and combining new therapeutic approaches, as well as researching factors related to the immune system that are linked to hypertension, new genes related to high blood pressure can be investigated (5)

Hypertension is a severe health problem that increases the risk of neurological, cardiovascular, and renal diseases. It is a major contributor to premature mortality on a global scale, affecting over a billion people, or one in four men and one in five women. Two-thirds of hypertension cases are found in countries with middle and low incomes, primarily as a result of a rise in risk factors among these populations in recent years (6)

In India 24% of individuals with essential hypertension are at risk for cardiovascular disease, coronary heart failure deaths and 57% of cerebral haemorrhage deaths are attributable to essential hypertension (EH). In addition to environmental factors, epigenetic also contributes to EH. The genes implicated in hypertension is difficult to be investigated (7).

Blood pressure is the leading cause of cardiovascular disease (CVD) and kidney failure, but its prevention and treatment remain challenging. The inadequate efficacy of hypertension treatment and the inter-individual variation in the response to antihypertensive medications have numerous causes, including noncompliance, but genetic variations may be significant contributory factors (8).

Hypertension is most likely a polygenic disorder’s combination of genes and environmental exposures have a small effect on BP in the majority of individuals. In addition, distinct subsets of genes may be associated with distinct hypertension-related phenotypes, such as dyslipidemia, obesity, and insulin resistance (IR). Twin, adoption, and family studies manifest that blood pressure levels and hypertension are substantially inherited. Candidate gene studies (CGS) and Genome-wide association studies (GWAS)

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

have recognized more than 25 rare mutations and more than 100 polymorphisms related to hypertension. These polymorphisms are involved in the regulation of arterial pressure-regulating pathways. However, BP-related polymorphisms only account for 3.5% of BP variance, whereas the heritability of hypertension is estimated to be between 30% and 40% based on family studies. The "missing heritability" explanation postulates that DNA epigenetic alterations are a factor in the heredity of blood pressure. Differences in the expressions of the genes are brought about by epigenetic mechanisms that do not involve DNA sequence alterations. In contrast to the DNA sequence, environmental exposures have a greater propensity to modify the epigenome (7)

Mechanisms regulating hypertension

Blood pressure is known scientifically as "lateral pressure applied on the vessel wall". The distributional pattern in the typical population resembles a bell curve. Hypertension is the term for an increase in blood pressure (10).

It is helpful to comprehend the variables that affect both normal and high arterial pressure. The two elements that affect arterial pressure are peripheral resistance and heart output. Heart rate and stroke volume together determine cardiac output; myocardial contractility and vascular compartment size both have an impact on stroke volume. The anatomical and functional alterations in arteries with small size (the diameter of lumen 10 to 400 mm) and arterioles have an impact on peripheral resistance. (7).

Extracellular matrix (ECM) and Vascular smooth muscle cells (VSMCs), are significant vascular wall constituents that influence hemodynamic vessel activities. They are essential for controlling blood pressure in both normal and hypertensive circumstances. VSMCs experience differentiation, contractile, proliferative, and migratory changes in pathological circumstances. These modifications impair the vessels' functionality and may hasten the development of the illness Extracellular matrix (ECM), a crucial component of the vascular wall, also contributes significantly to vascular function. The development of hypertension has been linked to a fundamental pathological process known as ECM remodeling (11,12).

According to the Multiple Risk Factor Intervention Trial (MRFIT), there is no clear cut blood pressure threshold that indicates when there may be an issue. Instead, the long-term risks of cardiovascular mortality increase steadily when the blood pressure (SBP & DBP) is high. As a result, the definition of hypertension varies, but the most popular one is a blood pressure level that is linked to a doubling of long-term risks. JNC states that a person's blood pressure considered normal when it is 120/80 mm Hg in adult (10).

A huge public health concern that affects people from all walks of life because it doubles the risk of CVD such haemorrhagic stroke, congestive heart failure, CHD, ischemic stroke ,peripheral arterial disease(PVD), and kidney failure. (13)

For the reason of classification, the majority of cases of hypertension are classified as "primary" rather than "essential" illnesses. Cardiac output and peripheral vascular resistance are used to calculate blood pressure (BP = CO x PVR). There may be

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

anomalies in one or more of the many factors that control either the cardiac output or the peripheral resistance that causes persistent Hypertension (12)

In more than 90 % of patients, there are no identifiable underlying causes of hypertension. It is considered that these people have Primary or Essential hypertension. Numerous variables, including as renal dysfunction, vascular tone, peripheral resistance, endothelial dysfunction, insulin resistance, autonomic tone and neurohumoral factors, may affect how blood pressure is regulated and how hypertension develops. The complication in the endocrine system, heart or renal system can cause secondary hypertension. Moreover, there are other types of hypertension, namely pulmonary hypertension (PH), pulmonary arterial hypertension (PAH), preeclampsia, gestational hypertension, portal hypertension, nocturnal hypertension and white coat hypertension (4).

There are many factors that contribute to primary Hypertension, including genetics and the environment, immunological which are all intertwined (15).

Genetic predisposition perform a significant role in the pathophysiology of EH. Examining the degree of genetic similarity and blood pressure level family aggregation, researchers have estimated that the genetic contribution to twins and family members ranges from 30% to 60%.According to epidemiological studies up to 60 percent of population variability in blood pressure is due to hereditary or genetic factors, the remaining percent is due to the common household environment, and non-family factors (16).

Those who are predisposed to hypertension could benefit from specialised environmental changes if genetic markers for the condition are discovered early. Various physiological conditions namely aging, sedentary lifestyle, hormonal imbalance, increases the possibilities of elevated blood pressure. In consequence of heavy alcohol use, 15-20% of adults in developed countries struggle with hypertension. The precise aetiology of hypertension in essential hypertension is unknown. In secondary hypertension, it usually disappears once the conditions are cured or controlled. Some of the conditions include endocrine or kidney disorders, cocaine use, sleep apnoea, smoking, pregnancy, very exhausting exercise, stress and long-term misuse of alcohol. Hypertension is now understood to be a complex illness because of its polygenic inheritance and interaction with a number of environmental variables. Cardiovascular disease is more likely to affect those with essential hypertension. (3).

Intravascular volume regulates blood pressure by controlling cardiac output and peripheral resistance. However, any factors that may increase these two main factors will lead to an increase in BP. One of the main factors affecting the amount of extracellular fluid is sodium, termed an extracellular ion. Sodium balance is preserved at the expense of an increase in BP when arterial pressure rises in response to high NaCl consumption, urinary sodium excretion rises and sodium excretion rises to maintain BP. The majority of nonachloride sodium salts do not affect blood pressure. People who have poor sodium excretion may have it due to intrinsic renal illness or increased secretion of the hormone

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

mineralocorticoid, which causes greater renal tubular reabsorption of sodium and, eventually, have higher BP (17)

Pressure, volume, and chemoreceptor signals establish cardiovascular haemostasis. The short-term regulation of blood pressure can be influenced by androgenic reflexes, but for long-term management of blood pressure both androgenic functions, together with hormonal and volume-related parameters, is important. The vasoconstrictor effects of angiotensin II and the salt retention effects of aldosterone are the main mechanisms by which the Renin-Angiotensin System (RAS) controls arterial pressure. Angiotensin I can only be produced by the enzyme Renin (13,17)

Resistance artery compliance and vascular radius are also significant(17) factors in determining arterial pressure. Small arteries and arterioles may have a smaller lumen in hypertensive patients due to mechanical, structural, or functional changes (7)

Angiotensin-converting enzyme II (ACE II), a component of the RAS, has been shown to counteract the effect of an activated RAS, thereby shedding new light on the treatment of HTN. Angiotensin II by the action of ACE II converts into angiotensin-(1-7), which binds to the Mas receptor with high affinity and exerts antihypertrophic, antifibrosis, and vasodilation. In turn, Angiotensin II inhibits ACE II activity and induces detrimental cardiovascular effects. 67% of the phenotypic variance in circulating ACE II could be attributed to heritability. Thus, genetic variants of the ACE II gene may affect the occurrence and progression of cardiovascular diseases. Several investigations conducted on various racial and ethnic groups revealed that genetic variants of ACE2 are associated with essential hypertension, coronary heart disease, and other cardiovascular events. The relationship may be owing to the effect of ACE II genetic variants on RAAS hormone levels. (18)

Aldosterone influences intravascular volume, sodium balance, and BP. The aldosterone synthase enzyme (CYP11B2) is a critical enzyme for aldosterone biosynthesis in the adrenal cortex zonaglomerulosa. CYP11B2 gene encodes a P450 cytochrome enzyme included in the final stages of the synthesis of aldosterone, potassium, and angiotensin II to regulate CYP11B2 expression. The CYP11B2 gene has been found in several forms, the CYP11B2 gene is essential for the production of aldosterone, which is connected to the kidney's reabsorption of sodium ions and water, a process that raises blood pressure. (19)

Studies have highlighted the significance of both environmental and genetic variables in understanding the origins of hypertension. Age, chronic stress, sodium intake, and obesity have been suggested as environmental causes of HTN. In addition, recent epidemiological and environmental studies have established a link between particulate matter (PM) and BP. Individual differences in susceptibility to the effects of pollution in the air on BP may be attributable to inherited differences. To explain how biological mechanisms influence BP characteristics, research on gene-environment interaction is essential. Recent epidemiological evidence suggests that both obesity and air pollution

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

contribute to HTN. Calcium–dependent cell adhesion protein, cadherin which is encoded by the CDH13 gene. Cadherin protein is expressed in various tissues, such as lung, vascular endothelial cells, brain, and smooth muscle cells, but predominantly in arteries in blood vessels. Effects of the influence of PM10 exposure and SNPs on the CDH13 gene on BP-related phenotypes in adult Korean men were investigated. (20)

Study the immunological factors that are associated with the illness and may be the factors of cardiac diseases and their association with BP. Knowing the mechanism of disease to BP. Synthesizing new treatment techniques to be studied for novel genes related to high BP. Additionally, mononuclear phagocyte cells of the first order create the inflammatory catalyst tumour necrosis factor (TNF). TNF-a stimulates the blood vessel lining to release vasoactive chemicals in the blood vessels through a paracrine or autocrine pattern. This results in vasoconstriction, or the contraction of blood vessels, which controls blood pressure. (5).

The final byproduct of purine catabolism is uric acid, which is associated with HTN, although the causality of this association is debatable. According to some specialists, the serum concentration of uric acid is frequently elevated in other conditions other than HTN, such as metabolic syndrome and obesity. Numerous studies have proposed plausible mechanisms by which increased BP and the onset of hypertension may be directly connected to uric acid (21)

Human Vitamin D is regulated by vitamin D Receptor (VDR), is encoded by one gene at 12q12-14 on chromosome 12. This protein mediates 1,25(OH)2D3's pleiotropic actions by influencing gene expression. 1,25(OH)2D3. Vitamin D is a negative RAS hormone, that decreases renin mRNA expression regardless of calcium metabolism, which is crucial for bone health. Since the biological actions of vitamin D are regulated by VDR. The presence of SNPs can affect arterial BP and cause HTN. Most of the cells in the human body have VDR and control 3% of human genes by activating target gene transcription. Thus, vitamin D's role in non-skeletal disorders such as diabetes mellitus, hypertension, autoimmune disease, and CVD has garnered attention. (22).

The genotype distribution of the Fok1 polymorphism in the VDR gene and EH were examined concerning vitamin D insufficiency. Vitamin D insufficiency was much more common in hypertensive people compared to control populations of the same age and gender. The researchers concluded that the prevalence of the recessive "ff" genotype is associated with lower serum vitamin D levels and causes noticeably higher systolic and diastolic blood pressure, which raises the risk of EH (19)

The class B scavenger receptor family includes a transmembrane glycoprotein with the name CD36. It is expressed in a variety of additional cell types in addition to monocytes and macrophages, including adipocytes, endothelial cells, and platelets. This receptor is linked to several different ligands and functions in a number of biological processes. Recent studies have revealed a connection between obesity and gene polymorphism on the CD36 gene on one hand, and obesity, hypertension, and CVDs on the other hand.

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

The CD36 gene, which is 32 kb in size and includes 15 exons, is found on chromosome 7 (q11.2). The SNP rs1761667 (G > A) is located in the exon 1A 5' flanking intron. The CD36 receptor, which has a high affinity for long-chain fatty acids (FAs), affects lipid metabolism. The A allele of rs1761667 lowers CD36 expression and reduces oral fat sensitivity, both of which are associated with higher recognition taste thresholds for fat. This lipid metabolism-related receptor has a high affinity for LCFAs. It is believed that CD36 polymorphisms enhance a person's chance of developing HTN or CAD because CD36 affects lipid metabolism, BP, and atherosclerosis (23)

In castrated rats, the Ephb6 gene deletion results in hypertension. In a testosterone-dependent way, EPHB6 controls catecholamine release by chromaffin cells of the adrenal gland (AGCCs). The first signaling process that results in catecholamine release by AGCCs is the activation of the ligand-gated Ca2+/Na+ channel known as Nicotinic acetylcholine receptor (nAChR). Due to the possibility that nAChR participates in EPHB6 signalling, sequence variations of the genes that make up this protein are linked to an increased risk of developing hypertension. In both human and rodent AGCCs, Nicotinic Acetylcholine Receptor Alpha 3 (CHRNA3) predominates as a nAChR component. CHRNA3 SNPs were not shown to be significantly associated with the risk of HTN in a number of GWAS(24).

Endothelin cells which are responsible for creating an endothelin material, it was first isolated from the supernatant of swine aortic endothelial culture and had considerable vasoconstrictive peptide activity. The endothelium distributes three separate genes that produce three isoforms of endothelin (ET-1, ET-2, and ET-3) and 21 amino acid peptides. Endothelin-1 (ET-1) is the most frequent and active endothelin isoform in the human cardiovascular system. It is now recognized that it is crucial in regulating local blood flow, cell proliferation, acid-base balance, and vascular tone. (25)

Obesity has immunogenetic traits, such as chronic inflammatory processes, that are linked to a certain genetic background. The specific genetic variations include polymorphism of the PPAR-2 gene (rs1801282, Pro12Ala, and rs3856806, C1431T), the -adrenergic receptor gene (3-AR; Trp64Arg, rs4994), and the Family With Sequence Similarity 13 Member A gene (FAM13A; rs7671167, rs1903003, rs2869967). According to this research, the cohabitation of PPAR-2 C1413C polymorphism and FAM13A variations determines how much and where body fat is distributed(26,27)

Urotensin II (UTS2 or UII) is a peptide that was initially discovered and studied in fish, and its gene, 1p36-p32, codes for it. UTS2 was found to have a vasoconstrictor effect in mammals in the endothelium-depleted rat thoracic aorta. This vasoconstrictor effect increased smooth muscle cell proliferation and vascular tone in vitro, revealing that this peptide may play a pathogenic role in EH. UTS2 is a potent vasoconstrictor in the arteries and veins of humans.10–12 Patients with EH have elevated levels of UTS2, a marker of arterial pressure.(28,29)

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

CD36 is considered as a scavenger receptor and member of the B family of scavenger receptors, binds oxidised low-density lipoprotein (ox-LDL) with high affinity. CD36 essential for the development of atherosclerosis (AS), according to research. It has been established that CD36 expression is markedly elevated in CHD patients and that this may, to some extent, indicate coronary artery AS severity. So far, 1372 SNPs have been identified within the human CD36 gene. Some SNPs, including rs3173798, rs3211892, and rs5956 have been linked to CHD, but the results are debatable. There are additional SNPs (such as rs1049673, rs1761667, and rs1527483), associated with HTN, T2DM and the metabolic syndrome (MetS), but do not have a direct association with coronary heart disease (CHD). The preponderance of these observations were also recorded in European communities. As a result, our study selected two SNPs, rs1761667 in the 59-flanking exon 1A region and in the intron 3 region (rs 317398), as candidate SNPs to evaluate the genetic and functional effects of CD36 gene polymorphisms on the development of CHD in the Chongqing Han population in China. 1372 single-nucleotide polymorphisms (SNPs) have thus far been identified within the human CD36 locus. Some SNPs, including rs3211892 rs3173798, and rs5956, have been linked to CHD, but the results are debatable. Other SNPs, such as rs1527483, rs1761667, rs3211931, and rs1049673, have been linked to metabolic syndrome or T2DM, although they are not directly associated with CHD. The preponderance of these observations were also recorded in European populations. As a result, our study selected two SNPs, rs1761667 in the 59 flanking exon 1A region and rs3173798 in the intron 3 region, as candidate SNPs to evaluate the genetic and functional effects of CD36 gene polymorphisms on CHD development in the Chongqing Han population of China. Recent research conducted in southeast Iranian population has revealed the association between CD36 gene polymorphisms (rs 1761667) with hypertension, and cardiovascular diseases (CVDs). The multifunctional CD36 scavenger receptor, an 88 kDa, 471 amino acid glycosylated membrane protein, was initially discovered in platelet membrane. A number of cell types express CD36, including adipocytes, hepatocytes, myocytes, macrophages, monocytes, macrophages, intestinal enterocytes and, vascular endothelial cells. According to the receptor's topology, an extracellular domain will consist of one hydrophobic sequence that may coil back into the membrane and two brief cytoplasmic sequences. Several recent papers have examined the role of the CD36 in encourage the uptake and oxidation of (FA) in humans and rodents, as well as its involvement in the pathophysiological mechanisms associated with dysfunctional FA metabolism. CD36 functions as a receptor and signalling molecule for a broad spectrum of ligands, binds to lipoproteins to facilitate the uptake and oxidation of high/low -density lipoprotein, cholesterol and the uptake of cholesteryl ester. CD36 may have an influence on a variety of obesity-related dysmetabolic diseases, including dyslipidaemia, DM, IR, AS, inflammation, and cancer, due to its multiple ligands and functions. In mammals, CD36 plays a crucial role in the orosensory perception of dietary lipids. In the buccal cavity, long-chain FA appear to be primarily responsible for dietary fat taste perception. Also, CD36 has been shown to influence the FA perception and involve in the initial steps of the cephalic phase in circumvallate papillae taste bud cells. In obese mice induced by a high-fat diet, in

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

circumvallate papillae the expression of CD36 has been observed to be significantly diminished. This demonstrated that decreased CD36 expression decreases taste sensitivity, leading to an increase in rich food consumption as a coping mechanism. Absolute deficiency, on the other hand, appears to reduce fat consumption due to delayed absorption. In human gustatory papillae, CD36 has been identify as a factor the primary long-chain FA receptor in taste bud cells and a factor in the fat preference by influences the orosensory perception of dietary lipid. Obese patients have been shown to prefer and consume more fatty foods, which may be indicative of a lowering in both oral and gastrointestinal FA sensitivity. The CD36 gene polymorphisms rs3840546, rs1761667, and rs1527483 are associated with taste perception, fat preference, and obesity. According to a number of studies, the polymorphism rs1761667 influences expression levels of CD36, which may make it possible to explain differences in the orosensory perception of lipids. flavour sensitivity for the acrid flavour of 6-n-propylthiouracil (PROP), considered a general oral marker for chemosensory perception, food preference, and BMI, influences lipid metabolism in individuals of normal weight (NW) and obesity (OB). Unusually, we discovered that those with exceptionally high PROP sensitivity, also known as super-testers, had higher BMIs and lower plasmatic endocannabinoid levels than those with lower PROP sensitivity (nontasters). OB super-tasters had lower levels of circulating retinol and non-esterified fatty acids (NEFA) than OB non-tasters, indicating a more favourable body fat distribution and lipid metabolism. Circulating levels of endocannabinoids are significantly associated with visceral obesity, ectopic fat deposition and inefficient mitochondrial function. Due to the important effect of the CD36 polymorphism rs1761667 on cellular lipid metabolism and preference for macronutrients in humans, we wanted to ascertain if it had an effect on fatty acid metabolism and endocannabinoid production in NW and OB participants (30–32)

A comprehensive medical history and physical examination of a patient with hypertension should confirm a diagnosis, screening for the secondary causes of HTN, identify cardiovascular consequences of HTN and other comorbidities, evaluate BP -related lifestyles, and determine the potential for intervention. Hypertension seldom causes symptoms. Headache is often associated with high blood pressure, although occurs only in severe hypertensives. A morning "hypertensive headache" is occipital. High blood pressure can also cause dizziness, palpitations, fatigue, and impotence. Hypertensive cardiovascular disease or secondary hypertension usually cause symptoms.

Attention to method and circumstances ensures accurate blood pressure readings. Observer training, patient placement, and cuff size are crucial. Most clinical measurements are conducted with aneroid sphygmomanometers or oscillometers due to mercury constraints. Periodically calibrate and verify these instruments. Before taking blood pressure, the patient should sit peacefully in a chair with their feet on the ground and must measure twice. JNC 7 advocates keeping an eye on patients for symptoms of symptomatic hypotension, episodic hypertension, and treatment resistance. On the floor for five minutes in a quiet, comfortable environment measuring of blood pressure should

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

be taken The first of at least two regular "tapping" Korotkoff noises is heard during the systole, and the last regular sound is heard during the diastole.(*7*)

DISCUSSION

A significant global risk factor for cardiovascular disease morbidity and death is essential hypertension. It is a specific kind of complex illness with hereditary and environmental roots. Even while some active measures have been taken to lessen the effects of hypertension, a sizeable percentage of individuals are still unable to attain the required blood pressure management. In order to improve the management and control of the condition, a unique treatment approach, hereditary variables, and precision medicine should be taken into consideration(18).

EH is a complex illness with interplaying genetic and environmental risk factors. Patients with EH often don't exhibit any symptoms, however, they occasionally deal with recurrent headaches, exhaustion, vertigo, or nosebleeds. Hypertension is considered a risk factor for CVD, stroke, and kidney disease. Additionally, a favorable family history, a sedentary lifestyle, and obesity are the main risk factors for EH. The identification of genetic variations throughout the entire genome that is prone to EH has started in several research. Researchers have discovered many EH risk loci utilizing a variety of methods and populations. The precise genetic origins of prevalent complex disorders are still poorly understood.

It's critical to take into account that gene variants that contribute to hypertension typically result in a slight increase in risk and are controlled by a variety of socioeconomic variables, eating patterns, and interactions with other genes. No one mutation in genes can fully explain how the problem manifests since hypertension is a complicated ailment that is impacted by both genetic and environmental variables.

Due to the combination of hereditary and environmental risk factors, essential hypertension is a complicated illness with sociodemographic variables playing a substantial role in its development. This has been shown in several epidemiological research. Finding the underlying molecular causes of EH and the genetic risk factors connected with it may open the door to more clinical treatment interventions and research into the disease's prevention. To understand the intricate pathophysiology of EH, researchers must pinpoint the susceptibility genes involved.

SUMARY OF THE STUDIES

Najafi and Mahdavi,2023	study conducted that according to the findings, COVID-19 symptoms may be more prevalent in ACE D/D homozygote individuals. In order to provide a population-based therapeutic development, ACE I/D SNP may be a biomarker that may be utilised to determine the severity of COVID-19 and may influence how it is treated. The severity of the illness was unaffected by the ACE2 rs2285666 mutation. (34)
(22)	Vitamin D insufficiency increases plasma renin activity, angiotensin II concentrations, and RAAS activity, which can be reduced by vitamin D3

ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

	treatment. These data suggest that vitamin D treatment may reduce RAAS activity and improve RAAS-related comorbidities such as HTN, IR, and nephropathy
Loscalzo et al., 2022	mentioned that It's a huge public health concern that affects people from all walks of life because it doubles the risk of CVD such coronary heart disease (CHD), ischemic stroke, haemorrhagic stroke, congestive heart failure (CHF), kidney failure, and peripheral arterial disease (PVD).
Ian Penman, Stuart Ralston, Mark Strachan, 2022	Intravascular volume regulates blood pressure via cardiac output and peripheral resistance. Sodium increases blood pressure. Sodium balance needs high arterial pressure, urinary sodium excretion, and BP management. Renal disease or mineralocorticoid secretion can reduce sodium excretion, raising blood pressure.
Melis et al.,2017; Toure et al.,2022	SNPs (such as rs1049673,rs1761667, and rs1527483),associated with HTN ,T2DM and the metabolic syndrome (MetS), but do not have a direct association with coronary heart disease (CHD). (31,32).
Touré *et al.*, 2022)	the important effect of the CD36 polymorphism rs1761667 on cellular lipid metabolism and preference for macronutrients in humans, we wanted to ascertain if it had an effect on fatty acid metabolism and endocannabinoid production in NW and OB participants
Preethi et al., 2022	Anti-miRNA drug development for the treatment of hypertension may enhance patients' therapeutic results (4).
Rajarajeswari and Ramalingam, 2022	Gene variations on CYP11B2 have been observed to influence Aldosterone, which is linked to Essential Hypertension (EHT).C-344T, CYP11B2,and IC polymorphisms that cause vulnerability to EHT and haplotype H1 (-344T-Conv-Lys173) as contributing component for predistortion of HTN were found to work together synergistically in the research. (19)
(Salim *et al.*, 2022).	The ET-1 gene also accelerated the etiology of a number of diseases, including arteriosclerosis, ischemic heart disease, diabetes and hypertension
Saxena et al.,2022	The severity of hypertension and vitamin D insufficiency were shown to have a strong inverse connection. This link may aid in the stage of hypertension, allowing for the use of early treatment interventions according to study conducted Utter Pradesh, north India(10).
Melton and Qiu, 2021	The CD36 gene polymorphisms rs3840546, rs1761667, and rs1527483 are associated with taste perception, fat preference, and obesity. Through inflammatory or genetic means, downregulation of this ACTN4-HLA-DPA1 regulatory axis promotes endothelial pathophenotypes, providing a mechanistic explanation for the association between this SNP and PAH outcomes.
Eweida et al.,2021	TaqI&BsmIVit D receptor gene polymorphisms increase the incidence of HTN & CVD
Van Oort et al.,2020	High-Density Lipoprotein Cholesterol (HDL), Body Max Index(BMI), Triglycerides(Tg), sleeplessness, drunkenness, and degree of education were all found to be risk factors for hypertension in this Mendelian randomization research. This implies that these changeable risk variables are essential targets for preventing hypertension as shown by the study conducted by(35).
Debiec et al., 2013; Xie et al.,2020	Examine the relationship between UTS2 and EH in northwest Chinese communities. (28,29)
Devaux, Rolain and Raoult,2020	The combined presence of the ACE I/D along with ACE2 G8790A polymorphisms in Brazilian subjects reveals HT susceptibility. ACE polymorphisms can modulate the RAAS pathway as well. Among African Americans with hypertension, an ACE polymorphism has been identified.

ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

Murshchak et al.,2019	research reveals that individuals with COPD may be more at risk for AH if the T allele of the AGT gene is present in the peptide chain at position 235 , both in heterozygous and homozygous situations. (36),
Momeni-Moghaddam *et al.*, 2019).	The polymorphisms of this gene, such as rs10499859, rs1761667, rs3173798, and rs1049673, have also been linked to lipid metabolism, type 2 diabetes mellitus (T2DM), cardiovascular risk, insulin resistance, body mass index (BMI), essential hypertension.). It is believed that CD36's role in regulating lipid metabolism, blood pressure and atherosclerosis confers susceptibility to CAD and/or hypertension
(Abdel Ghafar,219)	There was a substantial correlation between the polymorphism on CYP11B2 (344C/T) and the 344T allele and EH in the population of Egypt. Additionally, it was demonstrated that the CYP11B2 344C/T polymorphism and 344T allele may be associated with a predisposition to cardiovascular issues and hypertensive left ventricular hypertrophy
(Al-Awsi, Al-Garawi and Abdulhussein, 2019)	This study showed a significant association between genetic diversity G308 - of TNF and the prevalence of high blood pressure disorder
(Zhang *et al.*, 2019)	SNPs, rs1761667 in the 59 flanking exon 1A region and rs3173798 in the intron 3 region, as candidate SNPs to evaluate the genetic and functional effects of CD36 gene polymorphisms on CHD development in the Chongqing Han population of China
Cuevas, Villar, and Jose, 2019	Preventing and treating blood pressure, the major cause of cardiovascular disease (CVD) and renal failure, is difficult. Noncompliance and genetic differences may contribute to hypertension treatment inefficacy and inter-individual variance in responsiveness to antihypertensive medicines.
Prenissl et al., 2019	In India, hypertension is common, yet few individuals are diagnosed, treated, and controlled. Even after allowing for economic growth, state hypertension management health systems vary widely. Men, rural residents, and low-income people need better hypertension diagnosis and treatment(37)
Prenissl *et al.*, 2019)	In India, hypertension is common, yet few individuals are diagnosed, treated, and controlled. Even after allowing for economic growth, state hypertension management health systems vary widely. Men, rural residents, and low-income people need better hypertension diagnosis and treatment.
Luo et al.,2019	EH and the ACE2 variation rs2074192 were linked in south Chania (9)
(Ghosh and Kumar, 2019)	Hypertension prevalence among the population aged 15-49 years and associated risk factors in India. The prevalence of hypertension is becoming increasingly concentrated among those who live in poverty are more likely to have hypertension than other people. The intake of alcohol, high-calorie meals, dangerous working conditions, and rising societal demands to survive are examples of "lifestyle" changes that are risk factors that should be addressed by legislation that required to be taken to decrease the prevalence of hypertension in India.
(Kim *et al.*, 2019)	The CDH13 intronic SNP rs7500599 showed the greatest signals for BP characteristics or HTN when interacting with PM10. Additional research is required to fathom the pathogenesis of hypertension in this patient population in terms of gene-environment interactions
Kokubo et al.,2019	HTN called the "silent killer" because it doesn't show signs early on, but ignoring it can increase the risk of numerous significant health conditions. Hypertension causes heart disease, stroke, kidney damage, and organ damage, which increases mortality and morbidity.(15)

ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

Parchwani et al., 2018	The A/C transversion of the angiotensin II type 1 receptor (AT1R) gene at position 1166 has been linked to AT1R expression, even though it does not in and of itself indicate functional diversity. As a result, molecular variants of the gene may influence the potential risk of essential hypertension. Genetic variation at the AT1R locus affects the stratification of hypertension risk and may be a predictor of hypertension susceptibility in affected. (39)
(Parchwani et al., 2018)	The AT1R gene's A/C transversion at position 1166 may influence essential hypertension risk, potentially affecting risk stratification and predicting susceptibility in affected families.
(Carey *et al.*, 2018)	AHA and ACC in November 2017 created the most important recommendations are outlined regarding to classification of hypertension
Mannan et al.,2017	Among North Indian population, This study shows that people with the ACE DD 1 gene polymorphism are more likely to experience high blood pressure(3).
Vamsi *et al.*, 2016	Aldosterone, a hormone, affects intravascular volume, sodium balance, and blood pressure. The CYP11B2 gene, encoded by the adrenal cortex zonaglomerulosa, regulates CYP11B2 expression and is essential for aldosterone production. Variations in CYP11B2 have been linked to Essential Hypertension (EHT), with CYP11B2, C-344T, and IC polymorphisms contributing to EHT vulnerability and haplotype H1 as a risk factor for hypertension predisposition
(Scheepersa et al., 2016).	The SNPs rs11904439, rs2043013, and rs148756340 at the Xanthine Oxidoreductase (XOR) gene have been linked to an escalation in BP over time and/or an elevated risk of HTN
Krishnan *et al.*, 2016	Study conducted in the south Indian population, has demonstrated an association between essential hypertension and the I/D polymorphism in the ACE gene.

References

1) WHO. Hypertension. Hypertension https://www.who.int/news-room/fact-sheets/detail/hypertension Accessed: 2023-05-14. 2023.

2) AHA. Understanding Blood Pressure Readings What do your blood pressure numbers mean ? [Internet]. Aha. 2021 [cited 2023 May 14]. p. 2–4. Available from: https://www.heart.org/en/health-topics/high-blood-pressure/understanding-blood-pressure-readings

3) Mannan MA, Dhial S, Lall S, Singh J, Upadhyay AK. Hypertension and Genetic Polymorphism of Ace and Add1 Gene in North Indian Population. PONTE Int Sci Res J. 2017;73(7).

4) Preethi KA, Selvakumar SC, Ross K, Sekar D. Therapeutic aspect of microRNA inhibition in various types of hypertension and hypertensive complications. Gene Reports. 2022 Dec 1;29:101676.

5) Al-Awsi GRL, Al-Garawi EDC, Abdulhussein HH. Investigation of tumor necrosis factor-alpha (TNF-A) gene polymorphism in patients with hypertension in Al-Diwaniyah City, Iraq. J Glob Pharma Technol. 2019;11(2):144–8.

6) WHO. India Hypertension Control Initiative, a high impact and low-cost solution [Internet]. World Health Organisation. 2022 [cited 2023 May 13]. Available from: https://www.who.int/india/news/detail/02-06-2022-india-hypertension-control-initiative--a-high-impact-and-low-cost-solution

ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

7) Carey RM, Whelton PK, Aronow WS, Casey DE, Collins KJ, Himmelfarb CD, et al. Prevention, Detection, Evaluation, and Management of High Blood Pressure in Adults: Synopsis of the 2017 American College of Cardiology/American Heart Association Hypertension Guideline. Ann Intern Med [Internet]. 2018 Mar 6 [cited 2023 May 14];168(5):351–8. Available from: https://pubmed.ncbi.nlm.nih.gov/29357392/

8) Cuevas S, Villar VAM, Jose PA. Genetic polymorphisms associated with reactive oxygen species and blood pressure regulation. Pharmacogenomics J 2019 194 [Internet]. 2019 Feb 6 [cited 2023 May 28];19(4):315–36. Available from: https://www.nature.com/articles/s41397-019-0082-4

9) Longo, Fauci, Kasper, Hauser, Jameson L. HARRISON'S PRINCIPLES OF INTERNAL MEDICINE. 2021.

10) Saxena RR, Verma S, Gadpayle AK, Nandkeoliar MK, Al-azazi TAAA. Estimation Of Serum Calcium & Vitamin D Levels In Hypertension Patients And Its Correlation With Staging Of Disease. 2022;13(10):4576–82.

11) Luo Y, Liu C, Guan T, Li Y, Lai Y, Li F, et al. Association of ACE2 genetic polymorphisms with hypertension-related target organ damages in south Xinjiang. Hypertens Res [Internet]. 2019;42(5):681–9. Available from: http://dx.doi.org/10.1038/s41440-018-0166-6

12) Melton E, Qiu H. Interleukin-1β in Multifactorial Hypertension: Inflammation, Vascular Smooth Muscle Cell and Extracellular Matrix Remodeling, and Non-Coding RNA Regulation. Int J Mol Sci [Internet]. 2021 Aug 2 [cited 2023 May 12];22(16). Available from: https://pubmed.ncbi.nlm.nih.gov/34445357/

13) Loscalzo J, Fauci AS, Kasper DL, Hauser SL, Longo DL (Dan L, Jameson JL, et al. Harrison's principles of internal medicine. 2022;235.

14) Setters B, Holmes HM. Hypertension in the Older Adult. Prim Care [Internet]. 2017 Sep 1 [cited 2023 May 13];44(3):529. Available from: /pmc/articles/PMC5776734/

15) Kokubo Y, Padmanabhan S, Iwashima Y, Yamagishi K, Goto A. Gene and environmental interactions according to the components of lifestyle modifications in hypertension guidelines. Environ Health Prev Med [Internet]. 2019 Mar 11 [cited 2023 May 12];24(1):1–11. Available from: https://environhealthprevmed.biomedcentral.com/articles/10.1186/s12199-019-0771-2

16) Krishnan R, Sekar D, karunanithy S, Subramanium S. Association of angiotensin converting enzyme gene insertion/deletion polymorphism with essential hypertension in south Indian population. Genes Dis [Internet]. 2016;3(2):159–63. Available from: http://dx.doi.org/10.1016/j.gendis.2016.03.001

17) Ian Penman, Stuart Ralston, Mark Strachan RH. Davidson's Principles and Practice of Medicine. 2022.

18) Fan Z, Wu G, Yue M, Ye J, Chen Y, Xu B, et al. Hypertension and hypertensive left ventricular hypertrophy are associated with ACE2 genetic polymorphism. Life Sci [Internet]. 2019;225:39–45. Available from: https://doi.org/10.1016/j.lfs.2019.03.059

19) Rajarajeswari MPD, Ramalingam PAK. Status of Vitamin D Receptor Gene Polymorphism and 25-Hydroxy Vitamin D Deficiency with Essential Hypertension. Indian J Clin Biochem [Internet]. 2022;37(3):335–41. Available from: https://doi.org/10.1007/s12291-021-00984-z

20) Kim HJ, Seo YS, Sung J, Son HY, Yun JM, Kwon H, et al. Interactions of CDH13 gene polymorphisms and ambient PM10 air pollution exposure with blood pressure and hypertension in Korean men. Chemosphere [Internet]. 2019;218:292–8. Available from: https://doi.org/10.1016/j.chemosphere.2018.11.125

ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

21) Scheepers LEJM, Wei FF, Stolarz-Skrzypek K, Malyutina S, Tikhonoff V, Thijs L, et al. Xanthine oxidase gene variants and their association with blood pressure and incident hypertension: a population study. J Hypertens [Internet]. 2016 [cited 2023 May 26];34(11):2147–54. Available from: https://cris.maastrichtuniversity.nl/en/publications/xanthine-oxidase-gene-variants-and-their-association-with-blood-p

22) Awasthi R, Manger PT, Khare RK. Fok I and Bsm I gene polymorphism of vitamin D receptor and essential hypertension: a mechanistic link. Clin Hypertens. 2023;29(1):1–12.

23) Momeni-Moghaddam MA, Asadikaram G, Akbari H, Abolhassani M, Masoumi M, Nadimy Z, et al. CD36 gene polymorphism rs1761667 (G > A) is associated with hypertension and coronary artery disease in an Iranian population. BMC Cardiovasc Disord. 2019;19(1):1–10.

24) Wu T, Wang Y, Shi W, Zhang BQ, Raelson J, Yao YM, et al. A Variant in the Nicotinic Acetylcholine Receptor Alpha 3 Subunit Gene Is Associated With Hypertension Risks in Hypogonadic Patients. Front Genet [Internet]. 2020 Nov 27 [cited 2023 May 29];11. Available from: https://pubmed.ncbi.nlm.nih.gov/33329690/

25) Salim E, Ramachandran V, Ansari N, Ismail P, Mohamed MH, Mohamad NA, et al. Association of Endothelin-Converting Enzyme and Endothelin-1 Gene Polymorphisms with Essential Hypertension in Malay Ethnics. Genet Res (Camb). 2022;2022.

26) Grygiel-Górniak B, Ziółkowska-Suchanek I, Szymkowiak L, Rozwadowska N, Kaczmarek E. The Influence of FAM13A and PPAR-γ2 Gene Polymorphisms on the Metabolic State of Postmenopausal Women. Genes 2023, Vol 14, Page 914 [Internet]. 2023 Apr 14 [cited 2023 May 30];14(4):914. Available from: https://www.mdpi.com/2073-4425/14/4/914/htm

27) Marushchak M, Maksiv K, Krynytska I, Kozak K. Association between arterial hypertension and chronic obstructive pulmonary disease: Role of AGT gene polymorphism. Pneumologia. 2019 Dec 1;68(4):174–82.

28) Xie H, Wang X, He Y, Huang D, Qu X, Jiang Y, et al. Association between Plasma Urotensin II and Risk of Hypertension: Findings from a Prospective Study. Int J Hypertens. 2020;2020.

29) Debiec R, Christofidou P, Denniff M, Bloomer LD, Bogdanski P, Wojnar L, et al. Urotensin-II system in genetic control of blood pressure and renal function. PLoS One. 2013;8(12):6–13.

30) Zhang Y, Ling ZY, Deng SB, Du HA, Yin YH, Yuan J, et al. Associations between CD36 gene polymorphisms and susceptibility to coronary artery heart disease. Brazilian J Med Biol Res. 2019;47(10):895–903.

31) Touré M, Hichami A, Sayed A, Suliman M, Samb A, Khan NA. Association between polymorphisms and hypermethylation of CD36 gene in obese and obese diabetic Senegalese females. Diabetol Metab Syndr [Internet]. 2022;14(1):1–16. Available from: https://doi.org/10.1186/s13098-022-00881-2

32) Melis M, Carta G, Pintus S, Pintus P, Piras CA, Murru E, et al. Polymorphism rs1761667 in the CD36 gene is associated to changes in fatty acid metabolism and circulating endocannabinoid levels distinctively in normal weight and obese subjects. Front Physiol. 2017;8(DEC):1–9.

33) Longo, Fauci, Kasper, Hauser, Jameson L. Harrison's Principles of Internal Medicine, 18th Edition. 2011. 2042–2056 p.

34) Najafi M, Mahdavi MR. Association investigations between ACE1 and ACE2 polymorphisms and severity of COVID-19 disease. Mol Genet Genomics [Internet]. 2023;298(1):27–36. Available from: https://doi.org/10.1007/s00438-022-01953-8

Xi'an Shiyou Daxue Xuebao (Ziran Kexue Ban)/
Journal of Xi'an Shiyou University, Natural Sciences Edition
ISSN: 1673-064X
E-Publication: Online Open Access
Vol: 67 Issue 03 | 2024
DOI: 10.5281/zenodo.10876985

35) Van Oort S, Beulens JWJ, Van Ballegooijen AJ, Grobbee DE, Larsson SC. Association of Cardiovascular Risk Factors and Lifestyle Behaviors with Hypertension: A Mendelian Randomization Study. Hypertension [Internet]. 2020 [cited 2023 May 14];1971–9. Available from: https://www.ahajournals.org/doi/suppl/10.1161/HYPERTENSIONAHA.120.15761.

36) Marushchak M, Maksiv K, Krynytska I, Kozak K. Association between arterial hypertension and chronic obstructive pulmonary disease: Role of AGT gene polymorphism. Pneumologia. 2019;68(4):174–82.

37) Prenissl J, Manne-Goehler J, Jaacks LM, Prabhakaran D, Awasthi A, Bischops AC, et al. Hypertension screening, awareness, treatment, and control in India: A nationally representative cross-sectional study among individuals aged 15 to 49 years. PLOS Med [Internet]. 2019 May 1 [cited 2023 May 18];16(5):e1002801. Available from: https://journals.plos.org/plosmedicine/article?id=10.1371/journal.pmed.1002801

38) Ghosh S, Kumar M. Prevalence and associated risk factors of hypertension among persons aged 15-49 in India: a cross-sectional study. BMJ Open [Internet]. 2019 Dec 16 [cited 2023 May 18];9(12). Available from: https://pubmed.ncbi.nlm.nih.gov/31848161/

39) Parchwani DN, Patel DD, Rawtani J, Yadav D. Analysis of Association of Angiotensin II Type 1 Receptor Gene A1166C Gene Polymorphism with Essential Hypertension. Indian J Clin Biochem. 2018;33(1):53–60.