Journal of Population Therapeutics & Clinical Pharmacology

RESEARCH ARTICLE
DOI: 10.53555/jptcp.v29i03.3236

ROLE OF BMI AND GENETIC STUDY ON MATERNAL AGE OF MOTHERS

Dr. Shradha Suman Ghanto[1]*, Dr. Pawan Mahato[2]

[1]*Research Scholar, Malwanchal University, Indore
[2]Professor, Malwanchal University, Indore

***Corresponding Author:** - Dr. Shradha suman Ghanto
*Research Scholar, Malwanchal University, Indore

Abstract
Pregnancy outcomes are influenced by a complex interplay of factors, including maternal age, body mass index (BMI), and genetic predispositions. This study delves into the intricate relationship between these variables, aiming to unravel their impact on maternal-fetal health. This research explores how maternal age, BMI, and genetic factors intersect to influence pregnancy outcomes. The study investigates genetic markers associated with fertility, maternal age, and BMI-related traits. By understanding these relationships, the study aims to pave the way for personalized healthcare interventions. A prospective cohort study design was employed, involving pregnant women from diverse age groups and BMI categories. Anthropometric measurements were recorded, genetic analyses were conducted through advanced sequencing techniques, and detailed clinical data were collected. The study focused on identifying specific genetic markers associated with maternal age, BMI, and their combined impact on pregnancy complications. This study highlights the significance of considering maternal age, BMI, and genetic factors in prenatal care. Integrating genetic insights with BMI data allows for targeted interventions, enabling personalized healthcare approaches. By understanding the unique challenges faced by mothers of different ages and BMI categories, healthcare providers can tailor interventions, ultimately improving maternal and neonatal outcomes.

Keywords: Maternal age, Body mass index, Genetic study, Pregnancy outcomes, Personalized healthcare, Fertility, Maternal-fetal health.

INTRODUCTION

Pregnancy and childbirth are intricate biological processes influenced by a myriad of factors, including maternal age and body mass index (BMI). Maternal age at conception and maternal BMI have both been identified as significant determinants of pregnancy outcomes, maternal health, and the health of the newborn. Moreover, recent advancements in genetics have enabled researchers to explore the interplay between genetic factors and maternal age, shedding light on the complex relationship between genetics, maternal age, and various health outcomes in both mothers and infants.

1. Maternal Age and Pregnancy Outcomes: Maternal age is a critical factor that affects fertility, pregnancy complications, and the health of both the mother and the child. Advanced maternal age (usually considered over 35 years) is associated with a higher risk of chromosomal abnormalities, such as Down syndrome, as well as gestational diabetes and preeclampsia. Conversely, teenage pregnancies also present unique challenges, including increased risks of preterm birth and low birth

weight. Understanding the genetic underpinnings of these age-related risks is vital for personalized healthcare approaches.

2. BMI and Pregnancy Complications: Maternal BMI plays a pivotal role in pregnancy outcomes. Both underweight and obese mothers face elevated risks of complications. Obesity, in particular, is associated with gestational diabetes, hypertension, and larger birth weights, increasing the likelihood of cesarean section deliveries. Underweight mothers may experience challenges related to fetal growth and preterm birth. Genetic predispositions related to metabolism and body composition further complicate the relationship between BMI and pregnancy outcomes.
3. The Role of Genetics: Genetic studies have uncovered various susceptibility genes related to fertility, age at menopause, and metabolic health. Understanding the genetic basis of maternal age and BMI can provide essential insights into the biological mechanisms underlying fertility, maternal health, and fetal development. Genetic research helps identify individuals at higher risk of certain complications, allowing for targeted interventions and personalized healthcare strategies.
4. Importance of the Study: This study aims to explore the intricate connections between maternal age, BMI, and genetics, focusing on their combined impact on pregnancy outcomes. By deciphering the genetic factors contributing to age-related fertility decline and BMI-associated complications, healthcare providers can offer tailored guidance, early interventions, and potentially preconception genetic counseling. This knowledge is essential for empowering women to make informed decisions about family planning and prenatal care, ultimately enhancing the health and well-being of both mothers and their children.

LITERATURE REVIEW

Liyana Pathirana, Athula et.al (2021) The primary cause of mortality in hospitals in Sri Lanka is coronary heart disease (CHD). Tobacco use, poor nutrition, excessive alcohol use, a sedentary lifestyle, and a lack of physical exercise are all major contributors, as are disorders like high blood pressure, diabetes, obesity, and dyslipidemia. The purpose of this research was to identify CHD risk factors and the prevalence of CHD among adults in the Gampaha District of Sri Lanka. Methods: A community-based cross-sectional research was done among 1192 adults (30-64) in the Gampaha area using cluster sampling to ensure representativeness. The prevalence of coronary heart disease, high blood sugar, diabetes mellitus, abnormal lipid profiles, obesity, excessive use of alcohol, poor dietary habits, lack of exercise, tobacco use, and other risk factors, as well as anthropometric measures, were gathered via a series of interviews conducted by professional interviewers who used a pre-tested questionnaire. An electrocardiogram (ECG), blood pressure, fasting plasma glucose, and lipid panel were all performed to rule out any underlying conditions. SPSS-21 was used for the statistical analysis. The estimated prevalence of CHD based on diagnosed cases and Rose positive angina was 6.9% (95% CI 5.4% - 8.4%), CHD based on diagnosed cases and ECG was 6.4 (95% CI 4.9% - 7.8%), hypertension was 37.5% (95% CI 34.7% to 40.3%), diabetes mellitus was 17.4% (95% CI 15.2% to 19.6%), and dyslipidaemia was 66.5% (95% CI 63.8% - 69. Other modifiable risk factors include a body mass index (BMI) of 25.0 or higher (44.0%), a diet of sub-optimal quality (71.9%), a lack of regular physical activity (21.7%; 95%CI 19.3-24.1); excessive or risky drinking (11.4; 95%CI 9.56-13.2); and cigarette smoking (14.2; 95%CI 12.2-16.2). Conclusions- Gampaha District has a high estimated prevalence of CHD and selected risk factors, with a significant number of cases being undiagnosed. Public health measures, such as educating the public and educating healthcare providers on risk factor screening, are urgently required.

Kaur, Pupinder et.al. (2021). Blockage or interruption of the heart's blood flow, caused by a buildup of fatty substances in coronary arteries, is known as coronary heart disease. Blood flow is impeded when the arteries constrict from the inside due to the accumulation of fatty deposits after a given amount of time. The purpose of this research was to identify risk factors for coronary heart disease in the Malwa area of Punjab. In this analysis, male smoking prevalence was 30.2%, male alcohol consumption was 41.5%, and male and female obesity prevalence were respectively 70.8% and

55.3%. Males had more coronary risk factors than females did. Males may be at greater risk for coronary heart disease due to their higher rates of tobacco and alcohol use.

Aljefree, Najlaa et.al. (2015). Background. Cardiovascular disease (CVD) is a leading cause of death and disability worldwide. The goal of this study is to examine adult population data from Gulf nations to identify risk factors for coronary heart disease and stroke. Methods. Articles published between 1990 and 2014 were systematically reviewed. Results. 62 relevant studies were included in the meta-analysis. It has been estimated that 5.5% of the population in Saudi Arabia has CHD. Hypertension and diabetes are the most frequent risk factors among stroke and ACS patients, with yearly incidence rates ranging from 27.6 to 57 per 100,000 people in the Gulf region. Overweight and obesity were seen with a prevalence of between 31.2% and 43.3% and 22.0% and 34.1% in men and between 28.0% and 34.1% and 26.0% and 44.0% in women. Hypertension prevalence was 26.0% to 50.7% and diabetes prevalence was 9.3% to 46.8% in men and 20.9% to 57.2% and 6% to 53.2% in women. Males had a prevalence of inactivity ranging from 24.3% to 93.9% and females from 56.7% to 98.1%. Males were more likely to be smokers (13.4% to 37.4%) than females (0.5-20.7%). According to the statistics we have, people have terrible eating habits, with a heavy reliance on snacks, fatty meals, sugary foods, and fast food. Conclusion. The Gulf area urgently needs effective prevention methods and education initiatives to lower the risk of CVD mortality and morbidity in the years to come.

Mukhopadhay, Somnath et.al. (2021). Background Even fewer studies have looked at the incidence of CVD risk factors among Indian medical students, and none have focused on the country's eastern regions. Aim Among MBBS students in eastern India, we aimed to determine how common CVD risk variables are and how they relate to the risk ratio for CVD. In this study, we surveyed 433 pupils. Both physical activity (by the International Physical Activity Questionnaire-long form) and mental stress (via the Perceived Stress Scale) were measured. The WHtR (waist-to-height ratio) was determined. The ratio of total cholesterol to HDL was used to determine cardiovascular disease risk. Results There were 40.7% females and 68.6% juniors/sophomores in the sample. Only 22.4 percent of the sample had a high PSS, whereas 30.6 percent of the sample was inactive. There was a total of 29.3% regular smokers and 21.0% regular drinkers. One-fourth had a very high CVD risk ratio. Except for diabetes, juniors had a higher prevalence of most risk variables. Subjects who did not fall into the categories of overweight or obesity showed a positive association between WHtR and CVD risk score (R = 0.33, p 0.001). Weight-height-height ratio, body mass index, triglycerides, and low-density lipoprotein (LDL) all contributed to the variation in the CVD risk ratio (F (7, 425) = 296.085), but LDL (= 0.755) contributed the most. Conclusions It is alarming that such a high frequency of many modifiable CVD risk factors was found among the individuals in this research. Independent early prediction of CVD risk using WHtR in the Indian population shows promise. The youthful population requires a specific cardiovascular disease risk assessment method.

Krishnan, Anand et.al (2020). Objectives Our study's objective was to compare the prevalence of CHD and CVD risk in urban and rural parts of Delhi's NCR between the first survey, conducted in 1991–1994, and the second, conducted in 2010–2012. Methods The sample procedures and average participant ages were comparable across the two surveys. Survey 1 included 2,487 individuals from rural Ballabgarh, whereas Survey 2 included 1,917 people from metropolitan Delhi. Using a Minnesota coded electrocardiogram and the Roseangina questionnaire, a diagnosis of CHD was made. Standard procedures were used to gather data on behavioral, physical, clinical, and biochemical factors. The Framingham risk calculation, adjusted for gender, was used to determine each participant's risk of cardiovascular disease. Results Between the two surveys, the age- and gender-adjusted prevalence of CHD in urban Delhi rose from 10.3% (95% CI: 9.2-11.4) to 14.1% (95% CI: 12.6-15.6), whereas the corresponding figure for rural Ballabgarh rose from 6.0% (95% CI: 5.0-6.9) to 7.4% (95% CI: 6.3-8.6). Women living in urban areas had the greatest rise in CHD prevalence, from 10.1% to 16.6%. In urban regions, the percentage of the population at high 10-year CVD risk rose from 2.5% to 4.8%, whereas in rural areas, it rose from 1.2% to 4.1%. Conclusions Over a 20-

year period, CHD and CVD rates have risen in Delhi, with the highest increases seen among rural residents and women.

RESEARCH METHODOLOGY

Prospective Cohort Study: Conduct a prospective cohort study involving pregnant women from diverse backgrounds and age groups. This design allows for the collection of longitudinal data, facilitating the exploration of associations between BMI, genetic factors, and maternal age throughout pregnancy.

Inclusion Criteria: Include pregnant women in different trimesters, ensuring representation across various maternal age groups (adolescents, young adults, and advanced maternal age). Obtain informed consent from participants for genetic analyses and sharing of medical data.

Exclusion Criteria: Exclude women with pre-existing medical conditions or complications that might confound the results. Screen participants to exclude known genetic disorders affecting pregnancy outcomes.

Anthropometric Measurements: Record height, weight, and BMI of pregnant women during each trimester. Monitor changes in BMI over the course of pregnancy.

Genetic Analysis: Collect blood samples from participants for genetic analysis. Employ techniques such as whole-genome sequencing or targeted genetic testing to identify variations associated with fertility, maternal age, and BMI-related traits.

Clinical Data: Gather detailed clinical information, including pregnancy complications, gestational diabetes, preeclampsia, and neonatal outcomes. Correlate genetic findings with these clinical parameters.

DATA ANALYSIS

Body mass index (BMI) was estimated by formulae – BMI = weight/height^2 (kg/m^2).

According to the World Health Organization's (WHO) system of categorization, the participants' body mass indices were classed as follows: –

a. Underweight persons were categorized with weight <18.5 kg/m^2

b. Moderate weight persons were belong to 18.5-24.9 kg/m^2

c. Over weight persons were belong to 25-29.9 kg/m^2

d. Obese persons were corresponded to 30 kg/m^2

Table 1: BMI and Maternal Age parameters of mothers Mean and SD

Parameters	Cases (n=200)		Controls (n=200)		
	Mean	SD	Mean	SD	
Weight (kg)	62.44	6.95	60.07	5.67	0.000*
Height (feet)	5.48	0.20	5.48	0.19	0.73
BMI	22.57	3.42	21.60	2.63	0.002*
Maternal Age	24.83	3.76	23.85	2.14	0.001*

P-value is calculated by using independent t-test

There are 50 moms with CHD who are overweight, 146 who are of a healthy weight, and only 6 who are underweight. Cases had an average body mass index of 22.57 and a standard deviation of 3.42. But just 3% of moms in the control group are underweight, while 82% are overweight, and 189% fall somewhere in between. The average body mass index (BMI) of the controls is 22.60, with a standard deviation of 2.63.

Mothers who are 30 or older are classified as having Advanced Maternal Age. There are 15 incidences of CHD when the mother was above the age of 35. Cases had an average mother's age of 24.83, with

a standard deviation of 3.76 years. The advanced maternal age rate is 1 for control group moms. In the control group, the average mother age is 23.85, with a standard deviation of 2.14.

Genetic Study

After standardizing the NKX2.5 gene-specific primers, extracted DNA was put onto a 0.8% agarose gel for quality control before being subjected to conventional PCR. Using certain primers, we were able to amplify and sequence the whole exon as well as the intron-exon boundaries on each side.

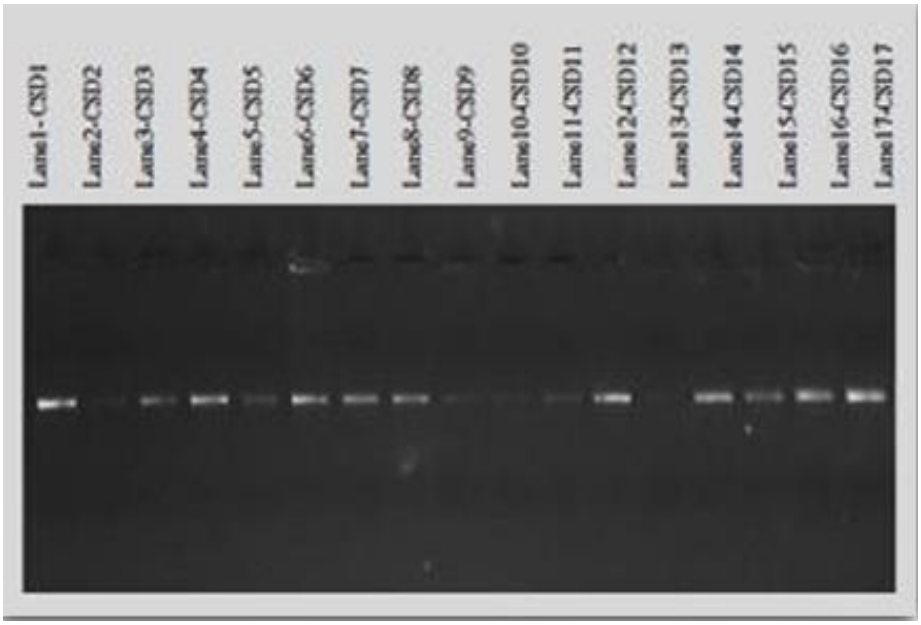

Figure 1: Representative image of isolated Genomic DNA on 0.8% agarose gel.

NKX2.5 sequence variations

Transcriptional factor NKX2.5 is characterized by the presence of a homeobox. The gene on chromosome 5q34 consists of two exons and codes for a 324 amino acid protein. It is essential in the development and maturation of the heart and in the maintenance of the atrioventricular node throughout life, and plays a key function in cardiogenesis by regulating the creation of the septum.
Based on the results of the molecular analysis of 200 samples. NKX2.5 primers (two sets of primers for two exons each) were used to amplify and sequence samples. Patients' DNA was sequenced directly alongside controls. The procedure includes polymerase chain reaction, agarose gel electrophoresis, purification of amplicons by gel elution, and DNA sequencing. Exon-specific primers were used in polymerase chain reaction to amplify a larger area.

NKX2.5 mutations in blood

There were 24 unrelated instances with CHD, and their lymphocyte DNA had nine sequence variations anticipated to change the encoded protein. Seven of the nine detected sequence variations were non-synonymous mutations, which affect just one amino acid rather than all of them. The control group showed no evidence of these alterations. With the use of a computer called Mutation Taster, researchers were able to speculate on whether or not a given sequence change really represented a disease-causing mutation or a harmless polymorphism. It was hypothesized that the c.723C>G sequence change, as well as the c.34T>C, c.600G>T, and c.609G>T sequence changes, would lead to illness.

All the instances that tested positive for the mutation had little or no family history and were the result of NCM.

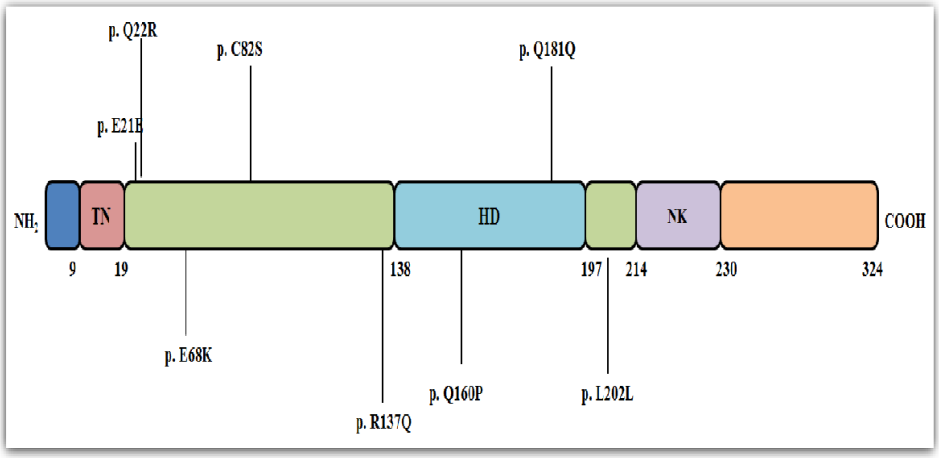

Figure 2: Conserved domains of *NKX2.5* protein showing the location of sequence variants indicates Tinman domain (TN), Homeobox domain (HD) and NK domain.

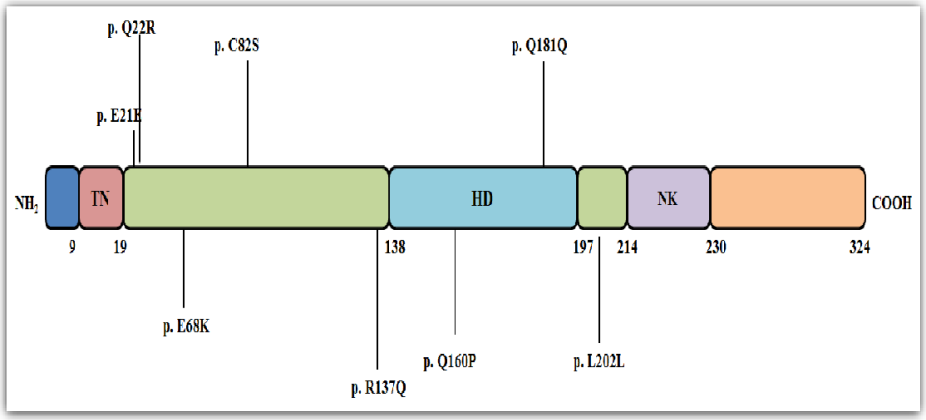

Figure 3: Conserved domains of *NKX2.5* protein showing the location of sequence variants indicates Tinman domain (TN), Homeobox domain (HD) and NK domain.

CONCLUSION

The intersection of maternal age, body mass index (BMI), and genetic factors represents a complex landscape that significantly influences pregnancy outcomes and maternal health. Through a meticulous exploration of these variables, this study has shed light on their interplay, offering valuable insights into the intricate mechanisms that underpin maternal-fetal health. The findings of this study underscore the nuanced relationship between maternal age and pregnancy outcomes. Adolescents, young adults, and advanced-age mothers each navigate distinct challenges and advantages. Advanced maternal age is associated with increased genetic abnormalities risk, while teenage pregnancies often entail heightened risks of preterm births and low birth weights. Recognizing these patterns is crucial for tailoring prenatal care to the specific needs of different age groups. The genetic study revealed a myriad of genetic markers associated with fertility, maternal age, and BMI-related traits. Understanding these genetic predispositions provides a basis for targeted interventions. Genetic screening can aid in identifying high-risk individuals, enabling personalized healthcare approaches and early interventions to mitigate potential complications. In conclusion, this study emphasizes the critical need for a holistic approach to maternal-fetal health, considering not only maternal age and BMI but also their intricate genetic underpinnings. By recognizing the multifaceted nature of these factors and integrating genetic insights, healthcare providers can offer targeted, personalized care, ushering in a future where maternal health disparities are mitigated, and every pregnancy has the best possible chance for a healthy outcome. Through continued research and implementation of personalized healthcare strategies, we can pave the way for a brighter and healthier future for mothers and their newborns.

REFERENCES

1. Doshi, Unnati & Wang-Giuffre, Elizabeth. (2022). Ventricular Septal Defects: A Review. 10.5772/intechopen.104809.
2. Borkar, Yashvanthi & Nayak, Krishnananda & K, RANJAN & Moka, Rajasekhar. (2019). ANALYSIS OF GENE COPY NUMBER VARIATIONS IN PATIENTS WITH CARDIAC SEPTAL DEFECTS USING MULTIPLEX LIGATION-DEPENDENT PROBE AMPLIFICATION. Asian Journal of Pharmaceutical and Clinical Research. 100-103. 10.22159/ajpcr. 2020.v13i1.36189.
3. Mahmoud, Hyam & Nicolescu, Alin & Filip, Cristina & Nicolae, Georgiana & Gabriela, Duica & Bălgrădean, Mihaela & Eliza, Cinteza. (2019). Complex atrial septal defect closure in children. Romanian journal of morphology and embryology = Revue roumaine de morphologie et embryologie. 60. 49-57.
4. Nova, Ria & Putra, Sukman & Nurmaini, Siti & Partan, Radiyati. (2021). Cardiac Septal Defects in Children: Hemodynamics, Clinical Manifestations and Detection. Bioscientia Medicina: Journal of Biomedicine and Translational Research. 5. 10.32539/bsm. v5i4.393.
5. Ozen, Betul & Ceyhan, Özlem & Kaya Erten, Zeliha & Soylu, Meltem. (2018). Determination of Risk Factors of the Youth for Coronary Heart Disease Based on Gender. International Journal of Contemporary Research and Review. 9. 20613-20620. 10.15520/ijcrr/2018/9/09/602.
6. Kaur, Pupinder & Mehta, Promila & Kaur, Ginjinder. (2021). A Study of Risk Factors of Coronary Heart Disease in Population of Malwa Region of Punjab. Studies on Ethno-Medicine. 13. 153-159.
7. Aljefree, Najlaa & Ahmed, Faruk. (2015). Review Article Prevalence of Cardiovascular Disease and Associated Risk Factors among Adult Population in the Gulf Region: A Systematic Review. Advances in Public Health. vol. 2015. 23 pages. 10.1155/2015/235101.
8. Mukhopadhay, Somnath & Mukherjee, Anindya & Khanra, Dibbendhu & Samanta, Biaus & Karak, Avik & Guha, Santanu. (2021). Cardiovascular disease risk factors among undergraduate medical students in a tertiary care centre of eastern India: a pilot study. The Egyptian Heart Journal. 73. 10.1186/s43044-021-00219-9.
9. Krishnan, Anand & Asadullah, Md & Roy, Ambuj & Praveen, Pradeep & Singh, Kalpana & Amarchand, Ritvik & Gupta, Ruby & Ramakrishnan, Lakshmy & Kondal, Dimple & Tandon, Nikhil & Sharma, Meenakshi & Shukla, Deepak & Dorairaj, Prabhakaran & Reddy, Kolli. (2020). Change in prevalence of coronary heart disease and its risk between 1991-94 to 2010-12 among rural and urban population of National Capital Region, Delhi. Indian Heart Journal. 72. 10.1016/j.ihj.2020.08.008.
10. Hinton, William & Mcgovern, Andrew & Coyle, Rachel & Han, Thang & Sharma, Pankaj & Correa, Ana & Ferreira, Filipa I M & de Lusignan, Simon. (2018). Incidence and prevalence of cardiovascular disease in English primary care: A cross-sectional and follow-up study of the Royal College of General Practitioners (RCGP) Research and Surveillance Centre (RSC). BMJ Open. 8. e020282. 10.1136/bmjopen-2017-020282.