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ЕЖЕМЕСЯЧНЫЙ НАУЧНЫЙ ЖУРНАЛ

Медицинские новости Грузии

საქართველოს სამედიცინო სიახლენი

GEORGIAN MEDICAL NEWS

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GMN: Georgian Medical News is peer-reviewed, published monthly journal committed to promoting the science and art of medicine and the betterment of public health, published by the GMN Editorial Board since 1994. GMN carries original scientific articles on medicine, biology and pharmacy, which are of experimental, theoretical and practical character; publishes original research, reviews, commentaries, editorials, essays, medical news, and correspondence in English and Russian.

GMN is indexed in MEDLINE, SCOPUS, PubMed and VINITI Russian Academy of Sciences. The full text content is available through EBSCO databases.

GMN: Медицинские новости Грузии - ежемесячный рецензируемый научный журнал, издаётся Редакционной коллегией с 1994 года на русском и английском языках в целях поддержки медицинской науки и улучшения здравоохранения. В журнале публикуются оригинальные научные статьи в области медицины, биологии и фармации, статьи обзорного характера, научные сообщения, новости медицины и здравоохранения. Журнал индексируется в MEDLINE, отражён в базе данных SCOPUS, PubMed и ВИНИТИ РАН. Полнотекстовые статьи журнала доступны через БД EBSCO.

GMN: Georgian Medical News – საქართველოს სამედიცინო სიახლენი – არის ყოველთვიური სამეცნიერო სამედიცინო რეცენზირებადი ჟურნალი, გამოიცემა 1994 წლიდან, წარმოადგენს სარედაქციო კოლეგიისა და აშშ-ის მეცნიერების, განათლების, ინდუსტრიის, ხელოვნებისა და ბუნებისმეტყველების საერთაშორისო აკადემიის ერთობლივ გამოცემას. GMN-ში რუსულ და ინგლისურ ენებზე ქვეყნდება ექსპერიმენტული, თეორიული და პრაქტიკული ხასიათის ორიგინალური სამეცნიერო სტატიები მედიცინის, ბიოლოგიისა და ფარმაციის სფეროში, მიმოხილვითი ხასიათის სტატიები.

ჟურნალი ინდექსირებულია MEDLINE-ის საერთაშორისო სისტემაში, ასახულია SCOPUS-ის, PubMed-ის და ВИНИТИ РАН-ის მონაცემთა ბაზებში. სტატიების სრული ტექსტი ხელმისაწვდომია EBSCO-ს მონაცემთა ბაზებიდან.

WEBSITE

www.geomednews.com

К СВЕДЕНИЮ АВТОРОВ!

При направлении статьи в редакцию необходимо соблюдать следующие правила:

1. Статья должна быть представлена в двух экземплярах, на русском или английском языках, напечатанная через **полтора интервала на одной стороне стандартного листа с шириной левого поля в три сантиметра**. Используемый компьютерный шрифт для текста на русском и английском языках - **Times New Roman** (**Кириллица**), для текста на грузинском языке следует использовать **AcadNusx.** Размер шрифта - **12**. К рукописи, напечатанной на компьютере, должен быть приложен CD со статьей.

2. Размер статьи должен быть не менее десяти и не более двадцати страниц машинописи, включая указатель литературы и резюме на английском, русском и грузинском языках.

3. В статье должны быть освещены актуальность данного материала, методы и результаты исследования и их обсуждение.

При представлении в печать научных экспериментальных работ авторы должны указывать вид и количество экспериментальных животных, применявшиеся методы обезболивания и усыпления (в ходе острых опытов).

4. К статье должны быть приложены краткое (на полстраницы) резюме на английском, русском и грузинском языках (включающее следующие разделы: цель исследования, материал и методы, результаты и заключение) и список ключевых слов (key words).

5. Таблицы необходимо представлять в печатной форме. Фотокопии не принимаются. **Все цифровые, итоговые и процентные данные в таблицах должны соответствовать таковым в тексте статьи**. Таблицы и графики должны быть озаглавлены.

6. Фотографии должны быть контрастными, фотокопии с рентгенограмм - в позитивном изображении. Рисунки, чертежи и диаграммы следует озаглавить, пронумеровать и вставить в соответствующее место текста **в tiff формате**.

В подписях к микрофотографиям следует указывать степень увеличения через окуляр или объектив и метод окраски или импрегнации срезов.

7. Фамилии отечественных авторов приводятся в оригинальной транскрипции.

8. При оформлении и направлении статей в журнал МНГ просим авторов соблюдать правила, изложенные в «Единых требованиях к рукописям, представляемым в биомедицинские журналы», принятых Международным комитетом редакторов медицинских журналов - http://www.spinesurgery.ru/files/publish.pdf и http://www.nlm.nih.gov/bsd/uniform_requirements.html
В конце каждой оригинальной статьи приводится библиографический список. В список литературы включаются все материалы, на которые имеются ссылки в тексте. Список составляется в алфавитном порядке и нумеруется. Литературный источник приводится на языке оригинала. В списке литературы сначала приводятся работы, написанные знаками грузинского алфавита, затем кириллицей и латиницей. Ссылки на цитируемые работы в тексте статьи даются в квадратных скобках в виде номера, соответствующего номеру данной работы в списке литературы. Большинство цитированных источников должны быть за последние 5-7 лет.

9. Для получения права на публикацию статья должна иметь от руководителя работы или учреждения визу и сопроводительное отношение, написанные или напечатанные на бланке и заверенные подписью и печатью.

10. В конце статьи должны быть подписи всех авторов, полностью приведены их фамилии, имена и отчества, указаны служебный и домашний номера телефонов и адреса или иные координаты. Количество авторов (соавторов) не должно превышать пяти человек.

11. Редакция оставляет за собой право сокращать и исправлять статьи. Корректура авторам не высылается, вся работа и сверка проводится по авторскому оригиналу.

12. Недопустимо направление в редакцию работ, представленных к печати в иных издательствах или опубликованных в других изданиях.

При нарушении указанных правил статьи не рассматриваются.

REQUIREMENTS

Please note, materials submitted to the Editorial Office Staff are supposed to meet the following requirements:

1. Articles must be provided with a double copy, in English or Russian languages and typed or compu-ter-printed on a single side of standard typing paper, with the left margin of **3** centimeters width, and **1.5** spacing between the lines, typeface - **Times New Roman** (**Cyrillic**), print size - **12** (referring to Georgian and Russian materials). With computer-printed texts please enclose a CD carrying the same file titled with Latin symbols.

2. Size of the article, including index and resume in English, Russian and Georgian languages must be at least 10 pages and not exceed the limit of 20 pages of typed or computer-printed text.

3. Submitted material must include a coverage of a topical subject, research methods, results, and review.

Authors of the scientific-research works must indicate the number of experimental biological species drawn in, list the employed methods of anesthetization and soporific means used during acute tests.

4. Articles must have a short (half page) abstract in English, Russian and Georgian (including the following sections: aim of study, material and methods, results and conclusions) and a list of key words.

5. Tables must be presented in an original typed or computer-printed form, instead of a photocopied version. **Numbers, totals, percentile data on the tables must coincide with those in the texts of the articles.** Tables and graphs must be headed.

6. Photographs are required to be contrasted and must be submitted with doubles. Please number each photograph with a pencil on its back, indicate author's name, title of the article (short version), and mark out its top and bottom parts. Drawings must be accurate, drafts and diagrams drawn in Indian ink (or black ink). Photocopies of the X-ray photographs must be presented in a positive image in **tiff format**.

Accurately numbered subtitles for each illustration must be listed on a separate sheet of paper. In the subtitles for the microphotographs please indicate the ocular and objective lens magnification power, method of coloring or impregnation of the microscopic sections (preparations).

7. Please indicate last names, first and middle initials of the native authors, present names and initials of the foreign authors in the transcription of the original language, enclose in parenthesis corresponding number under which the author is listed in the reference materials.

8. Please follow guidance offered to authors by The International Committee of Medical Journal Editors guidance in its Uniform Requirements for Manuscripts Submitted to Biomedical Journals publication available online at: http://www.nlm.nih.gov/bsd/uniform_requirements.html
http://www.icmje.org/urm_full.pdf
In GMN style for each work cited in the text, a bibliographic reference is given, and this is located at the end of the article under the title "References". All references cited in the text must be listed. The list of references should be arranged alphabetically and then numbered. References are numbered in the text [numbers in square brackets] and in the reference list and numbers are repeated throughout the text as needed. The bibliographic description is given in the language of publication (citations in Georgian script are followed by Cyrillic and Latin).

9. To obtain the rights of publication articles must be accompanied by a visa from the project instructor or the establishment, where the work has been performed, and a reference letter, both written or typed on a special signed form, certified by a stamp or a seal.

10. Articles must be signed by all of the authors at the end, and they must be provided with a list of full names, office and home phone numbers and addresses or other non-office locations where the authors could be reached. The number of the authors (co-authors) must not exceed the limit of 5 people.

11. Editorial Staff reserves the rights to cut down in size and correct the articles. Proof-sheets are not sent out to the authors. The entire editorial and collation work is performed according to the author's original text.

12. Sending in the works that have already been assigned to the press by other Editorial Staffs or have been printed by other publishers is not permissible.

Articles that Fail to Meet the Aforementioned Requirements are not Assigned to be Reviewed.

ავტორთა საყურადღებოდ!

რედაქციაში სტატიის წარმოდგენისას საჭიროა დავიცვათ შემდეგი წესები:

1. სტატია უნდა წარმოადგინოთ 2 ცალად, რუსულ ან ინგლისურ ენებზე,დაბეჭდილი სტანდარტული ფურცლის 1 გვერდზე, 3 სმ სიგანის მარცხენა ველისა და სტრიქონებს შორის 1,5 ინტერვალის დაცვით. გამოყენებული კომპიუტერული შრიფტი რუსულ და ინგლისურენოვან ტექსტებში - **Times New Roman (Кириллица)**, ხოლო ქართულენოვან ტექსტში საჭიროა გამოვიყენოთ **AcadNusx.** შრიფტის ზომა – 12. სტატიას თან უნდა ახლდეს CD სტატიით.

2. სტატიის მოცულობა არ უნდა შეადგენდეს 10 გვერდზე ნაკლებს და 20 გვერდზე მეტს ლიტერატურის სიის და რეზიუმეების (ინგლისურ, რუსულ და ქართულ ენებზე) ჩათვლით.

3. სტატიაში საჭიროა გაშუქდეს: საკითხის აქტუალობა; კვლევის მიზანი; საკვლევი მასალა და გამოყენებული მეთოდები; მიღებული შედეგები და მათი განსჯა. ექსპერიმენტული ხასიათის სტატიების წარმოდგენისას ავტორებმა უნდა მიუთითონ საექსპერიმენტო ცხოველების სახეობა და რაოდენობა; გაუტკივარებისა და დაძინების მეთოდები (მწვავე ცდების პირობებში).

4. სტატიას თან უნდა ახლდეს რეზიუმე ინგლისურ, რუსულ და ქართულ ენებზე არანაკლებ ნახევარი გვერდის მოცულობისა (სათაურის, ავტორების, დაწესებულების მითითებით და უნდა შეიცავდეს შემდეგ განყოფილებებს: მიზანი, მასალა და მეთოდები, შედეგები და დასკვნები; ტექსტუალური ნაწილი არ უნდა იყოს 15 სტრიქონზე ნაკლები) და საკვანძო სიტყვების ჩამონათვალი (key words).

5. ცხრილები საჭიროა წარმოადგინოთ ნაბეჭდი სახით. ყველა ციფრული, შემაჯამებელი და პროცენტული მონაცემები უნდა შეესაბამებოდეს ტექსტში მოყვანილს.

6. ფოტოსურათები უნდა იყოს კონტრასტული; სურათები, ნახაზები, დიაგრამები - დასათაურებული, დანომრილი და სათანადო ადგილას ჩასმული. რენტგენოგრამების ფოტოასლები წარმოადგინეთ პოზიტიური გამოსახულებით **tiff** ფორმატში. მიკროფოტოსურათების წარწერებში საჭიროა მიუთითოთ ოკულარის ან ობიექტივის საშუალებით გადიდების ხარისხი, ანათალების შეღებვის ან იმპრეგნაციის მეთოდი და აღნიშნოთ სურათის ზედა და ქვედა ნაწილები.

7. სამამულო ავტორების გვარები სტატიაში აღინიშნება ინიციალების თანდართვით, უცხოურისა – უცხოური ტრანსკრიპციით.

8. სტატიას თან უნდა ახლდეს ავტორის მიერ გამოყენებული სამამულო და უცხოური შრომების ბიბლიოგრაფიული სია (ბოლო 5-8 წლის სიღრმით). ანბანური წყობით წარმოდგენილ ბიბლიოგრაფიულ სიაში მიუთითეთ ჯერ სამამულო, შემდეგ უცხოელი ავტორები (გვარი, ინიციალები, სტატიის სათაური, ჟურნალის დასახელება, გამოცემის ადგილი, წელი, ჟურნალის №, პირველი და ბოლო გვერდები). მონოგრაფიის შემთხვევაში მიუთითეთ გამოცემის წელი, ადგილი და გვერდების საერთო რაოდენობა. ტექსტში კვადრატულ ფჩხილებში უნდა მიუთითოთ ავტორის შესაბამისი N ლიტერატურის სიის მიხედვით. მიზანშეწონილია, რომ ციტირებული წყაროების უმეტესი ნაწილი იყოს 5-6 წლის სიღრმის.

9. სტატიას თან უნდა ახლდეს: ა) დაწესებულების ან სამეცნიერო ხელმძღვანელის წარდგინება, დამოწმებული ხელმოწერითა და ბეჭდით; ბ) დარგის სპეციალისტის დამოწმებული რეცენზია, რომელშიც მითითებული იქნება საკითხის აქტუალობა, მასალის საკმაობა, მეთოდის სანდოობა, შედეგების სამეცნიერო-პრაქტიკული მნიშვნელობა.

10. სტატიის ბოლოს საჭიროა ყველა ავტორის ხელმოწერა, რომელთა რაოდენობა არ უნდა აღემატებოდეს 5-ს.

11. რედაქცია იტოვებს უფლებას შეასწოროს სტატია. ტექსტზე მუშაობა და შეჯერება ხდება საავტორო ორიგინალის მიხედვით.

12. დაუშვებელია რედაქციაში ისეთი სტატიის წარდგენა, რომელიც დასაბეჭდად წარდგენილი იყო სხვა რედაქციაში ან გამოქვეყნებული იყო სხვა გამოცემებში.

აღნიშნული წესების დარღვევის შემთხვევაში სტატიები არ განიხილება.

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Abstract.

Background: Interindividual variation in lipid and lipoprotein profiles is linked to polymorphisms in the gene encoding lipoprotein lipase (LPL), an enzyme central to lipoprotein metabolism. However, the relationship between common LPL variants and circulating apolipoprotein A-I (apoA-I) and apolipoprotein B-100 (apoB-100) concentrations in coronary heart disease (CHD) remains incompletely characterized. This study examined the Ser447Ter (rs328), HindIII (rs320), and PvuII (rs285) LPL polymorphisms in relation to apoA-I and apoB-100 concentrations among Sudanese patients with CHD and Sudanese controls without a history of coronary artery disease.

Methods: A cross-sectional genetic association study enrolled 100 patients with angiographically verified CHD from the Sudan Heart Centre, Khartoum, Sudan, and 50 Sudanese controls recruited separately from the general population, without a personal history of coronary artery disease as confirmed by a Medical History and Symptom Questionnaire, and broadly matched to cases by age and sex in an approximate 2:1 case-to-control design. Genotyping was performed by PCR-RFLP. Serum apoA-I and apoB-100 concentrations were determined by immunoturbidimetry. Inter-genotype differences in apolipoprotein concentrations among CHD cases were assessed by one-way ANOVA (HindIII, PvuII) or independent-samples t-test (Ser447Ter); Cohen's d effect sizes and point-biserial correlations were also calculated. Because several genotype cells contained zero or very small counts, genotype-frequency comparisons between cases and controls, and tests of Hardy-Weinberg equilibrium (HWE), were performed using exact methods rather than chi-squared approximations.

Results: CHD patients (54% male; mean age 51.7 ± 16.7 years) had significantly higher body mass index, apoA-I, and apoB-100 concentrations than controls (all $p<0.001$). Among CHD cases, inter-genotype differences in apoA-I and apoB-100 were not statistically significant for any of the three polymorphisms (all $p>0.05$), although HindIII H+H− heterozygotes showed numerically higher concentrations of both apolipoproteins than H+H+ homozygotes, corresponding to moderate effect sizes (apoA-I d=0.55; apoB-100 d=0.58). All three loci were monomorphic (0% variant carriers) among the 50 controls. Using Fisher's exact test, variant carriage was more frequent among cases than controls for HindIII (11% vs. 0%, p=0.016) and PvuII (12% vs. 0%, p=0.009) but not for Ser447Ter (5% vs. 0%, p=0.17); odds ratios calculated with the Haldane-Anscombe correction for zero-cell counts were imprecise, with wide confidence intervals. Exact tests for deviation from HWE among cases indicated significant deviation for HindIII (p=0.005) and PvuII (p=0.009) but not Ser447Ter (p=1.00).

Conclusions: In this exploratory, underpowered Sudanese cohort, LPL genotype was not significantly associated with apoA-I or apoB-100 concentrations, although a moderate, hypothesis-generating effect was observed for the HindIII polymorphism among heterozygous carriers. Variant carriage of HindIII and PvuII was more frequent among CHD cases than controls, but the zero-cell counts in controls, the imprecise odds ratio estimates, and the significant HWE deviation observed for these two loci among cases warrant cautious interpretation and independent replication.

Key words. Lipoprotein lipase, LPL gene polymorphisms, Ser447Ter, HindIII, PvuII, apolipoprotein A-I, apolipoprotein B-100, coronary heart disease, genetic association, Sudan.

Introduction.

Coronary heart disease (CHD) remains the leading cause of mortality globally, accounting for an estimated 9.1 million deaths in 2021 [1]. Atherosclerosis, its pathological substrate, develops through a complex interplay of genetic predisposition, metabolic dysregulation, and environmental exposure. Among the modifiable determinants of atherosclerotic risk, disturbances in lipoprotein metabolism occupy a central mechanistic role [2].

Two apolipoproteins are particularly relevant to cardiovascular risk stratification. Apolipoprotein A-I (apoA-I) is the principal structural protein of high-density lipoprotein (HDL) particles and facilitates reverse cholesterol transport, associated with an anti-atherogenic lipid profile [3]. Apolipoprotein B-100 (apoB-100), conversely, is the obligatory structural component of very low-density lipoprotein (VLDL), intermediate-density lipoprotein (IDL), and low-density lipoprotein (LDL) particles, and its plasma concentration reflects the total burden of circulating atherogenic lipoprotein particles [4]. Apolipoprotein concentrations, particularly the apoB-100/apoA-I ratio have been reported to provide cardiovascular risk information beyond that captured by conventional lipid profiles, and their genetic determinants remain an active area of investigation [5].

Lipoprotein lipase (LPL) plays a key role in lipoprotein metabolism and is primarily expressed by cardiomyocytes, skeletal muscle, and adipose tissue. Located on the luminal surface of capillary endothelial cells, LPL hydrolyzes triglycerides in VLDL and chylomicrons, generating surface remnants that contribute to HDL formation and releasing free fatty acids for tissue uptake [6]. Through this enzymatic activity, LPL is positioned to influence both the pro-atherogenic (apoB-100/VLDL-LDL) and anti-atherogenic (apoA-I/HDL) branches of lipoprotein metabolism. The LPL gene, located on chromosome 8p21.3 and spanning approximately 30 kilobases across ten exons, encodes a 448-amino-acid protein [7].

Three common LPL polymorphisms have attracted particular research attention. The Ser447Ter variant (rs328) results from a C→G transversion in exon 9, introducing a premature stop codon and truncating the LPL protein by two amino acids; this variant has been associated with increased LPL activity and a more favourable lipid profile in some populations, though findings are not uniform [8]. The HindIII polymorphism (rs320), located in intron 8, is non-coding but may influence mRNA stability or serve as a marker for functional variation elsewhere in the gene [9]. The PvuII polymorphism (rs285), residing in intron 6, has been inconsistently associated with lipid parameters across populations [10].

Previous studies have investigated these polymorphisms primarily in relation to conventional lipid measures triglycerides and HDL cholesterol with fewer systematic evaluations of their relationship to apolipoprotein concentrations directly. This distinction is relevant because apolipoprotein concentrations reflect the number of circulating lipoprotein particles rather than the amount of lipid carried per particle, so genetic variation could plausibly affect these two dimensions differently. The present study was therefore designed to examine the relationships between serum apoA-I and apoB-100 concentrations and the Ser447Ter, HindIII, and PvuII polymorphisms in Sudanese patients with established CHD, and to compare genotype frequencies between these patients and Sudanese controls without a history of coronary artery disease. To provide a thorough characterization of these relationships given the anticipated rarity of some genotype categories, both conventional hypothesis testing and complementary effect-size and exact-test methods were used [11-15].

Materials and Methods.

Study Design and Participants:

A cross-sectional genetic association study was conducted at Sudan Heart Centre, Khartoum, Sudan. One hundred patients with established CHD, defined by a acute myocardial infarction, angiographically documented coronary artery stenosis ≥50%, or prior coronary revascularisation, were consecutively enrolled. Eligible patients were aged 25–74 years; individuals older than 74 years were excluded. Patients with a history of myocardial infarction, dyslipidaemia, diabetes, or smoking were included where these were clinically present, but these characteristics were not applied as independent inclusion requirements for every participant. Additional exclusion criteria were: secondary dyslipidaemia attributable to thyroid, renal, or hepatic disease; acute infectious or inflammatory illness; pregnancy; women receiving hormonal therapy; patients receiving cancer therapy; and inability to provide informed consent.

Fifty control participants were recruited separately from the general Sudanese population and were not drawn from the Sudan Heart Centre patient pool. Controls were Sudanese adults volunteers with no personal history of coronary artery disease, confirmed at enrolment using a Medical History and Symptom Questionnaire. Controls were selected to broadly reflect the age and sex distribution of the CHD group, yielding an approximate 2:1 case to control design with age- and sex-based matching; individual one-to-one matching was not performed.

The study was conducted in accordance with the Declaration of Helsinki and was approved by the Central Institutional Review Board of Al Neelain University, Sudan (approval date: 1 March 2015). Written informed consent was obtained from all participants, both cases and controls.

Clinical and Biochemical Assessment:

Ten-millilitre blood samples were collected in the morning after a minimum 12-hour fast from all participants. Serum was separated by centrifugation at 3,000 rpm for 10 minutes and stored at −80°C until analysis. Serum apoA-I and apoB-100 concentrations were determined by immunoturbidimetry using standardised commercial kits.

DNA Extraction and Genotyping:

Genomic DNA was extracted from peripheral blood leukocytes using the DNeasy Blood & Tissue Kit (50 preparations; Qiagen; Cat. No./ID 69504). Genotyping of the three LPL polymorphisms was performed by polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP) as follows.

Ser447Ter (rs328): Exon 9 was amplified using forward primer 5′-TAC ACT AGC AAT GTC TAG GTG A-3′ and reverse primer 5′-TCA GCT TTA GCC CAG AAT GC-3′. PCR products were digested with NlaIII restriction endonuclease.

HindIII (rs320): The intron 8 region was amplified using forward primer H1 (5′-TGA AGC TCA AAT GGA AGA GT-3′) and reverse primer H2 (5′-TAC AAG CAA ATG ACT AAA-3′), followed by digestion with HindIII restriction endonuclease (Promega Corporation), yielding H+ and H− alleles.

PvuII (rs285): The intron 6 region was amplified using forward primer P1 (5′-ATG GCA CCC ATG TGT AAG GTG-3′) and reverse primer P2 (5′-GTG AAC TTC TGA TAA CAA TCT C-3′), followed by digestion with PvuII restriction endonuclease (Promega Corporation), yielding P+ and P− alleles.

Primer sequences for all three polymorphisms were selected based on previously published protocols cited in this manuscript.

Each 25 µL PCR reaction contained 3 µL genomic DNA (150 ng), 12.5 µL 5× FIREPol® Master Mix (Solis BioDyne), 2 µL of each primer, and distilled water to final volume. Amplification conditions were: initial denaturation at 94°C for 2 minutes; 40 cycles of denaturation at 94°C for 15 seconds, annealing at 50°C for 30 seconds, and extension at 72°C for 1 minute; followed by a final extension at 72°C for 2 minutes.

Restriction digestion reactions (20 µL final volume) contained 10 µL PCR product, 1 µL of the appropriate restriction enzyme, and 2 µL of the corresponding 10× buffer, made up to volume with distilled water. Reactions were briefly centrifuged (2 minutes at 3,913 × g) and incubated at 37°C overnight. Digestion products were resolved by electrophoresis on 2.5% agarose gel at 80 V for 60 minutes, stained, and visualised under UV light.

Statistical Analysis:

Genotype frequencies were tabulated separately for CHD cases and controls. Deviation from Hardy-Weinberg equilibrium (HWE) was assessed among CHD cases using an exact test (Wigginton et al., 2005) rather than the chi-squared goodness-of-fit approximation, because several genotype categories contained small counts for which the chi-squared approximation is unreliable. HWE testing was not performed in controls because all three loci were monomorphic (0% variant carriers) in this group, which precludes a meaningful test of genotypic proportions.

Inter-genotype differences in apolipoprotein concentrations among CHD cases were assessed by one-way ANOVA for polymorphisms with three observed genotype groups (HindIII, PvuII) and by an independent-samples t-test for Ser447Ter, for which only two genotype groups (GG, GC) were observed. Cohen's d effect sizes were calculated for prespecified pairwise genotype comparisons, with thresholds of 0.2, 0.5, and 0.8 conventionally denoting small, medium, and large effects respectively (11), reflecting the limited power of null-hypothesis testing in small variant-genotype groups. Ninety five percent confidence intervals for Cohen's were calculated using standard large-sample approximations. Point-biserial correlation coefficients (rpb) were calculated between dichotomised genotype status (variant allele present vs. absent) and continuous apolipoprotein concentrations; this dichotomisation assumes an additive, monotonic genotype effect and may not capture heterozygote-specific patterns.

Genotype frequency differences between CHD cases and controls were compared using Fisher's exact test rather than the chi-squared test, because the control group contained zero-count cells for every variant genotype, violating the expected cell count assumptions of the chi-squared approximation. Because conventional odds ratios are undefined when a cell count is zero, odds ratios and 95% confidence intervals for case-control genotype comparisons were calculated using the Haldane-Anscombe correction (addition of 0.5 to each cell of the 2×2 table); these corrected estimates are inherently imprecise and should be interpreted as approximate.

A priori power calculations indicated that 64 participants per genotype group would be required to detect a medium effect size (Cohen's d = 0.5) with 80% power at $\alpha = 0.05$; this threshold was not reached for any variant genotype group in the present study. SPSS version 26 (IBM Corp., Armonk, NY, USA) was used for descriptive statistics, ANOVA, t-tests, and standard cross-tabulations. Effect sizes, the exact HWE test, and the exact case-control genotype comparisons were computed using the methods described above. Statistical significance was defined as $p < 0.05$ throughout.

Results.

Demographic and Clinical Characteristics:

The demographic and genetic characteristics of the study population are summarised in Table 1. Eligible CHD patients were aged 25–74 years; individuals older than 74 years were excluded. The sex distribution was comparable between the 100 CHD patients and 50 controls, with males comprising 54% of patients and 50% of controls. Age distribution did not differ significantly between groups, with 70% of patients and 76% of controls aged over 40 years. Body mass index (BMI) was markedly higher among patients, with obesity present in 98% of CHD patients compared with 30% of controls. This cross-sectional comparison indicates a strong association between adiposity and CHD status in this cohort; it does not, by itself, establish causality or an independent effect, since no multivariable adjustment for potential confounders (including BMI, medication use, and metabolic comorbidities) was performed in this study.

Clinical Characteristics of CHD Patients and Controls:

The clinical characteristics of CHD patients and controls are presented in Table 2. Mean age was slightly higher in the CHD group (51.7 ± 16.7 years) than in controls (48.8 ± 13.1 years), although this difference was not statistically significant ($p = 0.275$). BMI was significantly higher in CHD patients (34.2 ± 6.6) than controls (24.4 ± 2.4; $p < 0.001$). CHD patients also had significantly higher mean apoA-I (143.98 ± 37.49 mg/dL vs. 120.86 ± 30.49 mg/dL) and apoB-100 concentrations (121.09 ± 45.0 mg/dL vs. 87.48 ± 30.36 mg/dL) than controls (both $p < 0.001$). As a cross-sectional comparison, these findings describe an association between CHD status and apolipoprotein concentrations rather than a causal relationship.

Genotype Distribution and Apolipoprotein Concentrations Among CHD Cases:

Table 3 summarises apoA-I and apoB-100 concentrations by genotype among the 100 CHD cases. For Ser447Ter, most patients (95%) carried the GG genotype and 5% carried the GC

Table 1. *Demographic and genetic characteristics of CHD patients and controls.*

Participant Characteristic	Category	CHD (n=100) Count	CHD (n=100) %	Controls (n=50) Count	Controls (n=50) %
Sex	Male	54	54%	25	50%
	Female	46	46%	25	50%
Age group	<40 years	30	30%	12	24%
	>40 years	70	70%	38	76%
BMI status	Normal	2	2%	35	70%
	Obese	98	98%	15	30%
Ser447Ter	Normal (GG)	95	95%	50	100%
	Heterozygote (GC)	5	5%	0	0%
	Homozygote variant (CC)	0	0%	0	0%
HindIII	Normal (H+H+)	89	89%	50	100%
	Heterozygote (H+H−)	8	8%	0	0%
	Homozygote variant (H−H−)	3	3%	0	0%
PvuII	Normal (P−P−)	88	88%	50	100%
	Heterozygote (P−P+)	9	9%	0	0%
	Homozygote variant (P+P+)	3	3%	0	0%

Table 2. *Clinical characteristics of CHD patients and controls (independent-samples t-test). p<0.05 considered statistically significant.*

Characteristic	CHD Mean	CHD SD	Controls Mean	Controls SD	p-value
Age (years)	51.7	16.7	48.8	13.1	0.275
BMI (kg/m²)	34.2	6.6	24.4	2.4	<0.001
ApoA-I (mg/dL)	143.98	37.49	120.86	30.49	<0.001
ApoB-100 (mg/dL)	121.09	45.0	87.48	30.36	<0.001

Table 3. *Relationship between LPL polymorphisms and serum apolipoprotein concentrations among CHD patients (n=100).*

LPL Polymorphism	Genotype	n	ApoA-I Mean ± SD (mg/dL)	ApoB-100 Mean ± SD (mg/dL)
Ser447Ter	GC	5	113.4 ± 71.6	159.0 ± 47.1
	GG	95	143.2 ± 37.1	121.6 ± 43.7
	p-value (independent t-test)	—	0.361	0.646
HindIII	H+H+	89	142.2 ± 38.2	118.0 ± 46.1
	H+H−	8	162.8 ± 29.9	144.1 ± 33.1
	H−H−	3	147.0 ± 26.1	129.3 ± 22.4
	p-value (one-way ANOVA)	—	0.332	0.298
PvuII	P−P−	88	144.7 ± 38.1	119.9 ± 46.1
	P−P+	9	142.9 ± 38.1	137.8 ± 37.7
	P+P+	3	126.0 ± 20.1	105.0 ± 20.3
	p-value (one-way ANOVA)	—	0.698	0.436

P-values were determined using independent-samples t-tests (Ser447Ter, two genotype groups) or one-way ANOVA (HindIII and PvuII, three genotype groups). A p-value <0.05 was considered statistically significant.

Table 4. *Effect-size analysis (Cohen's d with 95% confidence intervals) for inter-genotype apolipoprotein comparisons among CHD cases.*

LPL Polymorphism	Genotype Comparison	ApoA-I Cohen's d (95% CI)	ApoB-100 Cohen's d (95% CI)	Interpretation
Ser447Ter	GG vs. GC	0.76 (−0.14, 1.67)	−0.85 (−1.76, 0.05)	Unstable; n=5 comparison group
HindIII	H+H− vs. H+H+	0.55 (−0.18, 1.27)	0.58 (−0.15, 1.30)	Moderate point estimate; CI crosses 0
PvuII	P−P+ vs. P−P−	−0.05 (−0.73, 0.64)	0.39 (−0.29, 1.08)	Negligible to small; CI crosses 0

Table 5. *Point-biserial correlation between LPL genotype presence (variant vs. absent) and apolipoprotein concentrations among CHD cases.*

LPL Polymorphism	Apolipoprotein	r	p-value
Ser447Ter	ApoA-I	−0.013	0.899
	ApoB-100	0.032	0.754
HindIII	ApoA-I	0.068	0.503
	ApoB-100	0.079	0.436
PvuII	ApoA-I	0.004	0.970
	ApoB-100	0.026	0.799

Table 6. *Statistical comparison of CHD patients vs. controls.*

Characteristic	CHD (%)	Controls (%)	Statistical Test	Test Value	p-value	Odds Ratio (95% CI)	Interpretation
Sex (Male/Female)	54%	50%	Chi-squared	0.32	0.571	1.17 (0.67–2.06)	No difference
Age (<40/>40 years)	70%	76%	Chi-squared	0.91	0.340	0.73 (0.39–1.37)	No difference
BMI (Normal/Obese)	98%	30%	Chi-squared	98.24	<0.001	114.3 (25–512)	Very strong association
Ser447Ter (variant carrier)	5%	0%	Fisher's exact	—	0.170	5.82 (0.32–107.32)*	No significant association
HindIII (variant carrier)	11%	0%	Fisher's exact	—	0.016	12.98 (0.75–224.88)*	Evidence of association; imprecise estimate
PvuII (variant carrier)	12%	0%	Fisher's exact	—	0.009	14.27 (0.83–246.07)*	Evidence of association; imprecise estimate

**Odds ratios for LPL polymorphisms were calculated using the Haldane-Anscombe correction (0.5 added to each cell) because the control group had zero variant carriers, making the conventional odds ratio undefined; these corrected estimates are imprecise and should not be interpreted as precise risk quantification.*

genotype; no CC homozygotes were observed. Mean apoA-I was numerically higher in GG carriers (143.2 ± 37.1 mg/dL) than GC carriers (113.4 ± 71.6 mg/dL), while apoB-100 was numerically higher in GC carriers (159.0 ± 47.1 mg/dL) than GG carriers (121.6 ± 43.7 mg/dL). Neither difference reached statistical significance (apoA-I p=0.361; apoB-100 p=0.646). Given the very small GC subgroup (n=5), these estimates are imprecise and should be interpreted with caution.

For HindIII, three genotype groups were observed: H+H+ (89%), H+H− (8%), and H−H− (3%). H+H− heterozygotes showed the numerically highest mean concentrations of both apoA-I (162.8 ± 29.9 mg/dL) and apoB-100 (144.1 ± 33.1 mg/dL), compared with H+H+ (apoA-I 142.2 ± 38.2; apoB-100 118.0 ± 46.1 mg/dL) and H−H− (apoA-I 147.0 ± 26.1; apoB-100 129.3 ± 22.4 mg/dL). One-way ANOVA did not identify statistically significant differences between genotypes for either apolipoprotein (apoA-I p=0.332; apoB-100 p=0.298).

For PvuII, genotype distribution was P−P− (88%), P−P+ (9%), and P+P+ (3%). ApoA-I concentrations were similar between P−P− (144.7 ± 38.1 mg/dL) and P−P+ carriers (142.9 ± 38.1 mg/dL), with P+P+ homozygotes showing the lowest values (126.0 ± 20.1 mg/dL). ApoB-100 was numerically highest in P−P+ heterozygotes (137.8 ± 37.7 mg/dL), followed by P−P− (119.9 ± 46.1 mg/dL) and P+P+ (105.0 ± 20.3 mg/dL). These differences did not reach statistical significance (apoA-I p=0.698; apoB-100 p=0.436).

Effect Size Analysis:

Cohen's d effect sizes, calculated directly from the means, standard deviations, and sample sizes in Table 3, are presented in Table 4 (positive values indicate higher concentrations in the variant-carrying genotype). The HindIII comparison (H+H− vs. H+H+) showed moderate positive effects for both apoA-I (d=0.55, 95% CI −0.18 to 1.27) and apoB-100 (d=0.58, 95% CI −0.15 to 1.30); the wide confidence intervals, driven by the small H+H− subgroup (n=8), overlap zero, indicating that a null effect cannot be excluded despite the moderate point estimate. The Ser447Ter comparison (GG vs. GC) yielded recalculated effect sizes of d=0.76 (95% CI −0.14 to 1.67) for apoA-I and d=−0.85 (95% CI −1.76 to 0.05) for apoB-100; both intervals are wide and cross zero, and the extremely small GC subgroup (n=5) makes this estimate highly unstable. The PvuII comparison (P−P+ vs. P−P−) showed a negligible effect for apoA-I (d=−0.05, 95% CI −0.73 to 0.64) and a small-to-moderate effect for apoB-100 (d=0.39, 95% CI −0.29 to 1.08).

None of these effect-size estimates should be interpreted as evidence of a biologically or clinically meaningful association; all correspond to non-significant hypothesis tests (Table 3) and all 95% confidence intervals include zero. They are reported as descriptive, hypothesis-generating estimates only, consistent with the exploratory nature of this study.

Point-Biserial Correlation Analysis:

Results of the point-biserial correlation analysis (variant allele present vs. absent, dichotomised) are presented in Table 5. All correlation coefficients were weak (r range −0.013 to 0.079) and non-significant (all p>0.05). The largest coefficient was observed for HindIII and apoB-100 (r=0.079, p=0.436). These results indicate no linear relationship between the presence of a variant allele (in either heterozygous or homozygous form) and apolipoprotein concentrations when genotype is treated as a simple binary variable. This does not exclude a non-linear, heterozygote-dominant pattern of the kind suggested descriptively for HindIII in section 3.3: because dichotomisation of genotype as 'variant present vs. absent' combines heterozygotes and variant homozygotes into a single category, it assumes an additive and monotonic genotype effect, an assumption that this dataset does not clearly support (see section 4.4).

Genotype Frequency Comparison Between CHD Cases and Controls:

Statistical comparison between patients and controls is presented in Table 6. No significant differences were observed

for sex (χ^2=0.32, p=0.571, OR=1.17, 95% CI 0.67–2.06) or age group (χ^2=0.91, p=0.340, OR=0.73, 95% CI 0.39–1.37); these comparisons involved no zero-count cells and the standard chi-squared test and odds ratio are appropriate. BMI category showed a very strong association with CHD status (χ^2=98.24, p<0.001, OR=114.3, 95% CI 25–512); as noted in section 3.1, this cross-sectional association does not by itself establish an independent or causal effect of obesity on CHD risk.

For the three LPL polymorphisms, all variant genotypes were absent among the 50 controls (0%), precluding valid use of the chi-squared test or a conventional odds ratio. Using Fisher's exact test, variant carriage (heterozygous or homozygous combined) was more frequent among CHD cases than controls for HindIII (11% vs. 0%, p=0.016) and PvuII (12% vs. 0%, p=0.009), while the difference for Ser447Ter did not reach statistical significance (5% vs. 0%, p=0.170). Odds ratios calculated with the Haldane-Anscombe correction were: Ser447Ter, OR=5.82 (95% CI 0.32–107.32); HindIII, OR=12.98 (95% CI 0.75–224.88); PvuII, OR=14.27 (95% CI 0.83–246.07). All three corrected confidence intervals are wide and cross 1, reflecting the imprecision inherent in comparing a genotype frequency to a zero-count reference group; the point estimates should therefore be interpreted only as evidence that variant carriage was more frequent among cases, not as precise measures of the magnitude of that association.

Hardy-Weinberg Equilibrium:

Exact tests for deviation from Hardy-Weinberg equilibrium (Wigginton et al., 2005), calculated from the genotype counts among CHD cases (Table 1), indicated no significant deviation for Ser447Ter (p=1.00), but significant deviation for HindIII (p=0.005) and PvuII (p=0.009). In both cases, the deviation reflected fewer heterozygotes and more variant homozygotes than expected under equilibrium given the observed allele frequency. HWE testing was not performed in controls, as all three loci were monomorphic in this group (0% variant carriers), leaving no genotypic variation to test. The significant HWE deviation for HindIII and PvuII among cases is discussed as a methodological caveat in section 4.7.

Discussion.

This study examined the relationships between serum apoA-I and apoB-100 concentrations and three LPL gene polymorphisms (Ser447Ter, HindIII, and PvuII) in a cohort of 100 Sudanese patients with established CHD and 50 Sudanese controls without a history of coronary artery disease. Among CHD cases, effect-size analysis identified a numerically moderate pattern for the HindIII polymorphism, but conventional hypothesis testing did not reach statistical significance for any genotype-apolipoprotein comparison. Genotype-frequency comparisons between cases and controls, using methods appropriate for the sparse-cell structure of this dataset, suggested more frequent variant carriage among cases for HindIII and PvuII. The interpretation of all these findings requires careful contextualisation given the limitations inherent to the study design.

HindIII Polymorphism: A Possible Heterozygote-Associated Pattern:

The HindIII polymorphism produced the most notable descriptive pattern in this study. H+H− heterozygotes had the numerically highest mean concentrations of both apoA-I and apoB-100, corresponding to a moderate point-estimate effect size (d≈0.55–0.58) relative to H+H+ homozygotes; however, the 95% confidence intervals for these estimates were wide and included zero, and the corresponding ANOVA comparisons were not statistically significant. This pattern is consistent with, but does not establish, a heterozygote-associated effect, in which carriers of a single variant allele show a different phenotype from either homozygote group. Such patterns, when genuine, can arise from allelic complementation, differential regulatory activity of the two alleles, or linkage with functional variants elsewhere in the HindIII haplotype block. Because the HindIII polymorphism itself lies in intron 8 and is not thought to be directly functional, it more plausibly serves as a marker for a functional variant in linkage disequilibrium with it, potentially affecting LPL expression, mRNA stability, or post-translational regulation (9). Masana and colleagues previously reported an association between HindIII genotype and plasma triacylglycerol concentration in Spanish men with premature CHD, which is broadly consistent with a biological role for this locus (12), although that finding does not confirm the specific pattern observed here. Given the very small H+H− subgroup (n=8) in the present study, this finding should be regarded as hypothesis-generating rather than confirmatory.

Ser447Ter Polymorphism: An Unstable Estimate from a Very Small Subgroup:

The Ser447Ter comparison (GG vs. GC) yielded a moderate-to-large recalculated effect size for both apoA-I (d≈0.76) and apoB-100 (d≈−0.85, i.e., higher apoB-100 in GC carriers), but with wide confidence intervals crossing zero and a non-significant t-test for both outcomes. Because only 5 participants carried the GC genotype, and no CC homozygotes were observed, this comparison rests on an extremely small and potentially unstable subgroup; a single atypical value in this subgroup could substantially shift the estimated mean and SD. The broader literature on Ser447Ter has generally associated the Ter (minor) allele with increased LPL activity and a more favourable lipid profile (8), though findings vary across populations; the present dataset cannot meaningfully confirm or refute this relationship given its sample size. These findings should be considered exploratory and hypothesis-generating only, and we recommend that the underlying apoA-I/apoB-100 values for the five GC carriers be re-verified prior to final publication (see the Revision Note in section 3.4).

PvuII Polymorphism: Limited Association:

The PvuII polymorphism showed a negligible effect size for apoA-I (d≈−0.05) and a small-to-moderate effect for apoB-100 (d≈0.39), both with confidence intervals crossing zero, and near-zero point-biserial correlations. These findings are broadly consistent with the generally inconsistent and modest associations reported for this intronic variant in other populations (10). Gene-environment interactions for example, with physical activity or dietary fat intake — could plausibly modify PvuII effects, but this was not assessable within the present cross-sectional design (13).

Reconciling Non-Significant Hypothesis Tests with Moderate Point-Estimate Effect Sizes:

A central methodological theme of this study is the coexistence of non-significant ANOVA/t-test results with moderate Cohen's d point estimates, most notably for HindIII. This is mathematically expected: a p-value reflects both the magnitude of an effect and the sample size available to detect it. With only 8 H+H− and 3 H−H− carriers, and 5 Ser447Ter GC carriers, this study had limited power to detect even a true medium-sized effect a formal power calculation indicates that approximately 64 participants per genotype group would be required for 80% power at α=0.05. The non-significant hypothesis tests are therefore consistent with limited statistical power and do not, by themselves, demonstrate the absence of a true underlying effect; conversely, the moderate point estimates do not demonstrate the presence of one, given their wide confidence intervals. Reporting both statistics together, as done here, is intended to convey this uncertainty rather than to imply that a real effect has been established.

A related limitation concerns the point-biserial correlation used in section 3.5. By collapsing heterozygous and variant-homozygous carriers into a single 'variant present' category, this analysis assumes an additive, monotonic relationship between allele dosage and apolipoprotein concentration an assumption that appears inconsistent with the non-monotonic (heterozygote-associated) pattern described descriptively for HindIII in section 3.3. This is a known limitation of point-biserial correlation for detecting heterozygote-specific effects, and future studies with adequate sample sizes should instead use genotypic ANOVA, dominant/recessive model testing, or a formal test for heterozygote excess/deficiency.

Genotype Frequency Differences Between Cases and Controls:

All three LPL variant genotypes were entirely absent among the 50 controls. Using Fisher's exact test, appropriate for these small and zero-count cells, variant carriage was more frequent among CHD cases for HindIII (p=0.016) and PvuII (p=0.009), but not for Ser447Ter (p=0.170). It is important to note that the previously used chi-squared test and conventional odds ratio are not valid in the presence of zero-count cells, and produced overstated significance and biologically implausible point estimates (e.g., an apparent odds ratio in excess of 25) in the earlier version of this analysis. Even with the Haldane-Anscombe correction applied, the resulting odds ratios (5.82–14.27) carry very wide confidence intervals (all crossing 1), and should be interpreted only as suggesting that variant carriage was more common among cases, not as precise estimates of relative risk. Because no variant carriers were observed among controls, we also cannot exclude the possibility that this pattern partly reflects the relatively small control sample size (n=50) rather than a true absence of these variants in the broader Sudanese population without CHD; a larger control sample would be needed to estimate background variant frequency more precisely.

Deviation from Hardy-Weinberg Equilibrium:

Exact HWE testing among CHD cases indicated significant deviation from equilibrium for HindIII (p=0.005) and PvuII (p=0.009), reflecting fewer heterozygotes and more variant homozygotes than expected given the observed allele frequencies at these loci; Ser447Ter did not show significant deviation (p=1.00). Deviation from HWE in a case-only sample can arise from several distinct sources: genuine biological association between the variant and disease (if the variant itself, or a linked variant, contributes to CHD risk in a non-additive way), population stratification within the sample, small-sample sampling variation, or genotyping error (e.g., systematic misclassification of a subset of heterozygotes as homozygotes on the RFLP gel). This dataset alone cannot distinguish between these explanations. We recommend that genotyping quality-control steps (e.g., a proportion of samples re-genotyped or confirmed by an independent method) be reported if available, and that this deviation be explicitly acknowledged as a limitation of the genetic association findings for HindIII and PvuII (see section 4.7).

Limitations.

- The low frequency of variant alleles produced genotype subgroups (particularly HindIII H−H−, n=3; PvuII P+P+, n=3; and Ser447Ter GC, n=5) too small for statistically reliable inference.
- The cross-sectional design precludes causal interpretation of any association reported, including the BMI–CHD and apolipoprotein–CHD comparisons.
- The study was conducted at a single centre (Sudan Heart Centre) for CHD cases, and controls were recruited separately from the general Sudanese population rather than from the same clinical setting, which may introduce differences in ascertainment between the two groups beyond age and sex.
- Controls were matched to cases by age and sex at an approximate 2:1 case-to-control ratio rather than by individual one-to-one matching; residual imbalance in unmeasured characteristics between groups cannot be excluded.
- All three LPL variant genotypes were entirely absent among the 50 controls, which limited case-control comparisons to exact methods with wide confidence intervals and prevented meaningful HWE testing in this group.
- HindIII and PvuII genotype distributions among cases showed statistically significant deviation from Hardy-Weinberg equilibrium, which may reflect biological association, population stratification, sampling variation, or genotyping error; this cannot be resolved with the present data (section 4.6).
- No data on lipid-lowering medication use or other pharmacological treatment were available, limiting the ability to distinguish genetic effects from treatment-related influences on apolipoprotein concentrations.
- No multivariable-adjusted analysis was performed; consequently, BMI and other clinical differences between cases and controls should be regarded as potential confounders rather than as independently demonstrated effects.
- The overall statistical power of this study was limited for detecting the moderate effect sizes observed, particularly for the rare genotype comparisons.
- Restriction-fragment size data for RFLP genotype calls were not available for inclusion in this manuscript at the time of this revision (see section 2.3).

Clinical and Research Implications.

Despite these limitations, this study applies a multi-method analytical framework combining conventional hypothesis testing, effect-size estimation, and exact methods appropriate for sparse genetic data — and identifies the HindIII polymorphism as a candidate for further investigation in relation to apolipoprotein metabolism in CHD. We emphasise that this study does not establish a clinically meaningful or biologically confirmed effect of any LPL polymorphism on apolipoprotein concentrations or CHD status. Future studies should enrol substantially larger and, ideally, multicentre and ethnically diverse cohorts; incorporate formal gene-environment interaction testing; adjust for relevant confounders (including BMI, medication use, and metabolic comorbidities) using multivariable models; and include genotyping quality-control measures capable of detecting the kind of HWE deviation observed here.

Conclusion.

This exploratory, cross-sectional study of Sudanese CHD patients and controls found no statistically significant association between LPL genotype (Ser447Ter, HindIII, or PvuII) and serum apoA-I or apoB-100 concentrations among CHD cases, although a moderate, imprecisely estimated effect was observed for the HindIII polymorphism in heterozygous carriers. Variant carriage of HindIII and PvuII, but not Ser447Ter, was more frequent among CHD cases than controls using exact statistical methods appropriate for the sparse genotype data; these estimates carried wide confidence intervals, and HindIII and PvuII also showed significant deviation from Hardy-Weinberg equilibrium among cases, a finding that warrants further scrutiny of genotyping quality and sample composition. Given the small variant-genotype subgroups and the study's limited statistical power, these findings should be regarded as hypothesis-generating rather than confirmatory. Larger, adequately powered, multicentre studies in Sudanese and other populations are needed to determine whether LPL genetic variation makes a meaningful contribution to apolipoprotein metabolism or CHD risk in this population.

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Conflict of Interest.

The authors declare no conflicts of interest.

Informed Consent and Ethical Approval.

The study was approved by the Central Institutional Review Board of Al Neelain University, Sudan (Approval Date: 1 March 2015). All participants both CHD patients and controls were informed about the nature and purpose of the study and provided written consent for the use of their data for research purposes. The study was conducted in accordance with the Declaration of Helsinki.

Author Contributions.

A.A.A.N. and I.O.F. designed the research; A.A.A.N., H.E.M., and T.Y.E.Y. performed the experiments and collected samples; E.K.A., A.H., and A.H.A. performed statistical analysis; M.I.S. and S.E.O.H. wrote the original draft; A.H.A., E.I.A., H.O.E., A.A., and S.M.A. reviewed and edited the manuscript; I.A.M. and I.O.F. supervised the study. All authors contributed to and approved the final version of the manuscript.

Data Availability.

Available upon reasonable request.

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