SCHOOL OF PUBLIC HEALTH

COLLEGE OF HEALTH SCIENCES

UNIVERSITY OF GHANA

TRANSFUSION-TRANSMISSIBLE INFECTIONS AMONG BLOOD DONORS IN SUB-SAHARAN AFRICA: SYSTEMATIC REVIEW AND META-ANALYSIS

BY

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THIS IS THESIS WAS SUBMITTED TO THE SCHOOL OF PUBLIC HEALTH, UNIVERSITY OF GHANA, LEGON IN PARTIAL FULFILLMENT OF THE REQUIREMENT FOR THE AWARD OF MASTER OF PHILOSOPHY IN APPLIED EPIDEMIOLOGY AND DISEASE CONTROL

December 2021

DECLARATION

I, Yaw Asamoah Karikari, declare that except for other people's investigations which have been duly acknowledged, this research is the result of my original research undertaken under the supervision of Dr. Anthony Danso-Appiah and Dr. Bismark Sarfo and that it has neither in whole nor in part been presented for another degree in this university or elsewhere.

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ACKNOWLEDGEMENTS

This work was challenging because conducting a systematic review was new to me. I had to keep learning new skills and expanding on what I already knew. While I had my doubts about my ability to complete the work, I am glad I persevered and am proud of the knowledge and abilities I gained.

Dr. Anthony Danso-Appiah, my supervisor, has been invaluable mentor to me. His knowledge of systematic reviews was extremely useful in developing an objective review procedure and breaking it down into digestible components.

I would like to thank Mr. David Owiredu in particular for his assistance over the various stages of our systematic evaluation. I appreciate Miss Rebecca Oteng Gyanwaa's assistance with the data extraction. Mr. Yakubu Alhassan was helpful in taking me through the data analysis. Mr. Ernest Akyereko and Dr. Dora Dadzie, my mentors, provided me with valuable advice and encouragement. Without their help, this review would not have progressed to the point where it is now.

I would want to express my gratitude to the faculty members and staff of the Ghana Field Epidemiology and Laboratory Training Programme for their support and encouragement in seeing this project through. My training was made possible by the financing provided by the West African Health Organization.

On a more personal level, I would like to express my gratitude to my family and friends for their unwavering support and belief in me. Dr. Kenneth D. Sagoe has always been a great help to me at difficult times, and I owe him a great debt of gratitude. Mr. and Mrs. Afetsi have been a pillar of support for me. I would like to express my gratitude to Queenstar Edith Fuachie, a friend who encouraged me to apply to the AEDC program. I would also want to express my gratitude to my classmates for their help with many areas of this project.

DEDICATION

This work is dedicated to my son, Jayden Nyamekye Asamoah for giving me the strength and encouragement throughout this program as well as to my parents and siblings for always motivating me to be better and being my source of stress relief. I also dedicate this work to all blood donors across Sub-Saharan Africa.

TABLE OF CONTENT

LIST OF ABBREVIATIONS

BT	Blood Transfusion
CccDNA	Covalently closed circular Deoxyribonucleic acid
CD4	Cluster of differentiation 4
EMBASE	Excerpta Medica dataBASE
HBV	Hepatitis B Virus
HCV	Hepatitis C Virus
HIV	Human Immunodeficiency Virus
HTLV	Human T-Cell Lymphotropic Virus
ISBT	International Society of Blood Transfusion
NACP	The National AIDS Control Programme
PA	Particle agglutination
PRISMA	Preferred Reporting Items for Systematic Reviews and Meta-Analysis
RD	Replacement donor
RNA	Ribonucleic acid
SIVcpz	Simian Immunodeficiency Virus
SSA	Sub-Saharan Africa
TTI	Transfusion-Transmitted Infection
VNRBD	Voluntary non-replacement blood donor
WHO	World Health Organization
ZIKV	Zika Virus

LIST OF TABLES

LIST OF FIGURES

ABSTRACT

Background

Blood transfusion, as whole blood for a single patient or processed into blood products for multiple patients, is a life-saving intervention, saving millions of lives worldwide annually. Despite its importance and value, blood transfusion is associated with the risks of transmitting deadly infections such as Hepatitis B virus, Hepatitis C virus, Human Immunodeficiency Virus (HIV), and *Treponema pallidum* (Syphilis) to the recipients. Blood safety has been a major public health issue globally due to inadequate infrastructure, national blood transfusion policies and programs, personnel, and financial resources, predominantly in Sub-Saharan Africa with chronic resource constraints. This study aimed at comprehensively reviewing the prevalence of transfusion-transmissible infections among blood donors in Sub-Saharan Africa.

Methods

The systematic review and meta-analysis was designed, conducted and reported using best practices and validated tools and guidelines. Studies from 1st January 2000 to 31st October 2021 that reported transfusion-transmissible infections among blood donors in sub-Saharan Africa were retrieved from relevant electronic databases, including PubMed, SCOPUS, HINARI, Cochrane database library, Web of Science, Google Scholar, and Africa Journals Online, without language restrictions. The following search terms were used: blood transfusion-transmitted infections, blood transfusion-related infections, blood transfusion-transmissible infections, TTIs, blood transfusion infections, and each of the countries in Sub-Saharan Africa. Grey literature including conference proceedings, preprints repositories as well as references of retrieved studies were searched for additional studies. Experts in blood transfusion were contacted for unpublished studies. I (the candidate) screened title and abstract of articles and relevant data were extracted pretested eligibility criteria and data extraction form, respectively. The methodological quality of articles was assessed using Hoy et al critical appraisal checklist

for prevalence studies and the pooled prevalence of HIV, HBV, HCV and syphilis were determined using the random-effects model. Heterogeneity between the studies was assessed using the I^2 statistic. Sub-group analysis was performed by diagnostic methods used, country and geographical region to detect subgroup differences. The systematic review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA) Guidelines for reporting systematic reviews. The protocol was registered in the International Register: Prospective Register of Systematic Reviews (PROSPERO) with registration number: **CRD42021259042,** available at: https://www.crd.york.ac.uk/prospero/display_record.php?ID=CRD42021259042.

Results:

A total of 989 articles were retrieved, and after deduplication, 752 were screened for eligibility. One hundred and twenty-five full-text articles were assessed for eligibility of which 95 studies from different countries in Sub-Saharan Africa met the inclusion criteria. In the random effects model, the overall pooled prevalence (PP) of TTIs was 10.1% (95% CI; 8.4 to 11.7%; n=2,046,506, 95 studies, I^2 =99.9%). The pooled prevalence of the individual TTIs was: HBV (PP 6.9%, 95% CI 5.9 to 7.9%, , n=1,306,763, 75 studies , I^2 =99.9%), HCV (PP 2.0%, 95% CI 1.6 to 2.5%, n=1,228,214, 65 studies, I^2=99.9%), HIV (PP 3.2%, 95% CI 2.5 to 4.0%, n=1,633,198, 61 studies, I^2=99.9%) and syphilis (PP 2.8%,95% CI 1.9 to 3.6%, n=965,488, 43 studies, I^2=99.9%). Eastern Africa had the highest TTIs pooled prevalence (PP 11.2%, 95% CI, 7.3 to 15.1%, 29 studies, I^2=99.9%). Most individuals had co-infections: HBV and HCV co-infections (PP 0.7%, 95% CI 0.2% to 1.2%, 23 studies), HBV and HIV (PP 0.8%, 95% CI 0.3% to 1.3%, 19 studies, I^2=99.9%), HCV and HIV (PP 0.3%, 95% CI 0.1% to 0.4%, 16 studies, I^2=99.3%), HBV, HCV and HIV (PP 3.3%, 95% CI 3.0% to 9.6%, 2 studies, I^2=99.8%), HBV and Syphilis (PP 0.27%, 95% CI 0.1% to 0.4%, 11 studies, I^2=96.7%) and HCV and Syphilis (PP 0.2%, 95% CI 0.03% to 0.3%, 16 studies, I^2=99.4%). The systematic

review showed demonstrable declining trends in the pooled prevalence for the TTIs: HBV (PP of 16.8 % in 2001 to 6.9 % in 2021), HCV (PP of 4.0% to 2.1% in 2021), HIV (PP of 12.9% in 2000 to 3.2% in 2021) and Syphilis (PP of 7.5% in 2003 to 2.8% in 2021). The systematic review revealed the most widely used blood screening tests in Sub-Saharan Africa as Enzyme immunoassays (57.9%) and RDTs (49.5%). The most sensitive tool, PCR was hardly used. Replacement donors accounted for 99% of blood donors in Sub-Saharan Africa

Conclusion:

Despite, this systematic review and meta-analysis showing a huge decline in transfusion transmissible infections from 2001 to 2021 among blood donors in trends analyses, the pooled prevalence of 10.1% TTIs in Sub-Saharan Africa (which translates into 1 positive per every 10 donors screened) is high and has serious implications for public health and clinical practice. Worryingly, given that several studies from 2018 to 2021 appeared to show no further decline in the common TTIs, calls for intensified effort towards scaling down the TTIs among blood donors in SSA with the ultimate goal of ensuring the safety of recipients of whole blood or blood products in this region. Also, it is evident that the widely used diagnostic criteria for blood screening in Sub-Saharan Africa are the RDTs and Enzyme immunoassays which are less sensitive or specific, means the likelihood of some of the infections not being detected is high and calls for intensifying effort that will ensure screened blood products are safe for transfusion.

Keywords:

Transfusion-transmissible Infections, Blood donors, Sub-Saharan Africa, Systematic review, Meta-analysis, Pooled prevalence, Trends

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background

Blood transfusion is a life-saving intervention that saves millions of lives worldwide each year (Biadgo et al., 2017). Blood can be transfused for one patient as whole blood or maybe converted into multiple patient-specific blood products. Although the delivery of blood or its products as a therapeutic intervention helps to save lives, it is also a channel for the transfer of numerous microorganisms, resulting in infections of varying kinds and severity (Mandal & Mondal, 2016).

1.2 Blood Transfusion and blood donation

Blood transfusion is the intravenous administration of blood or blood products into a person's circulation (NHLBI, 2017) and serves as an intervention for medical conditions to replace lost components of the blood. Historically, whole blood has been used in transfusions, but increasingly blood components such red blood cells, white blood cells, plasma, clotting factors, and platelets are prepared for transfusion (Asif et al., 2013).

Transfusion can take two forms; autologous blood transfusion also referred to as autotransfusion, is when blood or its components are given back to the same person from whom it was obtained. Homologous blood transfusion is the transfer of blood or blood components obtained from a donor to another individual (Sansom, 1993). It was estimated that 118.5 million blood donations are collected globally each year of which 40% is collected in developed countries whilst 54% in low-income countries (WHO, 2018). In 2017, the global blood requirement was estimated at 304,711,244 blood product units, whilst supply was 272,270,243 blood product units (Roberts, James & Delaney, 2019), resulting in a need-to-supply ratio of 112. There was insufficient blood in 119 of the 195 countries (61%) of which every country in central, eastern, and western Sub-Saharan Africa, Oceania, and South Asia was short of blood (Roberts, Spencer, Delaney & Christina, 2019).

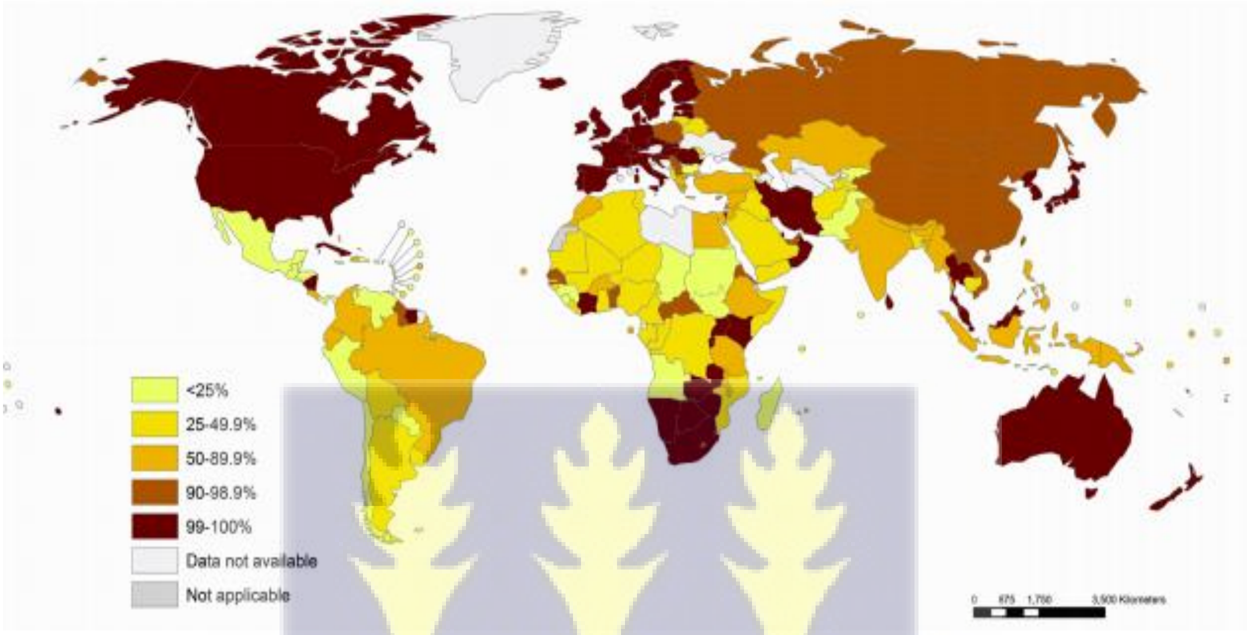

Figure 1: The percentage of global non-remunerated voluntary donations (whole blood and apheresis donations, 2013)

1.3 Transfusion Transmissible Infections

Transfusion-transmissible infection (TTI) is an infection that is transmitted from person to person via parenteral administration of blood or its products (Mohammed & Bekele, 2016). Blood transfusion has been associated with the risks of transmitting infections such as Human Immunodeficiency Virus (HIV), Hepatitis B and C viruses, Human T-Lymphotropic Virus Types I and II (HTLV), *Treponema pallidum* (syphilis), West Nile virus (WNV), Zika Virus (ZIKV), and malaria (ISBT, 2017). Hepatitis B Virus (HBV), Hepatitis C Virus (HCV), HIV, and Syphilis are the most common infectious agents among blood donors (Song, Bian, Petzold, & Ung, 2014).

Blood is an important healthcare resource used in a variety of situations. In developed countries, transfusion is most commonly used for supportive care in cardiovascular and transplant surgery, mass trauma, and the treatment of solid and haematological malignancies; in developing countries, it is most commonly used to treat pregnancy complications and severe anemia in children (WHO, 2016).

The frequency of transmission transmissible infections is directly related to the prevalence of transfusion-transmissible infections among the donor population (Apata & Averhoff, 2014). It is anticipated that if the WHO transfusion safety requirements are not met, transfusions alone will result in 28,595 hepatitis B infections, 16,625 hepatitis C infections, and 6650 HIV infections per year (Jayaraman et al., 2010).

In Sub-Saharan Africa, blood safety is still a major public health issue due to inadequate blood transfusion policies and programs, infrastructure, qualified personnel, and financial resources (Tessema et al., 2010a). According to data from Ghana's National Blood Bank, an average of 280,000 units of blood are required each year, but only 66% are obtained voluntarily. o keep blood banks stocked across the country, frequent voluntary blood donations are required (WHO, 2019).

The development of national blood transfusion guidelines through a set of published rules by the WHO has given rise to the establishment of National Blood Transfusion Services across countries (WHO, 1998). The national blood transfusion guidelines consist of action plans aimed at ensuring the availability of safe, accessible, and inexpensive blood donor units at all levels of the health system (WHO, 1998). However, many countries lack the resources (both material and human) that would enable the adoption of high technologies required for the effective implementation of national blood transfusion guidelines (Duits, 2013).

The prevalence of TTIs in blood donations is substantially higher in middle- and low-income countries than in high-income countries (Song et al., 2014). Globally, an estimated 257, 71, and 36.7 million persons have chronic HBV, HCV, and HIV infections, respectively. The prevalence of hepatitis B in the general population is estimated to be 6.1% and 6.2% in the WHO AFRO Region and the Western Pacific Region, respectively, and the infection accounts for an estimated 1.3 million attributable deaths hepatitis (WHO, 2017).

It is estimated that 12.5% of patients who undergo blood transfusions are at risk of acquiring post-transfusion hepatitis (Bartonjo & Oundo, 2019). The prevalence of Hepatitis C infection has been reported to be present in between 1.3% and 8.4% of blood donors, whereas HIV infection is present in between 1.5% and 3.8% of blood donors (Walana, Ahiaba, Hokey, & Vicar, 2014). Globally, blood transfusion-related HIV infection rate ranges from 80,000 to 160,000 people annually (Walana, Ahiaba, Hokey, Kofi Vicar, et al., 2014), with transfusion of blood being responsible for 5 to 10% of HIV transmission in Sub-Saharan Africa (SSA) (Yooda et al., 2019).

In Ghana, for example, TTIs are still on the upsurge, especially among blood donors with the prevalence of hepatitis B infection ranging between 9.6% to12.0% in urban areas and 13 o 21% in rural communities among blood donors (Walana, Ahiaba, Hokey, Kofi Vicar, et al., 2014). Similar patterns are observed in most Sub-Saharan African countries (Heyredin et al., 2019; M'Baya et al., 2019; B. M. Nagalo et al., 2012; Shiferaw et al., 2019; Siraj et al., 2018; Zerihun et al., 2018)TTIs continue to pose serious risks to blood safety in many developing nations, raising serious public health concerns (Song et al., 2014).

Monitoring the magnitude of TTI in blood donors is critical for ensuring safe blood and blood products to susceptible blood recipients and to help determine the effectiveness of screening programmes (Chassé et al., 2016). Estimation of the prevalence of TTIs among blood donors could also be directly linked to the prevalence of infections in the general community (Shiferaw et al., 2019). Monitoring the prevalence of TTIs can also provide baseline data for optimizing donor recruitment strategies and post-donation counseling services to reduce the spread of the infections (Shiferaw et al., 2019). It is therefore necessary to perform a systematic review on TTIs prevalence among SSA blood donors to provide synthesized and scientific evidences on prevalence of TTIs in donor populations for evaluating policies regarding safe blood transfusion to prevent the spread of infectious agents from blood recipients.

1.2 Problem statement

Transfusion-transmissible infections are major global public health problems and the transfusion of blood and blood products are the major modes of the spread of dangerous infections in high prevalence areas in SSA. Annually, over 81 million units of blood are donated worldwide, with 18 million not screened for infections (Chaudhary et al, 2014). In spite of the significant advancement made to ensure blood or blood product safety in the last 30 years when HIV and hepatitis HCV, blood safety has been a major public health issue in Sub-Saharan Africa with the highest prevalence but inadequate national blood transfusion policies and services, infrastructures, qualified personnel, financial resources, high levels of infections among blood donor population and capacity for donor and blood screening (Tessema et al., 2010a).

In low-income countries, the prevalence of HIV, HBV, HCV, and Syphilis infections is greater; 1.08, 3.70, 1.03, and 0.90 percent, respectively, compared to 0.003, 0.03, 0.02, and 0.05 percent, respectively, in high-income countries (WHO, 2017). Globally, it is estimated that the pooled prevalence of transfusion-transmitted infections ranges from 2.8% to 18.7% (Lakshmi, Devarashetty & Borugadda, 2016). Transfusion transmissible infections are potential risks for healthcare workers; the World Health Organization (WHO) estimates that about 3 million workers are exposed to these infections annually (Mengiste et al., 2021).

Every year, up to 16 million new hepatitis B infections and 5 million new hepatitis C infections are caused by contaminated blood transfusions (Chaudhary et al, 2014). The global HIV infection rate through blood transfusions alone ranges from 80,000 to 160,000 each year (Walana et al, 2014). In sub-Saharan Africa (SSA). An estimated 5–10% of HIV infections in Sub-Saharan Africa are caused by transfusion of infected blood (WHO, 2014)**,** and 12.5% of patients who receive blood transfusions are at risk of post-transfusion hepatitis (Okoroiwu et al., 2018a)**.** According to a study conducted by Adu-poku et al., 2020, the most affected age group affected by transfusion transmissible infections are those between the ages of 20 years and 49 years. Female donors are 30% less likely to be infected with Syphilis than males.

In Africa, where severe malaria, postpartum hemorrhages, malnutrition, and sickle-cell anemia are all common, blood transfusions are essential life-saving treatments (Loua et al., 2019) Candidate blood donors should be tested for HBV, HCV, HIV, and syphilis infections in order to ensure safe blood for transfusion and to prevent TTIs (Pruett et al., 2015). The process of transfusing blood is still difficult in poor nations, particularly in Sub-Saharan Africa (SSA) (Loua et al., 2019; Weimer et al., 2019). The main cause of this issue is the patchy availability of test kits, which is one of the most often mentioned screening-related obstacles (Loua et al., 2019; Weimer et al., 2019)**.**

Thus a systematic review and meta-analysis of data on the prevalence of TTIs among blood donors in SSA permit assessment of the accurate estimate of the risk of TTIs, which helps in the creation of long-term strategies to improve public health and to prevent the spread of disease in the local population (Adu-poku et al., 2020).

1.3 Justification

Despite strict donor screening and testing procedures, issues such as the 'window period,' false-negative results, the prevalence of asymptomatic carriers, viral genetic heterogeneity, and technical errors persist (Gagandeep et al., 2010), which continues to pose the risk of transfusion transmissible infections. A mathematical model that used three components to measure transfusion risks across 45 Sub-Saharan African countries found that the risk of a contaminated unit entering the blood supply, the risk of the unit being provided to a susceptible patient, and the risk of the recipient contracting an infection after receiving the unit indicated that in Sub-Saharan Africa, the risks of contracting HIV, HBV, or HCV from blood transfusion were 1, 4.3 and 2.5 infections per 1000 units, respectively (Jayaraman et al., 2010). According to a modeling exercise, transfusion of blood and blood products would be responsible for 28,595 HBV infections, 16,625 HCV infections, and 6650 HIV infections every year, if the WHO transfusion requirements are not met (Jayaraman, Chalabi, Perel, Guerriero, & Roberts, 2010). There is currently no available systematic review on transfusion transmissible infections in Sub-Sahara Africa even though several individual studies on TTIs have been conducted. The current study, therefore, sought to estimate the prevalence of TTIs in Sub-Saharan Africa, assess TTI-related factors, and provide the best evidence for sound and rational decision-making by Health care providers, patients, researchers, policymakers, and stakeholders involved in blood transfusion services.

1.4 Conceptual framework

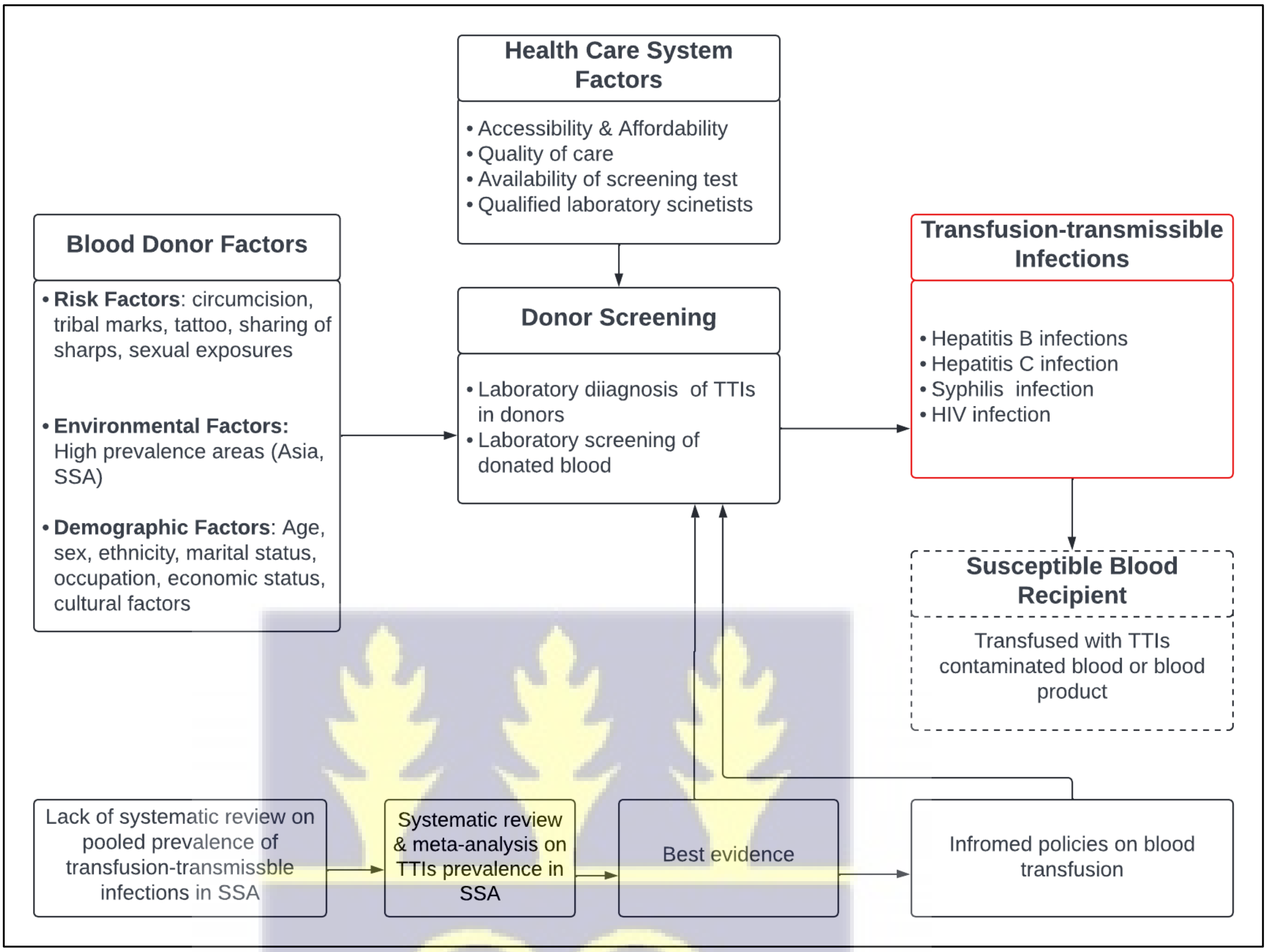

Figure 2: Conceptual Framework of systematic review and meta-analysis on TTIs prevalence in blood donors in SSA

1.5 Narrative to the conceptual framework of the systematic review and meta-analysis of TTIs among SSA blood donors

Donor factors, healthcare system factors, and health worker factors are interconnected and influence blood transfusion outcomes. Donor factors including: Risk factors including; tribal marks, circumcision, sharing sharps, sexual exposures, tattoos, etc. Environmental factors such as; high prevalence areas (Asia & Sub Sahara Africa), and Demographic factors comprising of; age, sex, ethnicity, economic, cultural factors have been identified as risk factors for a blood donor to be infected with transfusion-transmissible infections such as hepatitis B virus, hepatitis C virus, Treponema pallidum, and human immunodeficiency virus.

The healthcare system such as accessibility, availability of screening tests, and affordability of testing for transfusion-transmissible infections are heavily reliant on the health worker factors including; professional knowledge, professional experience, professional qualification, and professional skills for the outcomes (TTI's) for the identification or diagnosis of TTIs in blood donors and donated blood, to prevent the possibilities of transfusing infected blood to recipients.

Meanwhile, the availability of systematically synthesized data on transfusion-transmissible infections in Sub-Saharan Africa will enable the acquisition of evidence-based knowledge and aptitudes by the healthcare workers especially concerning screening for TTI's, among blood donors. This acquisition of knowledge and aptitudes is also a positive reinforcement and motivating factor which significantly influences proper and adequate donor and blood screening to prevent the possibility of transfusing infected blood to potential recipients to avoid morbidities and mortalities due to the transfusion of infected blood. Best evidence generated by systematic reviewed and meta-analyzed data of transfusion-transmissible infections will inform policies concerning health care factors such as the availability of screening and testing centers at all levels of the health system, affordability of donor screening, selection of donors which in turn will impact the effectiveness of blood screening to ensure no infected blood or blood products are given to recipients.

1.6 Research Questions

1. What is the prevalence of TTIs in blood donors in Sub-Saharan Africa?
2. What methods are available for screening blood and blood products donated for transfusion in Sub-Saharan Africa?

3. What are the trends of TTIs among blood donors in Sub-Saharan Africa?

1.5 Study Objectives

1.5.1 Main Objective

This study aims at reviewing the prevalence of transfusion-transmissible infections among blood donors in Sub-Saharan Africa.

1.5.2 Specific Objectives

1. To estimate the prevalence of transfusion-transmissible infections (TTIs) in the donor population to estimate the burden of TTIs through blood transfusions in Sub-Saharan Africa.
2. To explore screening methods used based on available literature in Sub-Saharan Africa.
3. To examine the trends of TTIs prevalence among blood donors in Sub-Saharan Africa

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Prevalence of Transfusion Transmissible Infections in Africa

Several studies have reported on transfusion transmissible infections in Sub-Saharan Africa. In a study conducted in Ethiopia involving 6,471 blood donors, 424 (6.6%) of the blood donors were positive for at least one transfusion-transmissible viral infection. Hepatitis B infection was positive for 3.6% of the participants, 2.2% were positive for HIV, and 0.8% were reactive for HCV infection. Co-infection was reported in 0.062% of the participants: 75% with HBV-HCV and 25% with HIV-HBV-HCV (Biadgo et al., 2017).

A study conducted in Ghana, also reported that the prevalence of HIV, HBV, HCV, and Syphilis were 3.9% 5.0%, 4.2%, and 5.2% respectively. Syphilis infection was shown to be 30% less common in females, donors between the ages of 20 and 29 were 60% less likely than those under the age of 20 to contract HIV, while persons aged between 30 and 39 years were 90 percent probable to contract Syphilis than those under the age of 20, and those aged 40-49 were twice as likely to contract HBV than those under the age of 20 (Adu-poku et al., 2020).

In another conducted in SSA, it was estimated that the median overall risks of contracting HIV, HBV, and HCV following a blood transfusion in Sub-Saharan Africa were approximately 1, 4.0, and 3.0 infections per 1000 units, respectively. Transfusions would be responsible for about 29,000 HBV infections, 17,000 HCV infections, and 7000 HIV infections every year if annual transfusion supplies projected by the WHO were met, sensitivity analysis reveals that the real risks could be substantially greater (Weimer et al., 2019).

2.2 Hepatitis B Virus

The Hepadnaviridae family includes the hepatitis B virus (HBV). It has a diameter of 30–42 nm and is made up of an outer lipid envelope containing hepatitis B surface antigen (HBsAg) and a protein-rich icosahedral capsid core (Song & Kim, 2016).The viral capsid contains the viral genome and reverse transcriptase-active DNA polymerase. The HBV genome is made up of a circular, partially double-stranded DNA with four open reading frames: (I) S for hepatitis B surface antigen (HBsAg); (II) pre-C/C for hepatitis B e antigen (HBeAg) and core protein (HBcAg); (III) P for polymerase, including reverse transcriptase; (IV) X for transcriptional transactivator factor (HBxAg) (Kramvis, 2014).

Hepatitis B Virus's transcriptional template is covalently closed circular DNA (cccDNA), which remains as a mini-chromosome inside the hepatocyte nucleus (Locarnini & Zoulim, 2010). The error-prone reverse transcriptase involved in HBV replication causes a high mutation rate, as seen in retroviruses and RNA viruses (Simmonds, 2001). According to existing figures, there are 250 million persons globally, chronically infected with the hepatitis B virus (Faure-Dupuy et al., 2018).

Cirrhosis and hepatocellular carcinoma can develop later in life as a result of immune-mediated liver damage in these people (Karayiannis, 2017). Annually, 800,000 people die as a result of the disease's chronic complications, including cirrhosis, hepatocellular carcinoma (HCC), or liver failure. (McGlynn, Evans, & London, 2012). Hepatitis B infection may be passed from one person to another in a variety of ways. The mode of transmission is determined by the number of chronic carriers in the population.

Transmission of HBV occurs primarily vertically, from a carrier mother to her infant, or through close contact between children in countries where HBV is endemic, such as Sub-Saharan Africa. Perinatal transmission of HBV occurs primarily during or shortly after birth when the newborn comes into touch with the mother's blood and other bodily fluids (WHO, 2006). While breast milk has not been linked to vertical transmission, carrier mothers are advised not to suckle other children but may breastfeed their babies (WHO, 2006).

Mothers who are carriers and test positive for the envelope antigen have a 90% chance of infecting their newborns (Hadziyannis, 2011). Children who are infected before the age of one year stand a 90% risk of becoming chronic carriers, whereas 10 percent of adults who are infected become chronic carriers (Hadziyannis, 2011).

2.3 Hepatitis C Virus

Hepatitis C Virus (HCV) belongs to the Flaviviridae family of viruses (Howard, 2002), having a single-stranded, positive-sense RNA genome of approximately 9.6 kb. The virus has a significant level of sequence heterogeneity due to the poor fidelity of HCV RNA-dependent-RNA-polymerase (NS5B protein) (Moradpour D, Penin F, 2007). Based on sequence homology, six genotypes of HCV (1-6) and several distinct subtypes (denoted by a little English alphabet suffixed after genotype, (e.g., 1b, 3a, etc.) have been identified (Umer & Iqbal, 2016). The genotype distribution of HCV is highly varied. Genotypes 1-3 are found all across the globe, while genotypes 4 and 5 are only located in the Middle East and Africa, and genotype 6 is predominantly found in Southeast Asian countries (Li, Chan, 2009; Ohno et al., 1997).

The hepatitis C virus transmission method is still a source of debate. In the vast majority of instances, infection occurs as a result of exposure to blood or blood products parenterally exposure, and the vast majority of intravenous drug users become infected as a result of repeated contact to contaminated injection equipment (Tibbs, 1995). Infection risk from a single need lipstick injury range from 5 to 15%, depending on the size of the inoculum. Traditional medicinal techniques and the use of infected medical equipment are two other parenteral ways of transmission (Tibbs, 1995).

Even though transmission within a family is uncommon, family members and sexual partners of carriers have a higher rate of hepatitis C virus antibodies than the general public. In certain situations, acute hepatitis C has been detected after a specific sexual experience (Tibbs, 1995). Vertical transmission is rare unless the mother has high amounts of HCV RNA in her blood, which can happen in HIV-positive individuals (Ward, 2018). The presence of hepatitis C in saliva and a higher-than-expected rate of infection among dentists may indicate the possibility of transmission via spit. There are still a considerable proportion of hepatitis C carriers for whom no infection pathway can be identified (Tibbs, 1995).

2.4 Human Immunodeficiency Virus

The human immunodeficiency virus (HIV) is still the top cause of morbidity and mortality in the world. About 76 million individuals have been infected with AIDS (acquired immunodeficiency syndrome) since the epidemic began, and AIDS-related illnesses have claimed the lives of 35.0 million individuals worldwide (UNAIDS, 2017). About 37 million individuals were living with HIV in 2016, there were 1.8 million new HIV infections reported, and 1 million individuals died from AIDS. (UNAIDS, 2017). In 2015, SSA was responsible for 76% of all HIV infections, 76% of new HIV infections, and 75% of all HIV/AIDS deaths (Wang et al., 2016). Furthermore, SSA accounts for two-thirds of the estimated 6000 new HIV infections per day. AIDS has disproportionately harmed women around the world (Ramjee & Daniels, 2013; Kharsany & Karim, 2016). It is estimated that every 60 seconds, a young woman contracts HIV (UNAIDS, 2012).

The situation is overwhelming in SSA (Gita Ramjee & Brodie Daniels, 2013; Kharsany & Karim, 2016), where females make up at least 56–59% of PLWHAs (Sia et al., 2016; UNAIDS, 2018). Currently, girls account for 75 percent of new infections in SSA among young people aged 15 to 19 years. Girls account for 75 percent of HIV incidence in SSA among young people aged 15 to 19 years. In addition, women in the sub-region aged HIV is twice as common in women aged 15–24 as it is in men of the same age range (NACP, 2019). In 2017, teenage females aged 10–19 years old accounted for 79 percent of HIV cases in southern and eastern Africa (UNAIDS, 2019).

Although HIV-1 infections continue to be a major problem in Sub-Saharan Africa, an increasing number of countries are reporting steady or declining prevalence (e.g., Kenya, Zambia, Ghana, Rwanda, Tanzania, Zimbabwe, and Burkina Faso) (NACP, 2019).

The human immunodeficiency virus (HIV) belongs to the Lentivirus genus, which is part of the Retroviridae family, subfamily Orthoretrovirinae (Seitz, 2016). HIV is classified into types 1 and 2 (HIV-1, HIV-2) based on genetic characteristics and differences in the viral antigens (Sharp & Hahn, 2011). Nonhuman primate immunodeficiency viruses (simian immunodeficiency virus, SIV) are also classified as Lentiviruses. Currently, available epidemiologic and phylogenetic research suggests that HIV entered the human population between 1920 and 1940 (Hebb et al., 1999; Nawrocki, 2015; Sharp & Hahn, 2011). HIV is spread when infected blood, sperm, vaginal secretions, or breast milk enters another person's body. Once within the body, the virus can propagate as a free viral particle or in a cell-associated form through target cells (Shane, Lewis, Zhang, Paul, 2012; Sourisseau, Sol-Foulon, Porrot, Blanchet, & Schwartz, 2007). The plasma virus is a cell-free virus, whereas the intracellular progeny virion that has been created but has not yet budded off the manufacturing T-cell is a cell-associated virus (Barreto-de-souza et al., 2014). In a cell-associated viral spread, the processes of budding, attachment and entry, proceed quickly at the sites of cell-to-cell contact (Mothes et al., 2010).

This shields the virus from the harsh extracellular environment while also concentrating viral particles at infection sites (Barreto-de-souza et al., 2014). The replicated viruses bud off from the producer cell, disseminate, identify a CD4 receptor on a CD4+ T cell, attach to the cell, and finally enter the cell in cell-free viral dissemination. Cell-free and cell-associated viruses are found in infected blood, sperm, vaginal fluids, and breast milk (Barreto-de-souza et al., 2014; Jonathan Posner and Bradley S. Peterson, 2008; Sagar, 2014). Markers for HIV screening of blood donations include the following markers: Serological markers: - Anti-HIV-1 against gp 41, including group O, + anti-HIV-2 against gp 36 - HIV p24 antigen (p24 Ag); viral nucleic acid: HIV RNA (Weber et al., 2002).

It is recommended that a test method capable of identifying both HIV-1 and HIV-2 subtypes be used. The great majority of donated blood from infected donors will be identified by screening for both antigen and antibodies. The antibody is detectable three weeks after infection, while the antigen is detectable six days after the first detection of antigen. Viral RNA may be identified 7-11 days after infection, however, HIV p24 antigen can be detected 3-10 days after viral RNA; its identification can shorten the serological window duration by 3-7 days before antibody detection (WHO, 2013b).

2.5 Syphilis (Treponema pallidum)

Treponema pallidum is a bacterium with a diameter of 0.10 to 0.18 micrometers and a length of 6 to 20 micrometers (Sambri et al., 2001). Syphilis is caused by *T. pallidum*, which is closely linked to other T. pallidum pathogenic strains that cause bejel, yaws, and pinta (LaFond & Lukehart, 2006). Until a distinct genetic signature is discovered, of *tpp15*, the four pathogenic strains of *T. pallidum* were indistinguishable (Noordhoek et al., 1989), a 15-kDa lipoprotein gene with a 5' and 3' flanking region can be used to distinguish between strains (Centurion-Lara et al., 1998).

Syphilis is usually contracted by sexual intercourse with someone who has active primary or secondary lesions. According to studies, the attack rate of syphilis is 16 percent to 30 percent within 30 days of sexual encounter with someone with syphilis (Schroeter, Turner & Lucas, 1971; Moore, Price, Knox, & Elgin, 1963). Oral intercourse is an excellent route for syphilis transmission (CDC, 2004; Marcus et al., 2006; Page-Shafer et al., 2002). When spirochetes pass through the placenta of an infected woman and infect the fetus, syphilis is transmitted congenitally (LaFond & Lukehart, 2006).

Syphilis can be passed from person to person through blood transfusions (Kaur & Kaur, 2015). While in high-income nations the risk of blood-borne transmission is almost non-existent, (Gardella et al., 2002)(Gardella et al., 2002), it remains in low- and middle-income countries (LMICs; (Efstratiou et al., 2000). Every year, almost 6 million new cases of syphilis are identified in people within the age group 15 to 49 years all across the world (Aabdien et al., 2020; Hao et al., 2011; Noubiap et al., 2013). Over 300,000 prenatal and neonatal deaths have occurred as a result of syphilis, and another 215,000 infants are at risk of dying prematurely (Noubiap et al., 2013). The incidence and prevalence of syphilis remain high among both volunteer and family/replacement blood donors in many parts of the world (Ji et al, 2013; Noubiap et al, 2013). In the literature, there are several reports in high-risk groups, both from developed and developing countries, demonstrating increased syphilis prevalence and incidence (Hao et al, 2011; Muldoon & Mulcahy, 2011).

2.6 Trends of transfusion-transmissible infections in Sub-Saharan Africa

The ability to monitor trends in the rate of transfusion-transmissible infections (TTIs) in blood donors is crucial to the safety of the blood supply and the success of donor screening. Globally, decreasing trends of TTIs have been reported by several studies. The frequency of transfusion-transmissible infections decreased significantly from 9.5% to 7.0% in a research conducted in Eastern Ethiopia between 2010 and 2013, with the lowest prevalence in 2012 (5.9%) (Zerihun et al., 2018). A similar decrease of TTIs prevalence was observed in studies conducted in Northwest Ethiopia (Tessema et al., 2010b). Transfusion-transmissible infections seroprevalence in Gondar increased from 3.6% to 5.5% year on year from 2014 to 2018 although it did not indicate a trend (Shiferaw et al., 2019). The decreasing trends of TTIs prevalence could be attributable to modifications and improvements instituted by the blood bank to ensure proper donor selection (Zerihun et al., 2018). From 2010 to 2012, there was a significant decrease in HBV prevalence, which subsequently rebounded in 2013. HCV infection rates increased from 0.35% to 1.46% between 2010 and 2012, but then fell to 0.7% in 2013 (Zerihun et al., 2018).

From 2010 through 2012, the HBV trend showed a steady decline, with a minor uptick in 2013 (Zerihun et al., 2018). Decreasing trends of HIV prevalence among blood donors have been recorded in Ethiopia (Sharew et al., 2017), Zerihun et al., reported a decreasing trend in HIV prevalence, which they attribute to the favourable effect of HIV prevention initiatives (Zerihun et al., 2018). There has been a declining trend of HIV infection for male and female blood donors (Sharew et al., 2017), between 2011 and 2015, Muktar et al., reported of decline in HIV prevalence among donors in the Northern Region of Ghana (Tikumah Muktar et al., 2019). During the study period, the prevalence of syphilis declined gradually (Zerihun et al., 2018). This finding is in line with the decreasing trend in syphilis infections among Gonder blood donors (Tessema et al., 2010b). Nigeria has documented a similar syphilis decline pattern (Salawu et al., 2010), an insignificant decline in syphilis has been documented by Muktar et al., in Ghana and The trend shows that not much has been being done to manage the risk factors and determinants of syphilis incidence over time (Muktar et al., 2019).

2.7 Blood availability and donor recruitment

In Africa, blood shortages are still widespread, with over 40 nations failing to meet the WHO's donation target of 10 units per 1000 people. Despite a 19% rise in blood donation in some SSA countries from 2011 to 2014, shortages persist (Michelle et al., 2016). This poses a range of health risks. Indeed, insufficient access to blood transfusion has been blamed for a quarter of peripartum maternal fatalities in SSA. Delay in transfusion has also been linked to an increased risk of death in children with malaria-related anemia(Bates, Chapotera, McKew, 2008).

A study revealed that extremely anaemic children who had not been transfused in the previous eight hours of diagnosis had a 52 percent mortality rate (Kiguli et al., 2015). Nonetheless, the overall projected blood supply in SSA will be insufficient to meet the theoretical transfusion needs for malaria-associated anaemia alone (Lund, Hume & Allain, 2013). In SSA, there has been a rise in VNRBDs (WHO, 2010). Even though it has been raised, it has not always been retained. Replacement donation (RD), the most common alternative to VNRBD, is controversial due to the presumed increased infectious risk. Despite a volunteer donor pool that is inadequate to satisfy demand, the WHO exclusively supports VNRBD (WHO, 2013). Evidence supporting the use of voluntary non-replacement blood donors NRBDs over replacement donors may be concealed by donor status (that is, first-time versus repeat donation), where the risk of infection in a repeat donor is reduced because of earlier transfusion-transmitted infections screening (Weimer et al., 2019).

As shown by a study in Zimbabwe, including repeat donors in VNRBD analyses artificially lowers TTI prevalence, with HIV rates in repeat VNRBDs of 0.42 % compared to 1.29 % in first-time VNRBDs (Mapako et al., 2013).The prevalence of TTIs among VNRBDs and RBs first-time donors do not vary much when repeat status is accounted for, as seen in Ghana, Guinea, and Cameroon (Karin et al., 2014). Males of secondary school age are consistently the leading donors in SSA (Tagny et al., 2010).

This is attributed to targeted recruiting focused on perceived good health and low infectious risk, resulting in repeated shortages during school breaks (Allain, 2011). Females continue to be inadequately represented in the donor population, owing to societal beliefs that men are healthier and iron-deficiency anaemia and pregnancy restrict donation capacity (Birhaneselassie, 2016; Olusola & Ogiogwa, 2020; Tagny et., 2009).

Few studies have been performed to characterize the sociocultural motivators for or deterrents to blood donation (Asamoah-akuoko, Hassall, & Bates, 2017; Koster, 2011). Altruism, family duty, or monetary and nonmonetary rewards such as free health screenings or gifts are all big motivators (Asamoah-akuoko et al., 2017; Muthivhi et al., 2016).Donor eligibility is influenced by regional health risks: in the South and East AFRO region, deferral rates for medical conditions such as low weight and anaemia (10.5 %) outnumber those for high-risk activities (1.5%). While medical deferral is not specific to SSA, it has a greater impact due to higher rates of endemic anemia (for example, due to malnutrition, iron deficiency, and parasitic infections) (Tagny, Owusu-Ofori, Mbanya & Deneys, 2010).

2.8 Blood donor screening methods

2.8.1 Pre-donation screening of donors

Pre-donation screening for TTIs is the process of testing a potential donor for the presence of one or more TTI agents using a single rapid or fast procedure, and deferring donation if the test is positive for any of the TTI markers (Shittu et al., 2014). The normal procedure is to administer a questionnaire and estimate the haemoglobin level. The purpose of pre-donation TTI testing is to conserve resources, supplies, and time that would have been spent to obtain donated blood that could not be used in transfusion and lower the percentage of donated blood that is discarded. Testing for TTIs among prospective donors avoids going through the donation process needlessly and the rate of donated blood that is discarded is reduced (Shittu et al., 2014).

Testing for TTIs before donation is the standard practice in many hospital-based blood transfusion facilities in SSA countries. The questionnaire on donor history assumes that donors understand the questions and that their responses to those activities are correct. Donation centers can use donor history questionnaires to determine the donor's current general health as well as his or her medical history (Dean et al., 2018). Some drugs and exposures revealed via the pre-donation questionnaire can result in the donor being deferred indefinitely or for a fixed period by the collection center. The questionnaire may be beneficial when laboratory testing is not accessible or possible to diagnose infectious disorders classified by the FDA as TTIs (Dean et al., 2018).

2.8.2 Post-donation screening of blood

As a supplementary precaution beyond the donor questionnaire, post-donation testing is employed to detect some TTIs for which FDA-approved tests are available (e.g., HIV, HBV, HCV, HTLV- and syphilis). Testing procedures for detecting TTIs in donated blood products have substantially improved over time. Serological screening tests are effective and cost-efficient in ensuring the blood supply's safety (Dean et al., 2018).

However, antibody formation can take several weeks after exposure to a pathogen, resulting in a window period between the time of infection and the first detection of infectious donors by testing. During this window period, seronegative donors account for the majority of HIV, HCV, and HBV transmission (Dean et al., 2018).Efforts were placed in the development assays in the 1990s to identify seronegative donors and to reduce the transmission rates of TTIs further. When compared to antibody testing, NAT to detect viral DNA or RNA showed promising results, lowering the window period for HCV by 50 to 60 days and for HIV by 11 to 15 days (Shimian et al., 2010).

The first serological tests for HBV detection in the USA were HBsAg and HBcAb detection, and they are still used as part of the research algorithm today. In 2007, HBV NAT was introduced to the HCV/HIV research platform, along with HBsAg and HBcAb assays, and in

2012, the FDA advocated testing all blood products using HBV NAT (Stramer et al., 2011). According to recent reports, the window time for detecting HBV will be reduced by 8 to 20 days as compared to antibody testing (Stramer & Edward, 2013). Individuals who test positive for HBV, HCV, HIV, or Syphilis are barred from ever giving blood. Following a 6-month deferral period and subsequent negative HBcAb, HBsAg, and NAT findings, individuals with false-positive HBV NAT results, similar to HIV and HCV NAT algorithms, may be eligible for readmission into the donor pool (U.S FDA, 2012).

2.9 Laboratory diagnostic methods for screening donor blood for TTI's

Throughout the previous three decades, a variety of assays have been developed for blood screening. Antibodies, antigens, and the infectious agent's nucleic acid are among the most commonly utilized assays. However, not every assay is appropriate for every case, and each assay has its own set of constraints. Therefore, when choosing assays, factors must such as critical assay characteristics, such as sensitivity and specificity, as well as cost and ease of use must be acknowledged and taken into account. The most common types of assay available for blood testing are Immunoassays (IAs) examples: Chemiluminescent immunoassays (CLIAs), Enzyme immunoassays (EIAs), Haemagglutination (HA)/particle agglutination (PA) assays, Rapid/simple single-use assays), and Nucleic acid amplification technology (NAT) assays (Amino , 1995; WHO, 2009).

2.9.1 Enzyme immunoassays (EIAs) and Chemiluminescent immunoassays (CLIAs)

The routinely used tests for screening blood for transfusion infections are enzyme and chemiluminescent immunoassays. The main difference between EIAs and CLIAs is the mechanism of detection of immune complexes created, which is color creation in EIAs versus measuring the light produced by a chemical reaction in CLIAs. If properly evaluate for blood screening and subsequently utilized in a quality setting, any of these forms of IA with high sensitivity will often identify the target signs of infection necessary. EIAs and CLIAs are appropriate for screening large quantities of samples and necessitate the use of a variety of specialized tools. Manually or using non-dedicated automated assay processing equipment, these assays can be carried out (open system). They could also be designed expressly for use on dedicated automated systems (closed systems) (WHO, 2009).

2.92 Haemagglutination (HA)/particle agglutination (PA) assays

Particle agglutination assays use the agglutination of particles coated with the complementary specific antigen or antibody to detect the presence of a specific antibody or antigen in a test sample. In agglutination assays, which are predominantly antibody assays, red cells (haemagglutination) and inert particles such as gelatin and latex are utilized (WHO, 2009). This method of using inert particles reduces non-specific reactivity to cross-reacting red cell antigens. Regardless of the type of particle used, the underlying principles of haemagglutination and particle agglutination are the same. Particle agglutination assays are still widely utilized for the detection of syphilis antibodies (WHO, 2009). For the detection of syphilis antibodies, Particle Agglutination tests are still widely utilized. PA tests do not require any additional processes or wash equipment.

The visual reading and interpretation of test results are subjective, and no permanent record of test results may be kept. PA tests are suitable for screening large volumes of blood samples in an automated manner. (WHO, 2009).

2.9.3 Rapid/simple single-use assays (rapid tests)

Single-use rapid or simple tests are disposable assays that are used once and then discarded. These tests are accessible in several different formats. A type of immunochromatography in which a sample is put to an inert strip and reacts with reagents that have been previously immobilized is used in many rapid tests (WHO, 2009).

In some situations, the specimen can be plasma, serum, or whole blood. A dot or a band positive represents a positive reaction on the device strip. Regardless of the specific test result, most assays have a control dot or band that is utilized to validate the results of each particular device (WHO, 2009).

Rapid tests are available in simple-to-use formats that usually just require the chemicals included in the test kit. They are visually read and provide a straightforward qualitative result in a matter of minutes. The results of tests are subjectively interpreted, and no permanent record of the original test results may be retained. Rapid Diagnostic Tests are not usually good for screening a big number of blood samples (WHO, 2009).

2.9.4 Nucleic acid amplification technology (NAT) assays

Nucleic acid amplification technology (NAT), detects the presence of viral nucleic acid, RNA, or DNA in blood samples. A specific RNA or DNA fragment of the virus is targeted and amplified in vitro using this method. The amplification stage aids the identification of low quantities of virus in the original sample (WHO, 2009). The presence of a certain nucleic acid shows that the virus is present and that the donated sample is likely to be infectious.

By increasing the amount of specific target-present to an easily identifiable level, the amplification stage allows low quantities of virus in the original sample to be detected. The presence of particular nucleic acid implies that the virus is present and that the contribution is likely to be infectious (WHO, 2009). The polymerase chain reaction (PCR) invented by Kary Mullis is the most relevant nucleic acid amplification technology (NAT) and has comprehensively revolutionized diagnostics in many areas (Roth, 2019).

2.10 Safety challenges associated with blood transfusion in sub-Saharan Africa

Bloody safety is still a concern in SSA, where many nations are resourced-constrained. Patient safety is further jeopardized by the infiltration of low-quality, untested in vitro diagnostic reagents into healthcare systems (Bloch et al., 2015).

Due to a variety of factors, including a lack of blood, improper implementation of blood transfusion guidelines, infrastructural deficiencies, and a high prevalence of transfusion-transmissible infections (TTIs), predominantly hepatitis and human immunodeficiency viruses, achieving blood transfusion safety in Sub-Saharan Africa remains a challenge (Abdella, Hajjeh, & Sibinga, 2018).

The WHO has been leading efforts in most parts of Africa to establish safe, accessible, and affordable blood transfusion services by encouraging adequate blood donor recruitment, testing, and collection, as well as establishing policies for the rational use of blood. Despite the efforts and successes achieved over the years, blood transfusion safety remains an uphill task (WHO, 2020).

Approximately 120 million units of blood are donated each year. However, this is insufficient to meet global demand, because many patients who require transfusion do not have timely access to safe blood. There is no way to keep blood for an infinite period (WHO, 2020).

CHAPTER THREE

3.0 METHODS

3.1 Study design and protocol registration

This dissertation used a systematic review design in synthesizing evidence on transfusion-transmissible infection among Sub-Saharan Africa's blood donors. It adopted PICOS (P-Patients, I-intervention, C-control, O-Outcomes, and S-Study) to describe the population, intervention, comparators, outcome of the intervention, and study types in the primary studies included in the systematic review. The protocol of this systematic review and meta-analysis was registered on PROSPERO (an international prospective register of systematic reviews) with registration number CRD42021259042. The entire report adhered to the guidelines set by the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA).

3.2 Criteria for including studies in this review

3.2.1 Inclusion and exclusion criteria for study selection

Studies that reported transfusion-transmissible infections among blood donors; between 16 years and 65 years, living in sub-Saharan Africa were eligible for inclusion. Case reports, abstracts with insufficient data, commentaries, and reviews were excluded. Also, studies with uncommon TTIs in sub-Saharan Africa such as West Nile virus, dengue fever, and human T-lymphocyte virus-1/2, studies with the frequency of TTIs in chronically transfusion-dependent patients of thalassemia major and haemophilia, were ineligible for inclusion.

3.2.2 Population

The population for the systematic review was blood donors in Sub-Saharan Africa. Even though the WHO age arrange for blood donation is between 18 years and 65 years, the study population included: persons aged between 16 years and 65 years, with bodyweight greater than 50kg, haemoglobin level greater than 12.5 g/dl whereby the exclusion criteria were: age less than 16 years or more than 65 years, bodyweight less than 50kg. Haemoglobin values less than 12.5 g/dl, history of jaundice, sickle cell disease, hypertension or current fever, recent illness or transfusion, high-risk sexual behavior, and lack of consent.

3.2.3 Intervention/Scope of the Meta-Analysis

The object of the study is to estimate the prevalence and trend of TTIs including HIV, HBV, HCV, and syphilis among blood donors in Sub-Saharan Africa. This is not a systematic review of intervention studies.

3.2.4 Control

The systematic review aimed at assembling all studies on TTIs in SSA but none of the studies retrieved and included in the analysis is a comparative study. Hence there is no control for this systematic review.

3.2.5 Outcomes

- Prevalence of TTIs among blood donors in Sub-Saharan Africa
- Trends of TTIs among donors in Sub-Saharan Africa
- Diagnostic methods used for screening blood donors in Sub-Saharan Africa

3.2.4.1 Primary outcome

Detection of transfusion-transmissible infections (HIV, HBV, HCV, and Syphilis) during screening.

3.2.4.2 Secondary outcome:

- Safety challenges associated with blood transfusion.
- Diagnostic methods used for blood donor screening in SSA

3.3 Search methods for identification of studies

3.3.1 Electronic database searches

The following electronic databases were searched from 1st January 2000 to 30th June 2021 without language restriction: PubMed, HINARI, WHO Global Health database, and Google Scholar for potentially eligible studies. The search was conducted using the terms Transfusion transmissible infections, TTI, TTIs, Human Immunodeficiency Syndrome HIV, Hepatitis B Virus, HBV, Hepatitis C Virus, HCV and Syphilis Blood Donors and Sub-Saharan Africa, SSA, LMIC's together with all other alternative terms and synonyms. The search was also extended to other search engines such as African Journals Online, Google, SCOPUS, Pre-print repositories, and Conference Proceedings. The detailed search strategy has been reported in the Appendix II section. References of retrieved studies were searched for additional published studies and experts in the field of blood transfusion were contacted for unpublished studies.

3.3.2 Other sources searched

The reference lists of all relevant studies were screened for potentially eligible studies, and their full texts were accessed for inclusion. A review of the references of published systematic reviews on the subject to identify potentially relevant primary studies that were missed by the search was conducted and assessed based on the pre-specified eligibility criteria for inclusion.

3.4 Study Selection

All records from the various searches were collated, deduplicated using Endnote, and then be exported to Rayyan QCRI- a systematic review web app, for screening. The titles and abstracts of the articles were screened independently by student and supervisor against each eligibility criterion in turn. Articles were screened advancing to full-text review. Any disagreements were resolved through discussion with my supervisors. The reasons for excluding potentially eligible articles were reported at both screening stages.

3.5 Data extraction and Management

Data were extracted using piloted data extraction form in Microsoft Excel. The following study characteristics were recorded: title, author, year study was conducted, year of publication, health facility in which the study was conducted, country and region where the study was conducted, study design, sample size, type of donors, as well as the number of seropositive HIV, HBV, HCV, Syphilis and co-infected individuals. Finally, all extracted data was re-checked for accuracy and consistency. Any disagreements and inconsistencies were resolved by cross-checking with results of the articles from which data was extracted.

3.6 Quality assessment of the included studies

The quality of each of the included studies was assessed using the checklist developed by Hoy et al (Appendix I) (Hoy et al., 2012). This quality assessment tool incorporates assessments of risk of bias across core domains including sampling, the sampling technique and size, outcome measurement, response rate, and statistical reporting. Any discrepancies were resolved through discussion between student and supervisors.

3.7 Data synthesis

Data synthesis and statistical analyses were performed using the Statistical Software Package (STATA) Version 15.0 (StataCorp, College Station, TX, USA). Proportions from each of the studies were estimated and presented with their 95% CI. The overall proportion for a particular TTI was obtained from pooling the weighted individual study estimates using a random-effects model and presented with their 95% CI. A random-effects model was used to generate the overall pooled estimate recommended to adjust for variability in the presence of between and within studies heterogeneity (Barth et al., 2010; White et al., 2008). Heterogeneity across studies was checked with I^2 test statistics that assess the percentage of variation across studies that is due to heterogeneity rather than chance

An I^2 less than 25% indicates less heterogeneity whereas I^2 greater than or equal to 75% indicates very high heterogeneity across studies (Higgins et al., 2019; Ried, 2006). Further, the presence of heterogeneity was assessed quantitatively by subgroup analysis.

3.8 Subgroup analysis

Where heterogeneity detected was significantly high (>75%), subgroup analysis was performed to address the possible sources using these variables, geographical area (African region), country, and diagnostic methods. However, potentially relevant subgroups such as type of health facility, number of donations, could not be analysed and reported because of insufficient data.

3.9 Dealing with missing and incomplete data

An attempt was made to collect sufficient data from all included studies. However, when data were missing, the original investigators were contacted to request for the missing data. Where original investigators were unable to be reached, the potential impact of missing data on the findings of the review was discussed in the discussion section.

3.10 Ethical issues

The study did not require ethical approval as it used data retrieved from published studies that are already in the public domain. However, the protocol of this systematic review and meta-analysis was registered on PROSPERO (an international prospective register of systematic reviews) with registration number CRD42021259042. The entire report adhered to the guidelines set by the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA).

CHAPTER FOUR

4.0 RESULTS

4.1 Eligible studies

A total of 989 studies were identified from various databases of which 755 remained after removing duplicates (Figure 1). After reviewing titles and abstracts using predefined inclusion/exclusion criteria, 627 studies were excluded. The full text was obtained for the 125 studies that were potentially eligible for inclusion. Thirty studies were excluded for reasons indicated in the PRISMA flow chart. Ninety-five studies met our inclusion criteria and were included in the systematic review.

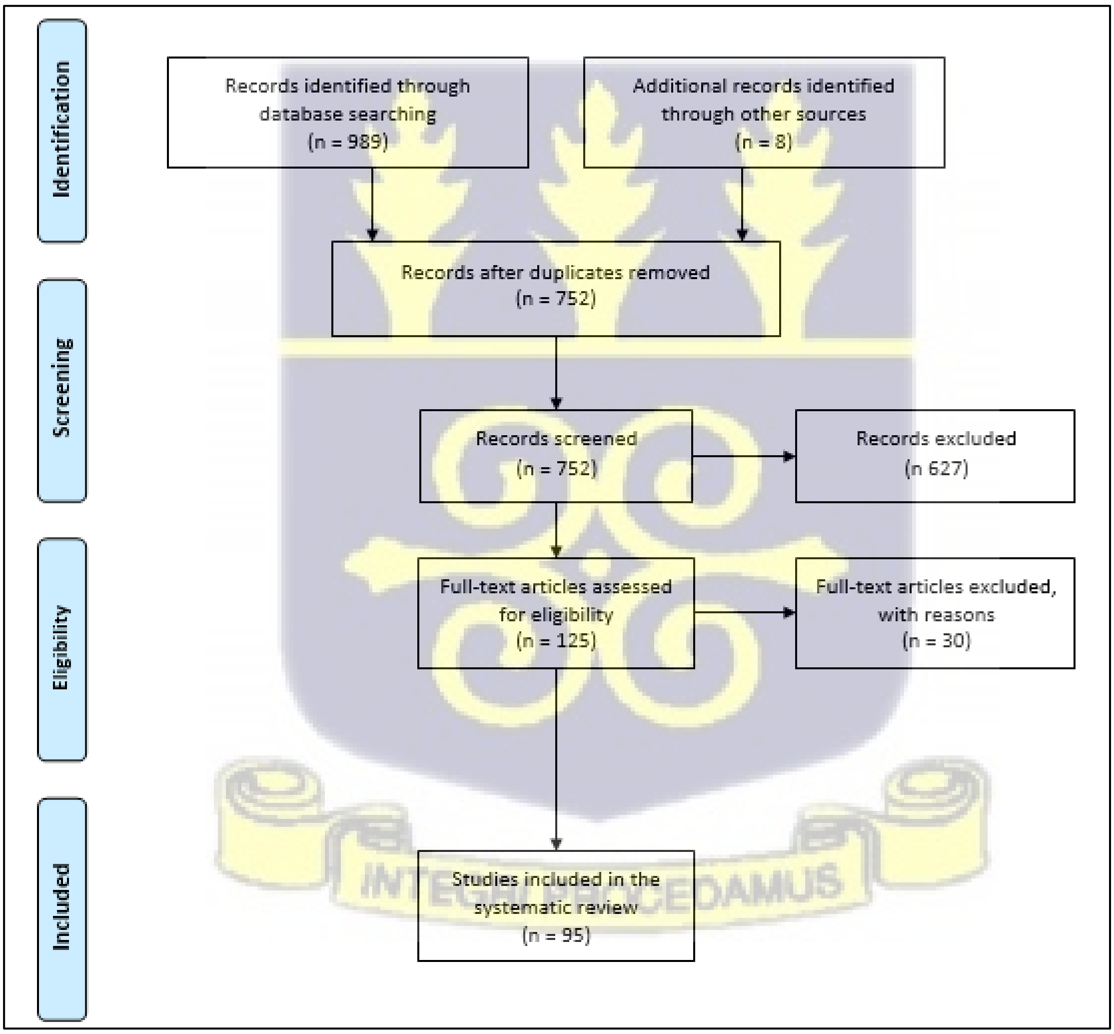

Figure 3: PRISMA flow diagram showing sources of studies and the selection process *(Adapted from: https://app.creately.com/diagram/X6DeP2Babld/edit)*

4.2 Characteristics of the included studies

Table 1 shows the characteristics of the studies included in the systematic review and meta-analysis. All included studies were conducted in twenty-two different countries in the five sub-regions of Africa; West Africa 45 (47.37%), Eastern Africa 31 (32.63%), Central Africa 9 (9.47%), Southern Africa 6 (6.32%), and Northern Africa 4 (4.21%) of which; the largest number 22 studies (23.16%) were conducted in Nigeria, 17 in Ethiopia, 10 in Ghana, six in Burkina Faso, five in Kenya, four each in Cameroon and DR Congo, three each in Mali, Tanzania and Zambia, two each in Cote d'Ivoire, Eritrea, Libya, Malawi, South Sudan, and Sudan, one each in Gabon, Mauritania, Mozambique, Namibia, Sierra Leone, and Zimbabwe.

The number of donors of eligible studies ranges from 90 to 550,753. All included studies were conducted between 1991 and 2019. Thirty-eight studies (n=724,846) evaluated the frequency of either HBsAg, Anti-HCV, HIV, and Syphilis together. Thirty studies (n=792,067) focused on the frequency of individual infections HBsAg, Anti-HCV, HIV, or Syphilis. Twenty-seven studies (n=530,453) assessed the prevalence of TTIs focusing on two or three of the infections (Table 1). Eighty-two studies (86.3%) were conducted between 2011and 2021, of which the highest number of studies on the prevalence of TTIs was in 2019. The age range of donors in the studies was between 15-75 years (Table 1).

Table 1: Characteristics of studies (n=95) included in the systematic review

Study ID	Year study conducted	Age of participants	Male (%)	Diagnostic method	Investigations conducted
Abebe et al., 2020	2015-2019	Not reported	70.1	ELISA	HBsAg, Anti-HCV
Adjei et al., 2003	2003	19-54	93.3	PAT	Syphilis
Adu-poku et al.,2020	2015-2016	Not reported	88.3	ELISA	HBsAg, Anti-HCV, Syphilis, HIV
Afolabi et al., 2013	2010	19-68	84.0	ELISA	HBsAg, HIV, Anti-HCV
Ahmed et al., 2020	2017	18-65	100.0	RDT	HBsAg, Anti-HCV, Syphilis, HIV
Ali et al., 2016	2008-2015	Not reported	Not reported	ELISA	HBsAg, Anti-HCV, Syphilis
Allain et al., 2003	1999-2000	16-56	88.9	RDT, EIA, PCR	HBsAg
Aluora et al., 2020	Not reported	16-65	59.3	CMIA, PCR	HBsAg
Ataro et al., 2018	2010-2013	18-65	85.2	ELISA	HBsAg, Anti-HCV, Syphilis, HIV
Awili et al., 2020	2019	18-52	61.8	CLIA	HBsAg
Azene et al., 2007	2006	18-60	87.4	ELISA, RDT	HIV, HBsAg, Anti-HCV, Syphilis
Babatunde et al., 2020	2013	Not reported	NA	ELISA, RDT, PCR	HIV
Bartonjo et al., 2019	2011- 2012	16-65	72.0	ELISA, RPR	HBsAg, Anti-HC, HIV, Syphilis
Biadgo et al., 2017	2010-2012	48	82.1	ELISA	HBsAg, HIV, Anti-HCV
Birhaneselassie, 2016	2009-2013	15-75	86.5	ELISA, RPR, RDT	HBsAg, Anti-HCV, HIV, Syphilis
Boushab et al., 2017	2010-2015	17-73	83.9	RDT	HBsAg, Anti-HCV, Syphilis, HIV
Chama et al., 2015	2012	Not reported	71.9	RDT	HBsAg, Anti-HCV, Syphilis, HIV
Coulibaly et al., 2020	2011-2014	18-55	87.0	ELISA	HBsAg, Anti-HCV, Syphilis, HIV
Damola et al., 2019	2002-2006	18-63	97.3	ELISA	Anti-HCV
Damulak et al., 2013	2007-2010	18-65	61.4	ELISA	Syphilis
Deressa et al., 2018	2014-2017	17-65	66.7	ELISA, RPR	HBsAg, Anti-HCV, Syphilis, HIV
Dionne-Odom et al.,2016	2014	Not reported	77.5	RDT	HBsAg, Anti-HCV, HIV, Syphilis
Elfaki et al., 2008	Not reported	20-40	100.0	RDT	HIV, HBsAg, Anti-HCV, Syphilis
Ezeonu et al., 2019	Not reported	18-60	94.1	ELISA, RDT, PCR	HBsAg
Fasola et al., 2008	2001-2006	Not reported	Not reported	RDT, ELISA	HBsAg, Anti-HCV, HIV
Fessehaye et al., 2011	2006- 2009	Not reported	Not reported	Not reported	HBsAg, HIV and Anti-HCV
Fithamlak et al., 2016	2015	18-60	74.6	ELISA, RDT	Anti-HCV, HBsAg, HIV, Syphilis
Gwarzo et al., 2018	2016-2017	18-55	100.0	RDT	HBSAG, Anti-HCV
Gwarzo et al., 2018	2016-2017	15-55	100.0	RDT	Anti-HCV, HBsAg
Heyredin et al., 2019	2018	18-65	81.2	ELISA	HBsAg, Anti-HCV, Syphilis, HIV
Hoogstraten et al., 2000	1991-1995	Not reported	Not reported	RDT	HIV
Hundie et al., 2017	Not reported	Not reported	Not reported	Not reported	HBsAg, Anti-HCV
Japhet et al., 2016	Not reported	Not reported	Not reported	RDT, ELISA	HIV
Jary et al., 2019	2018	Not reported	88.8	EIA, Western blot	HIV, HBsAg, Anti-HCV

Study ID	Year study conducted	Age of participants	Male (%)	Diagnostic method	Investigations conducted
Jean et al., 2013	2011-2012	18-65	82.0	RDT, ELISA, VDRL, TPHA	HIV, Anti-HCV, HBsAg, Syphilis
Kabebma et al., 2017	2015-2016	18-43	62.8	PRP	Syphilis
Kabebma et al., 2017	2014-2016	18-49	62.5	RDT, Abbot	HBsAg
Kambaba et al., 2021	2017-2019	18-65	71.5	RDT	HBsAg
Karoney et al., 2018	2010-2012	16-60	Not reported	ELISA	HBsAg, Anti-HCV, HIV
Kubio et al., 2012	2006	Not reported	Not reported	Not reported	HBsAg, Anti-HCV, HIV, Syphilis
Lokpo et al., 2017	2012-2016	18-58	88.4	RDT	Anti-HCV, HBsAg
M'baya et al, 2019	2011-2015	Not reported	82.0	RDT, EIA,	HBsAg, Anti-HCV, Syphilis, HIV
Mapako et al.,2013	2002-2010	Not reported	Not reported	RDT	HIV
Marfoua et al.,2016	2008-2015	Not reported	Not reported	RDT, ELISA	HBsAg, Anti-HCV, HIV, Syphilis
Matee et al., 2006	2004-2005	16-69	89.1	ELISA, EIA, TPHA	HBsAg, Anti-HCV, HIV, Syphilis[1]
Mba et al., 2018	2009-2016	15-65	76.4	RDT, ELISA	HBsAg
M'baya et al., 2019	2011-2015	Not reported	82.0	RDT, ELISA, EIA	HBsAg, Anti-HCV, HIV, Syphilis
Meda et al., 2018	2015	15-59	45.9	ELISA	HBsAg, Anti-HCV
Melese et al., 2016	2010-2014	17-65	97.4	ELISA, RPR	HBsAg, Anti-HCV, Syphilis, HIV
Mohamed et al., 2019	2016-2017	18-69	84.1	RDT, CMIA	HBsAg, Anti-HCV, Syphilis, HIV
Motayo et al., 2015	2013	20-57	96.9	EIA RAPID KIT	HIV, HBsAg, Anti-HCV, Syphilis
Motayo et al., 2015	Not reported	Not reported	96.4	RDT	HBsAg, Anti-HCV
Moukoko et al., 2014	2012	Not reported	79.9	RDT, ELISA, TPHA	HIV, HBsAg, Anti-HCV, Syphilis
Mremi et al., 2021	2017-2019	18-65	83.7	CMIA	HBsAg, Anti-HCV, HIV, Syphilis
Muhibi et al., 2014	2013	18-65	97.6	EIA	Anti-HCV
Mukendi et al., 2018	2016	Not reported	77.8	ANTI-HCVSCAN	Anti-HCV
Mwambungu et al., 2015	2012-2015	16-55	54.5	CMIA	HBsAg, Anti-HCV
N'guessan et al.,2013	2010	17-46	73.0	ELISA	HBsAg, Anti-HCV, HIV, Syphilis
Nagalo et al., 2012	2009	17-67	74.9	ELISA, RDT	HBsAg, Anti-HCV, HIV
Negash et al., 2019	2018	Not reported	63.8	ELISA	HBsAg, Anti-HCV, HIV
Nii-Trebi et al., 2019	Not reported	Not reported	Not reported	ELISA, PA, PCR	Anti-HCV
Njeru et al., 2009	Not reported	16-54	57.9	ELISA	HIV, Syphilis, HBsAg, Anti-HCV
Nkrumah et al., 2011	2006-2008	Not reported	92.2	RDT	HBsAg, Anti-HCV
Ogbodo et al., 2017	2009- 2011	18-50	92.9	ELISA	HIV, Anti-HCV
Okoroiwu et al., 2018	2005-2016	18-65	98.7	RDT	HBsAg, HIV, Anti-HCV, Syphilis
Olusola et al., 2021	Not reported	Not reported	Not reported	RDT, PCR	HIV

[1] **Abbreviations**: **ELISA** (Enzyme-Linked Immunosorbent Assay), **EIA** (Enzyme immunoassays), TPHA (Treponema pallidum haemagglutination), **RDT** (Rapid Diagnostic Test), **PCR** (Polymerase Chain Reaction), **PAT** (Particle Agglutination Test), **HIV** (Human Immunodeficiency Virus), **HBsAg** (Hepatitis B Surface Antigen), **Anti-HCV** (Hepatitis C Antibody)

Study ID	Year study conducted	Age of participants	Male (%)	Diagnostic method	Investigations conducted
Onoja et al., 2015	2011-2014	18-65	73.6	ELISA	HBsAg, Anti-HCV, Syphilis
Osaro et al., 2014	2010-2013	18-50	99.4	RDT, ELISA	HIV
Osaro et al., 2014	2010-2013	18-50	99.4	RDT	HIV
Osei et al., 2017	2014	Not reported	90.0	RDT	HBsAg
Owusu-Ofori et al., 2005	2002-2003	Not reported	Not reported	RDT, PCR	HBsAg, Anti-HCV, HIV
Ratib et al., 2014	2007-2011	16-58	64.9	RDT	HBsAg, Anti-HCV, HIV
Rooyen et al., 2014	2012	16-25	52.7	PCR, ELISA	HIV, HBsAg, Anti-HCV, Syphilis
Saleh et al.,2020	2018	18-57	Not reported	RDT, ELISA	Anti-HCV, Syphilis
Sarkodie et al., 2001	Not reported	16-52	Not reported	EIA	HBsAg, Anti-HCV, HIV
Sharew et al., 2017	2008-2012	18 +	80.1	ELISA	HIV
Shiferaw et al., 2019	2014-2018	Not reported	65.0	ELISA	HBsAg, Anti-HCV, Syphilis, HIV
Shittu et al., 2014	Not reported	Not reported	96.9	RDT	HBSAG
Shittu et al.,2019	2018	Not reported	Not reported	VDRL, RPR, TPHA	Syphilis
Simpore et al., 2014	2011- 2012	17-60	81.0	CMIA, PCR	Syphilis
Siraj et al., 2018	2010-2016	16-54	66.4	ELISA, TPHA,	HBsAg, Anti-HCV, Syphilis, HIV
Stokx et al., 2011	2009	25-65	89.0	RDT, PRP	HBsAg, Anti-HCV, HIV, Syphilis
Sube et al., 2014	2013	15-69	98.1	RDT	HBsAg, Anti-HCV, HIV, Syphilis
Tachalew et al., 2015	2014	15-75	40.0	RDT	HBsAg, Anti-HCV, Syphilis
Tagny et al., 2011	2008	18-58	84.3	RDT, ELISA	HIV
Tagny et al., 2020	2018	18-65	Not reported	RDT	HIV
Teklemariam et al., 2018	2008-2015	18–65	82.6	ELISA	HIV, Anti-HCV, HBsAg, Syphilis
Tessema et al., 2010	2003- 2007	17-65	87.9	ELISA, RDT, PCR	HBsAg, Anti-HCV, HIV, Syphilis
Tognon et al., 2020	2013-2016	Not reported	76.5	RDT	Anti-HCV, HBsAg
Tounkara et al., 2009	1993-2002	Not reported	87.6	ELISA, EIA	HIV
Umolu et al., 2005	Not reported	18-68	129	RDT	HBsAg, HIV
Yooda et al., 2019	2015-2017	17-65	71.2	RDT, CMIA	HBsAg, HVC, HIV
Yooda et al., 2019	2017	17-65	Not reported	CMIA, PCR	HBsAg, Anti-HCV, HIV
Zeba et al., 2014	2011	Not reported	Not reported	ELISA, PCR	Anti-HCV
Zeruhun et al., 2018	2011- 2012	18-65	85.2	ELISA, RDT	HBsAg, Anti-HCV, HIV, Syphilis

4.3 Blood Transfusion Donors in Sub-Saharan Africa

A total of 2,013,217 blood donors were screened for various TTIs. Twenty-six studies (26.9%) reported proportions of both Voluntary Non-Remunerated Donors (VNRDs) and Replacement Donors (RDs). The proportion of blood donations by VNRDs varied between 1.0% and 90.1

% and 10.0% and 99.0% by RDs across the twenty-seven studies of which 44.8% of all donations were due to VNRDs and 55.2% were due to RDs. Male donors comprised 40% to 100% of all blood donations. Donors were more prevalent in younger age groups. Female donors ranged between 0% and 60% in individual studies. Only one study reported a higher proportion of female (60%) donors.

4.4 Diagnostic Methods for TTIs screening in Sub-Saharan Africa

The diagnostic methods used for screening donors in the included studies in this systematic review are shown in Table 1. Overall, the proportions of diagnostic methods for screening donors for TTIs were 57.9% for (CMIA, EIA, and ELISA), 49.5% for RDTs, and 5.3% for PCR and NAT. The proportions of (CMIA, EIA, and ELISA) were 62.5%, 67.2%, 62.9%, and 19.6% for the diagnosis of HBV, HCV, HIV, and Syphilis respectively. The proportions of RDTs used for the diagnosis of HBV, HCV, HIV, and Syphilis were 40.3%, 32.8%, 37.1%, and 54.4% respectively. PCR testing ranged between 2.2% and 6.5% for the diagnosis of the various TTIs across all the studies (**Figure 4**).

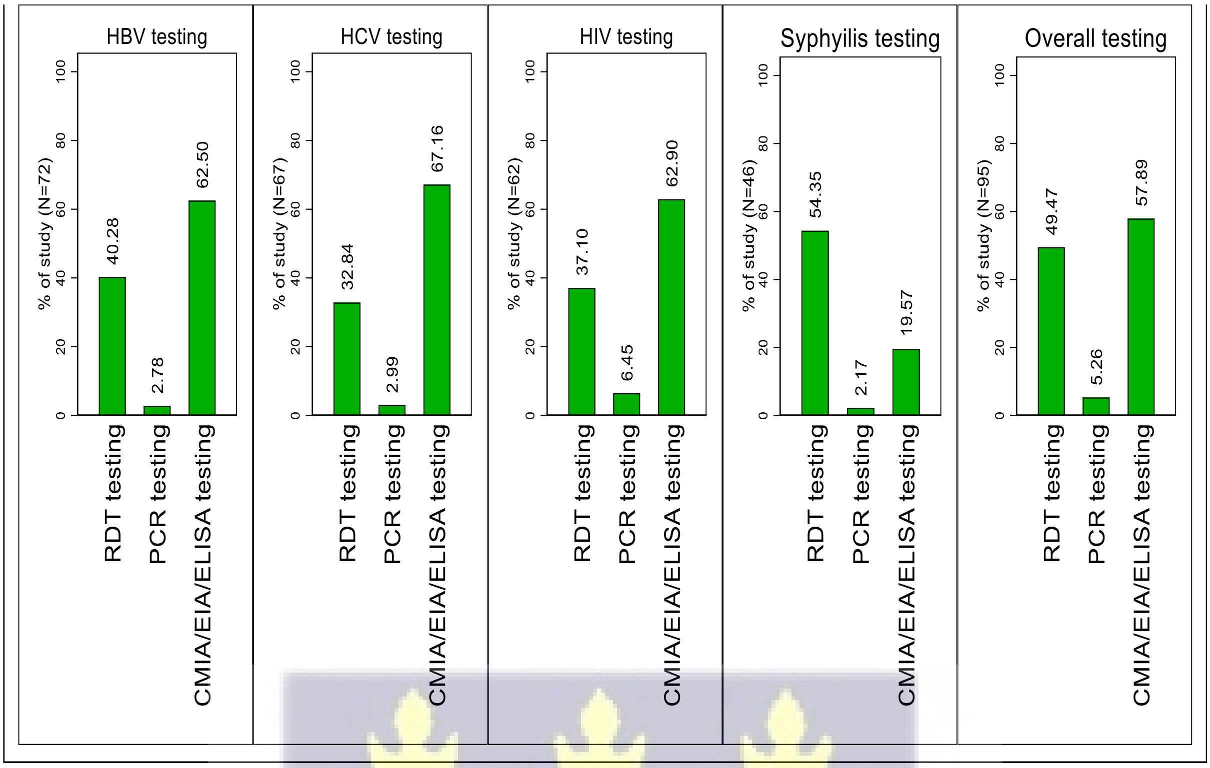

Figure 4: Proportions of study using the various diagnostic methods for TTIs screening

4.5 Pooled prevalence of TTIs

4.5.1 Overall pooled prevalence of TTIs

The occurrence of TTIs in blood donors varied among studies depending on donor types, number and type of TTI tested and screening method used. The overall prevalence of transfusion-transmissible infection was 10.1%, studies = 95 (95% CI; 8.4 to 11.7%, n= 2,047,302, I^2 =99.9%) (Table 2). The subgroup analysis revealed that there were considerable variations in TTIs estimate across regions in SSA. Eastern Africa had the highest (P=11.2%, 95% CI 7.3 to 15.1%, studies= 29, donors= 2,046,506, I^2 =99.9%), followed by West Africa 10.2%, studies = 41 (95% CI; 8.3 to 12.0%), Southern Africa 8.9%, studies = 6 (95% CI; 3.6 to 14.2%), Central Africa 8.6%, studies = 9 (95% CI; 4.4 to 12.7%), with lowest TTIs recorded among donors from Northern Africa 5.6%, studies = 3 (95% CI; -4.5 to 15.7%). Among individual SSA countries involved in this systematic review, Mozambique had the highest TTIs 18.7%, studies = 1 (95% CI 15.9 to 21.5%), followed by Mauritania 16.2%, studies = 1 (95% CI; 14.0 to 18.4%), Sudan 15.9%, studies = 1 (95% CI; 15.2 to 16.6), and Ghana 13.1% (95% CI; 9.0 to 17.3%). The lowest TTIs prevalence was among blood donors in Zimbabwe 1.7%, studies = 1 (95% CI; 1.7 to 1.7%) (Table 2).

Table 2: Subgroup analysis of the prevalence of overall infection among donor population in Sub-Saharan Africa countries

			Heterogeneity summary					Test of group differences	
Characteristics	**Proportion (95% CI)**	**P-value**	**df**	**Q-statistic**	**P (Q)**	**% I^2**	**H2**	**chi-square**	**P-value**
Overall	0.101 [0.084, 0.117]	<0.001	87	70217.05	<0.001	99.98	5560.39		
RDT testing								12.03	**0.001**
No	0.074 [0.057, 0.091]	<0.001	45	53762.54	<0.001	99.98	5738.96		
Yes	0.130 [0.103, 0.157]	<0.001	41	7124.80	<0.001	99.81	528.45		
PCR testing								0.25	0.619
No	0.102 [0.085, 0.119]	<0.001	82	69480.18	<0.001	99.98	5949.63		
Yes	0.084 [0.014, 0.153]	0.018	4	448.69	<0.001	98.62	72.36		
ELISA testing								1.90	0.168
No	0.114 [0.088, 0.141]	<0.001	36	38437.64	<0.001	99.98	4671.84		
Yes	0.091 [0.070, 0.111]	<0.001	50	31174.44	<0.001	99.97	3971.98		
African region								1.70	0.790
West Africa	0.102 [0.083, 0.120]	<0.001	40	30740.20	<0.001	99.78	458.60		
Central Africa	0.086 [0.044, 0.127]	<0.001	8	690.26	<0.001	99.57	235.01		
Southern Africa	0.089 [0.036, 0.142]	0.001	5	3320.69	<0.001	99.97	3934.22		
Eastern Africa	0.112 [0.073, 0.151]	<0.001	28	13614.48	<0.001	99.98	4584.14		
North Africa	0.056 [-0.045, 0.157]	0.274	2	1934.83	<0.001	100.00	65994.82		
Country								22809.62	**<0.001**
Burkina Faso	0.091 [0.049, 0.133]	<0.001	3	269.11	<0.001	98.22	56.26		
Cameroon	0.129 [0.054, 0.205]	0.001	3	429.96	<0.001	99.12	113.47		
Cote D'Ivoire	0.047 [0.042, 0.052]	<0.001	1	0.00	0.966	0.31	1.00		
DR Congo	0.047 [0.022, 0.072]	<0.001	3	66.86	<0.001	94.97	19.89		
Eritrea	0.037 [0.036, 0.039]	<0.001	1	0.55	0.460	0.00	1.00		
Ethiopia	0.123 [0.069, 0.177]	<0.001	16	1882.09	<0.001	99.96	2411.43		
Gabon	0.073 [0.071, 0.075]	<0.001	0	0.00	.	.	.		
Ghana	0.131 [0.090, 0.173]	<0.001	9	742.19	<0.001	99.05	105.37		
Kenya	0.051 [0.008, 0.095]	0.020	4	97.20	<0.001	98.53	68.22		
Libya	0.005 [0.004, 0.005]	<0.001	1	0.33	0.565	0.19	1.00		
Malawi	0.091 [0.089, 0.093]	<0.001	0	0.00	.	.	.		
Mali	0.120 [0.085, 0.156]	<0.001	1	10.08	0.002	90.08	10.08		
Mauritania	0.162 [0.140, 0.184]	<0.001	0	0.00	.	.	.		
Mozambique	0.187 [0.159, 0.215]	<0.001	0	0.00	.	.	.		
Namibia	0.013 [0.012, 0.014]	<0.001	0	0.00	.	.	.		
Nigeria	0.090 [0.063, 0.116]	<0.001	20	21886.01	<0.001	99.84	615.42		
Sierra Leone	0.108 [0.104, 0.112]	<0.001	0	0.00	.	.	.		
South Sudan	0.384 [0.355, 0.412]	<0.001	0	0.00	.	.	.		
Sudan	0.159 [0.152, 0.166]	<0.001	0	0.00	.	.	.		
Tanzania	0.114 [0.070, 0.158]	<0.001	2	63.84	<0.001	99.23	130.60		
Zambia	0.107 [0.086, 0.128]	<0.001	2	45.53	<0.001	97.81	45.74		
Zimbabwe	0.017 [0.017, 0.017]	<0.001	0	0.00	.	.	.		

Table 3: Frequencies of individual transfusion-transmissible infections among blood donors in SSA

			Frequency of Infections (%)			
Study ID	**Number of donors**	**Overall infection**	**Hep B (HBsAg)**	**Hep C (Anti-HCV)**	**Syphilis**	**HIV**
Abebe et al., 2020	17,810	3.7	3.1	0.6	NR	NR
Adjei et al., 2003	536	7.5	NR	NR	7.5	NR
Adu-poku et al.,2020	3,173	18.4	5.0	4.2	5.2	3.9
Afolabi et al., 2013	507	9.3	5.9	1.4	NR	2.0
Ahmed et al., 2020	10,897	15.9	5.6	1.4	5.7	2.6
Ali et al., 2016	78,987	0.5	0.2	0.2	0.0	0.0
Allain et al., 2003	3,587	15.5	15.3	NR	NR	NR
Aluora et al., 2020	300	2.3	2.3		NR	NR
Assih et al., 2016	440	NR	NR	NR	NR	NR
Ataro et al., 2018	6376	7.3	4.7	1.0	0.4	1.2
Awili et al., 2020	1,000	3.4	3.4	NR	NR	NR
Azene et al., 2007	324	43.2	25.0	13.3	1.2	11.7
Babatunde et al., 2020	1,028	5.4	NR	NR	NR	5.4
Bartonjo et al., 2019	594	14.1	5.6	3.2	1.2	3.5
Biadgo et al., 2017	6,471	6.6	3.6	0.8	NR	2.2
Birhaneselassie · 2016	6,337	7.1	4.8	0.6	0.5	1.6
Boushab et al., 2017	1,123	16.2	11.8	0.2	3.0	1.2
Chama et al., 2015	16,027	10.1	6.0	0.6	1.2	2.9
Coulibaly et al., 2020	11,373	10.4	8.9	1.5	NR	2.4
Damola et al., 2019	3,002	3.1	NR	3.1	NR	NR
Damulak et al., 2014	30,256	18.5	NR		0.9	NR
Deressa et al., 2018	8,460	2.4	1.2	0.3	0.7	0.3
Dionne-Odom et al.,2016	4,225	14.7	6.8	1.7	4.0	2.2
Elfaki et al., 2008	260	NR	10.0	NR	15.0	0.8
Ezeonu et al., 2019	550	11.7	11.7	NR	NR	NR
Fasola et al., 2008	33,628	24.6	13.2	3.7	NR	7.7
Fessehaye et al., 2011	29,501	3.8	2.6	0.6	0.5	0.2
Fithamlak et al., 2016	390	29.5	9.5	8.5	7.9	6.4
Gwarzo et al.,2018	12,333	7.1	6.7	0.5	NR	NR
Heyredin et al., 2019	500	12.4	6.6	1.0	3.4	1.4
Hoogstraten et al., 2000	4,044	12.9	NR	NR	NR	12.9
Hundie et al., 2017	56,885	4.4	3.9	0.5	NR	NR
Japhet et al 2016	169	5.9	NR	NR	NR	5.9
Jary et al., 2019	8,059	NR	14.8	2.3	0.0	2.2
Jean et al., 2013	543	21.2	10.1	4.8	5.7	4.1
Kabebma et al., 2017a	752	5.2	NR	NR	5.2[i]	NR
Kabebma et al., 2017b	1,145	3.9	3.9	NR	NR	NR
Kambaba et al., 2021	1,512	7.9	7.9	NR	NR	NR
Karoney et al., 2018	68,404	1.6	1.1	0.3	NR	0.3
Kubio et al., 2012	719	22.2	7.5	6.1	4.7	3.9

Study ID	Number of donors	Overall infection	Frequency of Infections (%) Hep B (HBsAg)	Hep C (Anti-HCV)	Syphilis	HIV
Lokpo et al., 2017	4,180	8.8	6.9	1.8	NR	NR
M'baya et al., 2019	125,893	NR	3.6	1.0	2.6	1.9
Mapako et al.,2013	550,753	1.7	NR	NR	NR	1.7
Marfoua et al.,2016	78,987	0.5	0.2	0.2	1.4	1.4
Matee et al., 2006	1,599	15.9	8.8	1.5	4.7	3.8
Mba et al.,2018	69,862	7.3	7.3		NR	NR
M'baya et al., 2019	125,893	9.1	3.6	1.0	2.6	1.9
Meda et al., 2018	14,886	12.7	9.1	3.6	NR	NR
Melese et al., 2016	6,827	14.8	9.5	0.7	0.7	3.2
Mohamed et al., 2019	6,402	8.4	4.1	1.0	2.2	1.7
Motayo et al., 2014	305	11.1	9.8	1.3	NR	NR
Motayo et al., 2015	130	NR	10.0	1.5	0.0	6.2
Moukoko et al., 2014	477	13.7	3.5	1.3	8.1	1.8
Mremi et al., 2021	101,616	10.1	5.2	1.1	1.9	1.9
Muhibi et al., 2014	290	2.1	NR	2.1	NR	NR
Mukendi et al., 2018	1,584	1.9	NR	1.9	NR	NR
Mukhtar et al., 2018	12,233	7.2	6.7	0.5	NR	NR
Mwambungu et al., 2015	22,007	9.2	6.7	2.5	NR	NR
N'guessan et al.,2013	3,823	4.7	4.7	NR	NR	NR
Nagalo et al., 2012	31,405	NR	13.4	6.3	2.1	1.8
N'dri et al., 2013	4,310	4.7	4.7	0.0	0.0	0.0
Negash et al., 2019	310	12.6	5.8	4.2	NR	2.6
Nii-Trebi et al., 2019	200	1.0	NR	1.0	NR	NR
Njeru et al., 2009	400	4.9	2.3	1.0	0.3	1.3
Nkrumah et al., 2011	2,773	13.8	10.5	5.6	NR	NR
Ogbodo et al., 2017	1,490	1.4	NR	0.6	NR	0.8
Okoroiwu et al., 2018	24,979	15.0	4.1	3.6	3.1	4.2
Olusola et al., 2021	1,028	5.4	NR	NR	NR	5.4
Onoja et al., 2015	500	15.5	7.5	2.7	NR	3.1
Osaro et al., 2014	15,061	5.8	NR		NR	NR
Osaro et al., 2014	15,061	5.8	NR	NR	NR	5.8
Osei et al., 2017	576	7.5	7.5	NR	NR	NR
Owusu-Ofori et al., 2005	9,372	16.7	13.4	0.5	NR	2.7
Ratib et al., 2014	496	NR	8.9	9.3	NR	6.7
Rooyen et al., 2014	24,761	1.3	0.6	0.1	0.3	0.3
Saleh et al.,2020	90	7.8	NR	5.6	2.2	NR
Sarkodie et al., 2001	3,263	20.2	16.8	1.7	NR	1.5
Sharew et al., 2017	9384	5.1	NR	NR	NR	2.1
Shiferaw et al.,2019	35,435	6.0	3.9	0.6	0.5	1.2
Shittu et al., 2014	350	10.9	10.9	NR	NR	NR
Shittu et al.,2019	98,478	0.8	NR	NR	0.8	NR

Study ID	Number of donors	Overall infection	Frequency of Infections (%)			
			Hep B (HBsAg)	Hep C (Anti-HCV)	Syphilis	HIV
Simpore et al., 2014	242	6.6	NR	NR	6.6	NR
Siraj et al., 2018	60,236	3.7	2.0	0.7	0.1	0.3
Stokx et al., 2011	750	18.7	10.6	0.0	1.2	8.5
Sube et al., 2014	1,095	38.4	NR	NR	NR	8.8
Tagny et al., 2011	2000	2.7	NR	NR	NR	2.7
Tagny et al., 2020	356	72.1	NR	NR	72.1	NR
Techalew et al., 2015	477	33.5	6.3	3.2	11.9	NR
Teklemariam et al., 2018	11,382	6.6	4.4	0.8	1.1	0.6
Tesseman et al., 2010	6,361	10.5	4.7	0.7	1.3	3.8
Tognon et al., 2020	29,713	10.8	10.8	1.2	NR	NR
Tounkara et al., 2009	1,000	14.0	NR	NR	NR	14.0
Umolu et al., 2005	130	15.4	5.8	NR	NR	10.0
Yooda et al., 2019a	84,299	NR	8.6	4.4	NR	1.8
Yooda et al., 2019b	989	12.5	7.3	2.7	NR	2.5
Zeba et al., 2014	2,200	4.4	NR	4.4	NR	NR
Zerihum et al., 2018	6,376	7.1	4.7	1.0	0.4	1.2

Notes: Overall infection was calculated based on the total donors positive for TTIs divided by the total number of donors screened multiplied by 100 for a study. The percentage of a single TTI was calculated based on the total number of donors positive for a particular TTI such as HBV, HCV, HIV or Syphilis divided by the total number of donors screened for that TTI multiplied by 100. Where a particular infection was not tested it was considered Not reported (NR)

4.5.2 The pooled prevalence of HBV

Regarding HBV among blood donors in Sub-Saharan Africa, 72 articles which included 1,306,763 study participants were used for estimation. These studies reported varying prevalence, ranging from 0.2% to 25.0%. In the random-effects model, the pooled seroprevalence of HBV was 6.9%, studies = 75, (95% CI 5.9 to 7.9%; n = 1,306,763, I^2, =99.9%) (Figure 5). The subgroup analysis revealed that there were considerable variations of HBV estimate across regions in SSA. Three studies had HBV frequency below 2% while 69 studies had frequency above 2%. Sub-group analysis by sub-region showed the highest prevalence of HBV infection 9.3%, studies = 29, n= 283,153 (95% CI; 8.0% to 10.6 %,) among blood donors was observed in West Africa; the lowest HBV infection 3.8%, studies = 6, n= 170,722 (95%CI; -0.7% to 8.2%) among donors was in Northern Africa. Eight percent (8.1%) of blood donors had a positive HBV test detected by RDT (95% CI; 6.9% to 9.2%). Among 21 countries, HBV infections were highest in donors from in Mali (studies=3, n= 20,432, P=11.8% (95%CI; 6.1% to 17.6%) and Malawi (study=1, n= 125,893; P=11.8% (95% CI; 9.9% to 13.7%) Mali and Malawi respectively. The least HBV prevalence was in Libya 0.2% (95% CI; 0.2% to 0.2%) (Table 4).

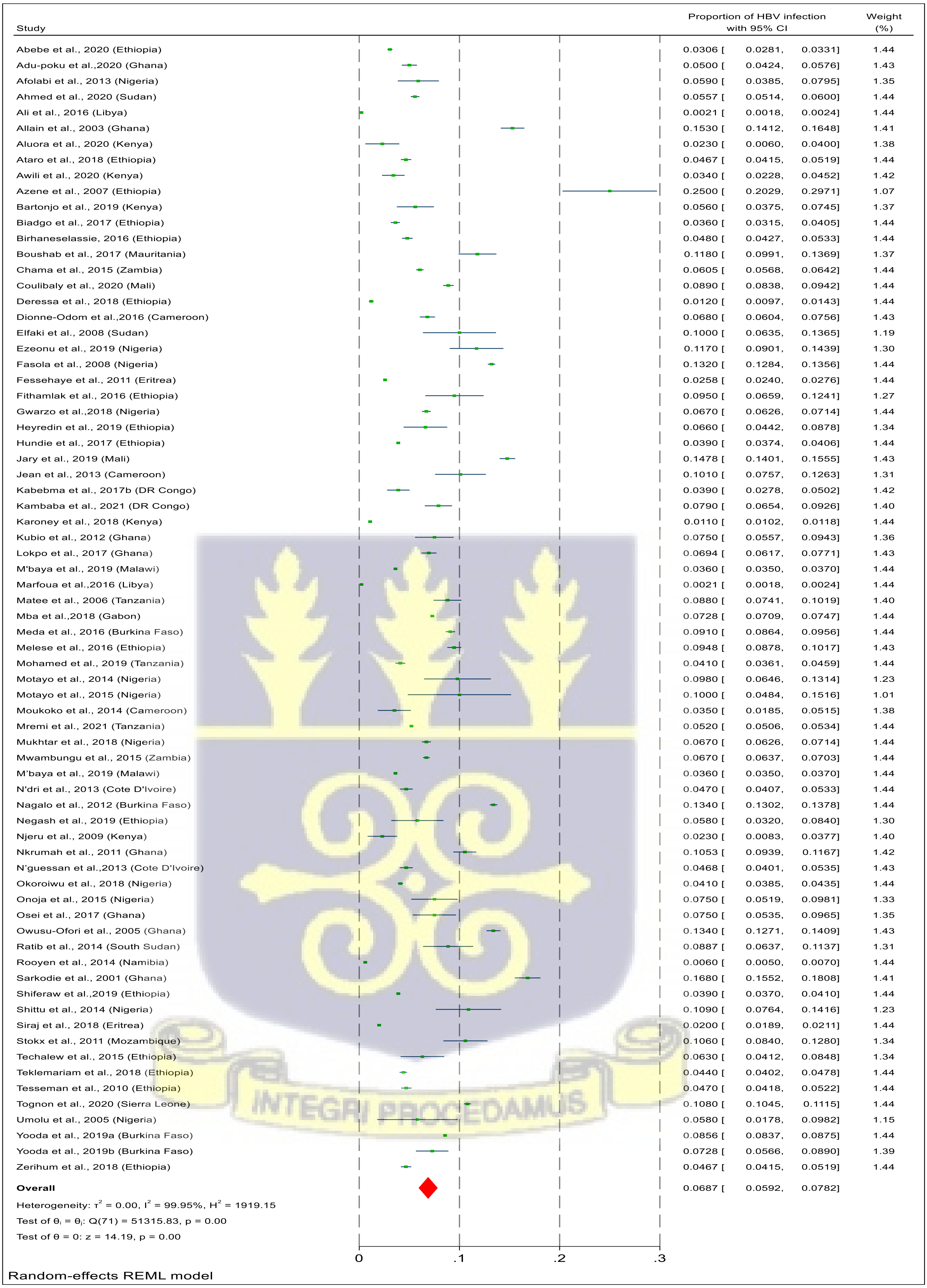

Figure 5: Pooled estimate of HBV using random-effect model among blood donors in SSA

Table 4: Subgroup analysis of the prevalence of hepatitis B virus infection among donor population in Sub-Saharan Africa countries

			Heterogeneity summary						
								Test of group differences	
Characteristics	**Proportion (95% CI)**	**P-value**	**df**	**Q-statistic**	**P (Q)**	**% I2**	**H2**	**chi-square**	**P-value**
Overall	0.069 [0.059, 0.078]	<0.001	71	51315.83	<0.001	99.95	1919.15		
RDT testing								4.95	0.026
No	0.061 [0.047, 0.074]	<0.001	42	43935.80	<0.001	99.97	3800.64		
Yes	0.081 [0.069, 0.092]	<0.001	28	1747.25	<0.001	98.80	83.37		
PCR testing								0.00	0.989
No	0.069 [0.059, 0.078]	<0.001	69	51256.14	<0.001	99.95	1958.76		
Yes	0.069 [-0.023, 0.162]	0.140	1	33.63	<0.001	97.03	33.63		
ELISA testing								1.58	0.209
No	0.076 [0.065, 0.086]	<0.001	26	4175.17	<0.001	99.17	120.85		
Yes	0.065 [0.051, 0.078]	<0.001	44	35593.87	<0.001	99.97	3850.08		
African region								23.17	<0.001
West Africa	0.093 [0.080, 0.106]	<0.001	28	3966.21	<0.001	99.32	146.43		
Central Africa	0.065 [0.046, 0.084]	<0.001	5	60.02	<0.001	96.19	26.21		
Southern Africa	0.059 [0.019, 0.099]	0.004	3	1930.52	<0.001	99.84	626.40		
Eastern Africa	0.051 [0.038, 0.064]	<0.001	28	5050.51	<0.001	99.89	916.86		
North Africa	0.038 [-0.007, 0.082]	0.096	3	621.18	<0.001	100.00	24892.74		
Country								16618.11	<0.001
Burkina Faso	0.096 [0.070, 0.122]	<0.001	3	516.65	<0.001	99.40	166.13		
Cameroon	0.067 [0.031, 0.103]	<0.001	2	21.06	<0.001	93.88	16.34		
Cote D'Ivoire	0.047 [0.042, 0.052]	<0.001	1	0.00	0.966	0.31	1.00		
DR Congo	0.059 [0.020, 0.098]	0.003	1	19.79	<0.001	94.95	19.79		
Eritrea	0.023 [0.017, 0.029]	<0.001	1	28.57	<0.001	96.50	28.57		
Ethiopia	0.061 [0.038, 0.083]	<0.001	15	923.30	<0.001	99.82	554.82		
Gabon	0.073 [0.071, 0.075]	<0.001	0	0.00	.	.	.		
Ghana	0.104 [0.074, 0.134]	<0.001	7	519.06	<0.001	98.54	68.56		
Kenya	0.028 [0.014, 0.043]	<0.001	4	42.95	<0.001	89.17	9.23		
Libya	0.002 [0.002, 0.002]	<0.001	1	0.00	1.000	0.11	1.00		
Malawi	0.036 [0.035, 0.037]	<0.001	1	0.00	1.000	0.15	1.00		
Mali	0.118 [0.061, 0.176]	<0.001	1	151.92	<0.001	99.34	151.92		
Mauritania	0.118 [0.099, 0.137]	<0.001	0	0.00	.	.	.		
Mozambique	0.106 [0.084, 0.128]	<0.001	0	0.00	.	.	.		
Namibia	0.006 [0.005, 0.007]	<0.001	0	0.00	.	.	.		
Nigeria	0.083 [0.064, 0.101]	<0.001	10	1688.21	<0.001	98.70	76.64		
Sierra Leone	0.108 [0.104, 0.112]	<0.001	0	0.00	.	.	.		
South Sudan	0.089 [0.064, 0.114]	<0.001	0	0.00	.	.	.		
Sudan	0.074 [0.031, 0.117]	0.001	1	5.59	0.018	82.12	5.59		
Tanzania	0.060 [0.033, 0.087]	<0.001	2	45.01	<0.001	98.95	95.00		
Zambia	0.064 [0.057, 0.070]	<0.001	1	6.70	0.010	85.07	6.70		

4.5.3 Pooled prevalence of HCV

For the estimation of HCV among blood donors, 65 studies with a total of 1,228,214 study participants were included. These studies reported varying prevalence, ranging from 0.1% to 13.3%. In the random-effects model, the pooled proportion of HCV was 2.0%, studies = 65 (95% CI, 1.6 to 2.5%; n=1,228,214, with I^2=99.9%) (Figure 6). The subgroup analysis revealed that there were considerable variations in HCV estimates across regions in SSA. Forty-two studies had HCV frequency below 2% while 23 studies had frequency above 2%. The highest prevalence of HCV infection 2.6% (95% CI; 1.9% to 3.2%) among blood donors was observed in West Africa; Northern Africa had the least HCV prevalence 0.6% (95% CI; -0.1 to 1.4%) among donors. 2.4% (95% CI; 6.9% to 9.2%) of blood donors had a positive HCV test detected by RDT. Among 18 countries, HCV infections was highest 9.3% (95% CI; 6.7% to 11.8%) among donors from South Sudan. The least HCV prevalence was in Namibia 0.1% (95% CI; 0.1% to 0.1%) (Table 5) (Figure 6).

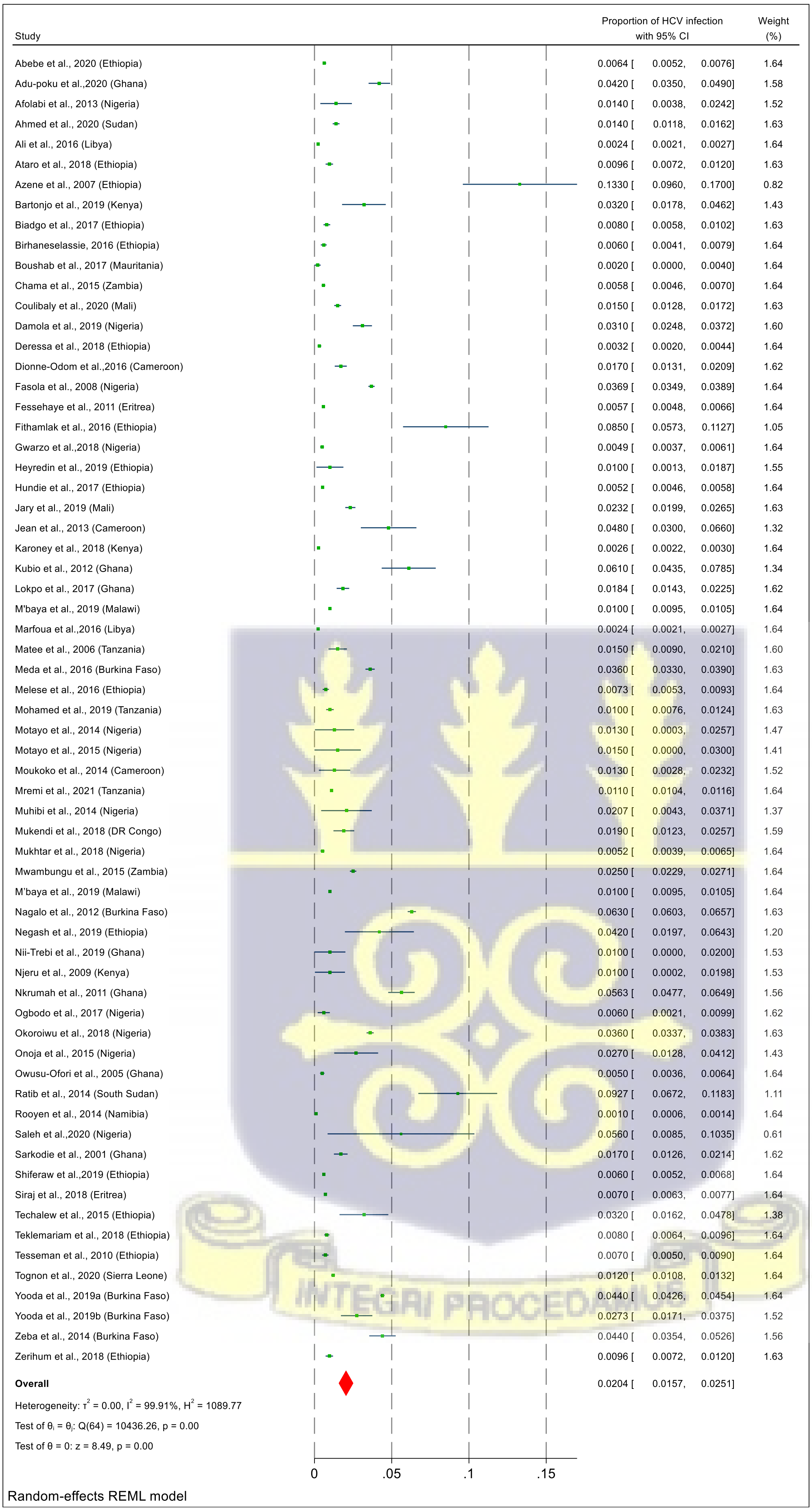

Figure 6: Pooled proportion of HCV among blood donors in SSA

Table 5: Subgroup analysis of the prevalence of HCV infection among donor population in Sub-Saharan Africa countries

			Heterogeneity summary					Test of group differences	
Characteristics	**Proportion (95% CI)**	**P-value**	**df**	**Q-statistic**	**P (Q)**	**% I2**	**H2**	**chi-square**	**P-value**
Overall	0.020 [0.016, 0.025]	<0.001	64	10429.68	<0.001	99.91	1090.31		
RDT testing								0.65	0.421
No	0.019 [0.014, 0.024]	<0.001	43	9328.24	<0.001	99.92	1217.87		
Yes	0.024 [0.014, 0.034]	<0.001	20	1049.25	<0.001	99.75	403.39		
PCR testing								1.74	0.188
No	0.021 [0.016, 0.026]	<0.001	62	10404.50	<0.001	99.91	1171.47		
Yes	0.016 [0.012, 0.021]	<0.001	1	0.90	0.344	0.02	1.00		
ELISA testing								0.67	0.414
No	0.023 [0.015, 0.032]	<0.001	20	1764.87	<0.001	99.80	488.06		
Yes	0.019 [0.013, 0.025]	<0.001	43	7929.81	<0.001	99.92	1280.10		
African region								15.96	0.003
West Africa	0.026 [0.019, 0.032]	<0.001	27	4774.03	<0.001	99.40	167.87		
Central Africa	0.022 [0.010, 0.035]	0.001	3	11.96	0.008	90.52	10.55		
Southern Africa	0.011 [-0.004, 0.025]	0.149	2	541.06	<0.001	99.81	528.79		
Eastern Africa	0.018 [0.009, 0.028]	<0.001	26	1141.72	<0.001	99.95	1938.83		
North Africa	0.006 [-0.001, 0.014]	0.106	2	104.97	<0.001	99.87	745.34		
Country								2161.92	<0.001
Burkina Faso	0.043 [0.032, 0.055]	<0.001	4	217.89	<0.001	98.49	66.18		
Cameroon	0.025 [0.005, 0.045]	0.016	2	11.85	0.003	92.19	12.80		
DR Congo	0.019 [0.012, 0.026]	<0.001	0	0.00	.	.	.		
Eritrea	0.006 [0.005, 0.008]	<0.001	1	5.50	0.019	81.80	5.50		
Ethiopia	0.020 [0.006, 0.035]	0.005	15	154.90	<0.001	99.92	1204.96		
Ghana	0.029 [0.013, 0.046]	<0.001	6	298.17	<0.001	98.75	80.31		
Kenya	0.014 [-0.003, 0.030]	0.106	2	18.76	<0.001	91.97	12.45		
Libya	0.002 [0.002, 0.003]	<0.001	1	0.00	1.000	0.00	1.00		
Malawi	0.010 [0.010, 0.010]	<0.001	1	0.00	1.000	0.01	1.00		
Mali	0.019 [0.011, 0.027]	<0.001	1	16.36	<0.001	93.89	16.36		
Mauritania	0.002 [-0.001, 0.005]	0.134	0	0.00	.	.	.		
Namibia	0.001 [0.001, 0.001]	<0.001	0	0.00	.	.	.		
Nigeria	0.020 [0.012, 0.028]	<0.001	11	1283.42	<0.001	98.67	74.99		
Sierra Leone	0.012 [0.011, 0.013]	<0.001	0	0.00	.	.	.		
South Sudan	0.093 [0.067, 0.118]	<0.001	0	0.00	.	.	.		
Sudan	0.014 [0.012, 0.016]	<0.001	0	0.00	.	.	.		
Tanzania	0.011 [0.010, 0.012]	<0.001	2	2.37	0.305	0.04	1.00		
Zambia	0.015 [-0.003, 0.034]	0.109	1	251.12	<0.001	99.60	251.12		

4.5.4 Pooled prevalence of Syphilis

With regards to syphilis, 43 studies involving 965,488 participants were eligible for estimating pooled prevalence. These studies reported varying prevalence, ranging from 0.0% to 15.0%. In the random-effects model, the pooled prevalence of syphilis was 2.8%, studies = 43, n=965,488 (95% CI; 1.9 to 3.6%) (Figure 7). The subgroup analysis showed considerable variation in the estimates for Syphilis across regions in SSA. Twelve studies reported syphilis in less than 1% of the donors, eight studies between 1% and 2% (Figure 7). Analysis by sub-region revealed the highest Syphilis 5.5% (95% CI; 3.9% to 7.1%) prevalence among donors in Central Africa with Southern Africa having the least syphilis infection 0.9% (95% CI; 0.2% to 1.5%) among donors. Sudan had the highest syphilis infection 10.1% (95% CI; 1.0% to 19.2%) among donors in seventeen SSA countries; only one study on syphilis testing was included in the systematic review and with a 0.0% prevalence of syphilis (Table 6).

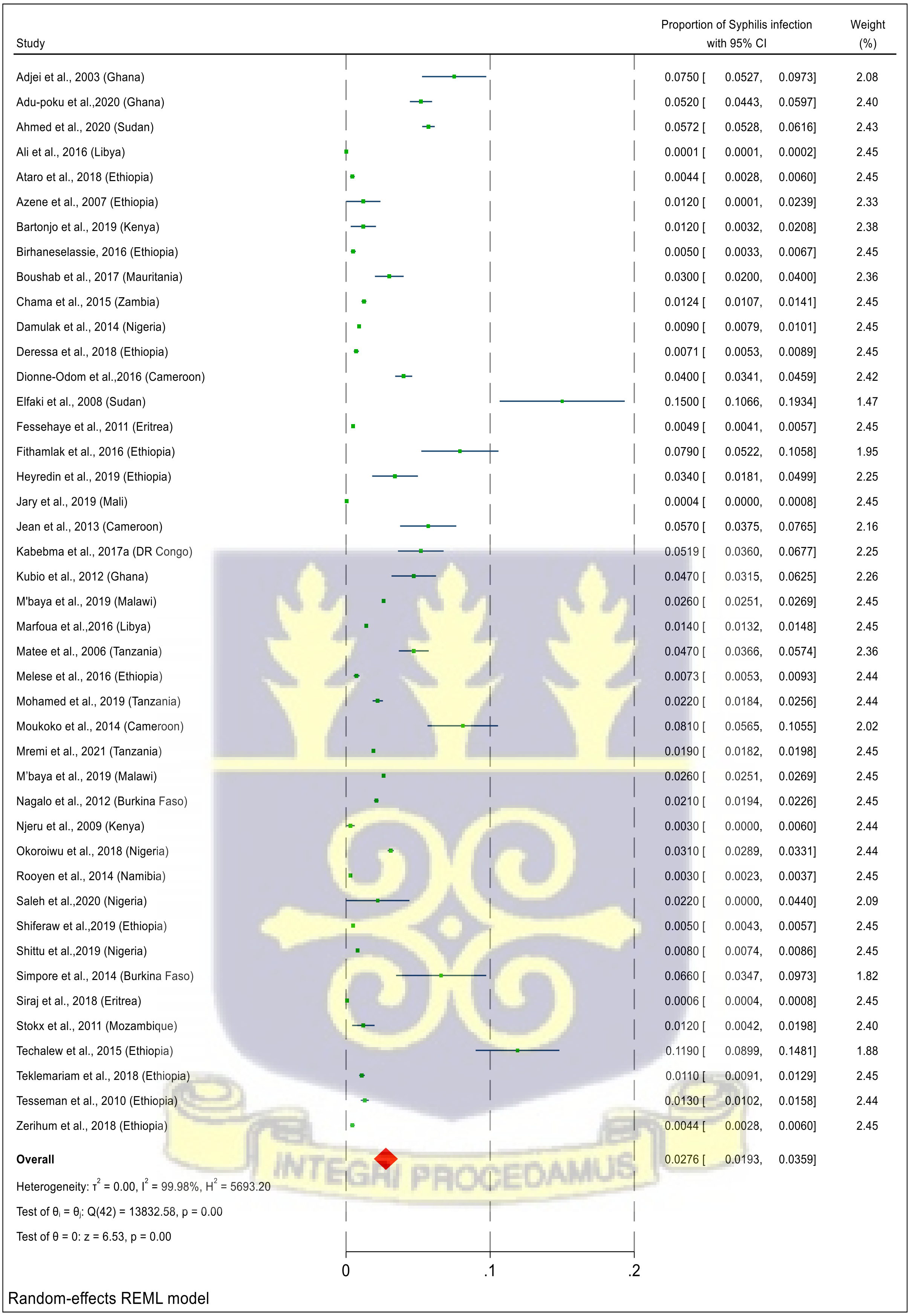

Figure 7: Pooled prevalence of Syphilis among blood donors in SSA, using random-effects model

Table 6: Subgroup analysis of the prevalence of syphilis infection among donor population in Sub-Saharan Africa countries

			Heterogeneity summary						
								Test of group differences	
Characteristics	**Proportion (95% CI)**	**P-value**	**df**	**Q-statistic**	**P (Q)**	**% I2**	**H2**	**chi-square**	**P-value**
Overall	0.028 [0.019, 0.036]	<0.001	42	13827.09	<0.001	99.98	5600.88		
RDT testing								5.22	0.022
No	0.018 [0.010, 0.025]	<0.001	18	10829.64	<0.001	99.98	4190.24		
Yes	0.036 [0.022, 0.049]	<0.001	23	2645.01	<0.001	99.87	786.81		
PCR testing								0.38	0.537
No	0.026 [0.017, 0.036]	<0.001	33	10673.36	<0.001	99.96	2693.03		
Yes	0.033 [0.013, 0.054]	0.001	8	540.38	<0.001	99.95	1825.50		
ELISA testing								5.60	0.018
No	0.027 [0.019, 0.035]	<0.001	41	13810.65	<0.001	99.98	5628.74		
Yes	0.066 [0.035, 0.097]	<0.001	0	0.00	.	.	.		
African region								32.73	<0.001
West Africa	0.031 [0.017, 0.045]	<0.001	10	1791.50	<0.001	99.91	1162.25		
Central Africa	0.055 [0.039, 0.071]	<0.001	3	13.17	0.004	77.51	4.45		
Southern Africa	0.009 [0.002, 0.015]	0.009	2	103.83	<0.001	97.18	35.46		
Eastern Africa	0.020 [0.010, 0.030]	<0.001	20	7598.71	<0.001	99.94	1638.22		
North Africa	0.053 [-0.011, 0.116]	0.102	3	1788.32	<0.001	99.99	15847.10		
Country								4760.59	<0.001
Burkina Faso	0.041 [-0.003, 0.084]	0.068	1	7.93	0.005	87.39	7.93		
Cameroon	0.057 [0.034, 0.080]	<0.001	2	12.20	0.002	83.45	6.04		
DR Congo	0.052 [0.036, 0.068]	<0.001	0	0.00	.	.	.		
Eritrea	0.003 [-0.001, 0.007]	0.204	1	105.51	<0.001	99.05	105.51		
Ethiopia	0.023 [0.005, 0.041]	0.014	11	168.97	<0.001	99.90	1020.02		
Ghana	0.055 [0.043, 0.068]	<0.001	2	4.38	0.112	55.98	2.27		
Kenya	0.007 [-0.002, 0.016]	0.126	1	2.95	0.086	66.13	2.95		
Libya	0.007 [-0.007, 0.021]	0.308	1	1088.17	<0.001	99.91	1088.17		
Malawi	0.026 [0.025, 0.027]	<0.001	1	0.00	1.000	0.00	1.00		
Mali	0.000 [0.000, 0.001]	0.073	0	0.00	.	.	.		
Mauritania	0.030 [0.020, 0.040]	<0.001	0	0.00	.	.	.		
Mozambique	0.012 [0.004, 0.020]	0.003	0	0.00	.	.	.		
Namibia	0.003 [0.002, 0.004]	<0.001	0	0.00	.	.	.		
Nigeria	0.017 [0.004, 0.029]	0.010	3	413.47	<0.001	99.68	310.44		
Sudan	0.101 [0.010, 0.192]	0.029	1	17.39	<0.001	94.25	17.39		
Tanzania	0.029 [0.012, 0.045]	0.001	2	30.05	<0.001	98.50	66.84		
Zambia	0.012 [0.011, 0.014]	<0.001	0	0.00	.	.	.		

4.5.5 Pooled prevalence of HIV

For the estimation of the pooled prevalence of HIV among blood donors, 61 articles with a total of 1,633,198 participants' data were used. These studies reported varying prevalence, ranging from 0.0% and 14.0%. In the random-effect model, the pooled size effect of HIV was 3.2% (studies= 61, n=1,633,198; 95% CI; 2.5, 4.0%) (Figure 8). The subgroup analysis revealed that there were considerable variations of HIV infection estimate across regions in SSA. Ten studies reported HIV less than 1% among donors, sixteen studies between 1% and 2%. Analysis by sub-region revealed highest HIV 5.2% (95%CI, 0.6%–9.8%) prevalence among donors in Southern Africa, with Northern Africa having the least HIV infection 1.2% (95%CI; 0.1%, 2.3%) among donors (Table 7). Analysis by countries showed Mozambique had the highest HIV infection 8.5% (95% C; 6.5%, 10.5%) among donors in eighteen SSA countries of included studies who reported on HIV, with Eritrea having the least HIV infection 0.2 % (95% CI; 0.1%, 0.4%) (Table 7).

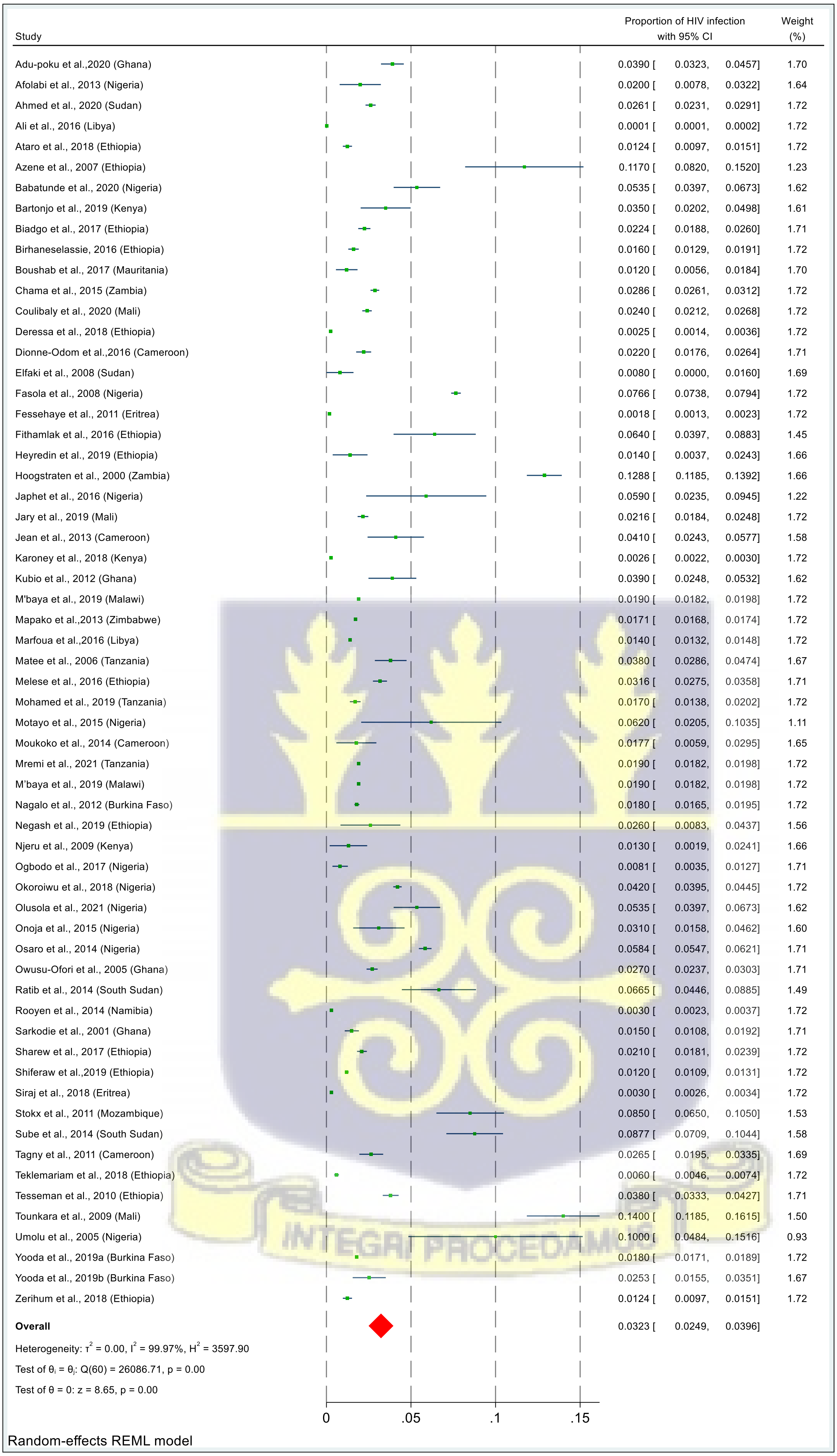

Figure 8: Pooled proportion of HIV among blood donors in SSA, random-effects model

Table 7: Subgroup analysis of the prevalence of HIV infection among donor population in Sub-Saharan Africa countries

			Heterogeneity summary					Test of group differences	
Characteristics	**Proportion (95% CI)**	**P-value**	**df**	**Q-statistic**	**P (Q)**	**% I2**	**H2**	**chi-square**	**P-value**
Overall	0.032 [0.025, 0.040]	<0.001	60	26085.83	<0.001	99.97	3596.88		
African region								12.48	0.014
West Africa	0.041 [0.028, 0.053]	<0.001	21	2345.12	<0.001	99.64	276.80		
Central Africa	0.024 [0.019, 0.029]	<0.001	3	6.29	0.098	34.19	1.52		
Southern Africa	0.052 [0.006, 0.098]	0.027	4	1950.25	<0.001	99.99	9854.91		
Eastern Africa	0.025 [0.016, 0.034]	<0.001	25	4952.35	<0.001	99.94	1573.75		
North Africa	0.012 [0.001, 0.023]	0.032	3	1375.72	<0.001	99.80	500.36		
Country								2184.09	<0.001
Burkina Faso	0.018 [0.017, 0.019]	<0.001	2	2.12	0.346	0.03	1.00		
Cameroon	0.024 [0.019, 0.029]	<0.001	3	6.29	0.098	34.19	1.52		
Eritrea	0.002 [0.001, 0.004]	<0.001	1	13.02	<0.001	92.32	13.02		
Ethiopia	0.025 [0.013, 0.036]	<0.001	13	653.13	<0.001	99.67	305.65		
Ghana	0.029 [0.018, 0.041]	<0.001	3	43.86	<0.001	94.29	17.50		
Kenya	0.016 [-0.003, 0.034]	0.093	2	21.80	<0.001	91.96	12.44		
Libya	0.007 [-0.007, 0.021]	0.308	1	1088.17	<0.001	99.91	1088.17		
Malawi	0.019 [0.018, 0.020]	<0.001	1	0.00	1.000	0.38	1.00		
Mali	0.061 [-0.015, 0.137]	0.114	2	113.95	<0.001	99.90	981.02		
Mauritania	0.012 [0.006, 0.018]	<0.001	0	0.00	.	.	.		
Mozambique	0.085 [0.065, 0.105]	<0.001	0	0.00	.	.	.		
Namibia	0.003 [0.002, 0.004]	<0.001	0	0.00	.	.	.		
Nigeria	0.048 [0.033, 0.062]	<0.001	10	753.83	<0.001	98.32	59.58		
South Sudan	0.078 [0.058, 0.099]	<0.001	1	2.25	0.133	55.63	2.25		
Sudan	0.018 [0.000, 0.036]	0.048	1	9.97	0.002	89.97	9.97		
Tanzania	0.024 [0.012, 0.036]	<0.001	2	17.32	<0.001	97.78	45.08		
Zambia	0.079 [-0.020, 0.177]	0.117	1	340.42	<0.001	99.71	340.42		
Zimbabwe	0.017 [0.017, 0.017]	<0.001	0	0.00	.	.	.		

4.6 Co-infections of TTIs among blood donors in SSA

Co-infections of HBV/HCV; HBV/HCV/HIV; HBV/HIV; HBV/Syphilis; HCV/Syphilis; HIV/Syphilis; HIV/HCV; HBV/HCV/Syphilis; HBV/HIV/Syphilis were reported among studies included in this systematic review. The proportion of HBV/HCV co-infection among blood donors ranged between 0.0% and 5.4% in 23 studies with a prevalence of 0.7% (95% CI, 0.2% to 1.2%). Ethiopia had the highest HBV/HCV coinfection 5.4% (95% CI, 5.2% to 5.6%). Six studies reported HBV/HCV coinfection less than 0.1% among donors (**Figure 9**). Two studies reported HBV/HCV/HIV coinfections with an overall prevalence of 3.3% (95% CI, -3.0% to 9.6%) (**Figure 10**). Nineteen studies reported HIV/HBV coinfection with an overall prevalence of 0.8% (95% CI, 0.3% to 1.3%) (**Figure 11**). Eleven studies reported HBV and Syphilis coinfection with an overall prevalence of 0.3% (95% CI, 0.1% to 0.4%) (**Figure 12**). Nine studies reported HCV and syphilis coinfection with an overall prevalence of 0.2% (95% CI, 0.0% to 0.3%) (**Figure 13**). Ten studies reported HIV and syphilis coinfection with an overall prevalence of 0.2% (95% CI, 0.1% to 0.2%) (**Figure 14**). Sixteen studies reported HIV and HCV coinfection, with an overall prevalence of 0.2% (95%CI, 0.1% to 0.4%) (**Figure 15**). Only one study reported HBV, HCV, and syphilis co-infection, with an overall prevalence of 2% (95% CI, 1.8% to 2.2%). One study reported HBV, HIV, and syphilis co-infection, with an overall prevalence of 31% (95% CI, 30.5% to 31.5%).

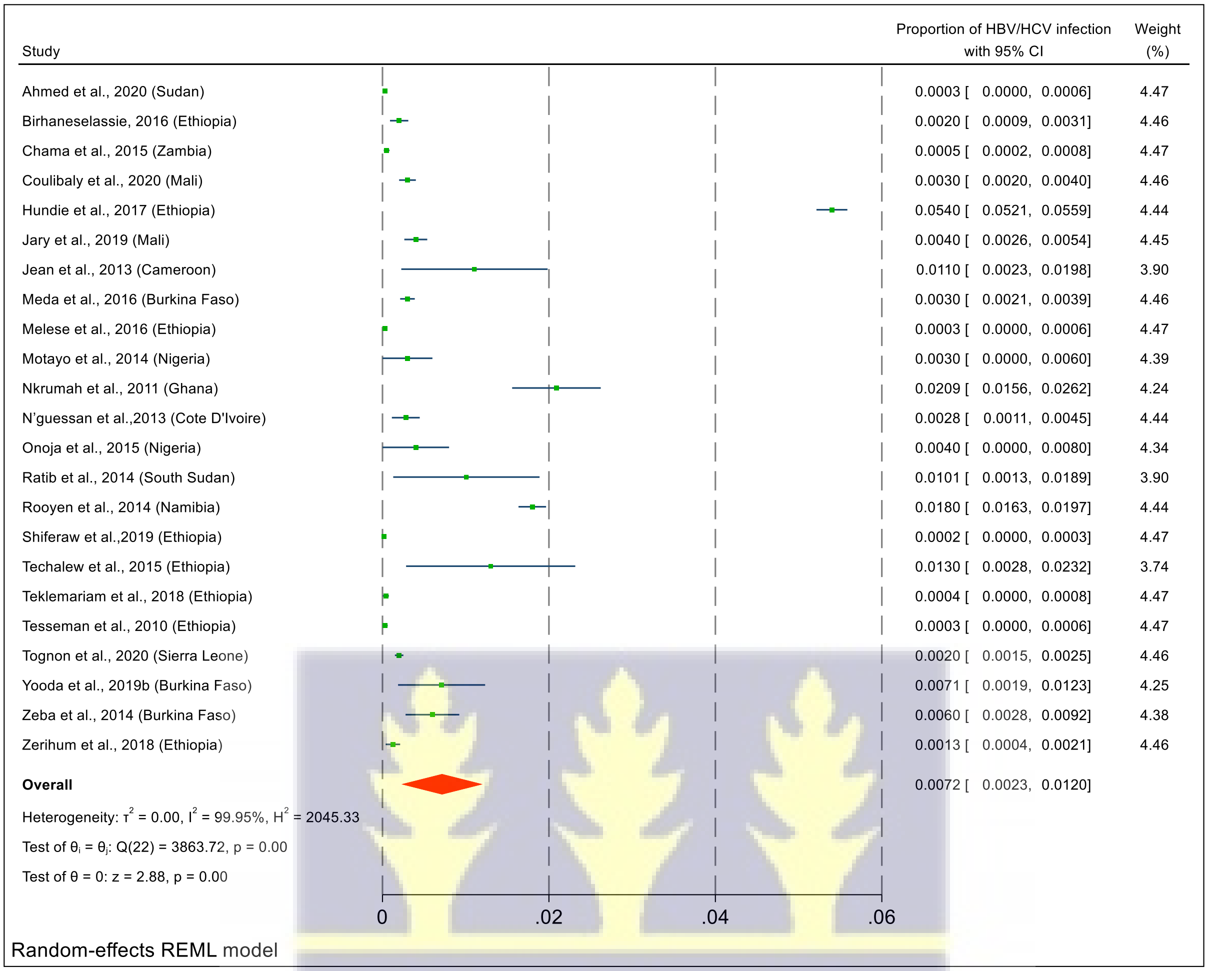

Figure 9: Forest plot of the proportion of HBV and HCV Co-infection among blood donors in Sub-Saharan Africa

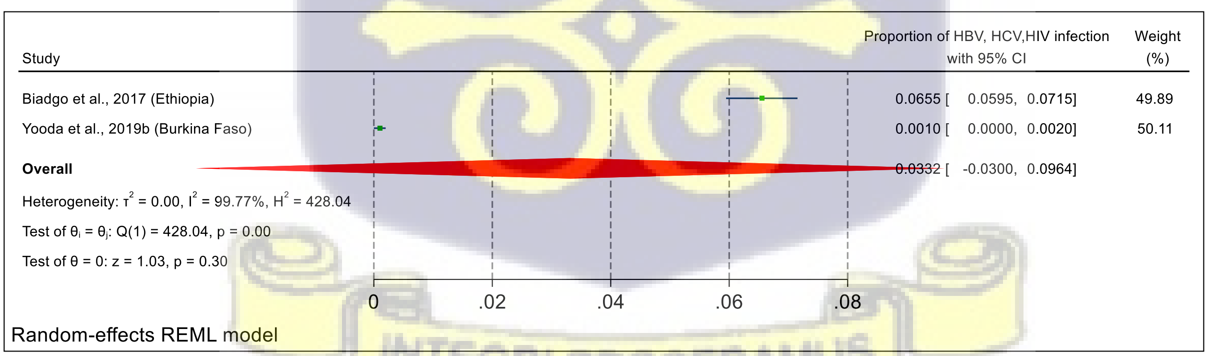

Figure 10: Forest plot of the proportion of HBV, HCV, and HIV Co-infection among blood donors in Sub-Saharan Africa

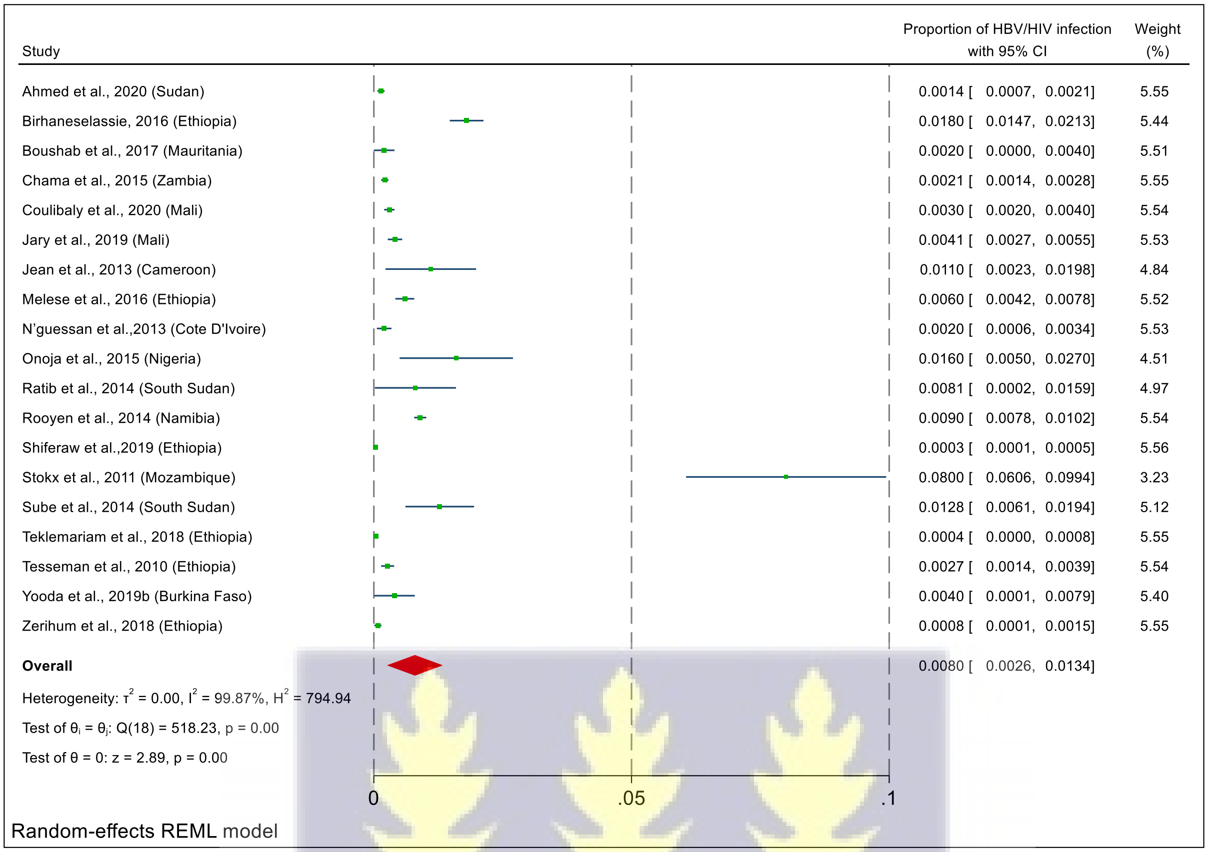

Figure 11: Forest plot of the proportion of HBV and HIV Co-infection among blood donors in Sub-Sahara Africa

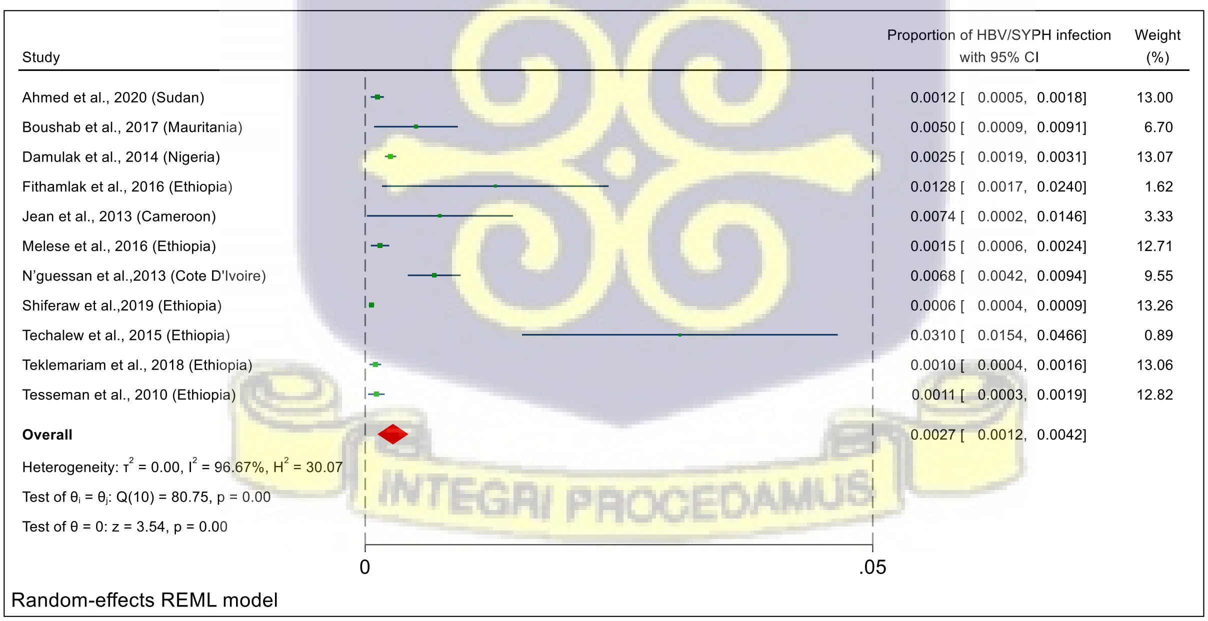

Figure 12: Forest plot of the proportion of HBV and Syphilis Co-infection among the donor population in Sub-Sahara Africa

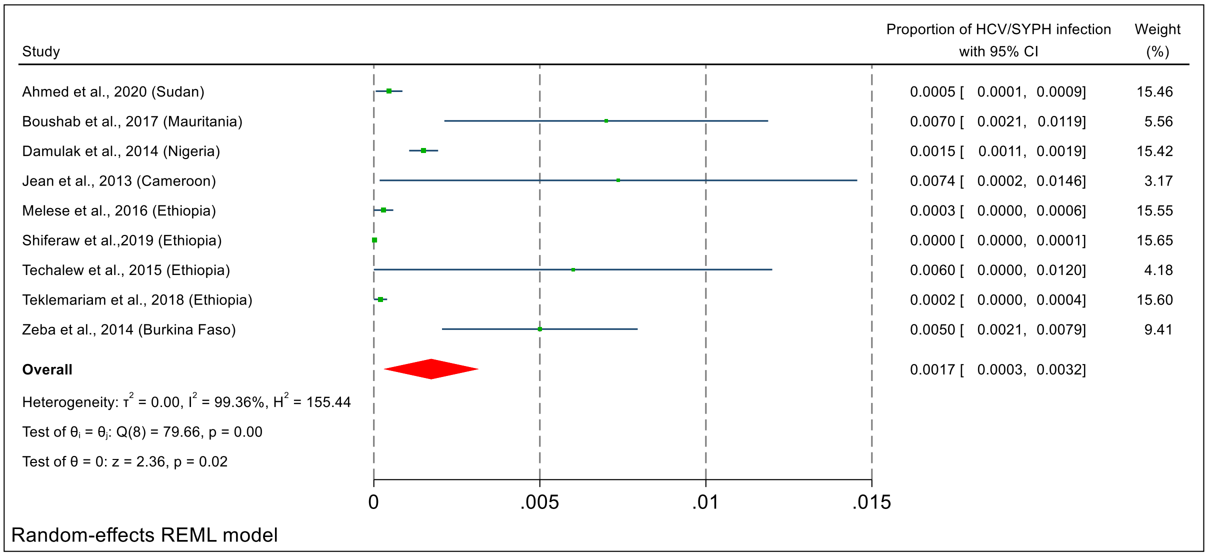

Figure 13: Forest plot of the proportion of HCV and Syphilis Co-infection among blood donors in Sub-Sahara Africa

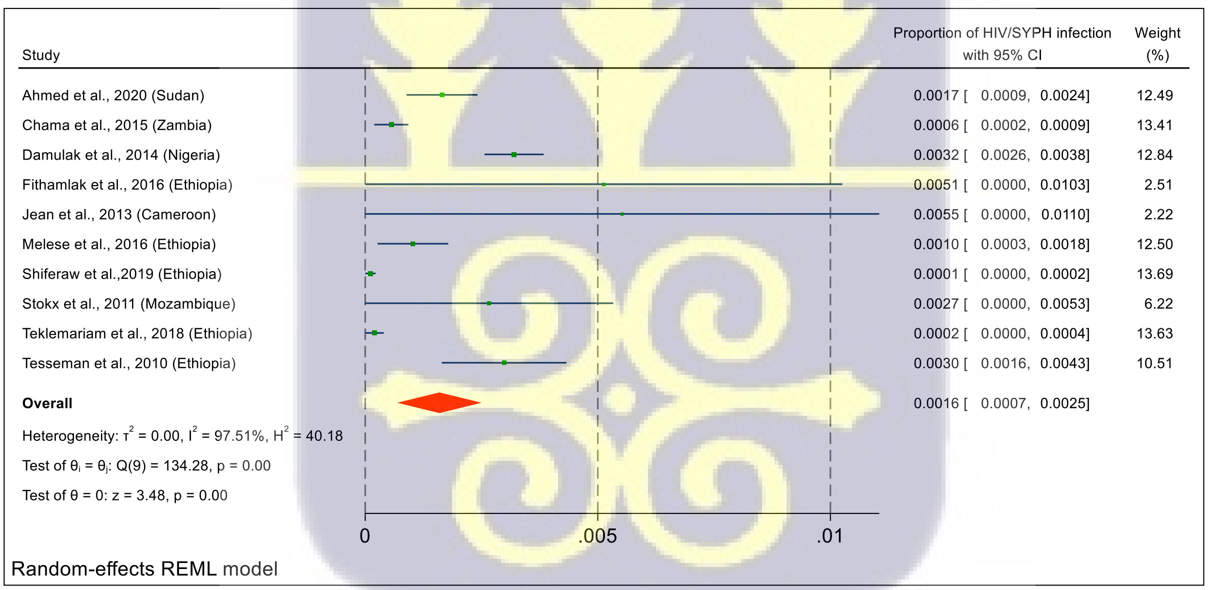

Figure 14: Forest plot of the proportion of HIV and Syphilis Co-infection among blood donors in Sub-Sahara Africa

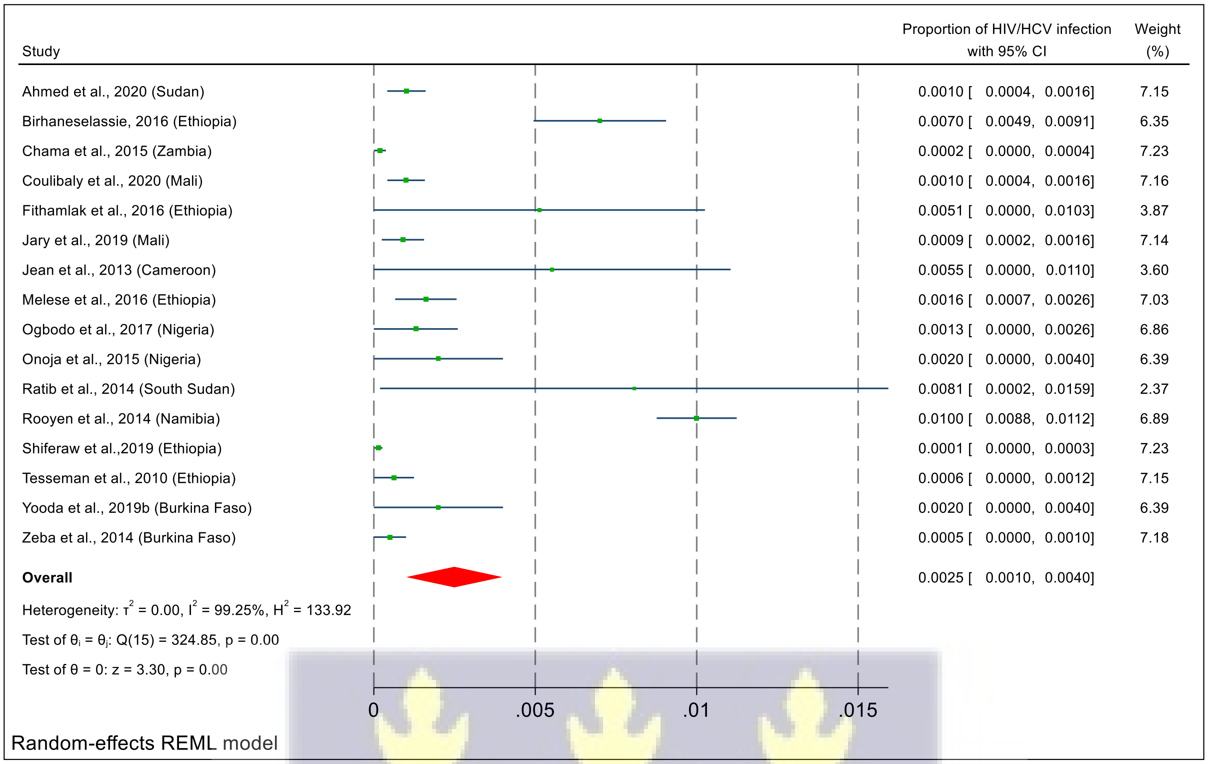

Figure 15: Forest plot of the proportion of HIV and HCV Co-infection among blood donors in Sub-Saharan Africa

4.7 Trends of TTIs in SSA from 2000 to 2021

4.7.1 Trend of HBV infection

Figure 16 shows the trend of HBV prevalence among blood donors and reveals a decreasing trend of HBV infections from research published from 2000 to 2021; 2000 (P=16.8%, 95% CI 15.5 to 18.1) and 2021 (P=6.9%, 95% CI 5.9 to 7.8). However, a 6.9% prevalence of HBV among blood donors have been reported in 8 studies conducted between 2020 and 2021.

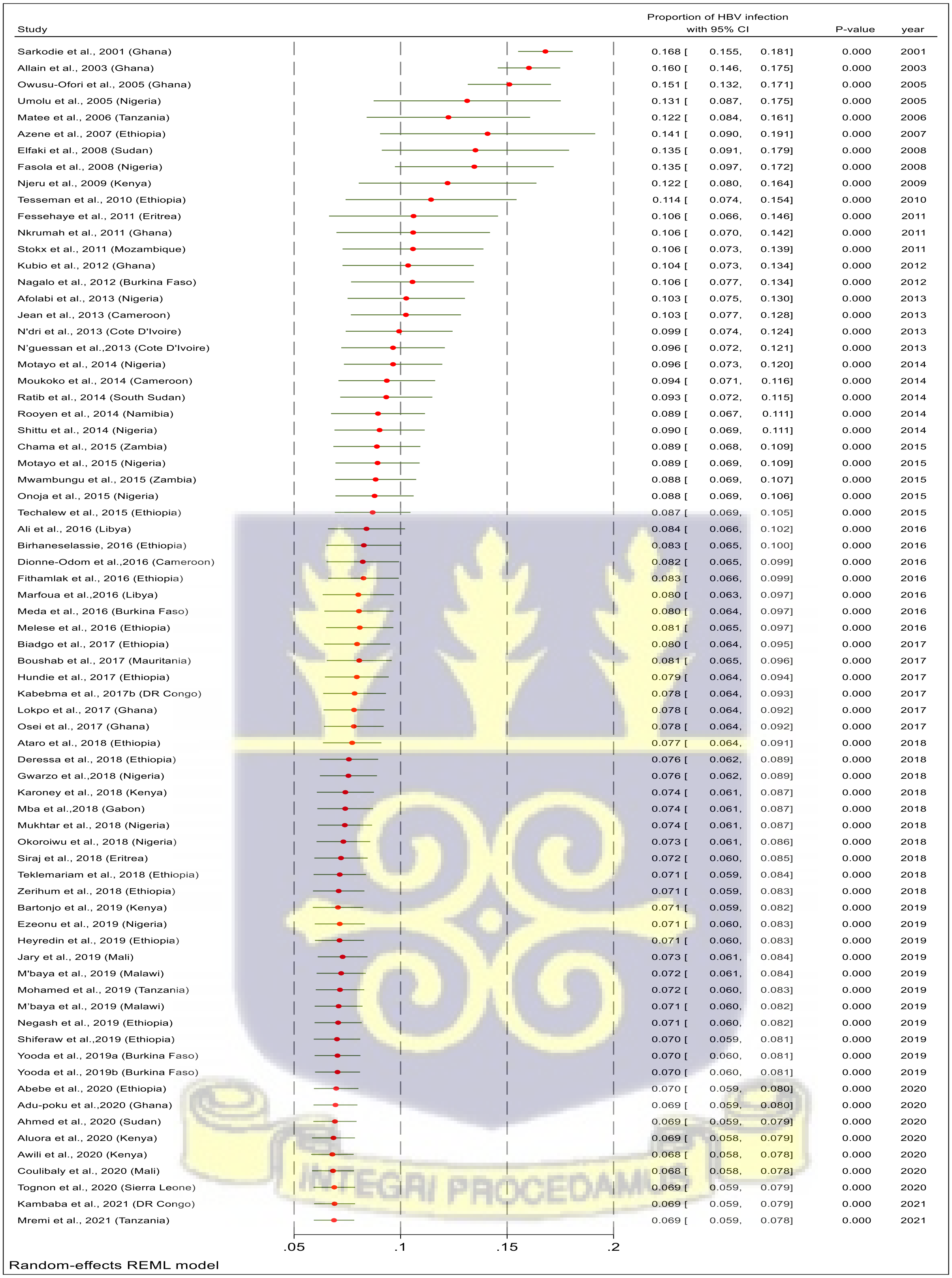

Figure 16: Trend of hepatitis B infection among donors by year of publication of study in SSA

4.7.2 Trend of HCV infection

Figure 17 shows the trend of HCV infection among blood donors by the year of publication of the study. Between 2001 and 2006, a 1.7% to 1.2% decreased trend was observed. However, there was a change in trend in 2007 with the prevalence rising to 4.0%. A decreasing trend in HCV prevalence from 4.0% in 2007 to 2.0% in 2021 was observed. A relatively constant trend of 2.1% to 2.0% was evident between 2018 and 2021.

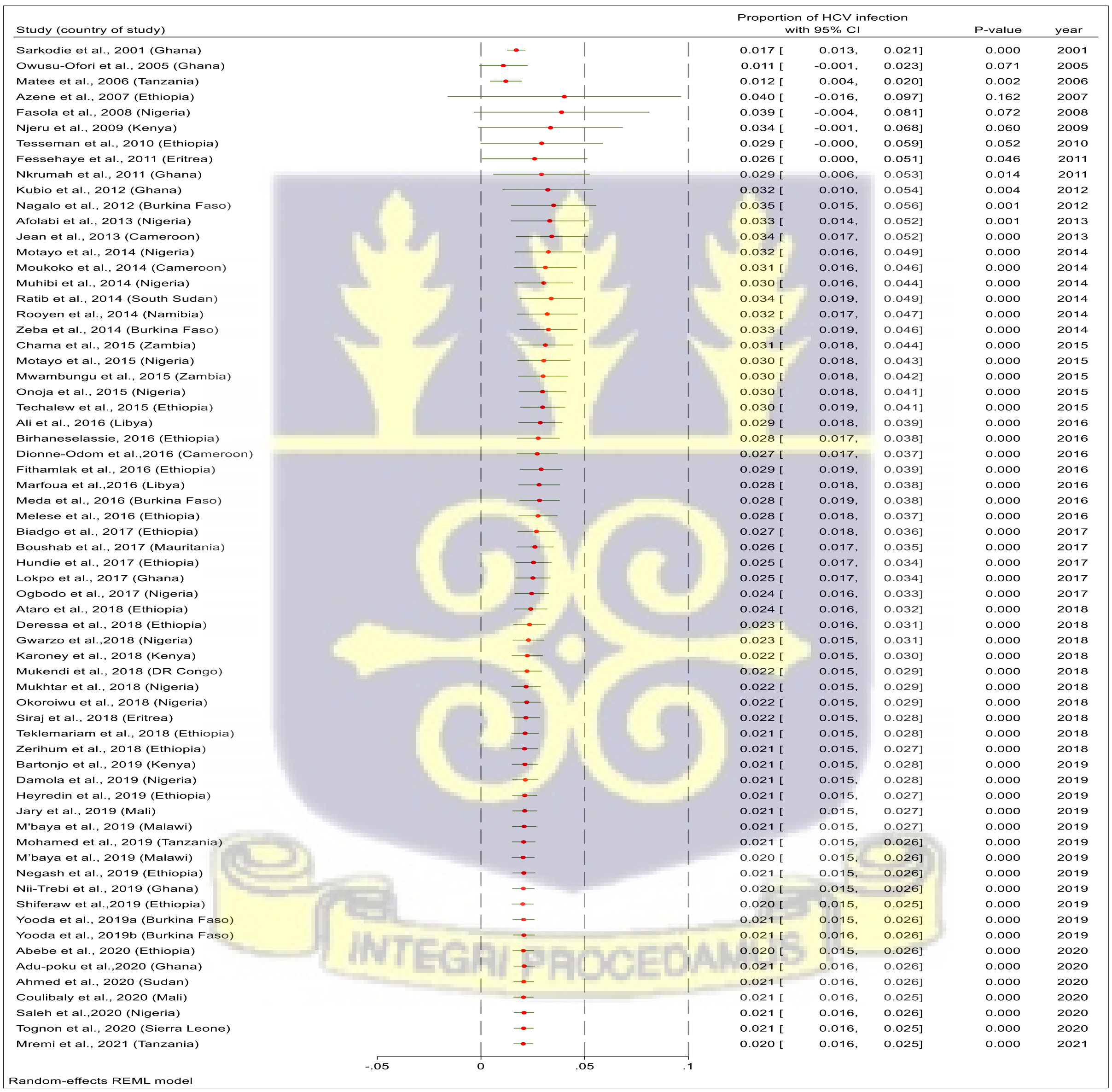

Figure 17: Trends of hepatitis C infection among donors by year of publications

4.7.3 Trend of HIV infection

Among the 43 studies included in this analysis comprising of 965488 blood donors, the trend of HIV prevalence shows a decline in HIV infection [12.9% (95% CI 11.9 to 13.9) to 3.2% (95% CI 2.5 to 4.0)] from 2000 to 2021 as shown in figure 18. Between 2019 and 2021 however, the decline in HIV prevalence saw a relatively stable trend (3.4% to 3.2%).

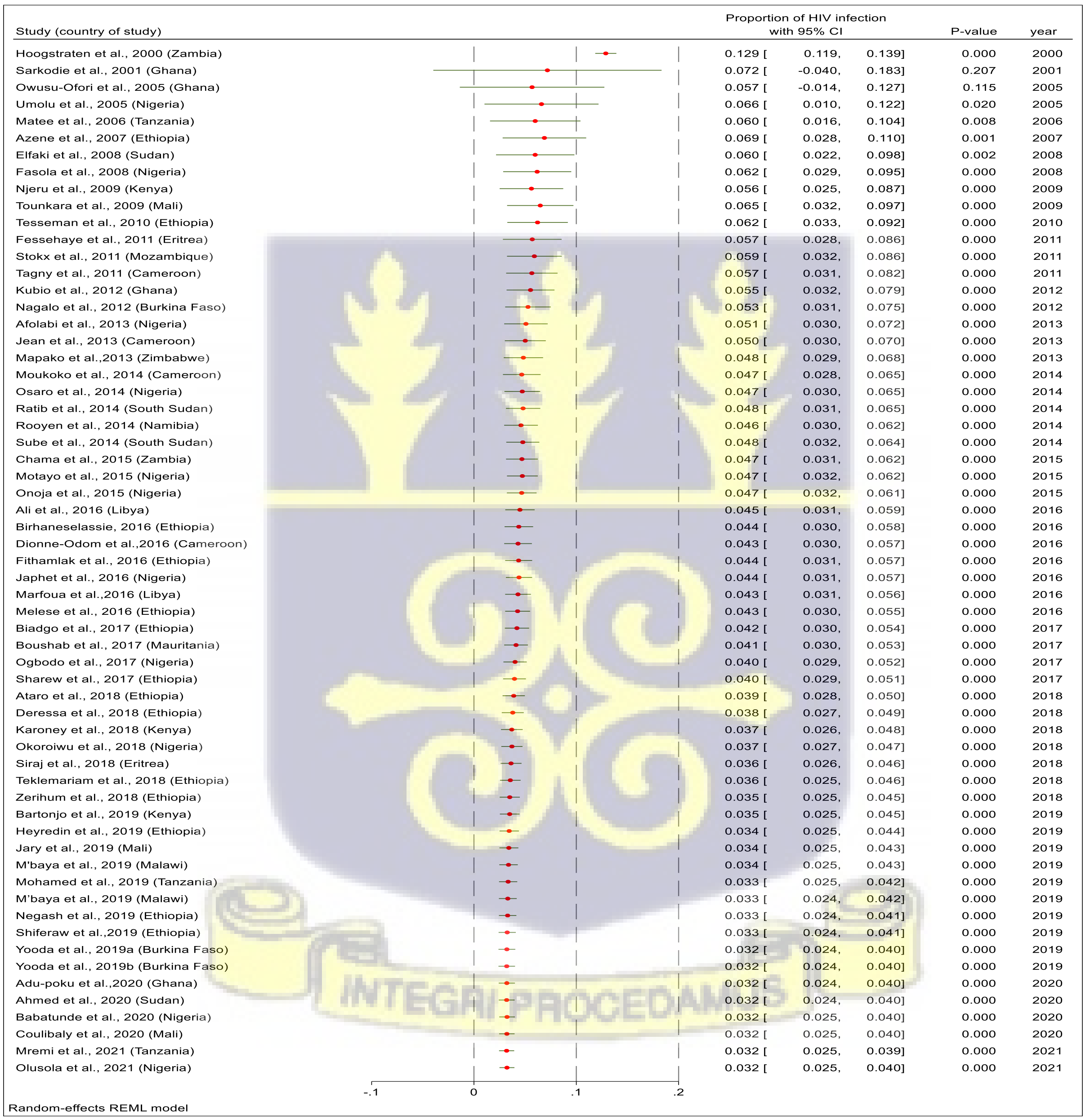

Figure 18: Trends of HIV infection among donors by year of publications

4.7.4 Trend of Syphilis infection

The prevalence of syphilis among blood donors generally shows a decreasing trend from published studies between 2003 and 2021 (Figure 19). The prevalence of Syphilis among blood donors decreased from 7.5% (95% CI 5.3 to 9.7) in 2003 to 2.8% (95% CI 1.9 to 3.5) in 2021. However, syphilis prevalence revealed relatively stable trend (2.9% and 2.8%) between 2018 and 2021.

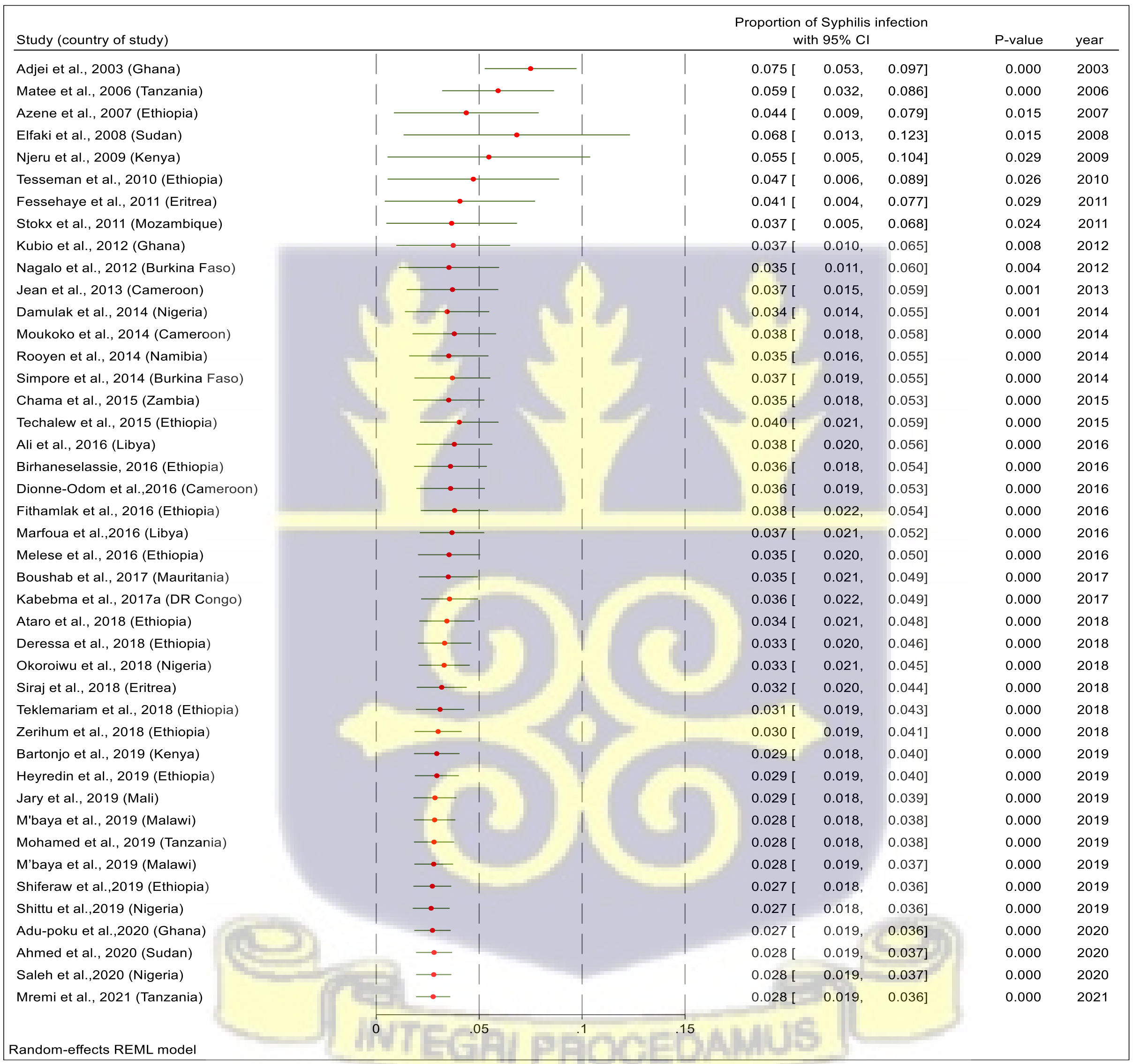

Figure 19: Trend of Syphilis among donors in SSA by year of publications of study

4.7.5 Trends of Hepatitis B and Hepatitis C co-infection

Figure 20 shows the trends in HBV and HCV co-infection among blood donors. Between 2011 and 2020, there was a general decrease in the trend of HBV and HCV co-infection from 1.0% to 0.72%. However, there were slight changes in the trends, especially, 0.92% in 2014 and 0.99% in 2018, where the prevalence of HBV and HCV co-infection increased, causing a deviation in the trend.

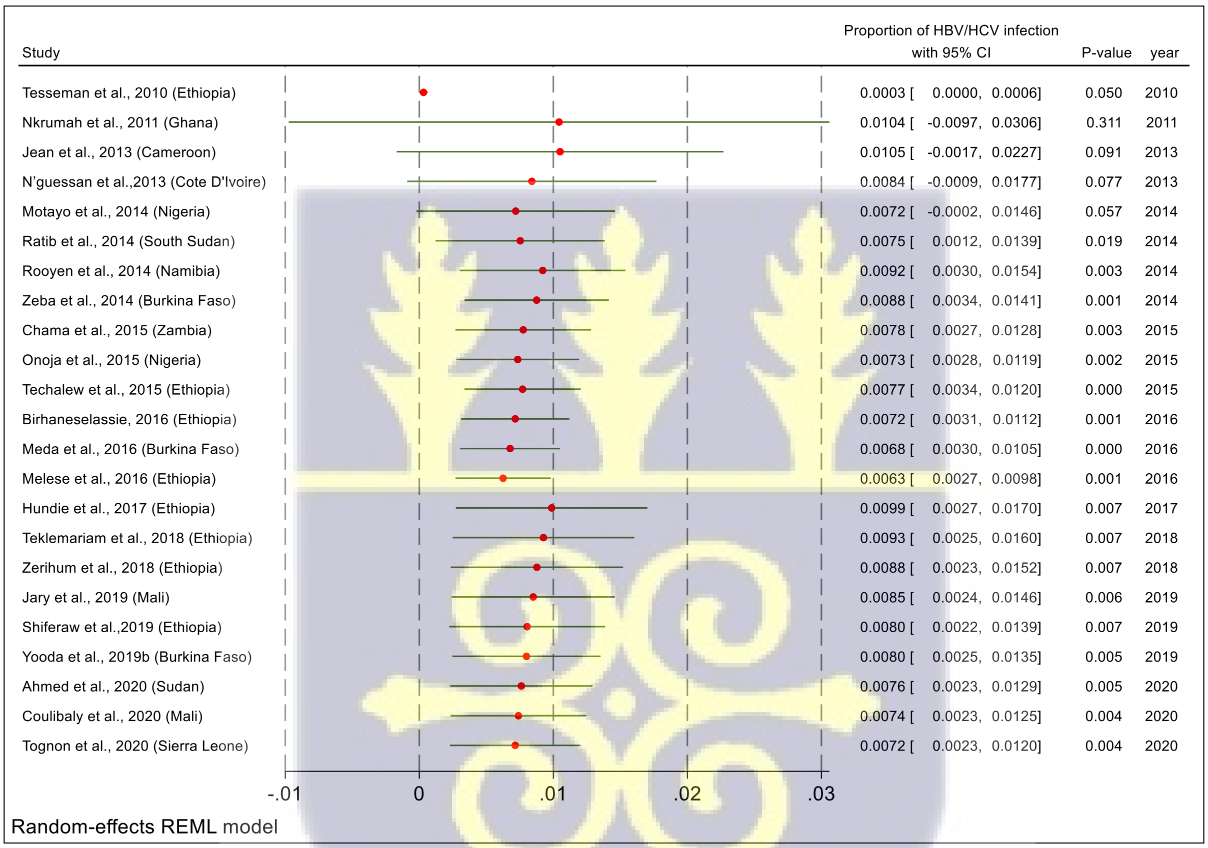

Figure 20: Trends of HBV and HCV infections among blood donors by year of publications

4.7.6 Trend of Hepatitis B and HIV Co-infection

Figure 21 shows the trend of HBV and HIV co-infections. HBV and HIV co-infections gradually decreased from 4.1% to 0.8% between 2011 and 2020. However, the prevalence has remained relatively stable in 2020.

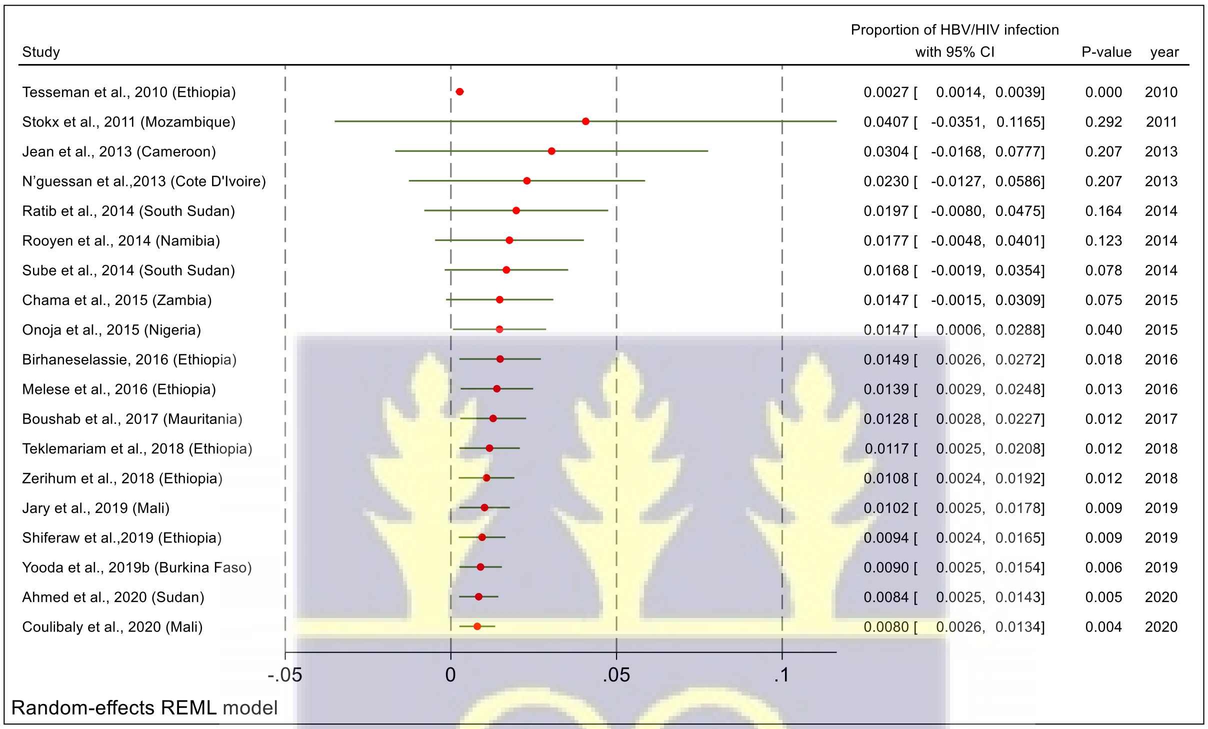

Figure 21: Trend of HBV and HIV co-infection by year of publication

CHAPTER FIVE

5.0 DISCUSSIONS

5.1 Discussion

In Sub-Saharan African countries, safe blood and blood products are in short supply, and sustainable and effective strategies to organize and maintain safe blood transfusion services are required (Christian et al., 2011). There is marked variability in the organization of transfusion services in sub-Saharan Africa. For many years, WHO has encouraged governments to develop national blood policies and create blood centre networks. To increase the quality of available blood, a lot of effort has gone into building quality assurance and standard procedures (Ambridge et al., 2004). The HCV, HIV, and HBV viruses, are among the three most important infections that can be transmitted to those receiving blood products. Moreover, HCV is still among the most common causes of post-transfusion hepatitis around the world and is the main cause of the end-stage liver disease (Okoroiwu et al., 2018b).

5.1.1 Pooled prevalence of TTIs in Sub-Saharan Africa

From the searches we conducted, this is the first systematic review on transfusion transmissible infection in SSA. This review showed an overall TTIs prevalence of 10.1% (n=2,047,302) among blood donors in SSA. Transmission of infectious pathogens such as HBV, HCV, HIV, and Syphilis through blood transfusion is a significant concern. The pooled TTIs prevalence in this systematic review is higher compared with the outcome of a study conducted in India with TTIs prevalence of 1.52% (Priya Poorana & Subhashree, 2013) and a similar studies in Pakistan with TTIs prevalence between 4% and 9% (Ehsan et al., 2020). In contrast, TTIs was found to be lower in our study as compared with others (Ahmed, et al., 2014; Nkrumah, Owusu, & Averu, 2011; Stokx et al., 2011) with TTIs prevalence of 13.7%, 13.8%, 15.9%, and 18.7% respectively. Our results showed a significant geographic difference in the prevalence of TTIs.

Comparing prevalence at the sub-regional level, Eastern and West Africa had relatively higher TTIs positivity rates among blood donors, accounting for 11.2% and 10.1% respectively. Meanwhile, the lowest prevalence was found in Northern Africa with a percentage of 5.6%. The disparities between these studies could be explained by differences in research region and population, sample size, socioeconomic position and cultural habits of study communities, and diagnostic methodologies, all of which are known factors influencing the occurrence and distribution of various disorders. Replacement donation contributed to the high prevalence of TTIs among donors (Stokx et al., 2011).

5.1.2 Prevalence of Hepatitis B virus in blood donors

In this review, the frequency of hepatitis B (HBsAg) in donors ranged from 0.2% to 25.0%. The pooled prevalence of HBV from 72 studies published between 2000 and 2021 was 6.9% (n=1,306,763). Our study finding for HBV is higher than similar studies 1.55% to 3.76% (Ehsan et al., 2020) in Pakistan, 4.9% in Ethiopia (Fite et al., 2020), and 2.0% in both Eastern Mediterranean Regional Office (EMRO) and middle eastern (E and M) countries (Babanejad et al., 2016). HBV infection is endemic in SSA, and the burden of HBV-related illness is substantial. HBV infection has a lifetime risk of over 60%, and more than 8% of the population is chronically infected, putting them at risk of liver disease and hepatocellular cancer (HCC) (Howell et al., 2014).

Sub-Saharan Africa has one of the world's highest incidences of HBV-related liver cancer (Parkin et al., 2005). The observed variances could be attributable to disparities in cultural norms regarding TTI prevention, as well as inequalities in economic status, which result in varying levels of vulnerability to sexually transmitted illnesses. Furthermore, differences in the period, the strength of preliminary screening of donors, and concerns related to the testing methodologies used for screening could all have a role in the HBV prevalence disparity (Shiferaw et al., 2019).

5.1.3 Prevalence of Hepatitis C Virus among SSA blood donors

Our study showed the prevalence of hepatitis C (anti-HCV antibodies) in blood donors ranged from 0.1% to 13.3%. The prevalence of HCV from 66 studies published between 2006 and 2021 was 2.0% (n= 1,228,214).Our finding was lower compared with estimates of similar studies 2.44% (n=17,660) (Ehsan et al., 2020), (2.83%) in Ethiopia (Melku et al., 2021), and (8.68%) in mainland China between 1990 to 2010 (Gao et al., 2011). Finding of our study was higher than prevalence of a systematic reviews conducted in Iran 0.5% (n=10,739,221) (Khodabandehloo, Roshani, & Sayehmiri, 2013) and Europe (0.74%) (Babanejad et al., 2016). HCV seroprevalence among blood donors ranges from 0.4% to 19.2% globally (Makroo et al., 2013).The differences could be due to a variety of factors, including differences in diagnosis methods; for example, the systematic review done in China included studies that used molecular techniques (Gao et al., 2011); disparities in demographic phenomena between countries, such as migration; and variances in safe sexual practice practices. Furthermore, one of the key causes of HCV prevalence variance is likely due to differences in safety standards and the degree to which they are enforced among nations.

5.1.4 Prevalence of Syphilis among blood donors in SSA

Based on this review, the prevalence of syphilis was 2.8% (95% CI; 1.9, 3.6%). This was higher compared to estimates of earlier studies in Pakistan 0.43% (Attaullah et al., 2012), India 0.43% (Makroo et al., 2015), Kenya 1.0% (Mahuro et al., 2017), 1.1% in Pakistan (Ehsan et al., 2020) and 1.5% in Ethiopia (Melku et al., 2021).On the other hand, our estimate was lower compared prevalence of syphilis reported in Burkina Faso 3.96% (M. B. Nagalo et al., 2011) and Nigeria

4.2% (Okoroiwu et al., 2018).The difference in syphilis magnitude between studies could be attributed to differences in risk behaviours in different geographical locations, or partly owing to differences in socio-cultural practices.

5.1.5 Prevalence of HIV among blood donors in SSA

The pooled seroprevalence of HIV in our study was 3.2% (95% CI; 2.5, 4.0%) and is higher than estimates of similar studies conducted in Ethiopia 2.83% (95% CI; 2.43, 3.23%) (Melku et al., 2021), 2.69% (95% CI; 1.79, 3.58%) (Mulugeta et al., 2019) Pakistan 0.038% (Ehsan et al., 2020), and 0.023% among Chinese voluntary blood donors (Yu & Xu, 2019). The reasons for these differences might be attributable to the type of donors recruited (volunteer versus replacement), the testing procedures, and the kits used for the diagnosis of HIV. The gap was further explained by the difference in the study period for which papers were included in the estimation, the Chinese included studies published since 2010, while our estimate covered studies published since 2000.

Furthermore, HIV prevalence among blood donors was unevenly distributed across Sub-Saharan Africa's sub-regions, with the highest HIV prevalence of 5.2% (95% CI; 0.6%, 9.8%) among donors in Southern Africa. This could be attributed to the fact that HIV prevalence is higher in the general population of East and Southern Africa than in other regions with about 21 million individuals infected with HIV and 730,000 new HIV infections in 2019, East and Southern Africa continues to be the world's most HIV-infected region (UNAIDS, 2020).

5.1.6 Transfusion Transmissible Co-infections among blood donors in SSA

This systematic review and meta-analysis also showed co-infection of TTIs in blood donors. The frequency of co-infections in our review were HBV and Syphilis 0.3%, HCV and Syphilis 0.2%, HIV and Syphilis 0.2%, HIV and HCV 0.2%, HBV and HCV 2.0%, Syphilis, HBV and HIV 31.0%, HBV and HIV 0.8%, HBV, HCV and HIV 3.3%, HBV and HCV 0.7%. In our study, the highest co-infection was with Syphilis, HBV, and HIV 31.0%.Coinfections were found in 0.135 percent of donors, with HCV and syphilis having the highest co-infectivity (0.09 percent) according to Sial et al., (Sial et al., 2016). Rauf et al. reported 0.22% of HBV and HCV coinfections as the highest co-infectivity (Rauf & Cheema, 2019). Consistent with our finding, other studies have also reported three concomitant TTIs co-infections, they reported 11 donors (0.16%) who were concomitantly reactive for HBV, HCV, HIV, and syphilis (Rauf & Cheema, 2019). Another author discovered three coexistent TTIs in two donors (Irfan et al., 2013).

5.1.7 Trends of TTIs among SSA blood donors

From published studies between 2001 and 2021, the results of this systematic review show a downward trend in the prevalence of all the major transfusion transmissible infections (HBV, HCV, HIV, and Syphilis). The decline in trends, however, remained relatively stable for the various infectious agents. HBV prevalence in published articles hovered around 6.9% between 2020 and 2021; HCV prevalence hovered between 2.1% and 2.0% between 2018 and 2021; HIV prevalence hovered between 3.4% and 3.2 % between 2019 and 2021 and syphilis prevalence hovered between 2.9 % and 2.8 % between 2018 and 2021. Similar decreasing trends have also been reported in previous studies from China revealed a decreasing trend of HIV prevalence between 2000 and 2002 (Li et al., 2012), in Iran, HBV and HCV seroprevalence rates decreased significantly from 0.460 % to 0.060 % and 0.329 % to 0.045 % between 2004 and 2014 (Farshadpour et al., 2016), in Argentina HBV decreased from 0.356% in 2004 to 0.198% in 2011 and HCV declined from 0.721% in 2004 to 0.460% in 2011 (Flichman et al., 2014). These decreasing trends could be due to a decline in the prevalence of these infections in the community. Other factors, such as HBV vaccination, increased public awareness about the mode of transmission of these viral infections, improvement in donor screening and selection through the use of more standard questionnaires and more effective procedures in physical examination by trained blood organisers, improvements in donor screening methods through the use of more sensitive diagnostic kits, and systematic screening of all donation for infectious agents, an increase in the number of voluntary non-remunerated donors, educational program regarding blood donation to improve the blood safety, and progress in preventive measures might also explain such declines in our study.

5.1.8 Diagnostic methods for TTIs screening in SSA

Rapid diagnostic tests (RDTs) for transfusion screening have been employed in the area which lacks the capacity to use more complex technologies. However, questions about the accuracy of some RDTs in the field have sparked discussion about their use in blood donor screening. In our study, the overall proportions of diagnostic methods for screening donors for TTIs were 57.9% for (CMIA, EIA, and ELISA), 49.5% for RDTs, and 5.3% for PCR. In a similar study in Iran, RDTs and third-generation ELISA were used in the majority of routine screening tests for HCV infection in blood banks (Khodabandehloo et al., 2013).Serological tests do not distinguish between acute, chronic, or resolved infection, making it impossible to determine the true prevalence of HCV. In this study, PCR testing ranged between 2.2% and 6.5% for the diagnosis of the various TTIs across all the studies. In instances where PCR was employed for diagnosis of TTIs, they were employed for research purposes and not for routine screening of blood donors.

In a study conducted by Aluora et al., they identified that seven samples were positives for HBsAg from negative samples already screened by chemiluminescent microparticle immunoassay when PCR was used (Aluora et al., 2020). In resource-limited countries, WHO advises anti-HCV antibody screening by rapid diagnostic immunoassay or a combination of HCV antigen-antibody assays (EIA/CLIA). CLIA/EIA-positive samples should be validated using nucleic acid amplification technology (NAT), the gold standard for HCV diagnosis. Blood donors should be tested for HBV using an EIA/CLIA, which is a highly sensitive and specific HBsAg immunoassay (Ehsan et al., 2020).

5.2 Limitation

There are certain limits to the review. A significant level of heterogeneity amongst included studies is one of the drawbacks, which can be related to variances in technique, study time, and geographic location. Furthermore, the diagnostic methods used in the research differed, which could be linked to the significant level of heterogeneity. Most articles reviewed did not assess the risk factor for transfusion transmissible infections among SSA blood donors. The factors described in most of the studies limited the scope of their analysis on factors such as gender and blood donor types. Given these limitations, the review followed the PRISMA-P 2015 statement methodology for preferred reporting items for systematic review and meta-analysis. Furthermore, a thorough search of databases and the engagement of experts boosted the quality of the evidence produced.

CHAPTER SIX

6.0 Conclusions and Recommendations

6.1 Conclusions

This study shows the prevalence of TTIs 10.1%, with pooled prevalence HBV of 6.9%, HCV of 2.0%, HIV of 3.2%, syphilis of 2.8% among screened donors. The rate of co-infections ranges from 0.0-5.4%. About 99% of blood donors in SSA are replacement donors. The widely used diagnostic methods for blood screening are the RDTs and Immunoassays. The prevalence of the various TTIs was high implying that initiatives to reduce the TTIs burden in the general population should be developed and implemented. Additionally, community knowledge of TTI prevention should be enhanced. Moreover, being a replacement donor has been associated to high levels of HBV, HIV, and HCV infection. Furthermore, modern and watchful blood screening measures should be strengthened before transfusion. Furthermore, national policies and strategies for post-donation counseling are urgently needed for the recruitment and retention of safe regular donors. Finally, performing a national population-based TTI survey is critical for monitoring the burden and trend of TTIs in the community.

6.2 Recommendations

6.2.1 Recommendations for Public Health Practice

The Ghana Health Service through the National Blood Service should make a concerted effort to raise community knowledge about TTI prevention and the importance of maintaining blood supply by encouraging voluntary blood donations.

6.2.2 Recommendations for Policy

Our findings support the creation of a universal quality-assured donor screening system, a haemovigilance system, standardized standard operating procedures, and a trained workforce for

BBs. To gain a better knowledge of the load of TTIs, the effect of screening processes, and the impact of mitigation measures such as haemovigilance systems and TTI tracking networks, large prospective multi-center epidemiological studies are needed in SSA countries.

To lower the risk of infection through the transfusion route, all whole blood and apheresis donations should be tested for evidence of infection before blood and blood components are released for clinical or manufacturing use. All blood donations should be screened for the following infections and utilizing the markers listed below: Hepatitis B: Screening for hepatitis B surface antigen (HBsAg), Hepatitis C: screening for either a combination of HCV antigen-antibody or HCV antibodies, HIV-1 and HIV-2: screening for either a combination of HIV antigen-antibody or HIV antibodies and Syphilis (*Treponema pallidum*): screening for specific treponemal antibodies.

Highly sensitive and specific assays that have been tested and validated for blood screening should be used for screening. Additionally, quality-assured serological screening of all donations should be in place before considering other technologies such as nucleic acid testing. Only blood and blood components from donors who pass all screening tests for all markers should be used in clinical or manufacturing settings.

All screen reactive units should be identified, removed from quarantined stock, and stored separately and securely until they are disposed of safely or maintained for quality assurance or research purposes. To reduce the risk of infection transmission through the transfusion method. Additionally, before the release of blood and blood components for clinical or manufacturing use, all whole blood and apheresis donations should be screened for evidence of infection.

6.2.3 Recommendations for Research

It is recommended that conducting a periodic national population-based survey for TTIs has of utmost importance to monitor the burden and trend of TTIs in SSA countries. Therefore, we recommend that periodic population-based surveys for TTIs be conducted periodically to assess the burden of infection in the general population compared with donor populations.

Finally, epidemiologic assessment research on the prevalence of TTIs among blood donors should be done to include all risk factors such as (number of sex partners, protected sex or unprotected sex, smoking history, body tattoo, needle stick history, vaccination history, etc.).

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APPENDICES

Appendix I:

Quality Assessment Checklist for Prevalence Studies

S2 Table. Quality assessment checklist for prevalence studies (adapted from Hoy et al [1])

Name of author(s):

Year of publication:

Study title:

Risk of bias items	Risk of bias levels	Points scored
1.Was the study's target population a close representation of the national population in relation to relevant variables, e.g. age, sex, occupation?	**Yes (LOW RISK)**: The study's target population was a close representation of the national population.	0
	No (HIGH RISK): The study's target population was clearly NOT representative of the national population.	1
2. Was the sampling frame a true or close representation of the target population?	**Yes (LOW RISK)**: The sampling frame was a true or close representation of the target population.	0
	No (HIGH RISK): The sampling frame was NOT a true or close representation of the target population.	1
3.Was some form of random selection used to select the sample, OR, was a census undertaken?	**Yes (LOW RISK)**: A census was undertaken, OR, some form of random selection was used to select the sample (e.g. simple random sampling, stratified random sampling, cluster sampling, systematic sampling).	0
	No (HIGH RISK): A census was NOT undertaken, AND some form of random selection was NOT used to select the sample.	1
4. Was the likelihood of non-response bias minimal?	**Yes (LOW RISK)**: The response rate for the study was ≥75%, OR, an analysis was performed that showed no significant difference in relevant demographic characteristics between responders and non- responders	0
	No (HIGH RISK): The response rate was <75%, and if any analysis comparing responders and non-responders was done, it showed a significant difference in relevant demographic characteristics between responders and non-responders	1
5. Were data collected directly from the subjects (as opposed to a proxy)?	**Yes (LOW RISK)**: All data were collected directly from the subjects.	0
	No (HIGH RISK): In some instances, data were collected from a proxy.	1
6.Was an acceptable case definition used in the study?	**Yes (LOW RISK)**: An acceptable case definition was used.	0
	No (HIGH RISK): An acceptable case definition was NOT used	1
7. Was the study instrument that measured the parameter of interest (e.g. prevalence of low back pain) shown to have reliability and validity (if necessary)?	**Yes (LOW RISK)**: The study instrument had been shown to have reliability and validity (if this was necessary), e.g. test-re- test, piloting, validation in a previous study, etc.	0
	No (HIGH RISK): The study instrument had NOT been shown to have reliability or validity (if this was necessary).	1
8. Was the same mode of data collection used for all subjects?	**Yes (LOW RISK)**: The same mode of data collection was used for all subjects.	0
	No (HIGH RISK): The same mode of data collection was NOT used for all subjects.	1
9.Were the numerator(s) and denominato r(s) for the parameter of interest appropriate	**Yes (LOW RISK)**: The paper presented appropriate numerator(s) AND denominator(s) for the parameter of interest (e.g. the prevalence of low back pain).	0
	No (HIGH RISK): The paper did present numerator(s) AND denominator(s) for the parameter of interest but one or more of these were inappropriate.	1
10. Summary on the overall risk of study bias	**LOW RISK**	0-3
	MODERATE RISK	4-6
	HIGH RISK	7-9

Appendix II

Search strategy

Search #	Query
#1	transfusion-transmitted infection*[Title/Abstract] OR transfusion-transmissible infection*[Title/Abstract] OR blood transfusion infection*[Title/Abstract] OR TTIs[Title/Abstract]
#2	blood donor*[Title/Abstract] OR donor*[Title/Abstract]
#3	(#1) AND (#2)
#4	sub-Saharan Africa sub-sahara Africa OR SSA OR Africa OR Angola OR Benin OR Botswana OR Burkina Faso OR Burundi OR Cameroon OR Cape Verde OR Central African Republic OR Chad OR Comoros OR Congo OR Cote d'Ivoire OR Djibouti OR Equatorial Guinea OR Ethiopia OR Gabon OR The Gambia OR Ghana OR Guinea OR Guinea-Bissau OR Kenya OR Lesotho OR Liberia OR Madagascar OR Malawi OR Mali OR Mauritania OR Mauritius OR Mozambique OR Namibia OR Niger OR Nigeria OR Rwanda OR Sao Tome and Principe OR Senegal OR Seychelles OR Sierra Leone OR Somalia OR South Africa OR Sudan OR Swaziland OR Tanzania OR Togo OR Uganda OR Zaire OR Zambia OR Zimbabwe
#5	(#3) AND (#4)