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Laboratory of Host-Pathogen Interaction in Livestock, Department of Biosystems, Division of Animaland Human Health Engineering, KU Leuven University, 3000 Leuven, Belgium. CRISPR-Cas12/Cas13: bibliometric analysis and systematic review of its application in infectious disease detection

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ADMINISTRATIVE INFORMATION

Support - This study was financially supported by the Global Minds Doctoral Scholarship Program, KU Leuven (project number 4520196970).

Review Stage at time of this submission - Data extraction.

Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 15 August 2023 and was last updated on 15 August 2023.

INTRODUCTION

eview question / Objective Regarding the CRISPR-Cas12/Cas13, there are numerous reviews conducted and there is indirect evidence of an increase in the number of research outputs especially since 2017. However, to our knowledge, no systematic review was conducted to assess the state of the art of this field of study and its application in infectious disease detection. Thus, this study aims to contribute to this growing area of research by systematically exploring the available data on the Web of Science to provide the art of the field and its evolution over time and its application in infectious disease detection.

Condition being studied Infectious diseases immensely burden global public health and the economy. It is estimated that about 15 million of 57 million annual deaths worldwide are estimated to be related directly to infectious diseases. Early detection of the etiologic agent of infectious diseases plays a crucial role in treating and preventing the further spread of pathogens. Polymerase chain reaction (PCR) is the most commonly used diagnostic assay to detect infectious diseases. PCR is very specific and sensitive, but time-consuming and requires expensive laboratory settings and well-trained personnel. The discovery of the clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated protein (Cas) (CRISPR-Cas) has revolutionized infectious diseases diagnostics. This study aims to trace the state of the art of CRISPR-Cas12/Cas13 research and its applications in infectious disease detection, and its evolution over time, using bibliometric analysis and systematic review.

METHODS

Search strategy Web of Science (https:// www.webofscience.com/) was used as a search engine. In this study, the terms "CRISPR-Cas13*, CRISPR/Cas13, Cas13*, CRISPR-Cas12*, CRISPR/Cas12, Cas1t2*" were used and the search equation was "TS=(CRISPR-Cas13*) OR TS=(CRISPR/Cas13*) OR TS=(Cas13*) OR TS=(C2c2) OR TS=(CRISPR-Cas12*) OR TS=(CRISPR/Cas12*) OR TS=(Cas12*) OR TS=(CRISPR/Cpf1)" with the the intention of refining the process of reporting scientific documents that had such terms in the title, abstract, author's keywords, and keywords plus of indexed publications. The search was performed on the 19th of January 2023.

Participant or population Studies on all infectious diseases of humans, animals, and plants are addressed in this systematic review.

Intervention Not applicable.

Comparator Not applicable.

Study designs to be included The systematic review was conducted according to The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement. Screening and data extraction were performed by two individuals independently.

Eligibility criteria To be considered, articles were required to meet the following inclusion criteria: (i) should be conducted on either CRISPR-Cas12 or CRISPR-Cas13, ii) should be conducted between 2015-2022 and (iii) should be conducted on infectious diseases. The study was refined to 2015-2022. Records before 2015 were removed as CRISPR-Cas12/Cas13 was first described in 2015 and records in 2023 were also removed for not having finished the year. Review articles were also removed from the systematic review.

Information sources Web of Science (https:// www.webofscience.com/) was used as a search engine. Web of Science is a subscription-based scientific database that provides access to multiple scientific records for many different academic disciplines. Web of Science was selected due to the availability of citation data. In this study, the terms "CRISPR-Cas13*, CRISPR/Cas13, Cas13*, CRISPR-Cas12*, CRISPR/Cas12, Cas1t2*" were used and the search equation was "TS=(CRISPR-Cas13*) OR TS=(CRISPR/Cas13*) OR TS=(Cas13*) OR TS=(C2c2) OR TS=(CRISPR-Cas12*) OR TS=(CRISPR/Cas12*) OR TS=(Cas12*) OR TS=(CRISPR/Cpf1)" with the intention of refining the process of reporting scientific documents that had such terms in the title, abstract, author's keywords, and keywords plus of indexed publications. The search was performed on the 19th of January 2023. All the identified articles

were exported in a Plain Text file (.txt) from Web of Science for further analyses.

Main outcome(s) The list of information extracted includes: Author, Journal, doi, publication year, CRISPR Protein/Effector protein type, CRISPR Protein/Effector protein subtype, target type, amplification method, signal readout method, target pathogen, the limit of detection, assay time and whether it is point-of-care testing or not.

Quality assessment / Risk of bias analysis To avoid bias two reviewers will assess each study independently. All disagreements will be discussed and resolved by consensus.

Strategy of data synthesis Descriptive statistical techniques and graphs were used to describe the results.

Subgroup analysis Not applicable.

Sensitivity analysis Not applicable.

Language restriction English.

Country(ies) involved Samson Leta from Ethiopia (Addis Ababa University), Jan Paeshuyse from Belgium (KU Leuven) and Tesfaye Rufael Chibssa from Ethiopia (Animal Health Institute).

Keywords bibliometric analysis; CRISPR-Cas12; CRISPR-Cas13; diagnostic assay; infectious disease; systematic review.

Contributions of each author

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