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ABSTRACT

A well-prepared abstract allows readers to quickly and accurately identify the basic content of a document, determine its relevance to their interests, and thereby decide whether to read the document in its entirety. The abstract must be informative and clear enough, written clearly, and provide a clear statement of the problem, research objectives, research methods, findings, and conclusions. Abstracts should consist of 100 to 200 words. The abstract must be written in the past tense. Standard nomenclature should be used, and abbreviations should be avoided. No literature may be cited. Keyword lists provide the opportunity to add keywords used by indexing and abstracting services in addition to the keywords already present in the title. Wise use of keywords can increase the ease with which interested parties find our articles (12pt).

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INTRODUCTION (Capital, bold, Times new romance 12 pt)

This section explains the three main components. First, to describe the phenomenon being studied, the introduction must contain the research background and research context. Second, the author explains the relationship between the phenomenon and existing theories (at least the journal cited must be less than ten years old), along with gap analysis and the novelty of the research, and finally explains the research objectives. All introductions should be presented in paragraph form, not pointers, with a proportion of 15-20% of the overall length of the article.

The introduction should not be divided into background sub-chapters, problem formulation, and objectives. Beginning of paragraph once tab. Citations are written in bodynote format and are relevant to the bibliography (recommended using the Mendeley application or other reference management application programs such as EndNote, Reference Manager, or Zotero) (12pt, spacing 1.5, spacing after paragraph 6pt).

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METHODS

The Methods section must be short but must include sufficient technical information and contain the type of research, research population, research samples or subjects, and data analysis techniques. Only new methods have to be described in detail. Cite previously published procedures in References.

Table 1. Search Strategy

Database	**Search Strategy**	***Hits***
Pubmed	*("acne" AND "microbiome")*	7
Science Direct	*("acne" AND "microbiome")*	79
Sagepub	*("acne" AND "microbiome")*	17

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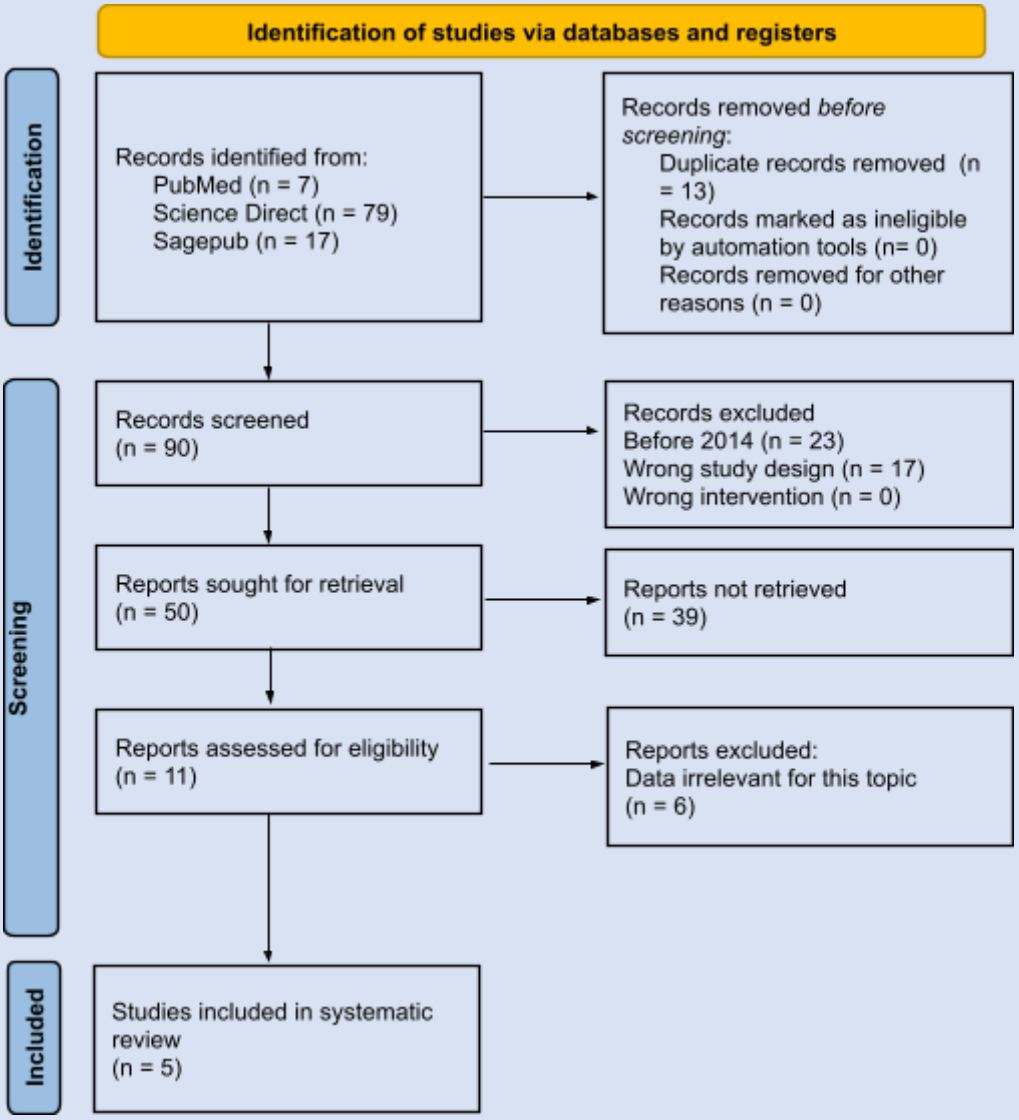


Figure 1. Article search flow chart

RESULT

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Results should include the rationale or design of the experiment as well as the results of the experiment. Results can be presented in the form of images, tables, and text. Research findings must be supported by adequate data. This section must answer the research hypothesis.

Avoid writing in the form of bullet numbering or item list style; it is best to write it in the form of a descriptive paragraph, even though it is a list item. If it contains tables and figures, the numbering is a continuation of the previous number. Each table and figure must be given a title.

Table

The table is in the middle. Use Times New Roman and font sizes 8 to 11. Horizontal lines in the middle of the table do not need to be displayed; only display the heading and the very end, and there should also be no vertical lines. Make sure you create the table correctly via the Insert Table menu. Tables should be referenced in the text by writing something like: '... (Tables are written with a capital 'T').

Table 3. The literature included in this study

Schneider, et al.[11] (2023)	USA	Cross sectional study	48 patients	A significant shift in microbial diversity emerged between early (T1-T2) and late (T3-T5) stages of puberty, coinciding with increased sebum production on the face. The overall relative abundance of C. acnes in both normal and acne skin increased during puberty and individual C. acnes strains were uniquely affected by pubertal stage

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				and the presence of acne. Further, an acne microbiome signature associated with unique C. acnes strain composition and metabolic activity emerges in late puberty in those with acne. This unique C. acnes strain composition is predicted to have increased porphyrin production, which may contribute to skin inflammation.
Cavallo et al.[12] (2022)	Italy	Cross sectional study	100 patients	Microbiota analysis showed a significantly lower alpha diversity in inflammatory lesions (LA) than in non-inflammatory (NI) lesions of acne patients and healthy subjects (HS). Differences at the species level were driven by the overabundance of C. acnes on LA than NI and HS. The phylotype IA1 was more represented in the skin of acne patients than in HS. Genes involved in lipids transport and metabolism, as well as potential virulence factors associated with host-tissue colonization, were detected

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				in all IA1 strains independently from the site of isolation. Additionally, the IA1 isolates were more efficient in early adhesion and biomass production than other phylotypes showing a significant increase in antibiotic tolerance.
Jusuf et al.[13] (2020)	Indonesia	Cross sectional study	40 patients	In non-inflammatory lesions, the growth of nine bacterial species was observed from 40 samples. In an anaerobic culture, Cutibacterium acnes (17,5%) was identified. In aerobic cultures, different bacterial species were found including Staphylococcus epidermis (52.5%), Staphylococcus hominis (12.5%), Staphylococcus haemolyticus (7.5%), Micrococcus luteus (7.5%), Leuconostoc mesentroides (7.5%), Staphylococcus aureus (5%), Kocuria varians (5%), and Staphylococcus vitulinus (2.5%). In inflammatory lesions, nine bacterial species were found, in which was the

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				anaerobic culture we identified Cutibacterium acnes (25.0%). Aerobic cultures have revealed the growth colonies of Staphylococcus epidermidis (42.5%), Staphylococcus hominis (22.5%), Staphylococcus aureus (12.5%), Staphylococcus haemolyticus (10.0%), Leuconostoc mesentroides (5.0%), Staphylococcus cohnii (2.5%), Staphylococcus arlettae (2.5%), and Dermacoccus nishinomyaensis (2.5%). Two mixed bacterial growths were observed in non-inflammatory lesions, while four mixed bacterial growths were found in inflammatory lesions.
Finotello et al.[14] (2018)	Italy	Cross sectional study	48 patients	Targeted amplicon sequencing of the 16S ribosomal RNA gene (16S-seq), are enabling the identification and quantification of human-resident microorganisms at unprecedented resolution, providing novel insights into the role of the

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				microbiota in health and disease. Once microbial abundances are quantified through NGS data analysis, diversity indices provide valuable mathematical tools to describe the ecological complexity of a single sample or to detect species differences between samples. However, diversity is not a determined physical quantity for which a consensus definition and unit of measure have been established, and several diversity indices are currently available.
Dagnelie et al.[15] (2019)	France	Cross sectional study	48 patients	Skin microbiota appears as a key player involved in several skin dermatoses physiopathology. Here, we show that inflammatory skin is associated with changes in the skin microbiota composition on the back of severe acne patients but also on the face of patients where acne was scored as mild to moderate, comparing with healthy controls. Changes were observed particularly

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				on skin commensals Propionibacteriaceae, Staphylococcaceae and Enterococcaceae families, suggesting the importance of the balance between skin commensals to maintain skin homeostasis and control skin inflammatory process.

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DISCUSSION

The discussion should be an interpretation of the results, not a repetition of the results. This discussion includes at least: an explanation of the meaning of the findings and why the findings are important; Support the answer with the results. Explain how your results relate to expectations and the literature; state clearly why the results are acceptable and whether there is any agreement or conflict with previous research results; consider alternative explanations for the findings; consider research implications; study limitations; and provide suggestions for further research.

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CONCLUSION

The conclusion must contain confirmation of the problems that have been analyzed in the results and discussion sections. Write a conclusion concisely and clearly. It is not recommended that the conclusion be written in several parts or points. The conclusion is intended to help readers understand why your research is important to them after they have finished reading the manuscript. A conclusion is not simply a summary of the main topics discussed or a restatement of your research problem, but rather a synthesis of the important points. It is important that the conclusion does not leave any questions unanswered.

DISCLOSURE STATEMENT

Disclosure Statement : The authors have no conflicts of Interest to declare.

REFERENCES

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References should be listed in the order of their appearance in the text. Each cited source must include the author's name, article title, journal name, year of publication, volume, issue number, page numbers, and DOI (if available). Example of reference format:

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