

Supplementary Materials

The microbiome bone axis in osteomyelitis integrating evidence from bone oral and gut microbiota

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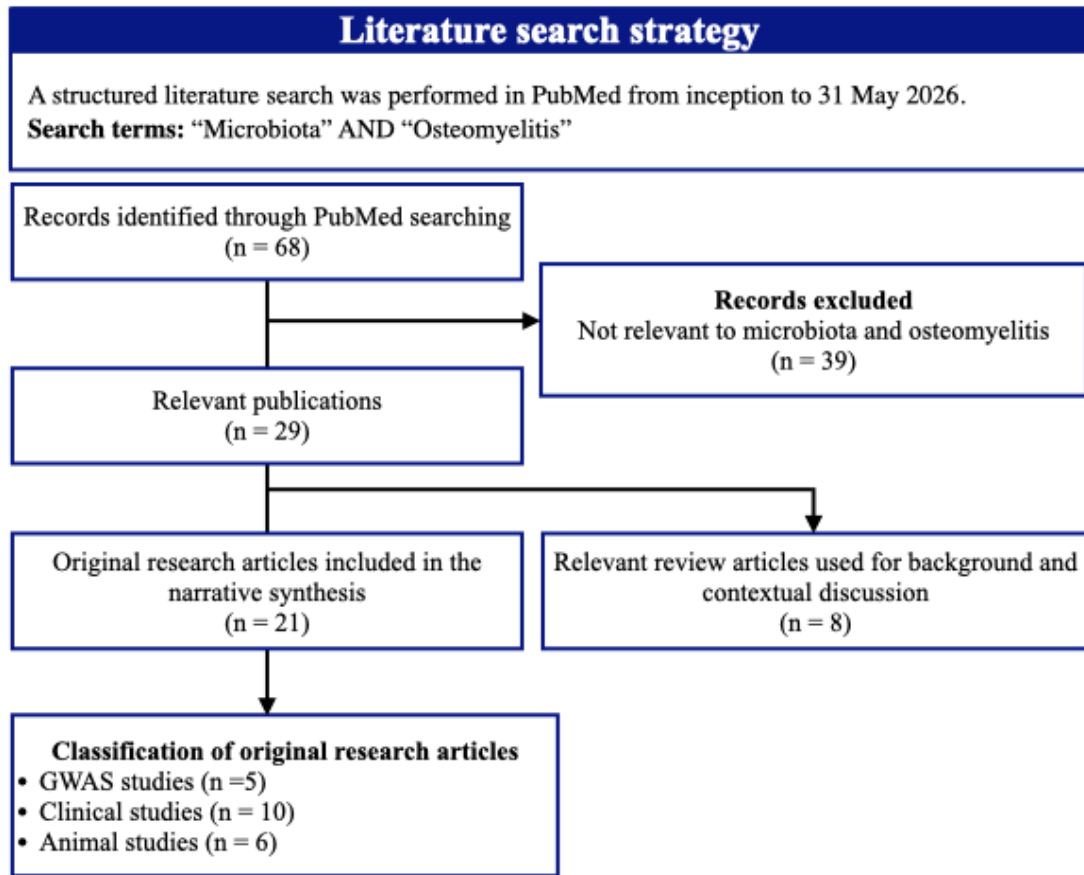
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Supplementary Figure 1. Literature search and study selection process for this narrative review. The figure was created by the authors using Keynote.

Supplementary Table 1. Effect estimates from GWAS and Mendelian randomization studies investigating associations between microbiota and osteomyelitis

Taxa	Outcome	Direction	OR (95% CI)	P-value	Ref
Skin Microbiome					
<i>Staphylococcus</i>	Osteomyelitis	↑ Risk	1.067 (1.007–1.131)	0.027	(1)
<i>Propionibacterium</i>	Osteomyelitis	↑ Risk	1.068 (1.010–1.129)	0.021	(1)
<i>Corynebacterium</i>	Osteomyelitis	↑ Risk	1.072 (1.013–1.135)	0.016	(1)

Micrococcaceae	Osteomyelitis	↑ Risk	1.090 (1.027–1.157)	0.0045	(1)
Clostridiales	Osteomyelitis	↓ Risk	0.958 (0.926–0.991)	0.013	(1)
<i>C. glutamicum</i>	Osteomyelitis	↓ Risk	0.959 (0.933–0.987)	0.0037	(1)
<i>Finegoldia</i>	Osteomyelitis	↓ Risk	0.964 (0.931–0.998)	0.038	(1)
<i>Betaproteobacteria</i>	Osteomyelitis	↓ Risk	0.941 (0.902–0.980)	0.0038	(1)
Gut Microbiome					
<i>Bacilli</i>	Osteomyelitis	↑ Risk	1.361 (1.127–1.644)	0.011*	(2)
<i>Bacteroidia</i>	Osteomyelitis	↑ Risk	1.295 (1.051–1.594)	0.023*	(2)
<i>Butyricimonas</i>	Osteomyelitis	↑ Risk	1.227 (1.028–1.465)	0.023*	(2)
Lactobacillales	Osteomyelitis	↑ Risk	1.295 (1.051–1.594)	0.023*	(2)
Bacteroidales	Osteomyelitis	↑ Risk	1.295 (1.051–1.594)	0.023*	(2)
<i>Lachnospira</i>	Osteomyelitis	↓ Risk	0.666 (0.478–0.928)	0.023*	(2)
Bacteroidales S24.7	Osteomyelitis	↓ Risk	0.795 (0.656–0.965)	0.023*	(2)
<i>Bacilli</i>	Osteomyelitis	↑ Risk	1.36 (1.13–1.64)	0.022*	(3)
<i>Butyricimonas</i>	Osteomyelitis	↑ Risk	1.23 (1.03–1.46)	0.023	(4)
<i>Coprococcus</i> 3	Osteomyelitis	↑ Risk	1.37 (1.03–1.82)	0.029	(4)
<i>Tyzzarella</i> 3	Osteomyelitis	↑ Risk	1.15 (1.01–1.30)	0.036	(4)
<i>Lachnospira</i>	Osteomyelitis	↓ Risk	0.77 (0.61–0.98)	0.032	(4)

* p-values for Ref. 18 and 19 represent FDR-adjusted P-values (pFDR)

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