Table 1: Description of the articles included in this systematic review

S. No	Author, Year, Country	Mean Age	Gender	Type Of Study	Study Population	Cancer Staging	Risk Factor	Samples Examined	Oral Site	Microbiota Detection Method	Associated Bacterial Species	Alpha & Beta Diversity	Result
1.	Yamamoto Y et al, 2023, Japan (19)	68.6	M-44 F- 21	Retrospective study	case = 65 control =93	I -28 II-18 III-7 IV -12	A-77 S-57	Tissue sample, Saliva, Dental plaque Tongue plaque	Tongue, Floor of mouth Gingiva Buccal mucosa	16S rRNA Sequencing, Shotgun Sequencing, FISH Immunostaining	Fusobacterium species	α-Diversity had a marked distinction between bacterial communities in the saliva, tongue plaques and tumor tissue	Increased Diversity of Fusobacterium species in Tisue samples compared to saliva, plaques.
2.	Benjamin WJ et al, 2023, USA (26)	59.1	M -34 F - 9	Case-control study	Case - 52 control -102	I&II-18 III & IV - 34	A-23 S - 6	Saliva samples	Tongue, Buccal mucosa	16S rRNA Sequencing	Community 1- Streptococcus, Rothia, Prevotella Community 2 - Veillonella, Neisseria, Fusobacterium, Pasteurellaceae	Beta – Diversity was significantly higher between the cases than between the controls	Increased Diversity of Lachnospiracee and Eikenella families in the case group
3.	Li Z et al, 2023, China (13)	60.52	M-76 F-36	Cross-sectional study	Case - 112 Control – 20	I - 7 II - 22 III - 16 IV - 55	A -76 S-109	Tissue samples	The floor of the mouth, Buccal & Alveolar mucosa, Tongue	Whole–exome sequencing (WES) & Whole genome sequencing (WGS)	P-Firmicutes, p.Actinobacteriac_Fuso bacterium species	Not analysed	Increased Abundance of fusobacterium species at all levels
4	Zhou J et al, 2023, China (20)	61.1	M-19 F-5	Observational	Case - 24	I – 4 II – 12 III – 7 IV – 1	A – 9 S -5	Tissue samples	Tongue, Floor of mouth Gingiva	16S rRNA Sequencing	Fusobacterium Treponema, Streptococcus, Peptostreptococcus, Carnobacterium, Parvimonas and Filifactor	Detect significant differences in alpha-diversity	Identified a microbial signature comprising 12 bacteria associated with OSCC
5	Mäkinen AI et al, 2023, Finland (24)	68	M-54 F- 45	Cross-sectional study	Case - 99 Control - 101	I - 57 II - 42	A -62 S- 43	saliva samples		DNA Extraction 16S rRNA Sequencing	Streptococcus anginosus, Abiotrophia defective, and Fusobacterium nucleatum	Significant decrease in alpha diversity	Microbial profiles in saliva indeed were different when comparing OSCC patients to healthy controls
6	Kaliamoorthy S et al, 2023, India (14)	67	M- 7 F- 5	Pilot case-control study	Case - 12 Control - 12	II – 3 III – 7 IV - 2	Not analysed	Tissue samples	Right and left also buccal - complex	RNA extraction PCR amplification, gel electrophoresis	Fusobacterium Nucleatum	Not analysed	Among OSCC tissue samples, positive for F. nucleatum, while none of the control samples showed its presence.
7	Zhu H et al, 2023, China (11)	45.5	M-26 F- 65	Case-control study	Oscc-91 Escc- 49 Control -91	Not mentioned	A -17 S-22	Oral rinse samples	-	16 S rRNA sequencing	Fusobacterium, Selemonas, Peptoanaerobacter, Peptostreptococcus	No significant changes were seen in alpha and beta diversity	Abundance of Prevotella, Fusobacterium, and depletion of Streptococcus and Neisseria were responsible for changes in pathways in OSCC.
8	Yan K et al, 2023, USA (12)	66	M-21 F-14	Case-control study	Case – 35 Control -31	I, II – 22 III, IV - 13	A -23 S - 8	Oral swabs	Buccal mucosa, Tongue	16S rRNA sequencing	Fusobacteria, Peptostreptococcus, Parvimonas, Neisseria, and Treponema	No significant difference in alpha diversity between the case and control group	Increases in bacteria that correspond with tumor stage
9	Lan Q et al, 2023, China (27)	54.1	M- 8 F- 10	Case-Control study	OSCC - 18 OLK – 21 Control-21	Not mentioned	A - 5 S - 5	Saliva samples	-	DNA extraction, library construction, metagenome sequencing, taxonomic profiling	Streptococcus sp., Gemella haemolysans, and Gemella morbillorum.	A significant difference in beta diversity among the three groups	G.haemolysans was significantly correlated with all metabolic pathways. Microbiome composition differed with varying degrees of epithelial dysplasia.
10	Haider K et al, 2023, India (15)	57.4	M-31 F- 29	Cross-sectional study	Case – 60 Control - 60	Not mentioned	Not analysed	Oral swab	Tongue, Buccal mucosa	DNA Extraction 16 S rRNA sequencing	Firmicutes Bacteroides Fusobacterium Porphyromonas	Significant reduction in alpha diversity and separation in beta diversity between case & control group	Increased abundance of Fusobacterium species in oral cancer compared to control
11	Yang J et al, 2022, China (21)	61.9	M-16 F-13	Cross-sectional study	OSCC-29 OLP-32 HC-30	I-7 II-10 III-6 IV-6	A–16 S - 14	Saliva sample Oral swab Tumor tissue	Tongue, Buccal mucosa Gingiva Palate Floor of mouth	DNA Extraction 16 S rRNA sequencing	Fusobacterium, Prevotella, Porphyromonas, Streptococcus, Fusobacterium, Neisseria, Porphyromonas, and prevotella	Microbiome of outer tumor tissue had a greater alpha diversity	Tumour group showed an increased abundance of periodontitis-related pathogens.
12	Michikawa C et al, 2022, USA (25)	58.7	M-20 F-17	Observational study	Case - 37 Control - 37	I- 6 II-23 III-3 IV-5	A -10 S - 21	Tissue samples	Tongue	16 S rRNA sequencing, Whole Exome sequencing (WES)	Fusobacterium, Rothia Streptococcus	Alpha diversity was significantly lower between the species group	Fusobacterium was significantly enriched in oral tongue cancer
13	Zhang Z et al, 2022, China (16)	Young – 37.55 – 65.6	F- 20 M - 20	Cross-sectional study	Case - 20 Control -20	I &II – 26 III & IV - 14	No history of Smoking, Alcohol	Tissue samples	Tongue	PCR Amplification, 16 S rRNA sequencing.	Ralstonia and Prevotella were significantly enriched in younger OSCC tissue. Pedobacter was more abundant in elderly OSCC tissues.	A significant difference in both alpha and beta diversity is seen.	The microbiota of younger OSCC tissues differed from that of elderly OSCC tissues. Fusobacterium had

													high relative abundance in both cohorts
14	Nie F et al , 2022 , China (22)	57.9	M -41 F - 24	Cross-sectional study	Case – 65		Not analysed	Tissue sample, saliva sample, Tongue niches	Mucosa, Tongue, gingiva , Floor of mouth	16 S rDNA Amplification, sequencing	Fusobacterium, Prevotella, Porphyromonas, Campylobacter, Aggregatibacter, anaerobic bacteria	Significant higher alpha diversity in tumor tissue compared to niches	Periodontitis-related flora and anaerobes were significantly enriched in tumor tissue.
15	Hashimoto K et al , 2022 , Japan (23)	67.7	M-30 F-11	Cross-sectional study	OSCC - 41 Post – 20	I, II – 23 III, IV - 18	A -41 S - 5	Saliva samples	Tongue , Gingiva , Buccal mucosa	DNA Extraction DNA library construction, sequence	Streptococcus, Aggregatibacter, prevotella Fusobacterium, Bacteroidetes	Alpha diversity showed a difference between the early and late stages of OSCC	Fusobacterium was significantly associated with early recurrence of OSCC. Streptococcus and phylum Firmicutes were decreased.
16	Ganly I et al, 2022, USA (17)	63	M-19 F-23	Case-control study	Case – 42 Contro l - 45	I-20 II-4 III-6 IV-12	A -27 S – 0	Mouthwash sample	Tongue. Floor of mouth Gingiva Retromolar trigone	DNA Extraction 16 S rRNA sequencing	Bacteroidetes, Actinobacteria Firmicutes, Fusobacterium	No Significant difference in alpha diversity and Significant separation of Beta diversity between OSCC and the control	Taxonomic composition of the oral microbiome in patients with OSCC is significantly different from that of non-smoker control patients
17	Saxena R et al, 2022 , India (18)	54	M-26 F- 8	Cross-sectional study	Case – 34 Contro l - 32	Higher than Stage -III	A – 3 S – 4 T - 24	Swab samples, Dental plaque samples	Tongue , Buccal mucosa , Gingiva	16 S rRNA sequencing Amplification	Prevotella, Capnocytophaga, Fusobacterium, Streptococcus.	A significant decrease in alpha diversity and a Higher in beta diversity are seen	Deterministic shift of oral microbiome composition in healthy to OSCC samples in consumption of smokeless tobacco
18	Liu Y et al , 2022 , China (28)	60.3	M-27 F-13	Case-control study	Case- 40 Contro l-10		A -9 S-16	Oral swab samples	Tongue, Gingiva Floor of mouth Palate Buccal mucosa	16S r DNA sequencing	Fusobacterium, Capnocytophaga, Porphyromonas, Gemella Sp. P. endodontalis, Prevotella,Neisseria Haemophilus	A significant difference in beta diversity between OSCC and the control group	The microbiome of patients with oral cancer changes as the disease progresses to a more advanced stage
19	Zhu W et al, 2022, China (29)	65	M-90 F-88	Case-control study	Case – 70 Contro l - 108	Not mentione d	A -32 S -33	Saliva samples		16S r DNA sequencing FISH	Streptococcus, Capnocytophaga, Peptostreptococcus Lactobacillus Capnocytophaga gingivalis	Significant difference in Beta – diversity between case and control group	C.gingivalis might invade OSCC tissues and play an important role by promoting invasion and metastasis by inducing EMT
20	Pandey D et al, 2022, Australia (30)	63.6	M-16 F- 5	Case-control study	Case - 21 Contro l -27	Not mentione d	A – 8 S - 8	Saliva samples Swab samples	Buccal mucosa , Tongue , Hard palate Faucial pillars	DNA extraction 16S rRNA sequencing.	Prevotella, Streptococcus, salmonella, Fusobacterium, Porphyromonas, Leptotrichia, Rothia	Beta-diversity analysis showed microbiome was compositionally distinct between cancer and healthy controls	OSCC salivary samples demonstrate stability and have the richest diversity.

*M - MALE ; F – FEMALE ; A – ALCOHOL; S - SMOKING