The microbial community shifts of subgingival plaque in patients with generalized aggressive periodontitis following non-surgical periodontal therapy: a pilot study

Supplementary Material

Table S1 Demographic patient data and clinical parameters at baseline pre- and post-treatment. Two patients were females, non-smokers with generalized aggressive periodontits GAgP.For every tooth clinical parameters (PD, BOP) were determined from six sites.

Patient	G	Z	
Age(years)	29	27	
Num of teeth	27	30	
Percent of sites with PD≤3mm (pre/post intervention)	15.43/93.21	13.33/55.56	
Percent of sites with PD 4~6mm (pre/post intervention)	54.94/6.79	52.78/40.56	
Percent of sites with PD≥7mm (pre/post intervention)	29.63/0	33.89/3.89	
Percent of sites with BOP (pre/post intervention)	100/0	100/9	

Table S2 Filtration and quality evaluation of original data. Raw PE-reads meant the original paired-end reads after amplification. Combined meaned the number of tags after merging paired-end reads. Qualified meant the number of tags after filtering. Nochime meant number of tags after filtering chimera, which were used for the subsequent analysis (clean tags). Base meant the number of base of clean number.

AvgLen meant the average length of the clean tags. Q20 meant the percentage of base

whose error rate of sequencing less than 1% and 0.1% respectively. GC (%) meant the percentage of GC base in clean tags. Effective (%) meant the rate of tags in clean tags and the paired-end reads in raw data.

Sample Name	Raw PE-reads	Combined	Qualified	Nochime	Base(nt)	AvgLen(nt)	Q20	Q30	GC%	Effective%
G1	63,256	62,606	62,161	61,062	15,433,413	253	98.18	94.9	53.11	96.53
G2	40,214	39,832	39,588	38,841	9,819,301	253	98.24	95.04	52.49	96.59
G3	31,160	30,879	30,687	30,046	7,593,432	253	98.27	95.03	52.39	96.42
G4	47,249	46,734	46,440	45,307	11,446,912	253	98.27	95.06	53.18	95.89
GT1	95,594	94,588	94,049	91,527	23,146,405	253	98.38	95.34	52.66	95.75
GT2	100,089	98,879	98,214	95,122	24,050,849	253	98.19	94.9	53.21	95.04
GT3	74,434	73,665	73,201	70,914	17,926,909	253	98.35	95.24	53.66	95.27
GT4	73,753	72,993	72,522	70,684	17,860,257	253	98.23	94.99	54.44	95.84
Z 1	61,163	60,655	60,324	58,797	14,857,091	253	98.32	95.2	51.79	96.13
Z 2	47,946	47,453	47,177	46,158	11,657,141	253	98.3	95.16	51.08	96.27
Z 3	67,923	67,230	66,804	65,444	16,532,347	253	98.16	94.83	52.38	96.35
Z 4	44,534	44,095	43,821	42,540	10,747,502	253	98.18	94.93	52	95.52
ZT1	12,564	12,443	12,370	12,171	3,076,014	253	98.25	95.03	54.12	96.87
ZT2	76,962	76,333	75,930	74,646	18,872,811	253	98.2	94.87	54.49	96.99
ZT3	77,586	76,915	76,438	75,552	19,106,478	253	98.1	94.65	55.71	97.38
ZT4	37,845	37,509	37,238	36,815	9,313,307	253	98.04	94.47	56.04	97.28

Table S3 The percentage of shared OTUs among groups. The G and Z represented the samples from the patient G and Z before treatment; the GT and ZT represented the samples from the patient G and Z after treatment. The shared OTUs in sample of G1-G3 and Z1-Z4 decreased after treatment. While, the shared OTUs in sample of G4 increased after treatment.

Group percentage number	1	2	3	4
G	82.3	79.1	80.8	42.6
GT	62.5	64.7	60.9	63.0
Decline	\downarrow	\downarrow	\downarrow	↑
Z	76.0	76.6	76.3	79.6
ZT	50.8	67.2	63.4	42.5
Decline	\downarrow	\downarrow	\downarrow	\downarrow

Table S4 The top 6 most abundant bacteria in phylum level in each sample. G and Z represented the samples from the patient G and Z before treatment; G and G represented the samples from the patient G and G after treatment.

(G1\G2\G3\G4)	percentage	(GT1\GT2\GT3\GT4)	percentage
Bacteroidetes	0.2017-0.3810	Bacteroidetes	0.1121-0.1508
Firmicutes	0.2646-0.3512	Firmicutes	0.1654-0.3858
Spirochaetes	0.0597-0.1894	Spirochaetes	0.0150-0.0186
Proteobacteria	0.0638-0.2047	Proteobacteria	0.2110-0.5134
Fusobacteria	0.0507-0.1279	Fusobacteria	0.0325-0.0669
Synergistetes	0.0213-0.0391	Actinobacteria	0.0951-0.1708
$(Z1\Z2\Z3\Z4)$	percentage	$(ZT1\ZT2\ZT3\ZT4)$	percentage
Bacteroidetes	0.2808-0.3918	Bacteroidetes	0.0076-0.0139
Firmicutes	0.2140-0.3223	Firmicutes	0.0695-0.3277
Fusobacteria	0.0996-0.2556	Fusobacteria	0.0023-0.0040
Spirochaetes	0.0688-0.1504	Spirochaetes	0.0095-0.0109
Proteobacteria	0.0497-0.0763	Proteobacteria	0.0642-0.3914
Synergistetes	0.0156-0.0342	Actinobacteria	0.3415-0.8339

Table S5 The shift of the most dominant microbial in genus level pre- and pot-treatment and their belonging in phylum level. G and Z represented the samples from patients G and Z before treatment; GT and ZT represented the samples from patients G and Z after treatment.

	Before treatment	After treatment		Before treatment	After treatment	
Z1-ZT1	Johnsonella	Streptococcus	G1-GT1	Syntrophomonas	Neisseria	
	(Actinobacteria)	(Actinobacteria)	GI-GII	(Actinobacteria)	(Proteobacteria)	
Z2-ZT2	Fusobacterium	Streptococcus	C2 CT2	Megamonas	Aggregatibacter	
	(Fusobacteria)	(Actinobacteria)	G2-GT2	(Actinobacteria)	(Proteobacteria)	
Z3-ZT3	Sharpea	Rothia	C2 CT2	Hylemonella	Kingella	
	(Actinobacteria)	(Actinobacteria)	G3-GT3	(Proteobacteria)	(Proteobacteria)	
Z4-ZT4	Moryella	Rothia	C4 CT4	Selenomonas	Parascardovia	
	(Actinobacteria)	(Actinobacteria)	G4-GT4	(Actinobacteria)	(Actinobacteria)	

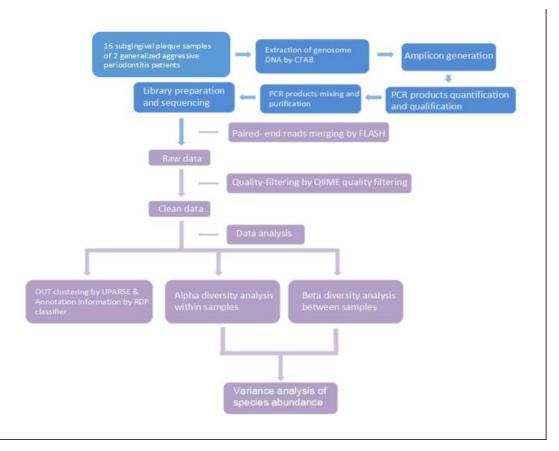


Figure S1. The schematic overview of the experimental work-flow and applied bioinformatic procedure. The blue color meaned the part of sequencing, and the purple color meaned the part of bioinformatic analysis.



Figure S2. The intraoral photos and panoramic radiographs of patient G. (A) showed the intraoral photo before treatment. (B) showed the panoramic radiograph before treatment. (C) showed the intraoral photo after treatment.

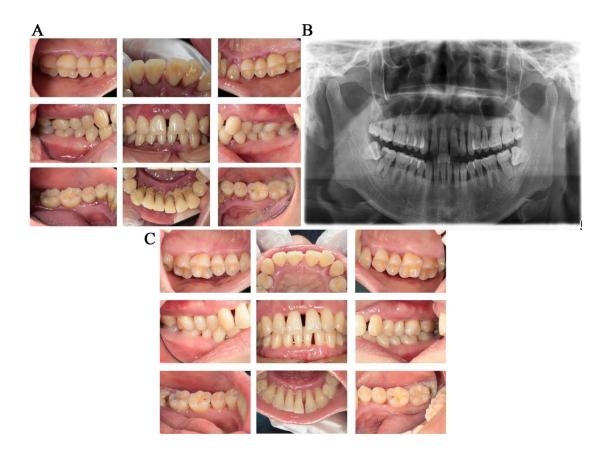


Figure S3. The intraoral photos and panoramic radiographs of patient Z. (A) showed the intraoral photo before treatment. (B) showed the panoramic radiograph before treatment. (C) showed the intraoral photo after treatment.