

Analysis and characterization of an SGB from the oral microbiome

Virginia Leombruni

magID	sampleID	sex	bmi	age	smoking_state	st
M1260886280	BP01007	female	25.7116620752984	64	non-smoker	mu
M1873802605	BP01023	male	24.6913580246914	65	non-smoker	mu
M1194372573	BP01030	female	25.390625	62	non-smoker	mu
M1114272019	BP01053	male	22.4913494809689	70	ex-smoker	mu
M1282899885	BP02008	male	24.6913580246914	73	smoker	pe
M1847318425	BP02019	female	25.7116620752984	77	smoker	mu
M1681596460	BP02027	male	26.2345679012346	60	smoker	he
M1707521290	BP02044	male	28.7273771904625	43	non-smoker	mu
M1397010834	BP03017	female	19.1326530612245	37	non-smoker	mu
M1499940801	BP04010	female	19.3624726594715	57	ex-smoker	pe
M1651786238	BP05009	female	24.2214532871972	62	smoker	he
M1517296339	BP07023	female	21.0771952275208	40	ex-smoker	mu
M1127218052	BP08040	female	18.491124260355	66	non-smoker	mu
M1188148053	BP08044	male		33	smoker	mu
M1397343304	BP08062	male	30.4218496484586	63	ex-smoker	pe
M1421637969	BP08066	female	21.9261258222297	70	non-smoker	mu
M1048341381	BP10004	female	16.0230732254446	55	non-smoker	he
M1052895688	BP11007	male	24.2122933884298	72	smoker	pe
M1362480498	BP11012	male	21.1463199091024	77	non-smoker	pe
M1829024632	BP11023	male	24.2122933884298	65	ex-smoker	pe
M1000973172	BP11027	male	29.0123456790123	73	non-smoker	pe
M1494835367	BP11028	female	26.8923231381548	38	smoker	he
M1586570985	BP11029	female	22.7244034844085	57	smoker	mu
M1992796799	BP11043	female	24.65483234714	80	non-smoker	he
M1173671022	BP11046	male	23.2459847844463	83	smoker	he
M1394460324	BP11058	female	25.4766600920447	70	non-smoker	mu
M1182440883	BP12006	male	23.3747260774288	72	non-smoker	he
M1831405370	BP13021	female	26.3146353230121	79	non-smoker	pe
M1290119613	BP14004	male	24.7842575173938	60	ex-smoker	mu
M1504735909	BP14017	female	26.9896193771626	50	smoker	he

SET OF 30 MAGS

Taxonomic assignment (PhyloPhlAn)

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M1992796799
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Quality checking (CheckM)

Bin Id	Marker lineage	# genomes	# markers	# marker sets	0	1	2	3	4	5+	Completeness
PI1651786238	Prevotella (5)	65	522	281	3	519	0	0	0	0	98,93
H1282899885	Prevotella (5)	65	522	281	3	519	0	0	0	ë	98.93
M1194372573	Prevotella (5)		522	281	3	519	0		8	0	98.93
PI1127218052	Prevotella (5)		522	281	3	518	1	10	8	0	98.93
P1681596460	Prevotella (5)	65	522	281	5	513	4	100	0	0	98.75
M1052895688	Prevotella (5)	65	522	281	21.	500	1	100	0	0	98.73
PH\$17296339	Prevotella (5)	65	522	291	4	518	0	100	0	0	98.58
PI1829824632	Prevotella (5)	65	522	281	8	514	0	8	0	0	98.22
H1114272019	Prevotella (5)	65	522	281	7	509	6	100	8	0	98.00
PI1362488498	Prevotella (5)	65	522	281	8	511.	3	100	8	0	97.39
PI1873882685	Prevotella (5)	65	522	281	9	584	9	100	0	0	97.15
M1397010834	Prevotella (5)	65	522	281	16	586	0	10	8	0	95.37
P11499948881	Prevotella (5)	65	522	281	19	583	0		0	0	94.66
PI1394460324	Prevotella (5)	65	522	281	22	499	1		0	0	94.66
M1173671022	Prevotella (5)	65	522	281	52.	454	16	100	0	0	92.96
PH298119613	Prevotella (5)	65	522	281	38	463	21	-	0	0	92.52
PI1504735909	Prevotella (5)	65	522	281	44	479	8	100	0	0	88.42
PI1397343384	Prevotella (5)	65	522	281	49	482	0		8	0	88.26
M1992796799	Prevotella (5)	65	522	281	58	455	9		8	0	86.44
M1182440883	Prevotella (5)	65	522	281	82	435	5	10	8	0	85.53
M1707521290	Prevotella (5)	65	522	281	74	434	14		0	0	84.40
PI1831405370	Prevotella (5)	65	522	281	81.	441	0		0	0	84.34
PH000073172	Prevotella (5)	65	522	291	99	419	5	100	8	0	80.86
PI1260996290	Prevotella (5)	65	522	291	117	396	9		0	0	79.82
PI1494835367	Prevotella (5)	65	522	281	137	376	9		0	0	76.83
PI1586570985	Prevotella (5)	65	522	281	214	292	16		8	0	62.17
PI1648341381	Prevotella (5)	65	522	281	182	339	1		8	0	61.21
M1421637969	Prevotella (5)	65	522	281	175	347	0	0	8	0	58.90
H1847318425	Prevotella (5)	65	522	281	243	275	4	0	e	0	55.84
M1188148053	Prevotella (5)	65	522	281	221.	361	0	0	0	0	51.42

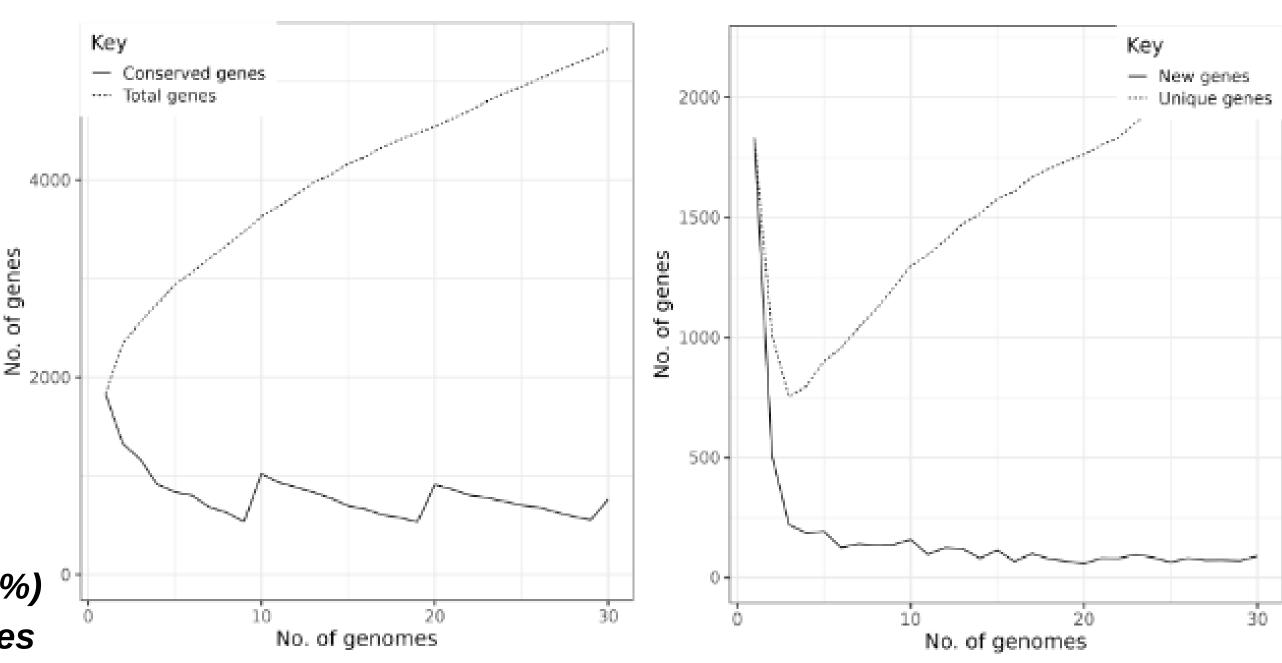
# High quality genomes (>90% completeness and <5% contamination)	16/30			
# Medium quality genomes (>50% <90% completeness and <5% contamination)	14/30			
# Low quality genomes (<50% completeness or >5% contamination)	0/30			
Average completeness	86.5%			
Average contamination	0.754%			
CG content ± std	0.452 ± 0.003			
Average genome size	~ 2.1 Mb			
Average # predicted genes	~ 2059			

Genome annotation (Prokka)

A total of 54,103 proteins were detected in the MAGs:

- about 1800 proteins/genome (compatible with quality-checking)
- 25,013 known proteins
- 29,090 hypothetical (about 54% of the proteome).

Pangenome analysis (Roary)

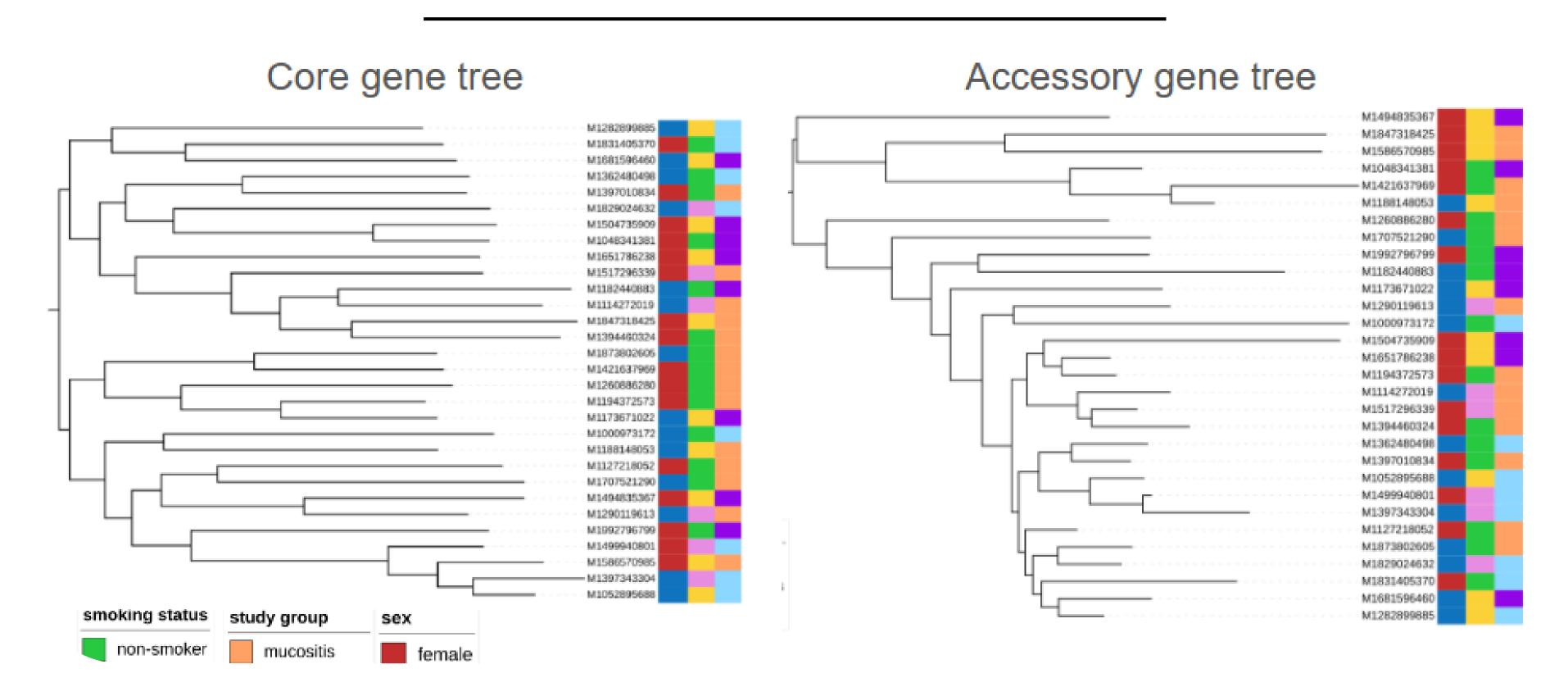


Total genes: 5336

• 764 core genes (~14%)

• 4572 accessory genes

Phylogenetic data (Roary/FastTreeMP)



Conclusions

PANGENOME ANALYSIS

Detected extensive genetic plasticity

GENOMIC ANNOTATION

Shown that most of the genome content has yet to be characterised

THANK YOU FOR THE ATTENTION