

**Title: Microbiome analysis reveals the abundance of bacterial pathogens in
Rousettus leschenaultii guano**

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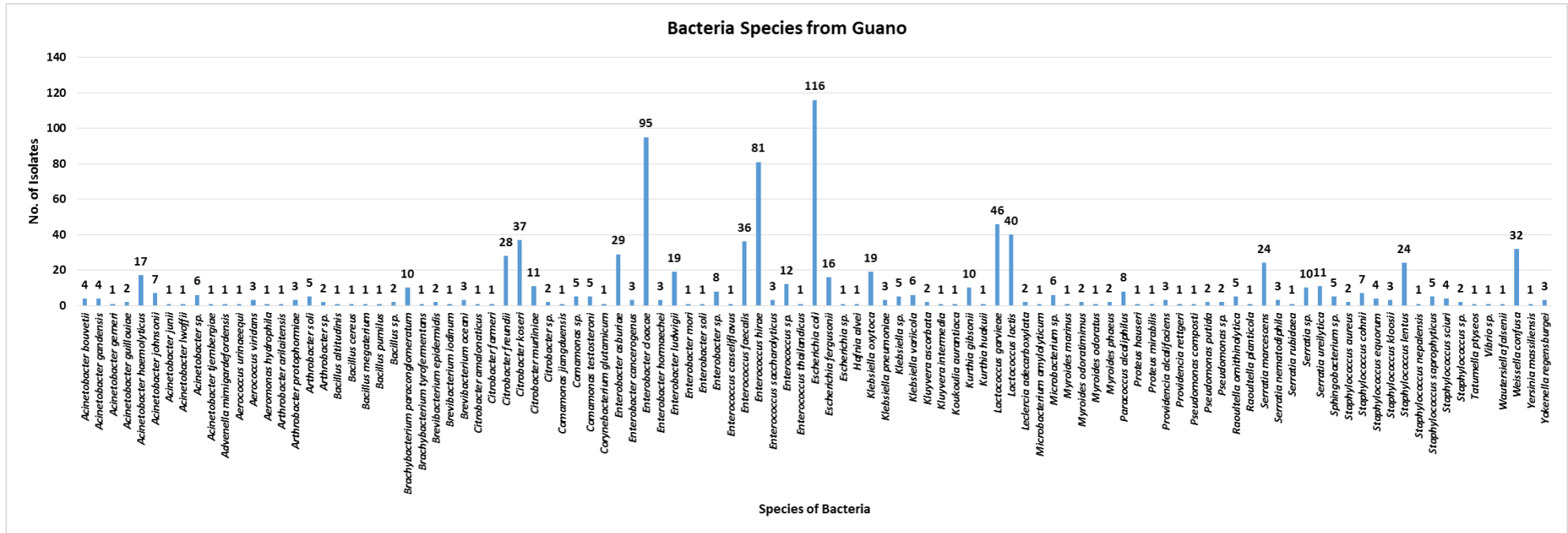
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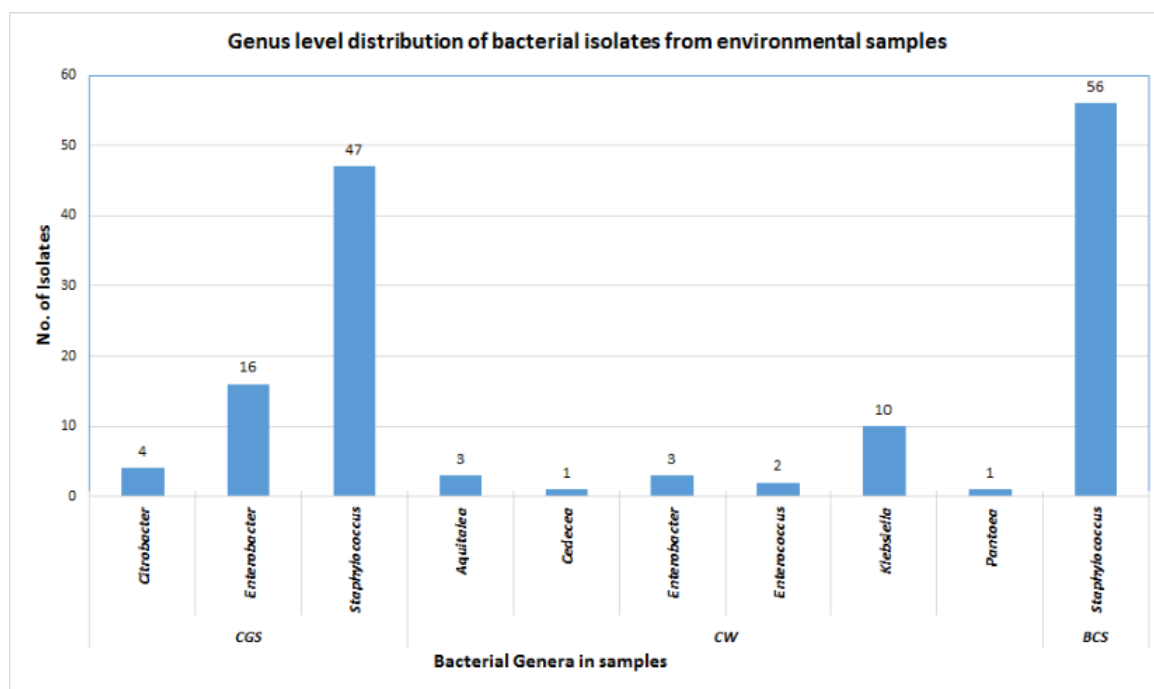
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Supplementary Table-S1. Supplementary Table-S1.pdf file attached separately



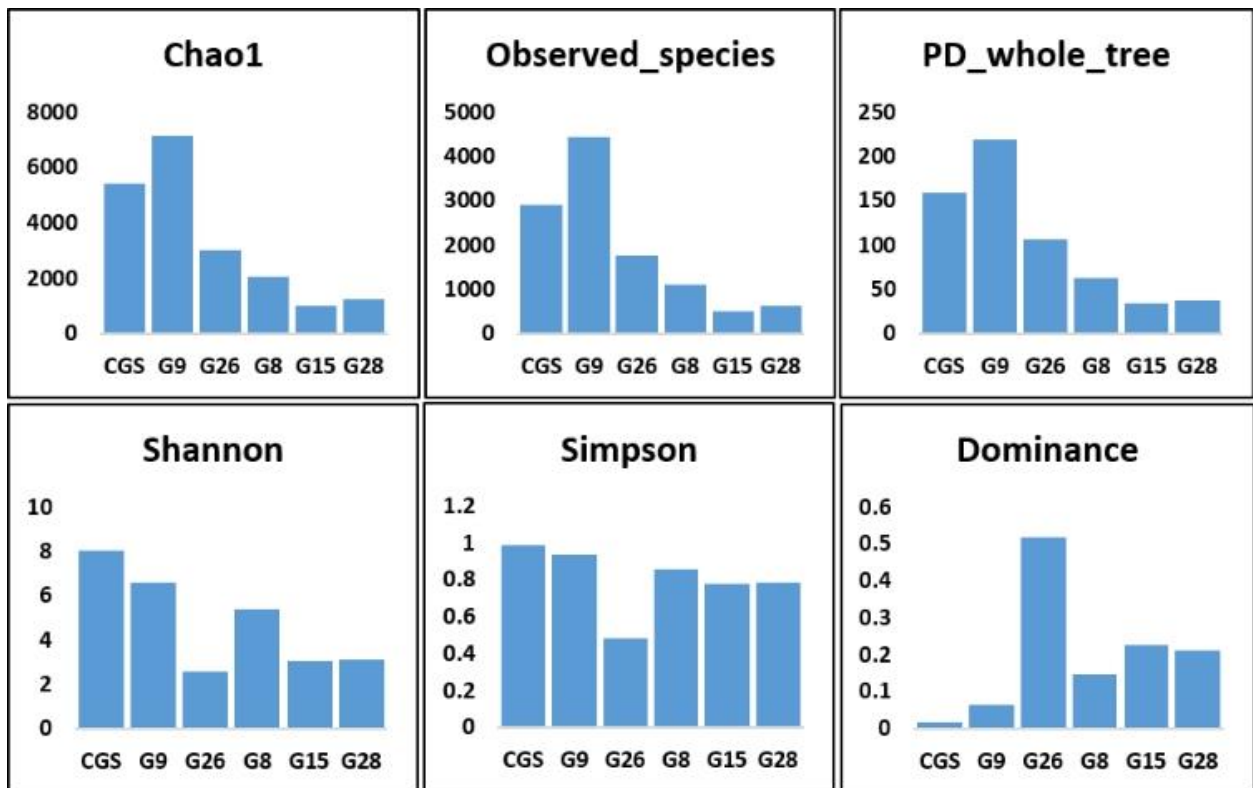
Supplementary Figure-S2. The different bacterial species isolated from the bat guano.



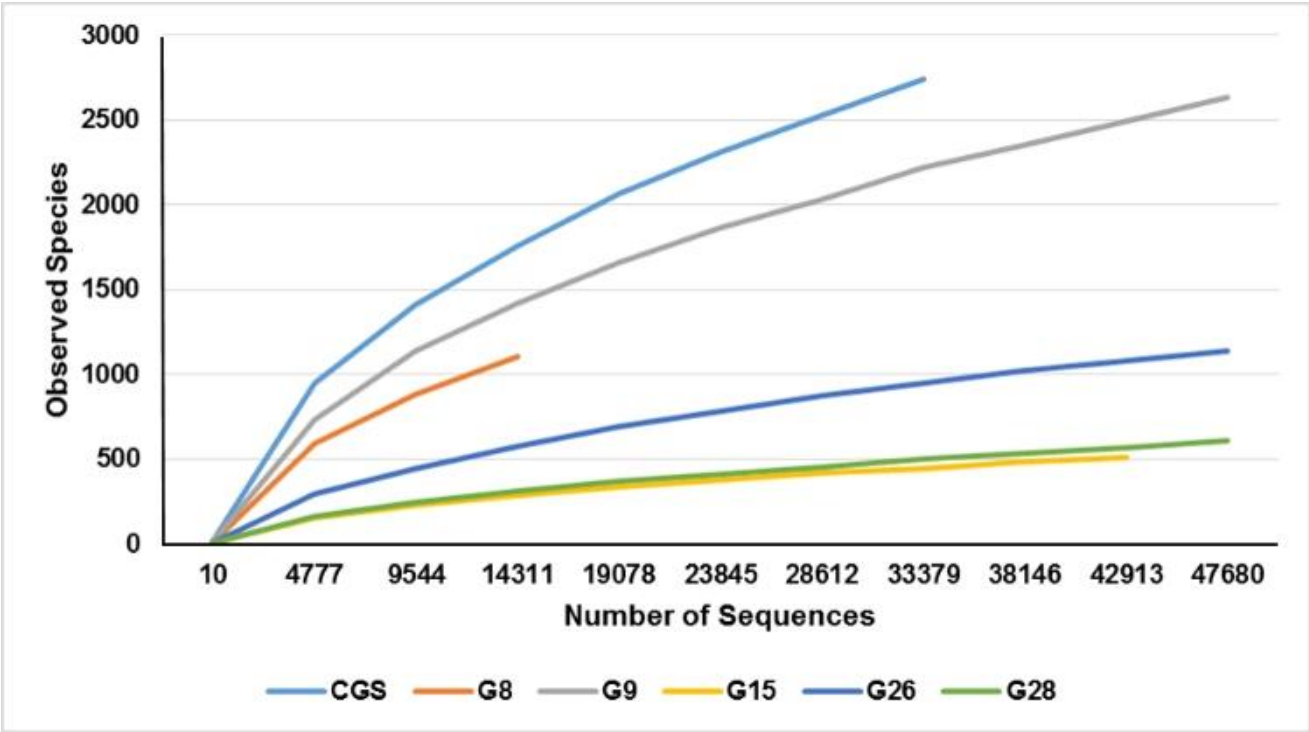
Supplementary Figure-S3. The bacterial genera obtained from the cave environment. A single bacterial genus *i.e.* *Staphylococcus* was obtained from BCS sample.

Supplementary Table-S4: The list of primers used for the identification of *E. coli* pathotypes.

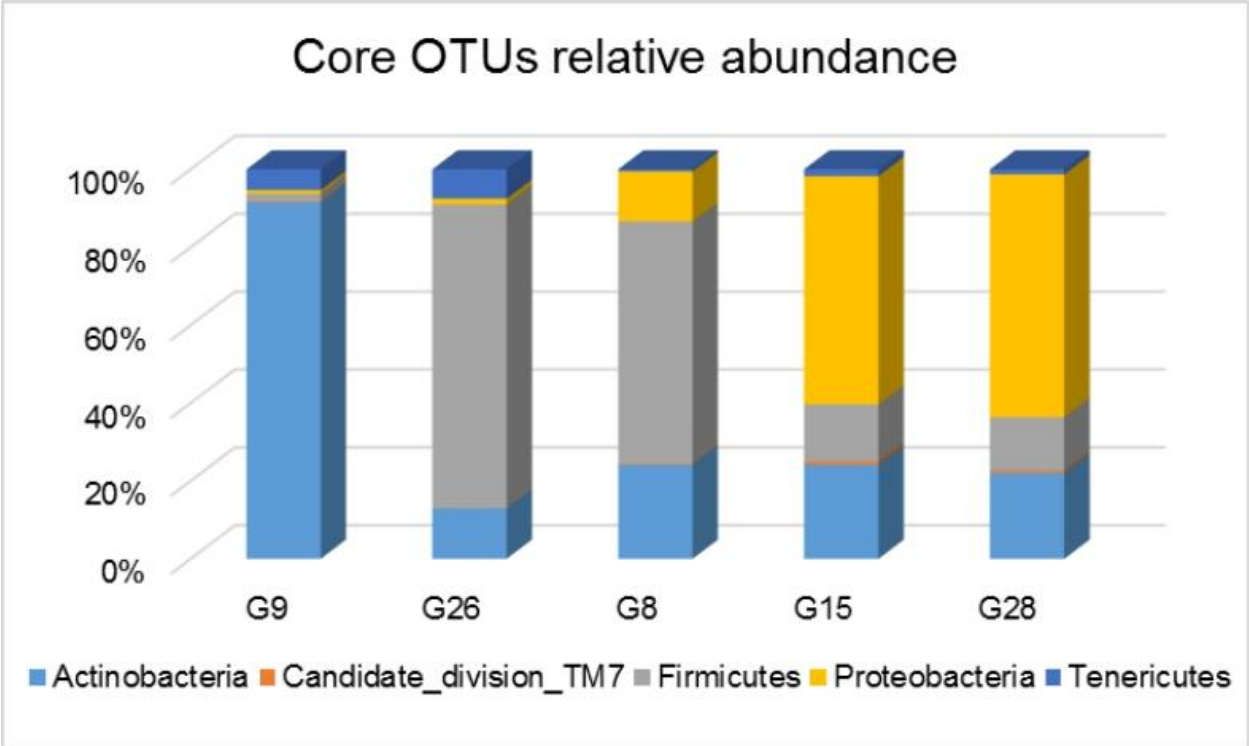
Sr. No.	virulence gene	Primer name	DNA Sequence (5' to 3')	Pathotype	Pathogenity type	Description
1	<i>hlyA</i>	hly-F	AACAAGGATAAGCACTGTTCTGGCT	ExPEC	extraintestinal (ExPEC)	Alpha-Hemolysin
		hly-R	ACCATATAAGCGGTCATTCCCGTCA			Invasion of brain endothelium
2	<i>ibeA</i>	ibe10-F	AGGCAGGTGTGCGCCGCGTAC	EaggEC	entero-aggregative (EaggEC)	heat-stable enterotoxin
		ibe10-R	TGGTGCTCCGGCAAACCATGC			
3	<i>east1</i>	east 11a	CCATCAACACAGTATATCCGA	EHEC	enterohemorrhagic (EHEC)	Shiga toxin-1
		east 11b	GGTCGCGAGTGACGGCTTTGT			Shiga toxin-2
4	<i>stx1</i>	stx1-F	ATAAATCGCCTATCGTTGACTAC	EIEC	enteroinvasive (EIEC),	Invasion Plasmid antigen
		stx1-R	AGAACGCCCACTGAGATCATC			
5	<i>stx2</i>	stx2-F	GGCACTGTCTGAAACTGCTCC	ETEC	enterotoxigenic (ETEC)	Heat stable toxin-b
		stx2-R	TCGCCAGTTATCTGACATTCTG			Heat stable toxin-a
6	<i>ipah</i>	ipaHIII	GTTCTTGACCGCCTTTCCGATACCGTC	ETEC	enterotoxigenic (ETEC)	Heat stable toxin-b
		ipaHIV	GCCGGTCAGCCACCCTCTGAGATAC			Heat stable toxin-a
7	<i>estII</i>	STb-2	ATCGCATTTCTTCTTGATC	ETEC	enterotoxigenic (ETEC)	Heat stable toxin-b
		STb-2	GGGCGCCAAAGCATGCTCC			Heat stable toxin-a
8	<i>estI</i>	STa1	TCTTTCCCCTCTTTTAGTCAG	ETEC	enterotoxigenic (ETEC)	Heat stable toxin-b
		STa1	ACAGGCAGGATTACAACAAG			Heat stable toxin-a



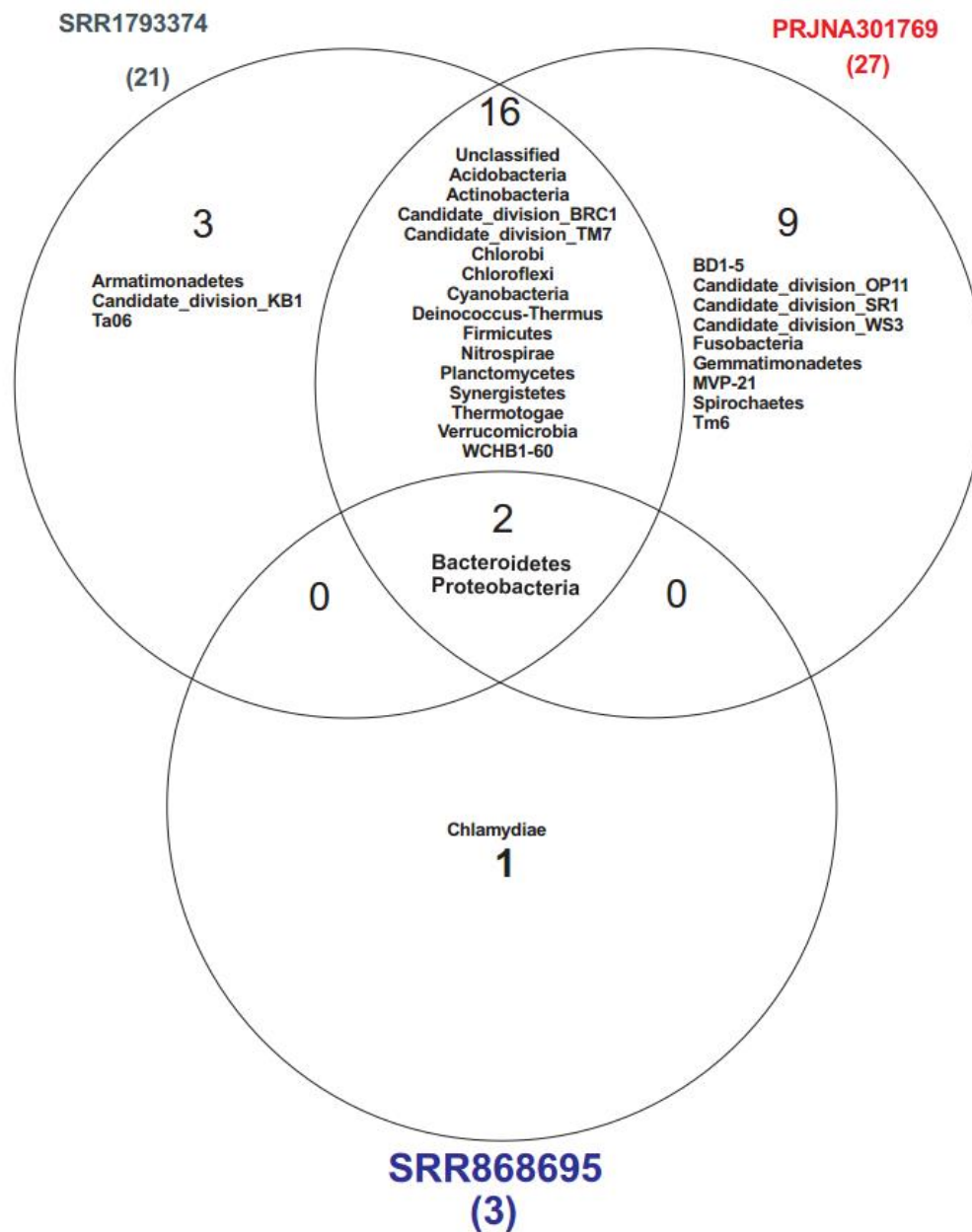
Supplementary Figure-S5. The alpha diversity indices showing the diversity of bacterial communities in different guano samples and a composite (decaying) guano *i.e.* CGS.



Supplementary Figure-S6. The rarefaction curve between observed OTUs (Operational Taxonomic Units) and number of Ion Torrent sequence.



Supplementary Figure-S7. Relative proportions of different bacterial phyla constituting the 'core microbiome'.



Supplementary Figure-8. The common bacterial phyla obtained in the comparison of three studies. SRR1793374 = DeMandal et.al.,2015; PRJNA301769 = This Study; SRR868695 = Veikkolainen et.al.,2014.