

**a. Acidobacteria sequence, prevalent and enriched at low pH****b. Pasteurella sequence, specific for animal surface/secretion****c. S24-7 sequence, specific for animal proximal gut**

# EMP Trading Card

TACGGGGGGGCAAGCGTTCTCGGAATTACTGGCGTAAGGGCTCGTA  
GGCGGCCAAGTCAGACGTAAATCCCTCGCTTAAAC

**TAXONOMY:** Assigned Greengenes taxonomy & most common taxonomy of 100% ID matches to RDP.

Greengenes lineage: k\_Bacteria; p\_Acidobacteria; c\_Acidobacteria-6; o\_ii-1-15; f\_g\_s\_

RDP lineage: d\_Bacteria; k\_p\_Acidobacteria; c\_Acidobacteria\_Gp6; o\_f\_g\_Gp6  
(4/4)

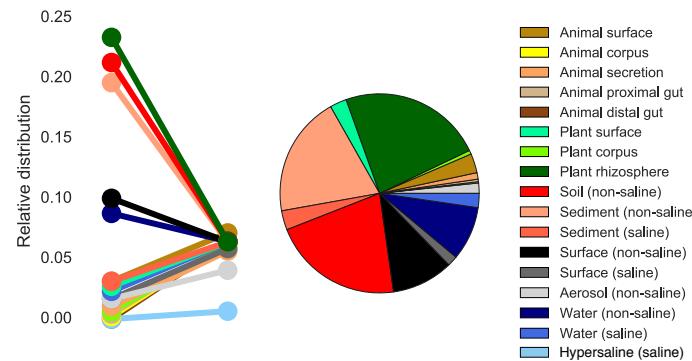
RDP species: unidentified bacterium (2/4) agricultural soil (1/4) Acidobacteria bacterium (1/4)

**PREVALENCE:** Found in 23.95% of samples, rank #4 out of 153302 tag sequences.

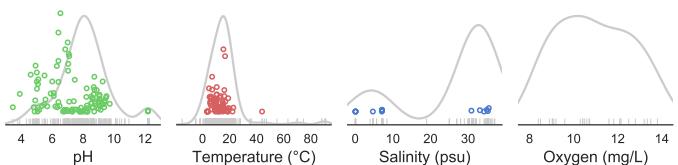
**ABUNDANCE:** Composes 0.140% of observations, rank #77 out of 153302 tag sequences.

**METHODS:** Amplicon PCR with 16S rRNA V4 primers 515f-806rB. Sequencing with Illumina HiSeq 90/100-bp or MiSeq 150-bp single reads. Sequences error-checked with Deblur, trimmed to 90 bp & rarefied to 5000 obs./sample. Showing 2000 samples evenly distributed by habitat & study.

**PREVALENCE BY HABITAT:**



**ABUNDANCE BY ENVIRONMENTAL PARAMETERS:**



# EMP Trading Card

TACGGAGGGTGCAGCGTTAACCGAATAACTGGCGTAAGGGCACGCA  
GGCGGACTTTAAGTGAGATGTGAAATCCCCGAGCTTAAC

**TAXONOMY:** Assigned Greengenes taxonomy & most common taxonomy of 100% ID matches to RDP.

Greengenes lineage: k\_Bacteria; p\_Proteobacteria; c\_Gammaproteobacteria; o\_Pasteurellales; f\_Pasteurellaceae; g\_Pasteurella; s\_multocida

RDP lineage: d\_Bacteria; k\_p\_Proteobacteria; c\_Gammaproteobacteria; o\_Pasteurellales; f\_Pasteurellaceae; g\_Pasteurella (263/264)

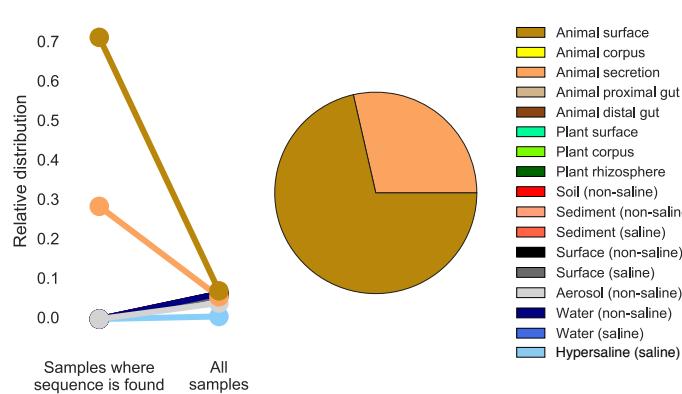
RDP species: Pasteurella multocida (226/264) Pasteurella sp. (17/264) Pasteurella canis (9/264)

**PREVALENCE:** Found in 0.70% of samples, rank #12271 out of 153302 tag sequences.

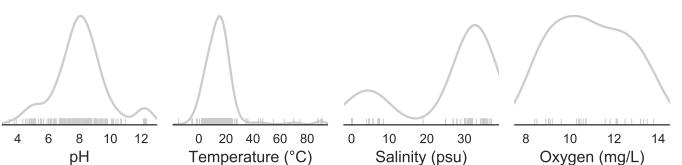
**ABUNDANCE:** Composes 0.030% of observations, rank #501 out of 153302 tag sequences.

**METHODS:** Amplicon PCR with 16S rRNA V4 primers 515f-806rB. Sequencing with Illumina HiSeq 90/100-bp or MiSeq 150-bp single reads. Sequences error-checked with Deblur, trimmed to 90 bp & rarefied to 5000 obs./sample. Showing 2000 samples evenly distributed by habitat & study.

**PREVALENCE BY HABITAT:**



**ABUNDANCE BY ENVIRONMENTAL PARAMETERS:**



# EMP Trading Card

TACGGAGGATGCGAGCGTTATCCGGATTATGGGTTAAAGGGCGCA  
GGCGCGCGAAAGTCAGCGGCTCAAAGTCCGGCTCAAC

**TAXONOMY:** Assigned Greengenes taxonomy & most common taxonomy of 100% ID matches to RDP.

Greengenes lineage: k\_Bacteria; p\_Bacteroidetes; c\_Bacteroidia; o\_Bacteroidales; f\_S24-7; g\_s\_

RDP lineage: d\_Bacteria; k\_p\_Bacteroidetes; c\_Bacteroidia; o\_Bacteroidales; f\_Porphyromonadaceae; g\_Dysgonomonas (3/6)

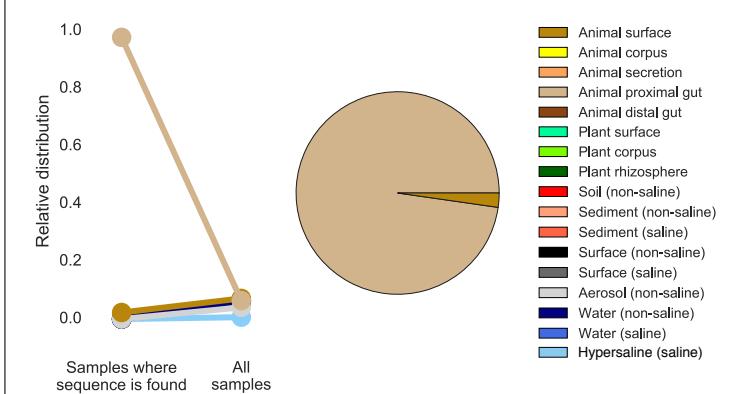
RDP species: bacterium enrichment (2/6) bacterium NLAE-zl-C249 (1/6) Dysgonomonas hofstadii (1/6)

**PREVALENCE:** Found in 2.20% of samples, rank #2759 out of 153302 tag sequences.

**ABUNDANCE:** Composes 0.143% of observations, rank #76 out of 153302 tag sequences.

**METHODS:** Amplicon PCR with 16S rRNA V4 primers 515f-806rB. Sequencing with Illumina HiSeq 90/100-bp or MiSeq 150-bp single reads. Sequences error-checked with Deblur, trimmed to 90 bp & rarefied to 5000 obs./sample. Showing 2000 samples evenly distributed by habitat & study.

**PREVALENCE BY HABITAT:**



**ABUNDANCE BY ENVIRONMENTAL PARAMETERS:**

