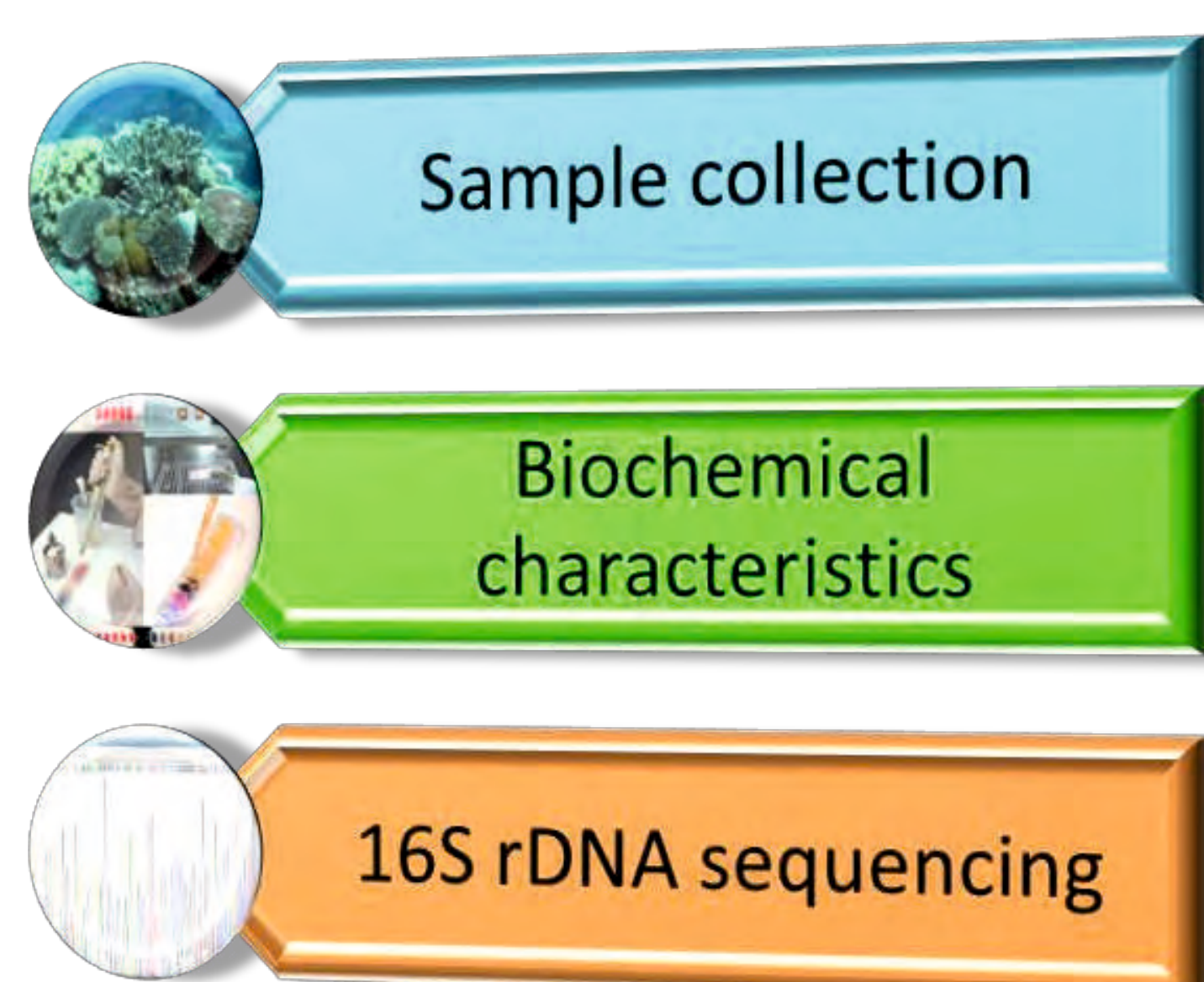


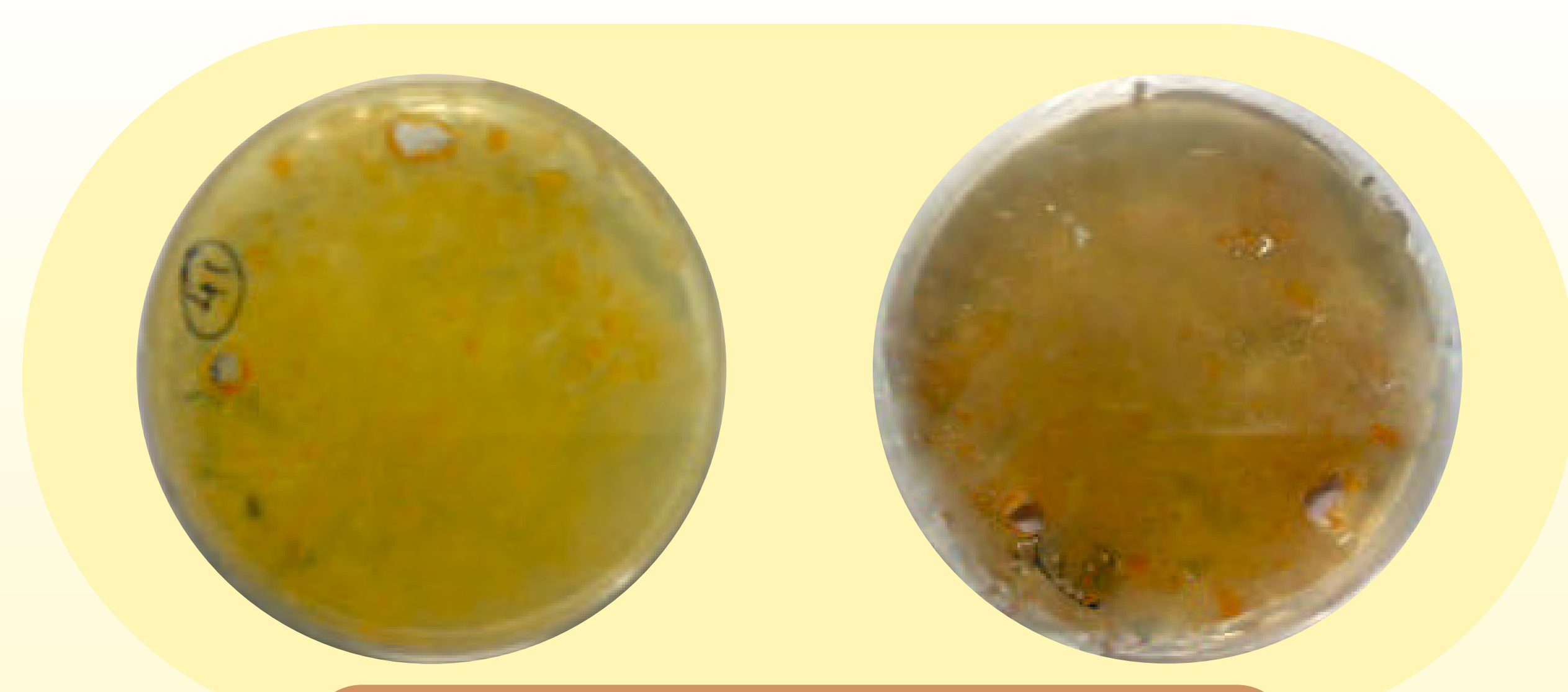
INTRODUCTION

Coral reefs are the precious resources in the ocean and the most biodiverse and productive ecosystems on earth. Bacterioplankton forming a major component of the picoplankton community in coral reefs are the primary producers and primary consumers in these ecosystems which drive the biogeochemical cycling of elements essential for life. Recent advances in microbiology aided by molecular tools have come in the form of discoveries of novel microorganisms as well as amazing genetic diversity in the marine microbial world. The present study reports isolation and characterization of an agarolytic bacterium *Vibrio* sp. BP4-6A from bacterioplankton samples collected from the coral reef ecosystem off Tuticorin, southeast coast of India. The bacterium was isolated on Marine agar (Difco) and the agarolytic activity was pronounced as colonies of the bacteria formed pits on agar plates, which sometimes progressed to big holes. Partial sequence of the 16S rRNA gene showed 99% sequence identity with the agarolytic bacterial strain *Vibrio astriarenae* isolated from water samples collected from the coral reef in Okinawa, Japan.

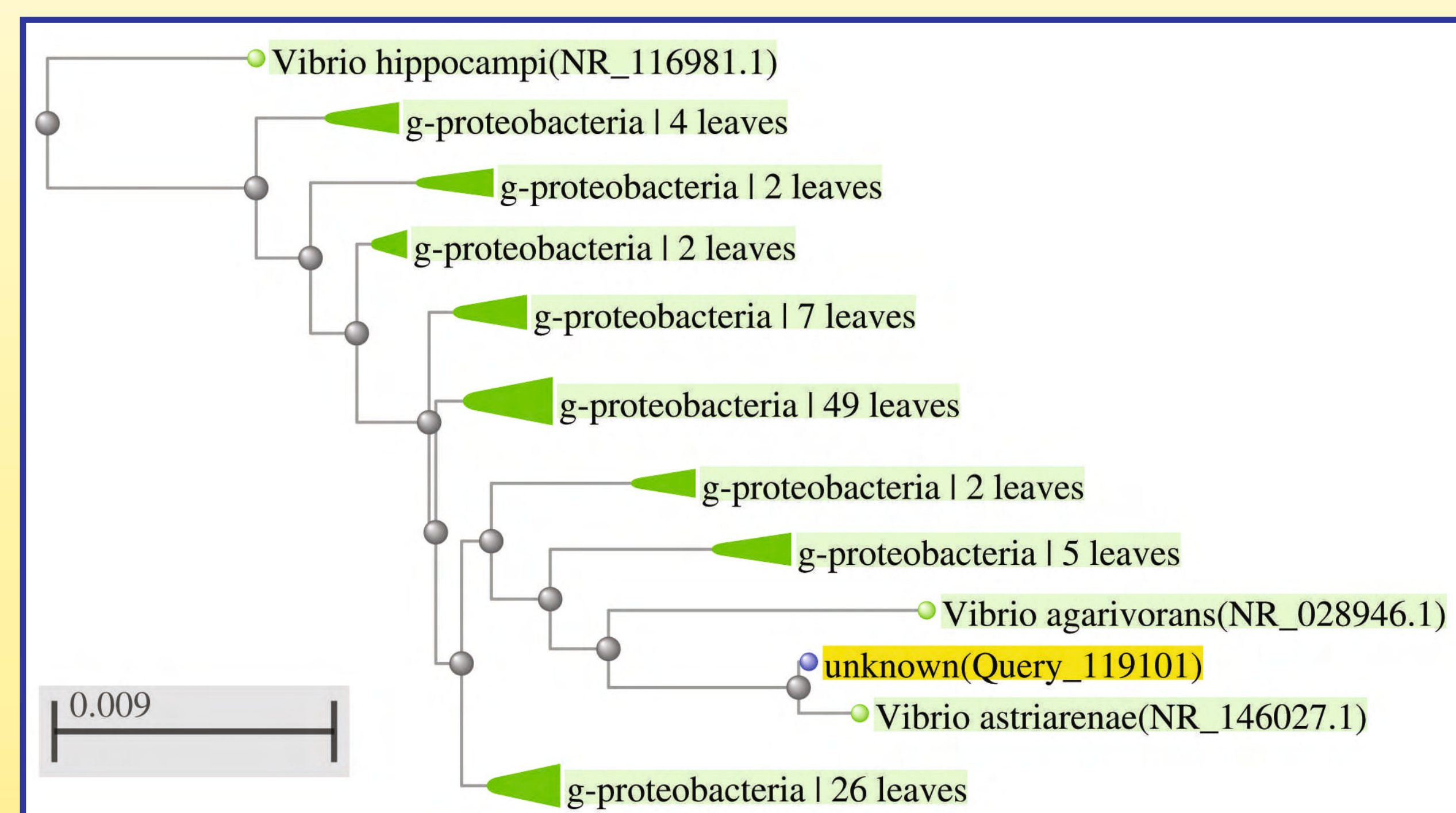
METHODOLOGY



RESULTS

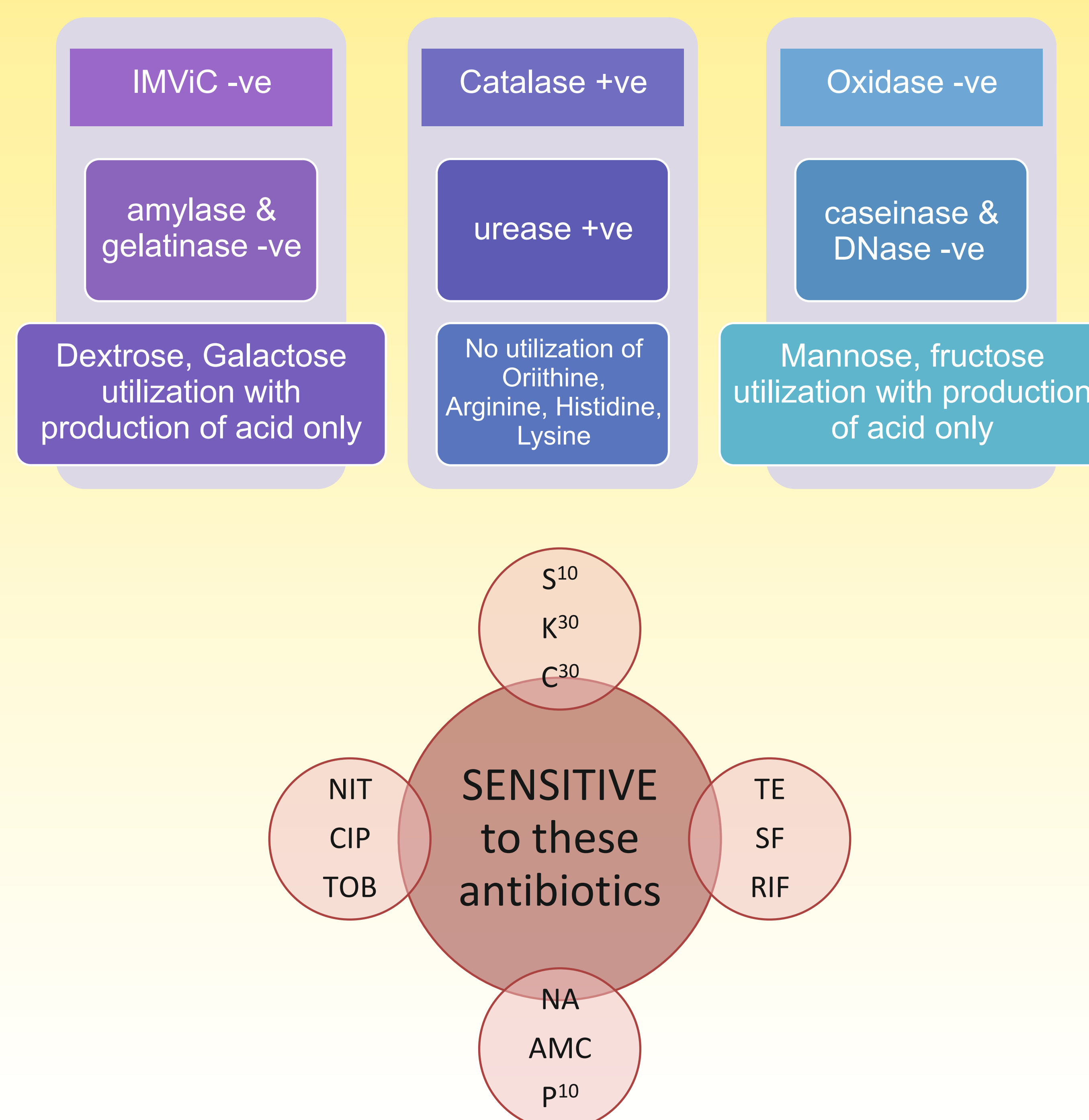


Agarolytic colonies on MA agar plates



Phylogenetic tree of *Vibrio* sp. BP4-6A

BIOCHEMICAL CHARACTERISTICS - V.BP4-6A



Comparison of characteristics of *Vibrio* sp. BP4-6A and *V. astriarenae* C7T

Characteristics	V.BP4-6A	V.AC7T	Characteristics	V.BP4-6A	V.AC7T
Gas production from glucose	-ve	-ve	Growth in 6.0% (w/v) NaCl	+ve	-ve
Growth in 3.0% (w/v) NaCl	+ve	+ve	Trehalose Utilisation	-ve	+ve
Growth at 40°C	-ve	-ve	Lipase	-ve	+ve
pH6-10	+ve	+ve	Dnase	-ve	+ve
pH>10	-ve	-ve	Gelatinase	-ve	+ve
Oxidase	-ve	-ve	Amylase	-ve	+ve
Catalase	+ve	+ve	Urease	+ve	-ve
Nitrate reduction	-ve	-ve			
Caseinase	-ve	-ve			

V.BP4-6A: *Vibrio* sp. BP4-6A, V.AC7T: *V. astriarenae* C7T

CONCLUSION

The agarolytic bacterium *VIBRIO* SP.BP4-6A isolated in the bacterioplankton samples collected from coral reef ecosystem showed 99% sequence identity with the agarolytic bacterial strain *Vibrio astriarenae*. However the strain exhibited differential results with respect to many of the phenotypic and biochemical characteristics and hence appears to be novel strain in the Agarivorans clade.

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