

Bacterial in microalgal cultures: Community composition



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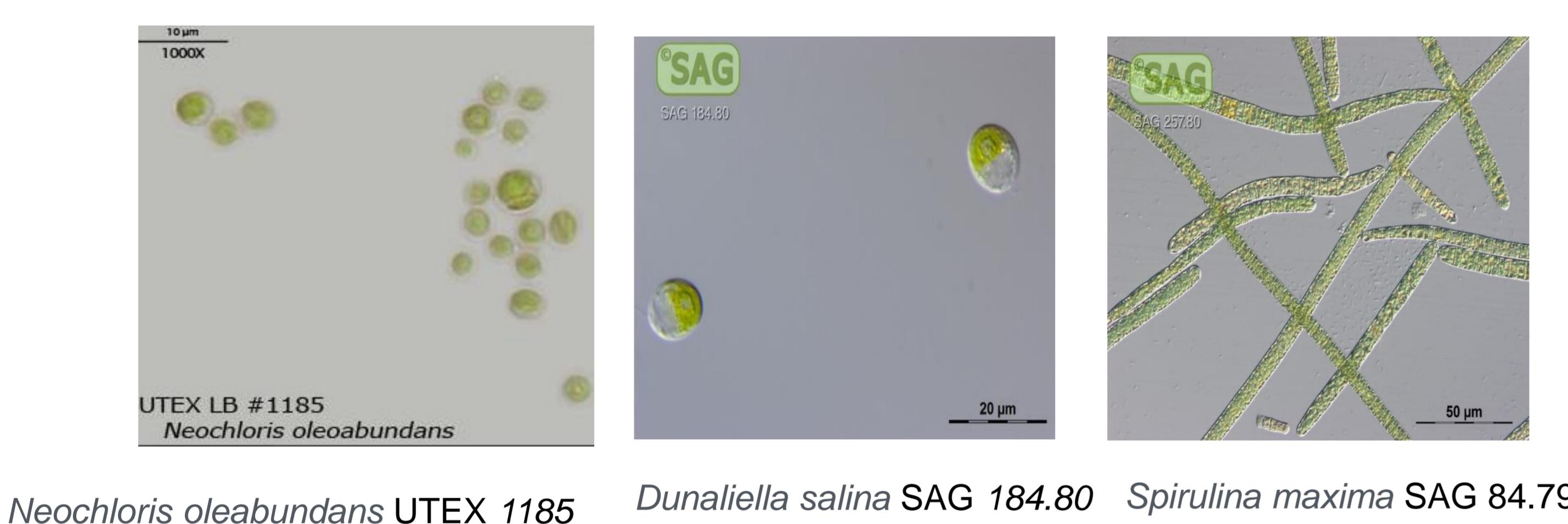
INTRODUCTION

Phycologists regard any organisms with α-Chlorophyll and a thallus not differentiated into roots, stem and leaves to be an alga (Lee and Shen 2004; Abeliovich et al. 2005). Nowadays, algae biomass can be produced in open systems and photobioreactors. These biomass is used in different industries: dietary supplements, pigments, biofuels, cosmetics, pharmaceuticals (Day et al. 2012a; Huang et al. 2014a). At present, one of the most important problem in the algae production is the contamination. But in some cases xenic or polyculture are one relevant approach in the analysis of the population dynamics using different molecular techniques.

OBJECTIVES

Identify possible prokaryotic contaminants present in the cultures of *Neochloris oleoabundans* UTEX 1185 and *Dunaliella salina* SAG 184.80, and two strains of cyanobacteria *Spirulina platensis* (*Arthrospira*) SAG 257.80 and *Spirulina maxima* (*Arthrospira*) SAG 84.79.

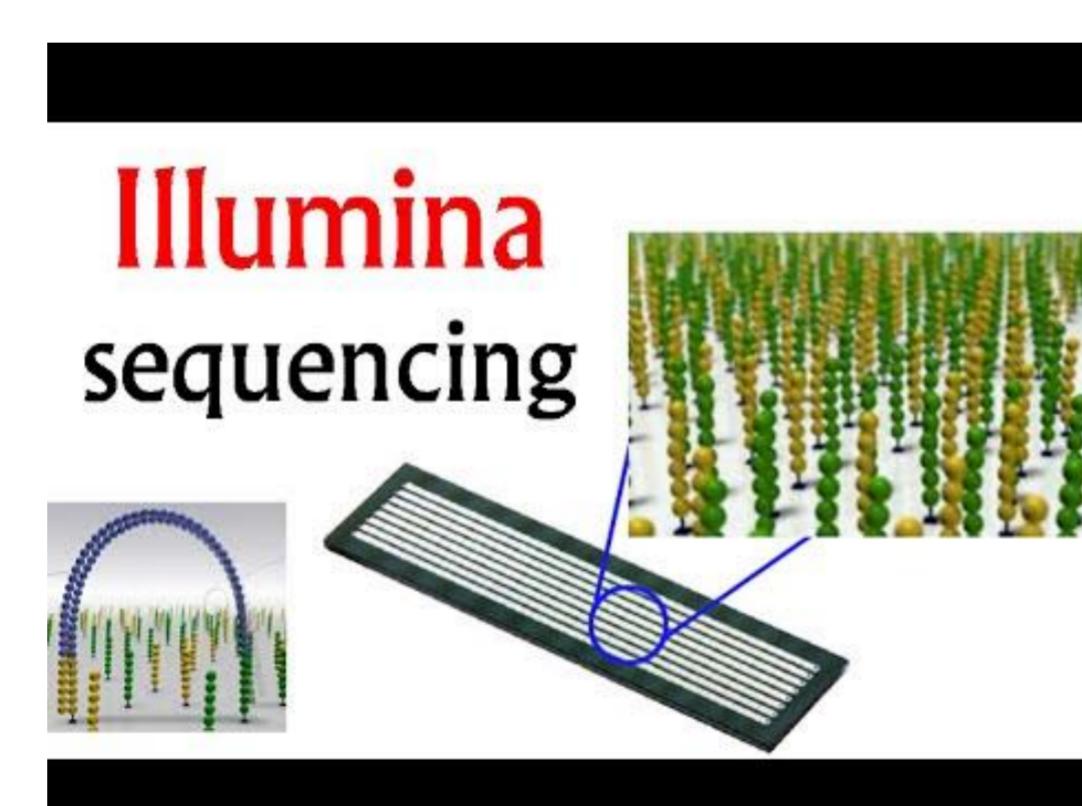
MATERIALS AND METHODS



Neochloris oleoabundans UTEX 1185 Dunaliella salina SAG 184.80 Spirulina maxima SAG 84.79



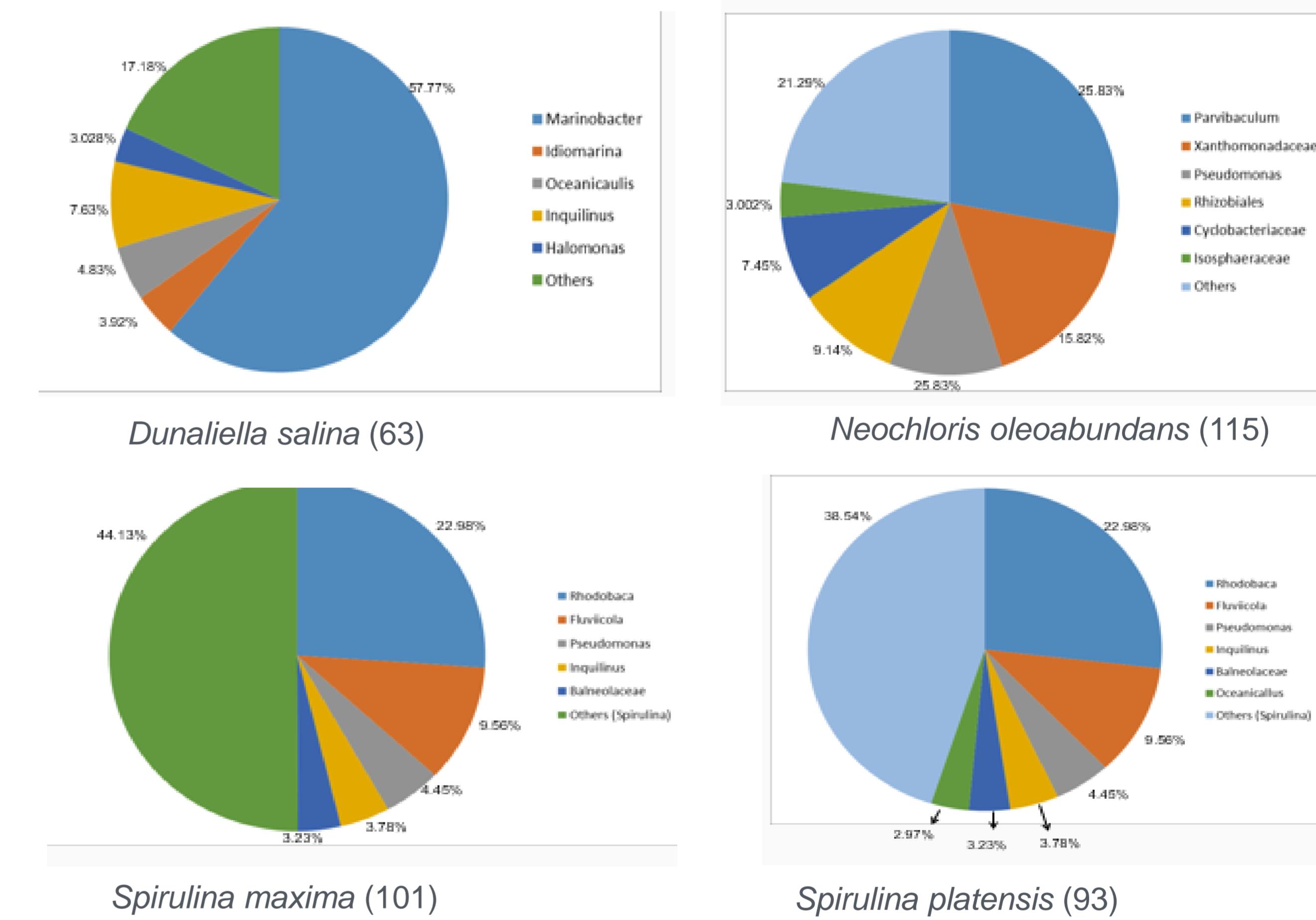
Spirulina platensis SAG 257.80



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RESULTS E DISCUSSION



CONCLUSION

Metagenomic assay identified 372 microorganisms: *Dunaliella salina* (63), *Neochloris oleoabundans* (115), *S. platensis* (93), *S. maxima* (101). The biological contaminants with the greatest abundance were: *Dunaliella salina*: *Marinobacter* 57.67%, *Neochloris oleoabundans*: *Parvibaculum* 25.83%, *S. maxima* and *platensis*: *Rhodobaca* 44.99% and 22.98% mass of bacteria contaminant.

