


Chapter 2

Halophiles

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ABSTRACT

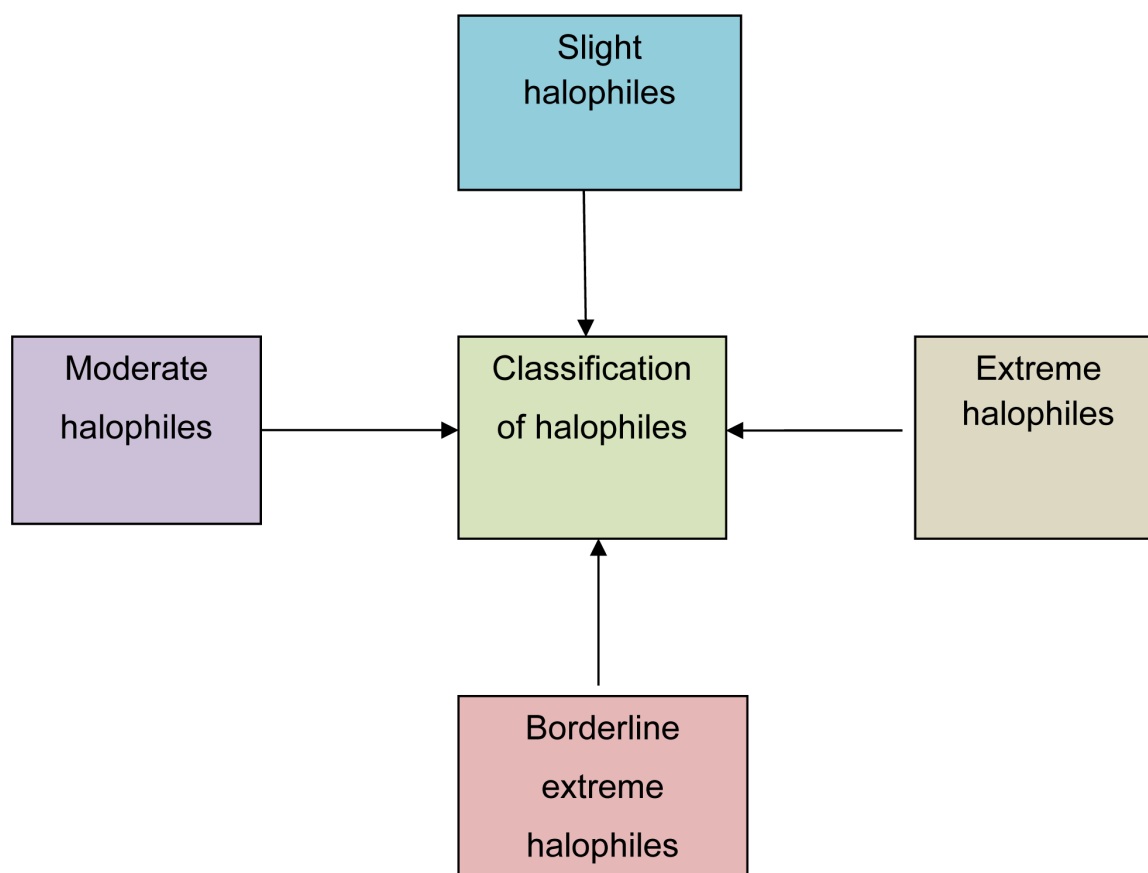
Halophiles are extremophilic salt-loving microorganisms that can survive in an extremely high level of salinity (10-30% NaCl). They belong to all three groups (i.e., bacteria, archaea, and eukaryotes). Halophiles tolerate high salt concentration due to unique cellular adaptations like salt-in strategy, compatible solute strategy, and enzyme adaptations. The chapter describes the classification, physiology, ecology, and mechanisms of adaptations and biotechnological applications of halophiles.

INTRODUCTION

Halophiles include diverse group of organisms which include Archaea, Bacteria, and Eukarya and grow in presence of salt (Oren, 2015). The halophiles are isolated mainly from saline soil, water, springs, marshes, brines and lakes. These are classified viz., slight halophiles (0.2-0.5 M salt tolerance), moderate halophiles (0.5-2.5 M salt tolerance), borderline extreme halophiles (2.5-4.0 M salt tolerance) and extreme halophiles (4.0-5.9 M salt tolerance) based on their ability to tolerate salinity (Fig. 1). The ability to tolerate salt depends on parameters such as temperature, pH, nutrients, etc. (Corral et al., 2020). In this way, the halophiles are adapted and limited by specific environmental factors. Halophiles belong to family Halomonadaceae and class Gammaproteobacteria. The halophiles can be aerobes, anaerobes, chemo heterotrophs, photo heterotrophs, or photoautotrophs (Edbeib et al., 2016). The halophiles have been reported to be isolated from Dead Sea of Israel (Wei et al., 2015), lake Urmia near Iran (Mehrshad et al., 2015a), Tuzkoy salt mines of Turkey (Mutlu & Guven, 2015), Great salt lake, Utah in United States of America (Tazi et al., 2014), Rambla Salada, Murcia, Spain (Luque et al., 2014), etc. The sources for isolation of halophiles are represented in Fig. 2.

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Figure 1. Classification of group of halophiles



HISTORY OF HALOPHILES

The first halophilic microorganism came into account in 2700 BC (Bass-Becking, 1931) and found in hyper saline area. In 1920s and 1940s halophilic bacteria were isolated from different sources, e.g., fish, animal hides, and anchovies. Elazari isolated various extreme halophiles, *Halobacterium trapanicum* and *Micrococcus morrhuae* and moderate halophiles *Chromohalobacterium marismortui*, *Pseudomonas halestrogus*, and *Flavobacterium halmephium* from the Dead Sea (Edbeib et al., 2016). The ecology, physiology and biochemistry of halophiles have been reported (Oren, 2015). The genome sequencing of halophiles has immense interest. The first genome sequence has been studied of *Halobacterium* NRC-1 (Ng et al., 2000). During the last three years, the genome sequence of eight halophiles has been reported. From these, four halophiles belong to the *Halomonas* genus. The *in-silico* studies help to know exact biology of halophiles (Oren, 2014). The *in-silico* post-genomic and genetic engineering studies have developed new pathways of growth optimization for halophilic microorganisms (Yue et al., 2014).

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