

## 2 OBJECTIVES

Optimal living conditions for microorganisms exist under their normal physiological environments. If any changes occur, this inflicts the microorganism as a stress factor. The type and the severity of the stress factor determine their survival possibilities. Known environmental changes are differences in temperature, pH, salt concentration, pressure and nutrition.

One group of microorganism named halophiles inhabit hypersaline environments, an extreme condition for most of other microorganisms. Halophiles can resist the denaturing effect of salt by balancing the osmotic pressure of the environment and overcome the denaturing effect of salt.

Although there is a growing interest in extremophilic microorganisms due to their potential industrial usage and their interesting living capabilities in the diversity point of view, only very few moderate halophiles have been studied so far. Until now, researchers' interests are driven to archaea and extreme halophilic bacteria and this leads to a growing data flow including whole genome databases. Collected data about moderate halophiles are limited to some partial genomic information. This led us to the challenging work to gather information about their proteomes. It is known that, with known genomic knowledge, proteome studies can provide detailed functional and cellular information about an organism. This is achieved by the aid of several sensitive identification techniques. However, when it comes to study organisms, which are regional, and isolates or type strains for which entire genomes are not yet collected in databases, it becomes hard to identify data about their proteomes.

This study was planned to add more information about moderate halophiles whose industrial importance have been recognized. Thinking about global changes that our world is facing, cellular knowledge of these organisms could help us to understand how the survival capabilities of these organisms work and how they may adapt to changes in the environment. Sensitive techniques have been used, to see whether the proteins from moderate halophilic bacteria can be identified with satisfying and

unambiguous results. On the other hand, this study supplies information about halophilic bacteria living in saltern parts of Anatolia.

The microorganisms were isolated from soil samples, which are collected from Çamaltı saltern area, which is located very near to Izmir at the west coast of Turkey. The photograph of the area where the isolates are taken is given below (Figure.2.1). Totally 11 isolates were collected and studied in order to gain information about their biochemical characteristics. The isolates were determined as moderate halophiles with optimal living conditions at salt concentrations of 5-20 % NaCl.



Figure 2.1 Çamaltı saltern area, Izmir/ Turkey

This study is focused on two main microorganisms, namely *Halomonas salina*, a type strain and the moderately halophilic isolate (Isolate No 6) from Çamaltı saltern area. Protein expression patterns of the isolates under given physiological conditions (growth at different temperatures of 45°C and 37°C, and at different salt concentrations, as 20 % and 5 %) are studied by comparing whole cell protein profiles by 2-DE (high resolution two-dimensional gel electrophoresis). Different protein identification techniques are applied to obtain data where possible from limited genome database sources.

In parallel to this work, foot printing studies of isolated moderate halophiles were performed to initiate a preliminary fast phenotypic characterisation of newly and closely related isolates and to visualize the relation of the isolates to type stains *Halomonas salina* (DSMZ 5928) and *Halomonas halophila* (DSMZ 4770) by global analysis of the metabolites in culture media (metabolic footprinting) [108].