



STUDY OF ECOPHYSIOLOGY OF ALGAE LIVING IN HIGHLY ACIDIC ENVIRONMENT IN HAJIPUR DISTRICT

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ABSTRACT

Some microalgae are adapted to extremely acidic environments in which toxic metals are present at high levels. However, little is known about how acidophilic algae evolved from their respective neutrophilic ancestors by adapting to particular acidic environments. To gain insights into this issue, we determined the draft genome sequence of the acidophilic green alga *Chlamydomonas eustigma* and performed comparative genome and transcriptome analyses between *C. eustigma* and its neutrophilic relative *Chlamydomonas reinhardtii*. The results revealed the following features in *C. eustigma* that probably contributed to the adaptation to an acidic environment. Genes encoding heat-shock proteins and plasma membrane H⁺ ATPase are highly expressed in *C. eustigma*. This species has also lost fermentation pathways that acidify the cytosol and has acquired an energy shuttle and buffering system and arsenic detoxification genes through horizontal gene transfer. Moreover, the arsenic detoxification genes have been multiplied in the genome. These features have also been found in other acidophilic green and red algae, suggesting the existence of common mechanisms in the adaptation to acidic environments.

KEY WORDS: microalgae , acidic environments.

INTRODUCTION:

Extremely acidic environments are scattered worldwide, and their ecosystems are supported by acidophilic microalgae as primary producers. To understand how acidophilic algae evolved from their respective neutrophilic ancestors, we determined the draft genome sequence of the acidophilic green alga *Chlamydomonas eustigma* and performed comparative genome analyses between *C. eustigma* and its neutrophilic relative *Chlamydomonas reinhardtii*. The results suggest that higher expression of heat-shock proteins and H⁺ ATPase, loss of some metabolic pathways that acidify cytosol, and acquisition of metal-detoxifying genes by horizontal gene transfer have played important roles in the adaptation to acidic environments. These features are also found in other acidophilic green and red algae, suggesting the existence of common mechanisms in the adaptation to acidic environments.

ECOPHYSIOLOGY OF ALGAE LIVING IN HIGHLY ACIDIC ENVIRONMENTS

Highly acidic environment is inhabited by acidophilic as well as acid tolerant algae. Acidophilic algae are adapted to pH value as low as 0.05 and unable to grow at neutral pH. A prerequisite for thriving at low pH is the reduction of proton influx and an increase in proton pump efficiency. In addition, algae have to cope with a limited supply of carbon dioxide for photosynthesis because of the absence of bicarbonate pool. Therefore, some algae grow mainly in near terrestrial situations to increase the CO₂ availability or actively move within the water body into areas with high CO₂. Beside these direct effects of acidity, high concentrations of heavy metals and precipitation of nutrients cause indirect effects on algae in many acidic environments. Algae are the main the primary producers in all kinds of water bodies and they are involved in

water pollution in a number of significant ways. Firstly, enrichments of the algal nutrients in water through organic effluents may selectively stimulate the growth of algal species producing massive surface growth or "blooms" that in turn reduce the water quality and affect its use.

However certain algae flourished in water polluted with organic wastes play an important part in self participation of water bodies. Some pollution algae may frequently be toxic to fish and also mankind and animals using polluted water. In fact, algae can play significant part of food chain of aquatic life thus whatever alters the number and kinds of algae strongly affects all organisms in the chain including fish.

Algae are also known to be cause of tastes and odours in water. In fact, a large number of algae are associated with tastes and odours that vary in type. Certain diatoms, blue-green algae and coloured flagellates (particularly chrysophyta and ecoglenophyta) are the best known algae to pose such problems in water supplies, but green algae may also be involved. Some algae produce an aromatic odour resembling to that of particular flowers or vegetables. In addition, a spicy, a fishy odour and a grassy odour can also be produced by odour algae.

Extremely acidic environments are scattered worldwide and their ecosystem are supported by acidophilic microalgae as primary producers. To understand how acidophilic algae evolved from their respective neutrophilic ancestors, we determined the draft genome sequence of the acidophilic green alga *Chlamydomonas eustigma* and performed comparative genome analysis between *C. eustigma* and its neutrophilic relative *Chlamydomonas reinhardtii*. The result suggests that higher expression of heat shock proteins and H⁺ ATPase, loss of some metabolic pathways that acidity cytosol and acquisition of metal-detoxifying genes by horizontal gene transfer have played important roles in the adaptation to acidic environments. These features are also found in other acidophilic green and red algae, suggesting the existence of common mechanisms in the adaptation to acidic environments.

Some microalgae are adapted to extremely acidic environments in which toxic metals are present at high levels. However, little is known about how acidophilic algae evolved from their respective neutrophilic relative *Chlamydomonas reinhardtii*. The result revealed the following features in *C. eustigma* that probably contributed to the adaptation to an acidic environment. Genes encoding heat – shock proteins and plasma membrane H⁺ ATPase are highly expressed in *C. eustigma*. This species has also lost fermentation pathways that acidity the cytosol and has acquired an energy shuttle and buffering system and arsenic detoxification genes through horizontal gene transfer. Moreover, the arsenic detoxification genes have been multiplied in the genome –these features have also been found in other acidophilic green and red algae, suggesting the existence of common mechanisms in the adaptation to acidic environments.

Several eukaryotic microalgae have been identified in acidic environments (pH < 4.0) such as acid mine drainage (AMD) geothermal hot springs.

- (i) In this pH range, cyanobacteria are not present and only acidophilic eukaryotic phototrophs are capable of photosynthesis.
- (ii) The extremely low pH of these water is due to the dissolution and oxidation of sulphur that is exposed to water and oxygen and produces sulphuric acid.
- (iii) The low pH facilitates metal solubility in water; therefore, acidic water tends to have high concentrations of metals.
- (iv) Thus, acidophilic eukaryotic algae usually possess the ability to cope with toxic heavy metals in addition to low pH both of which are lethal to most eukaryotes.

Among different extreme environments acidic habitats are rather peculiar because in most case they are the product of metabolism of active microorganisms. The microbial diversity characterization of Rio Tinto allowed for detection of a high level of eukaryotic diversity, which contrasts with the rather low level of prokaryotic diversity, which contracts with the rather low level of prokaryotic diversity found in the system. The highest concentration of biomass of the ecosystem corresponds the photosynthetic algae.

Since, some of these acidophiles are closely related to coloured neutrophiles, we can conclude that eukaryotes must have the ability to adopt from neutral to acidic environments over relatively short periods of time. Thus eukaryotic extremophiles are more widely distributed and phylogenetically diverse than previously thought.

CONCLUSION

Algae can grow in virtually any environment that has carbon dioxide, sunlight, minerals and enough water. The limiting factor in algae growth is often sunlight or minerals. When sunlight is limited, some kinds of algae can take in organic substances, like plant matter, as food.

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