

Evolutionary processes of the hydrothermal vent species

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Abstract

In the past 40 years, a large number of species have been discovered around hydrothermal vents. These new discoveries raise questions. For example: how is the process of hydrothermal vent species evolution occurring? These creatures have to adapt to adverse conditions like extreme temperatures and pressure. Most of these animals belong to the same taxonomic groups as species of the sunlit zone. The purpose of this review paper is to compare these two groups of animals in order to determine differences and similarities between their evolutionary processes and to focus on specific traits common for the vent inhabitants only. The severe hydrothermal vent environment resulted in specific morphological features of the vent species. Another very unique phenomenon of these animals is proteins that can function at extremely high temperatures. At the same time, one of the most important studies of the evolution of the hydrothermal vent species is a study of genomes because it can reveal the evolutionary history of species.

Introduction

In the last several decades there has been extensive research into the evolution of marine taxa. With new technologies developed, the area of research has spread. Scientists can conduct research deeper into the ocean. In this way, a large number of species were discovered around hydrothermal vents. Many of these animals belong to the same taxonomic groups as species of the sunlit zone. However, there are differences between these groups of animals. For example, creatures that live in hydrothermal vent areas are usually eyeless or have a specific eye structure. Extensive research exists into the adaptive evolution of other eyeless species like deep-water worms or cave fish, but around hydrothermal vents, species have to adapt to other conditions like temperature extremes and high pressure, about which less is known. That is why the evolutionary processes of the hydrothermal vent species remain unclear.

Hydrothermal vents and their inhabitants were first discovered in 1977 during exploration along the Galapagos Rift (Hui et al. 2017). Even now, conducting field work near these deep-water phenomena is very expensive. Considering the fact that the studying of this discovery started not long ago, and the high costs of research, there are many gaps in our knowledge of hydrothermal vents.

Specific characteristics of hydrothermal vent environments are extremely high or low temperature, and gases and minerals released by black and white smokers to the water. Black and white smokers are two most common types of the hydrothermal vents. They are named this way because of the colour of water they emit. Black smokers release iron and sulfur which turn black after combining. Water that comes out of white smokers contains barium, silicon, and calcium. The color of these elements is white.

Because of the chemicals emitted in the water, low oxygen concentration, high pressure, and extreme variations of temperature, the environment around the vents would generally be considered unfavourable for life. However, due to the special conditions created by the hydrothermal vents, several theories and hypotheses have been developed. For example, the “Iron-sulfur world hypothesis” by Günter Wächtershäuser states that the first organisms originated in a hydrothermal vent flow with high pressure and high temperature. Researchers nowadays study different aspects of the evolutionary processes of the hydrothermal vent species. Structures of bodies, the shape of genomes and some other adaptations have already been studied. Since the scientific community does not have enough data about the hydrothermal vents, theories and research often are contrasting. As an example, the “Iron-sulfur world hypothesis” is being criticized. Considering the paper “Two-dimensional life?” by de Duve et al. (1991), the hypothesis raises several questions of kinetic and thermodynamic nature.

Knowing the origin of life is very important for solving a number of biological and philosophical issues and studying evolutionary processes of the hydrothermal vent species may help in discovering it. Addressing my research issue can bring light to a number of scientific questions and help in farther studies of the evolution of all living creatures. If researchers don’t pay enough attention to the evolution of the hydrothermal vent species, lots of information about the evolution of all the species can be missed.

Some studies also reveal data about conditions in the ocean at different periods of time. Hydrothermal vent ecosystems are some of the oldest on the planet and have already been a source of revolutionary discoveries. For example, before the vents were found, photosynthesis was considered the only basis of primary production. The discovery of chemosynthetic organisms, which live in the hydrothermal vent environment and use chemicals as the source of energy, gave a new understanding of the life on Earth.

My goal is to compare, combine and summarize studies in order to get holistic, complete understanding of the research that has been done. In order to achieve this purpose, several significant areas of the adaptation of the hydrothermal vent fauna have been selected. The data about evolutionary changes the species went through can be collected by studying genomes. Reviewing the morphological features deep-water animals developed is also important because they demonstrate adaptations essential for surviving in the hydrothermal vent environment. Temperature is a factor that influences all organisms, and vent inhabitants have developed unique and rare thermal adaptations. Although I cannot run my own experiments or develop new research techniques, the uniqueness of my paper is a specific way of summarizing and comparing studies that correspond my issue. To achieve the purpose of my review I will collect data from research articles in the biological literature.

Genome studies

A phenomenon of the hydrothermal vent environment is a specific ecosystem based on microbial chemoautotrophic production (Brown et al. 2001). Chemoautotrophic microorganisms obtain energy from chemical reactions of elements released by black and white smokers like iron and sulfur. These organisms are the primary producers of the hydrothermal vent ecosystem. The concentrations of elements emitted by black and white smokers would be highly toxic for most

organisms (Hui et al. 2017). However, the inhabitants of this environment have developed a variety of mechanisms that let them survive (Hui et al. 2017).

One of the main adaptive features of some hydrothermal vent species is shown in genes. During several studies, animals of the hydrothermal vents were collected by submarines in the South China Sea and the Lau back-arc basin (Tui'Malin, 2015). Researchers determined that these organisms adapted both for extremely hot and cold temperatures during the evolutionary processes that occurred a long time ago. The research by Fontanillas et al. (2017) is based on comparing two groups of species that belong to the *Alvinellidae* family, but inhabit completely different types of hydrothermal vents. The first group, which includes species such as *A. pompejana* or *Paralvinella sulfincola*, lives in the environment with temperatures up to 100 °C. The second group includes species such as *P. grasslei* and *Paralvinella pandorae*. These animals live in the colder types of the hydrothermal vents with the temperature around 2–5 °C. The groups of species were expected to have different thermal adaptations demonstrated in their genomes. However, detailed studying of their amino acid and nucleotide compositions showed that species that belong to one family produce nearly the same genome imprints after adapting to different extreme environmental conditions (Fontanillas et al. 2017). This information can possibly mean that the species that share common ancestors save the genomes developed during the variety of evolutionary processes. If this assumption is accurate, then it may be possible to determine common genomes between the hydrothermal vent and sunlit environment inhabitants by conducting detailed studies in the future.

A different study by Zhang et al. (2017) compared the genomes of the deep-sea scale worms *B. pettiboneae* and *Lepidonotopodium* and the shallow-water scale worm *Harmothoe imbricata*. This research revealed a variety of genomic differences between these types of worms. For example, only the deep-sea species were determined to carry genes responsible for DNA repair, recombination, and integration. The study also shows that two tested deep-water species developed alternative ways to adapt to the hypoxic (low oxygen) environment. Therefore, there are differences between genomes of species from closely related environments. Even less common features were found when comparing the deep-sea species to the shallow-water ones. Only future similar comparative research and more data about genomes of both the hydrothermal vent inhabitants and sunlit zone species can give the possibility to construct a holistic theory of the evolution of marine organisms (Zhang et al. 2017).

Other research shows that hydrothermal vent species can have unique genomes. A study of the vent crab *Austinograea alayseae* showed that these animals have unique sets of genes related to hypoxia, metal detoxification, high osmotic pressure and pathogens (Hui et al. 2017). Considering the hypothesis that most of the sunlit zone marine species are ancestors of hydrothermal vent inhabitants, it is possible that many sunlit environment inhabitants still carry the unique genes from the early stages of adaptive evolution. Future studies based on identifying these unique genes can confirm or disprove this hypothesis.

Three different studies on genomes of the species from the deep-water extreme environments have been reviewed. These studies have different results. However, this discrepancy can be explained in part by methods used in each of the studies. In the first study, genomes of worms that belong to one family but live in different thermal conditions were compared. Researchers

focused on comparing the influence of the thermal adaptation on base compositions, amino acid compositions, and nucleotide compositions (Fontanillas et al. 2017). The second study by Zhang et al. (2017) is more general, comparing hemoglobins, highly expressed genes and possibly duplicated genes of the deep-sea species and shallow-water ones. The third study, by Hui et al. (2017), is mostly focused on the expression and sequence analysis of the genes of the hydrothermal vent crab. However, all three studies include identification of the orthologous genes of the selected species, which means genes shared by different organisms that evolved from the common ancestor. Since the studies are focused on the different aspects of the genome of the hydrothermal vent species, different conclusions of the researchers are not unusual. However, in order to get a holistic understanding of the adaptations and evolutionary processes of the deep-water organisms, more studies should be conducted. Choosing one family of hydrothermal vent species, studying its genome from all the aspects listed above, and comparing it to the genome of the related sunlit zone inhabitants can bring light to this issue.

Morphology of the hydrothermal vent species

The hydrothermal vent environment forced animals to adapt to very extreme conditions. Consequences of these processes are still noticeable in genomes and should be noticeable in morphological features. The main adaptive feature that is common for all the hydrothermal vent species is that eyes of these creatures are absent or have a very special structure. An important part of a light-sensitive receptor in the eyes of arthropods is called rhabdom. By measuring the rhabdom volume density, it is possible to determine the light sensitivity of the particular arthropod's vision system. It is also important to analyze a microvillar surface area in order to understand how the lens of a specimen's eye works.

These methods were used by Gaten et al. (1998) when studying the eye of the *bresiliid* shrimp. Rhabdom volume density and microvillar surface area were measured on light micrographs. The researchers also measured diameters of microvilli on electron micrographs to determine the microvillar surface area accurately. The research showed that the eyes of these shrimps do not have enough optics to produce an image, but have many other important features. Gaten et al. (1998) concluded that the eye of the *bresiliid* shrimp is most likely an "extremely sensitive and highly directional photoreceptor", that is intended to detect quanta of light coming out from a hydrothermal vent. It had previously been suggested that vent shrimps are able to see black-body radiation (Van Dover et al. 1989, 1994).

Thermal adaptation

The ecosystems around hydrothermal vents are diverse and environmental conditions near the different types of vents can be dramatically different. Fontanillas et al. (2017) studied a family of worms called *Alvinellid*. Methods of this research are partly explained in the “Genome studies” section. Species of the *Alvinellid* family live near all the hydrothermal vents of the Pacific Ocean, including hot and cold vents. Two of the *Alvinellid* family species are the most thermophilic multicellular organisms on Earth (Fontanillas et al. 2017). The temperature of the water near the hot hydrothermal vents they inhabit can be as high as 464 °C (Hui et al. 2017) and the temperature near the cold vents is usually around 0°C.

Temperature influences the evolutionary process of all species. Organisms that live in such an environment must have strong adaptive features. Protein composition tests and comparisons of the hot- and cold-adapted species were conducted. Even though several similarities in genomes of these organisms were found, animals that have been adapting for different thermal conditions show contrasting patterns of protein compositions (Fontanillas et al. 2017). The analysis of the evolutionary gene development of both hot- and cold-adapted species indicates significant amino acid changes which are likely to affect proteins in many aspects. The studies of changes in amino acids and protein compositions revealed that adaptation for cold temperatures happened secondarily and independently to adaptation to high temperatures, which occurred very early in the history of the species (Fontanillas et al. 2017). The ability to survive in the extremely hot environment was maintained by natural selection (Fontanillas et al. 2017).

Another study was conducted by Jollivet et al. (2012) and it is based on the detailed studying of the adaptive features of the *Alvinella pompejana* that allow this worm to live in extremely high temperatures. As a part of the research, evolutionary changes of amino acid positions of *A. pompejana* and *P. grasslei* species were compared. 355 orthologous proteins of these two species yielded 2844 different changes out of 40338 amino acid positions (Jollivet et al. 2012). These data gave researchers the opportunity to examine differences between amino acids of these two species and to determine features that allow the worms to adapt to the different temperature regimes. Testing the changes showed important differences between thermal adaptations of *A. pompejana* and *P. grasslei*. During the parallel evolutionary processes when these species were evolving from the shared ancestor, the amino acids of *Alvinella pompejana* were replaced to be more charged and to have higher hydrophobicity than amino acids of *P. grasslei*. Because of these replacements, *A. pompejana* demonstrates better thermal adaptation. A simplified graph visually demonstrates this process for the example of 10 amino acid classes (Figure 1).

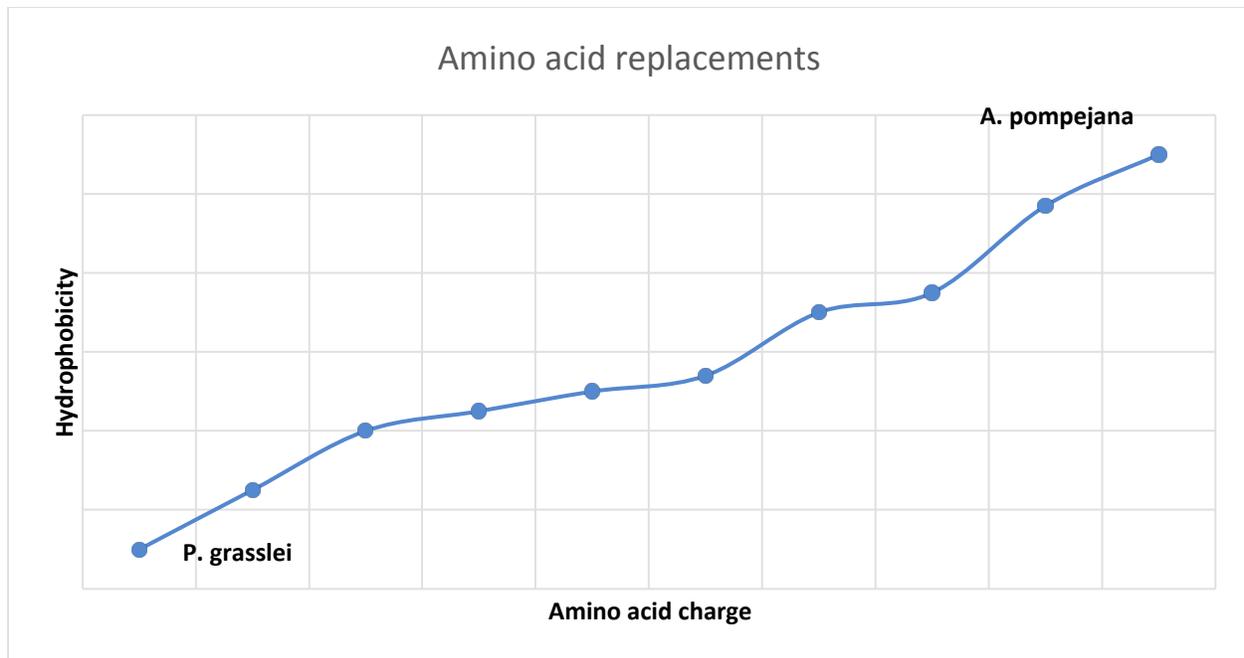


Figure 1- The graph visually demonstrates the process of the amino acid replacement during the adaptation to the extremely hot environment. This graph does not present the exact data but demonstrates a general process. The graph is based on the research paper “Proteome Adaptation to High Temperatures in the Ectothermic Hydrothermal Vent Pompeii Worm” by Jollivet et al. (2012).

The study conducted by Jollivet et al. (2012) revealed that thermal adaptations are possible because of higher hydrophobicity and more charged amino acids.

Further studying of thermal adaptation of hydrothermal vent inhabitants can show many details about conditions on Earth long periods of time ago and history of the evolution of all the species on Earth.

Conclusion

Conducting research at hydrothermal vents is expensive and dangerous. That is why there are still many gaps in our knowledge of these unique underwater ecosystems. By comparing and summarizing studies, several significant aspects of the deep-sea organisms have been reviewed. Referring to one of the main purposes of the paper, very few similarities with shallow-water species were found currently. However, deep-sea species possess many unique genes and adaptive features like, for example, sets of genes related to hypoxia or high osmotic pressure.

Based on the information I could find it is possible to make several conclusions:

- 1) Genome studies and thermal adaptation research show that most of the hydrothermal vent species have a long evolutionary history and went through many changes and adaptations. Amino acid replacement during the long evolution of the *A. pompejana* is an example of it.
- 2) Some species that inhabit the hot areas of the hydrothermal vents share genome features with cold-adapted animals. For example, different species of worms from the *Alvinellidae* family live both in cold and extremely hot environments but share a common genome. This observation

shows that at a particular period of time both of the species had to adapt to the same conditions. Only future studies can show the exact time frames of this period.

Studying evolutionary processes of the hydrothermal vent species can fill in many gaps in the modern science. However, a variety of studies is still required in order to get a full understanding of these processes. Numerous unique traits of the deep-sea species need to be discovered and lots of research needs to be conducted around hydrothermal vents. In order to get a complete evolutionary picture, scientists should focus on studying easily available sunlit zone inhabitants and identify features that can confirm or disprove relations between these species and vent inhabitants. Researchers should also focus on studying the geology of the hydrothermal vent environment. This knowledge can reveal facts about conditions on Earth at different periods of time.

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