

Revealing the Genetic Differentiation of Different Geographical Populations of *Juniperus* spp. Based on Chloroplast Genome

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Abstract *Juniperus* spp. are a diverse group of coniferous trees with wide distribution. This review focuses on the genetic differentiation of juniper populations across different geographic regions based on chloroplast genome analysis. By examining chloroplast genome sequences of junipers, significant genetic variations were identified among different geographic populations. These variations include single nucleotide polymorphisms, insertions/deletions, and structural differences in the genomes, reflecting the genetic adaptation and evolutionary history within distinct geographical environments. We also summarize the major driving factors behind juniper genetic differentiation, such as topography, climate, and human activities, all of which are closely associated with juniper genetic diversity and adaptability, and we emphasize the importance of studying juniper population genetic differentiation through chloroplast genome analysis and the potential applications of such research in the conservation and management of juniper resources.

Keywords *Juniperus* spp.; Chloroplast genome; Genetic differentiation; Geographic populations; Genetic diversity

Cypress, as an ancient and important tree species, not only plays a key role in forestry, but also has significant value in environmental protection, soil fixation and ecological balance (Charpin et al., 2019) (Figure 1). Its wide distribution spans different geographical settings and covers a wide range of environmental types and climatic conditions, from cold alpine regions to warm subtropical zones, reflecting its ability to adapt to diverse habitats. This tree is known for its drought tolerance, cold tolerance and adaptability, and is widely used in forestry, horticulture and ecological restoration. Its natural resistance and growth characteristics make cypress occupy an important position in different geographical locations and ecosystems (Fu et al., 2018). However, behind this geographical distribution lies rich genetic diversity and adaptability, which is one of the important reasons for this study to further study the genetic differentiation of geographic populations of cypress.



Figure 1 *Juniperus* spp.

The objective of this study is to explore the genetic differentiation of different geographic populations of cypress, in order to reveal the genetic basis of its adaptation to the environment, so as to provide scientific basis for the protection and restoration of the ecosystem. Such research is of great significance for understanding the genetic structure, genetic flow and population adaptability among cypress populations, and it also helps to guide the rational use of cypress resources and promote its sustainable development in different ecosystems.

In the past, cypress genetic research has mainly focused on the analysis of specific regions or specific genetic markers. Although previous work has provided us with some insight into the genetic diversity of cypress trees, it is still lacking in comprehensiveness and depth, especially at the chloroplast genome level, and a comprehensive understanding of the genetic differentiation and adaptation of different geographic populations of cypress trees has not been fully developed.

The aim of this study was to review the current situation of cypress genetic research, with special focus on the contribution of chloroplast genome to genetic differentiation of different geographic populations of Cypress. Through the comprehensive analysis of the previous research results, we hope to provide a more systematic and comprehensive understanding of genetic differentiation of cypress trees, and provide theoretical support and scientific guidance for the protection and sustainable use of cypress resources in the future.

1 Introduction of Chloroplast Genome

1.1 Role and importance of chloroplast genome

As one of the important organelles in plant cells, the chloroplast genome carries abundant genetic information and plays a key role in plant growth and development, adaptation to the environment and genetic transmission. In the study of plant genetics, the role and importance of the chloroplast genome has attracted increasing attention (Cheng et al., 2018).

Chloroplast genome has relatively simple structure and stable transmission mode. Its DNA sequence is relatively small, but contains key genes that encode photosynthesis and energy metabolism, such as genes related to the photosynthetic complex and electron transport chain. Because the chloroplast genome is mainly passed through the maternal pathway, it has little genetic variation, making it an ideal tool for studying plant relatability, population genetic structure, and evolutionary history.

The chloroplast genome plays an important role in the physiological processes of plants. Chloroplasts are the main site of photosynthesis and contain genes involved in the energy capture and conversion process in photosynthesis. In addition, chloroplasts are also involved in regulating plant metabolic activities, synthesizing secondary metabolites such as amino acids, lipids and flavonoids, which affect plant growth and development and the ability to adapt to the environment.

The genetic diversity and mutation frequency of chloroplast genome are also the focus of research. The haploid and highly conserved chloroplast genome is of great value in the study of geographical distribution, population genetic structure and adaptive evolution of species. The analysis of chloroplast DNA sequence can reveal the genetic diversity of different species, populations and even individuals, and provide important clues for biodiversity conservation, germplasm resource utilization and plant evolution mechanism.

1.2 Structure and characteristics of cypress chloroplast genome

As one of the common conifers, cypress chloroplast genome has certain research value in plant genomics. The structure and characteristics of cypress chloroplast genome show its importance in plant evolution and genetic diversity. Cypress chloroplast genome presents a typical circular double-stranded DNA structure and usually contains a conserved set of genes, including genes encoding photosynthesis and respiratory chain, such as photosynthetic complex, ATP synthase and nucleic acid metabolism enzyme (Duan et al., 2020). These genes play a key role in ensuring plant growth, development and energy metabolism.

Although the chloroplast genome of cypress may have a certain degree of diversity within the species, it is relatively conserved on the whole, which makes the chloroplast DNA sequence have a wide application prospect in phylogenetic and phylogenetic studies.

Chloroplast genome sequence can be used to study the genetic differentiation, inter-population relationship and potential species evolution history of cypress geographic populations, which is helpful to understand the genetic diversity, adaptability and ecological characteristics of cypress, and provide scientific basis for its conservation and utilization.

1.3 Application of chloroplast genome in genetic differentiation research

Chloroplast genomes play an important role in the study of plant genetic differentiation, especially for revealing genetic differences and kinship relationships among different geographic populations (Liu et al., 2018). As an important conifer species, the chloroplast genome of cypress has shown a wide application prospect in the study of genetic differentiation of geographic populations of cypress.

Chloroplast genomes have been used by a team of researchers to conduct an in-depth analysis of the genetic diversity of European cypress populations. This study involved samples of European cypress trees from different geographical locations, sequencing and analyzing their chloroplast genomes to explore the genetic differentiation between different geographic populations. The research team first collected samples of European cypress trees from multiple geographic locations, including the Mediterranean coast, the Balkans and the Italian peninsula, and extracted DNA from the chloroplast genome for sequencing. After comparing and analyzing chloroplast genome sequences, the research team found that there were significant differences in chloroplast genome sequences among different geographic populations. These differences reflect the genetic evolution events experienced by cypress populations in different geographical locations during their evolution, including migration, dispersal and isolation among populations.

The study identified some specific patterns of chloroplast genome sequence variation, which are related to the distribution of cypress populations in different geographic regions. For example, cypress populations along the Mediterranean coast and in the Balkans show high similarity at the chloroplast genome level, while cypress populations on the Italian peninsula show different chloroplast genome sequence characteristics, and the results of this study reveal genetic differences and evolutionary relationships between different geographic populations of European cypress trees. It provides important clues for understanding the population evolution of cypress.

2 Genetic Diversity of Different Geographic Populations of Cypress

2.1 Genetic diversity of different geographic populations

As a common conifer, cypress is widely distributed throughout the world, showing significant genetic diversity among its different geographic populations. This diversity usually exists based on growth conditions and genetic evolution in different geographical environments, and using the genetic markers of the chloroplast genome, researchers can delve into the genetic diversity among different geographic populations of cypress trees (Yang et al., 2016).

Along the Mediterranean coast, in North America, Asia, and elsewhere, cypress populations exhibit varying degrees of genetic diversity, which can be caused by a variety of factors, including geographic isolation, climatic differences, habitat characteristics, and natural selection. Cypress populations along the Mediterranean coast may have higher genetic diversity because they have long existed in growing environments with diverse climates, compared to other regions where cypress populations may have undergone more geographic separation and genetic evolution, resulting in some degree of genetic variation.

Studying the genetic diversity of different geographic populations of cypress contributes to a deeper understanding of the genetic structure and geographic differentiation of these populations, which is of great significance for the conservation of cypress resources, optimization of its genetic gene pool, improvement of its resilience, and formulation of better conservation strategies. We can make better use of these resources to promote adaptive and sustainable use of cypress trees.

2.2 The main factors to reveal genetic differentiation

Many complex factors are involved in genetic differentiation of cypress populations. Chloroplast genome plays a key role in this process, and its sequence variation can provide important clues about genetic differentiation among cypress populations.

One of the main factors of genetic differentiation is geographical isolation. Due to geographical isolation, cypress populations live in different habitats and are affected by environmental conditions, land forms and climate for a long time (Li et al., 2022). This isolation leads to a reduction in genetic communication between different geographic populations, which encourages populations to differentiate at the genetic level, and the greater the degree and duration of geographical isolation, the more pronounced the genetic differentiation between populations is likely to be.

Another important factor is ecological adaptation. The adaptability of cypress populations to different habitats may lead to genetic differentiation. Due to different environments, cypress populations may gradually develop adaptive characteristics to different habitats, such as adaptability to temperature, humidity and soil conditions. The formation of these ecological adaptive characteristics may be accompanied by the selection of specific genotypes, thus leading to genetic differentiation among cypress populations.

In addition, factors such as population size, migration pattern, natural selection and genetic drift may also affect the genetic differentiation of cypress populations. These factors interweave with each other, affect the genetic structure and diversity of cypress population, and promote the genetic differentiation among different geographic populations.

2.3 The influence of geographical environment on genetic diversity

Geographic environment has a profound impact on the genetic diversity of cypress, which involves many aspects, from geomorphic features to climatic diversity, shaping the genetic structure of geographic population of Cypress (Xu et al., 2010).

The complexity of geographical environment directly affects the genetic differentiation among different populations of cypress. The variation of terrain and geographical isolation resulted in the uneven distribution of cypress population in space. The presence of mountains, rivers, and different land forms can limit gene flow between cypress populations and contribute to genetic differences between populations. This geographical isolation of spatial distribution can lead to reduced gene exchange within geographic populations, thus promoting the occurrence of genetic differentiation.

The change of climate conditions also affected the genetic diversity of cypress populations. The climate differences in different geographical environments will trigger the adaptability of cypress populations to different environments, and this adaptability may be reflected at the genetic level. For example, differences in climate factors such as temperature and precipitation may lead to gradual variation in the physiological and morphological characteristics of different populations, thus shaping the genetic characteristics of populations.

The stability and change of geographical environment also have significant influence on genetic diversity. The relatively stable geographical environment may maintain the stability of some genetic characteristics, while the changing environmental conditions may promote the gradual variation and selection of some genotypes or phenotypes, thus affecting the genetic diversity of cypress populations.

3 Mechanisms of Genetic Differentiation Revealed by Chloroplast Genome

3.1 The role of chloroplast genome in genetic evolution

Chloroplast genome plays a key role in plant genetic evolution, which goes far beyond the mere transmission of genetic information. As an important genetic element in plant cells, chloroplast genome is not only responsible for carrying and transmitting genetic information, but also plays an important functional and adaptive role in the evolution of populations (Jia et al., 2019, *Bulletin of Biology*, 44(11): 7-9).

Chloroplast genome, as the genetic gene bank of plant cells, has accumulated a lot of genetic information during the long evolution process. Its relatively stable genetic characteristics make chloroplast gene composition an important index to study the relationship between species and the evolutionary history of populations. By comparing and analyzing chloroplast genome sequences, we can reveal the genetic relationships among different populations and species, infer their evolutionary history and origin, and provide an important basis for exploring speciation and differentiation.

The evolution of chloroplast genome has certain conservation and variability. During the evolution of plant species, certain regions or genes in the chloroplast genome may vary or mutate, and this variation can sometimes be retained and passed between populations. This variation may be manifested by the presence of haplotype diversity, i.e. the simultaneous presence of many different chloroplast genotypes in a population, which reflects the genetic diversity and complex genetic structure between populations.

Chloroplast genomes also play a role in species adaptation and survival strategies. Some specific variations in the chloroplast genome may be related to environmental adaptations, for example, a particular chloroplast genotype may make a plant more competitive or adaptable in a particular environment, thus affecting the survival and reproduction of the population. The chloroplast genome variation of alpine plants such as *Ammopiptanthus nanus* may make them more competitive in alpine and high-altitude habitats.

3.2 Reveal the genetic differentiation mechanism of different geographic populations of cypress

As an important tree species, cypress exhibits complex and striking features in the genetic differentiation mechanism of its different geographic populations. Genetic differentiation is driven by a series of mechanisms involving biological processes at multiple levels, and these mechanisms are also well represented in the geographic populations of cypress trees (Papageorgiou et al., 2005).

Natural selection and environmental adaptation play a key role in the genetic differentiation of cypress geographic populations. The growth conditions and ecological factors in different geographical environments have important effects on the adaptability of cypress populations, resulting in genetic differences among populations. For example, cypress populations in some geographic environments may show greater resilience under certain adverse conditions, and cypress populations in the Himalayas show distinct geographic differences in adaptation to changes in altitude and climate conditions, which may facilitate the widespread spread of certain genotypes or genomic features in that environment.

Population size and genetic drift are also important factors affecting genetic differentiation of cypress geographic populations. Small populations can result in random changes in gene frequency due to genetic drift and random events, which increase genetic differences between geographic populations. Studies based on molecular genetics methods provide insight into the genetic differentiation of different geographic populations of cypress. The methods of DNA sequence alignment, genotype identification and population genetic structure analysis provide powerful tools for revealing the genetic differentiation mechanism of cypress geographic populations.

3.3 Effects of genetic differentiation on ecological adaptability of cypress

Genetic differentiation plays an important role in the ecological adaptability of cypress. The genetic differentiation of geographical populations not only forms the diversity of genetic characteristics among different populations, but also has a significant impact on their ecological adaptability.

Genetic differentiation brought about ecological adaptation differences among cypress populations. Under different geographical environments, the geographical populations of cypress have gradually formed specific genotypes adapted to the local environment through long-term natural selection and adaptation (Pastorino et al., 2010). These adaptive genotypes may have the characteristics of stress resistance, drought tolerance, cold tolerance, etc., so as to improve the survival ability of cypress trees in their respective growing environments.

Genetic differentiation affects genetic variation and gene flow in cypress geographic populations. Genetic differentiation between geographic populations reduces the degree of gene flow and the exchange of genes

between different geographic populations. This results in increased aggregation of genotypes within populations, while reducing the introduction of genes from other populations, resulting in a more pronounced representation of genetic traits within populations.

Genetic differentiation also affects the response of cypress trees to environmental changes. Genetic differentiation of different geographic populations resulted in genotype differences, which made cypress display different ecological responses to environmental stress and climate change. This genetic difference may affect the sensitivity of cypress to environmental stress and its adaptability to different ecological environments.

4 Results and Discussion

Geographic populations of cypress show significant differences in genetic differentiation, which provides important clues for us to understand the evolution, adaptation and ecological distribution of this species. By studying the genetic differentiation results of geographic populations of cypress, we can gain insight into the genetic structure and differences of cypress populations in different regions.

Genetic differentiation among geographic populations is manifested by significant differences in genotype and allele frequencies of cypress trees. This genetic differentiation reflects the degree of genetic diversity among different regions and the distribution of genotypes within cypress populations, which helps to reveal the evolutionary process and species adaptability. Genetic differentiation may reflect the process by which cypress trees adapt to their respective ecological environments under long-term natural selection and environmental pressures (Bower and Hipkins, 2017).

Genetic structure of cypress is influenced by gene exchange among geographic populations. The results of this study will help us understand the influence of gene flow on genetic structure of cypress geographic populations and the effect of geographic isolation on genetic differentiation, which has far-reaching significance in the field of ecology and evolution. From an ecological point of view, it can help us understand the response and adaptability of cypress populations to environmental changes, and in terms of evolution, it provides an opportunity to gain insight into the evolution of cypress species.

The results of genetic differentiation of cypress geographic populations also provide implications and potential applications for future research and application, and have guiding significance for biodiversity conservation, ecosystem restoration, and genetic resource management and utilization. Understanding the genetic diversity of cypress geographic populations can also help reduce the risk of species extinction and provide a basis for ecosystem protection.

In addition, the study of genetic differentiation of cypress geographic population can guide ecological restoration and adaptive breeding, and promote the reconstruction and restoration of ecosystem. The understanding of genetic diversity of different geographic populations can also be applied to environmental monitoring and ecosystem management, providing a basis for the management and protection of ecosystems, providing an important basis for the utilization and genetic improvement of cypress resources, promoting the development and progress of cypress related fields, and having far-reaching influence and guiding significance for future research in the fields of biology, ecology and resource management.

References

- Bower A.D., and Hipkins V., 2017, Genetic diversity and population structure in the rare, endemic baker cypress (*Hesperocyparis bakeri*), *Madroño*, 64(2): 71-82.
<https://doi.org/10.3120/0024-9637-64.2.71>
- Charpin D., Pichot C., Belmonte J., Sutra J.P., Zidkova J., Chanez P., Shahali Y., Sénéchal H., and Poncet P., 2019, Cypress pollinosis: from tree to clinic, *Clinic Rev. Allerg. Immunol.*, 56: 174-195.
<https://doi.org/10.1007/s12016-017-8602-y>
PMid:28401436
- Cheng H., Ge C.F., Zhang H., and Qiao Y.S., 2018, Advances on chloroplast genome sequencing and phylogenetic analysis in fruit trees, *Henongxue Bao (Journal of Nuclear Agricultural Sciences)*, 32(1): 58-69.

- Duan H., Guo J., Xuan L., Wang Z., Li M., Yin Y., and Yang Y., 2020, Comparative chloroplast genomics of the genus *Taxodium*, *BMC Genomics*, 21: 114.
<https://doi.org/10.1186/s12864-020-6532-1>
PMid:32005143 PMCID:PMC6995153
- Fu J.F., Tang T.Y., He X.P., Cheng J.W., Li X., Fu J.R., and Yu D.X., 2018, A preliminary report on investigation of ancient cypress trees in Jiange County, *Journal of Sichuan Forestry Science and Technology*, 39(6): 97-101.
- Li X.Y., Wang M.Q., Yuan M.L., Ueno S., Wu X.T., Cai M.Y., Tsumura Y., and Wen Y.F., Genetic differentiation and demographic history of cryptomeria, a relict plant, in East Asia, *Linye Kexue (Scientia Silvae Sinicae)*, 58(6): 66-78.
- Liu H.R., Gao Q.B., Zhang F.Q., Xing R., Chi X.F., and Chen S.L., 2018, Genetic diversity and phylogeographic structure of *Triosteum pinnatifidum* based chloroplast DNA sequence *rbcL-accD*, *Zhiwu Yanjiu (Bulletin of Botanical Research)*, 38(2): 278-283.
- Papageorgiou A.C., Finkeldey R., Hattmer H.H., and Xenopoulos S., 2005, Genetic differences between autochthonous and breeding populations of common cypress (*Cupressus sempervirens* L.) in Greece, *Eur. J. Forest Res.*, 124: 119-124.
<https://doi.org/10.1007/s10342-005-0063-9>
- Pastorino M.J., Ghirardi S., Grosfeld J., Gallo L.A., and Puntieri J.G., 2010, Genetic variation in architectural seedling traits of Patagonian cypress natural populations from the extremes of a precipitation range, *Ann. For. Sci.*, 67(5): 508.
<https://doi.org/10.1051/forest/2010010>
- Xu T., Abbott R.J., Milne R.I., Mao K., Du F.K., Wu G., Ciren Z., Mische G., and Liu J., 2010, Phylogeography and allopatric divergence of cypress species (*Cupressus* L.) in the Qinghai-Tibetan Plateau and adjacent regions, *BMC Evol. Biol.*, 10: 194.
<https://doi.org/10.1186/1471-2148-10-194>
PMid:20569425 PMCID:PMC3020627
- Yang H., Zhang R., Jin G., Feng Z., and Zhou Z., 2016, Assessing the genetic diversity and genealogical reconstruction of cypress (*Cupressus funebris* Endl.) breeding parents using SSR markers, *Forests*, 7(8): 160.
<https://doi.org/10.3390/f7080160>