

The Asian Connection

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While Arboretum horticulturists have tested the hardiness of east Asian plants in the Boston climate, botanists have been theorizing about the causes of their similarities to eastern North American plants, employing a range of methods to investigate their relationships to one another.

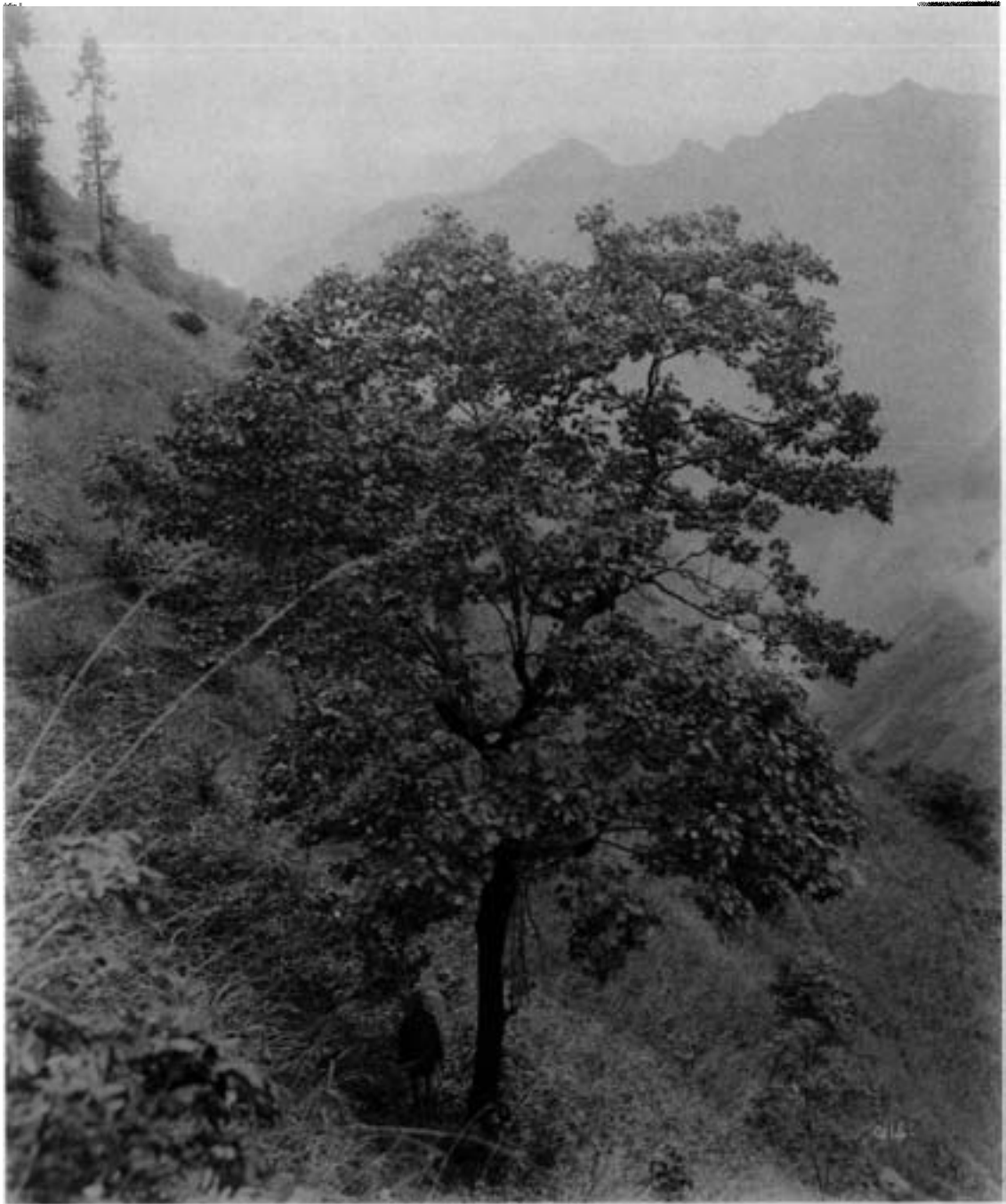
Harvard botanists have long been entranced by the flora of east Asia. Although the floristic similarity of eastern Asia and eastern North America was first noted by Linnaeus in the middle of the eighteenth century, it was Harvard's Asa Gray who in 1859 focused scientific attention on the many common or closely related species found in the two regions and nowhere else. This disjunct pattern of distribution seemed to suggest a once more extensive flora now broken up into two smaller regions by geological and climatic causes.

Gray has been followed by numerous students and staff (Sargent, 1894; Fernald, 1931; Hu, 1935; Li, 1952; Wood, 1971; Boufford and Spongberg, 1983; Tiffney, 1985) who have studied and written about the causes of this relationship. Inevitably, alternative explanations have been postulated to account for the similarities of the floras. Perhaps a distinct flora found in one region migrated as a whole across a land bridge connection to the other region. The similarity might also result from the random but repeated dispersal of individual species across great ocean barriers. Or the apparent similarity may not be real at all. Unrelated species could have evolved similar morphologies because the climate and soils of the two regions are similar.

Over the last half century our understanding

of past climatic and geological history has deepened. We believe that whole continents, now separated by thousands of miles of ocean, were once connected as a single land mass. We know that major changes in the earth's climate have brought about repeated periods of glaciation in northern regions of the world as well as cycles of wet and dry periods in tropical regions, leading to massive dislocations of flora and fauna. Changes in sea level and the uplifting of mountain ranges have completely altered the shape of terrestrial land and inland seas. Plant fossils discovered in high latitude regions such as Greenland, northern Europe and Asia, and the arctic lands of North America clearly demonstrate that many southern species were once more widely distributed.

Each new piece of evidence about climate, geology, or historical plant distributions has been used by botanists to argue for one over another cause of the striking similarity of the floras on the two continents and the apparent close relations of many of their species. As is so often the case in science, the real explanation for such a complex but distinct pattern is likely to be a combination of several factors interacting over long spans of time. The similarities seen in one group of plants may have its own distinctive history of causes when compared with a different group.



Liriodendron chinense photographed in Patung Hsein, China, altitude 4,000 feet, by E. H. Wilson in June 1910. At 60 feet in height this individual is at the upper end in stature for its species. From the Archives of the Arnold Arboretum.

A Common Ancestry

Underlying all of this, and at the heart of the perceived pattern, is the belief that species found in the two regions are indeed closely related and that the pattern represents the remnants of a shared evolutionary history. It could be otherwise. Two species can appear very similar in many characteristics and yet be quite unrelated as in the case of *Acer pseudoplatanus* (Sycamore maple) and *Platanus occidentalis* (Sycamore). This phenomenon has been called convergent evolution by botanists who strive to distinguish this misleading similarity from true relationship.

What does it mean to say that two species are closely related? What constitutes a true relationship? To an evolutionary botanist it means that they share a large number of genes in common because at some time in the past they shared a common ancestor. In essence, the two species were once one species, which subsequently split into two. Our most common definition of a species is a group of interbreeding individuals that do not interbreed with any other such group. The members of a species all share genetic information in a way analogous to the sharing of information among members of a human population who use a



Liriodendron tulipifera, the American tulip tree, photographed in North Carolina, is a far taller plant than its Chinese relative. For this individual, the height to the first limb alone is 65 feet. From the Archives of the Arnold Arboretum.

common language or dialect. And just as isolation over time can lead to the development of distinct language dialects, so too can isolation trigger the process of speciation in plants. If parts of a species' population become isolated from each other—perhaps by a geographical barrier such as a mountain range or a river—then the exchange of genetic information is interrupted and the two isolated parts begin to develop genetic differences. If this isolation continues long enough, the two isolated parts may no longer be capable of interbreeding. Speciation has occurred.

The goal of the plant systematist is to organize the diversity of plant species in such a way that their degree of relatedness (in the sense of shared genes due to shared common ancestors) is revealed in the classification. Ideally, then, the names given to species and the way they are placed in genera and families will reflect our understanding of the history of speciation events during evolution that led to the diversity we see today.

Measuring Relatedness

How have systematists tried to measure this degree of relationship among species? The earliest efforts, beginning with Linnaeus two hundred years ago, examined the degree of morphological similarity under the assumption that this accurately revealed the underlying genetic similarity. But we now know that very similar plant morphologies can develop from very different sets of genes. Therefore, morphology may in many cases be misleading.

In their search for the characteristics that more closely represent the genetic identity of species, botanists turned to the proteins that constitute the building blocks of tissues, organs, and mature morphologies. Through biochemical isolation and separation they were able to evaluate a new set of characteristics believed to be the direct products of genes.

In recent years this approach has been further eclipsed by the revolution in molecular biology, which allows one to identify individual genes and compare sequences of genes as they are represented in two presumably

related species. Therefore, in theory, one can directly measure the degree of genetic similarity. Molecular systematics, as it is called, promises to bring a higher order of evidence to questions of the relationship between species that may or may not have once shared a common ancestor.

Genes can best be analyzed when they are extracted from living plant tissue that has been quickly frozen in extremely cold temperatures. Researchers use a liquified form of nitrogen to achieve such temperatures. The need for living tissue close at hand from a wide diversity of plant species has greatly increased the importance and value of well-documented collections of trees such as are maintained with great care in the Arnold Arboretum. Samples from these specimens can be supplemented with fresh collections obtained on expeditions to the native habitat of the species under consideration.

History of Two Tulip Trees

The value of this new, molecular approach can be seen in recent work on a classic case of a Chinese–eastern North American disjunct distribution, the tulip tree. *Liriodendron tulipifera*, which ranges from New England to northern Florida, appears closely related to *Liriodendron chinense* of central and eastern China. In addition to sharing a great deal of morphological similarity in leaf, flower, and fruit characteristics, these two species are capable of cross pollination to form viable hybrid offspring. By these criteria, they might almost be judged a single species. Yet the vast geographical distance separating them clearly prevents such hybrids from forming naturally. Based only on morphological evidence, one might conclude that these two species were once part of a large, interbreeding population (that is, sharing a common ancestor) and that the split into two populations had occurred relatively recently.

To obtain new evidence on the true genetic similarity between these species, Clifford Parks and Jonathan Wendel at the University of North Carolina extracted the genetic material (DNA) in leaf tissue from a large number of

samples throughout the range of both species, which would directly determine the degree of difference in selected genes. The result of their analysis revealed that approximately one and one-quarter percent of the genetic material differed between the two species. Using statistical models based on the rates at which genetic material changes over time, these botanists were able to estimate how long ago these two species shared a common ancestor. They concluded that *L. tulipifera* and *L. chinense* were part of a single interbreeding population twelve and a half million years ago.

A Confirmation from Fossils

Parks and Wendel then turned to the fossil record to assess the historical evidence for past distributions of *Liriodendron* and other temperate deciduous species found in both Asia and North America. They wished to test their estimate based on genetic analysis against the actual dated presence of the species in particular locations. Reviewing the discovery of fossil plants in western Canada and Alaska, and taking into account the position of the continents ten to twenty million years ago, they concluded that a broadly distributed, temperate forest existed in a band across North America through Alaska and into central Asia at the start of this time period. A global cooling trend around the middle of this time brought the invasion of coniferous forests into Alaska and northeastern Russia, displacing deciduous forests to the south and effectively severing the Asian connection. Fossil dating showed that this disjunction occurred about thirteen million years ago.

Despite the great morphological similarity between *L. tulipifera* and *L. chinense* and their ability to produce hybrid offspring, the molecular and fossil evidence reinforce each other and suggest that they have been separated for more than twelve million years. While their genes have continued to evolve during this separation, their morphologies have remained relatively unchanged, thus giving a false picture of their degree of relatedness.

Parks and Wendel argue the need for similar studies of other genera, such as maples (*Acer*), silverbells (*Halesia*), witchhazels (*Hamamelis*), and ginsengs (*Panax*), all of which show an Asian–North American disjunct distribution. Clearly molecular systematics, utilizing the rich living collections of institutions such as the Arnold Arboretum, will provide a powerful tool for illuminating our ancient Asian connection.

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