植物学通报 2001，18（6）：635～642
Chinese Bulletin of Botany

综述与专论

植物分子生态学进展（Ⅰ）——遗传结构和杂交①

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摘要 从物种遗传结构和杂交的角度介绍了当前植物分子生态学研究的新进展。对于物种遗传结构，文章分析了物种生物学特性、生态因子对它的影响，强调了种群不同世代遗传结构研究的重要性。而在杂交研究领域，文章揭示了分子生物学手段有着比传统形态分析方法更多的优越性。

关键词 分子生态学，遗传结构，杂交

Advances of Plant Molecular Ecology（Ⅰ）—— Genetic Structure and Hybridization

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Abstract This paper reviews advances in studies on genetic structure and hybridization in plant molecular ecology. Besides discussing the species biological characteristics and ecological factors influencing genetic structure, this paper further emphasizes the importance of demographic genetic structure study. Meanwhile, molecular techniques are much better than traditional morphological methods in hybridization study.

Key words Molecular ecology, Genetic structure, Hybridization

Molecular methodologies are becoming more and more popular. A lot of new methods have been used to save time and money, and more problems are solved (Valsecchi, 1998; Hu and Wang, 2000). Sometimes we are surprised for their applications. For example, one can analyze DNA of plant which had been used in building, furniture, handcrafts or barrels.

Then, what can molecular ecology do in plant researches? Let us see some study problems in plant ecology first.

Traditionally, gene flow estimation was based on marked dyes or pollinators. But this study in

① Foundation items: Guangzhou Branch of Chinese Academy of Sciences and Academy of Sciences of Guangdong Province (No. 99B05902X), Natural Science Foundation of Guangdong Province (003031).
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收稿日期：2000-11-14 接受日期：2001-05-29 责任编辑 刘 晖

measuring apparent rather than total gene flow might substantially underestimate the true rate of gene flow (Boshier *et al*, 1995).

By only relying on morphological traits, we sometimes may not differentiate between two closely related germplasm because the morphological traits are partitioned into phenotypic plasticity and genetic variability (Yun *et al*, 1998a; Kolliker *et al*, 1998; Kuehn *et al*, 1999).

For many plants the concept of individuality is straightforward. For many other plants that propagate vegetatively, however, it is difficult to identify individuals (Paul *et al*, 1997).

Nevertheless, the use of DNA analysis offers new opportunities of addressing these important questions and the others, which become known as "molecular ecology".

Therefore, this article is not intended to be comprehensive across all contemporary fields in plant molecular ecology, but rather illustrative of the diversity of applications.

1 Genetic Structure

The genetic structure of natural population is one of the core issues in plant population studies (Wang *et al*, 1996; Ge *et al*, 1997; Wang *et al*, 1997; Yun *et al*, 1998b; Ge and Hong, 1999; Meikle *et al*, 1999; Hu and Wang, 2000). Genetic structure, simply saying, is the genetic diversities (variations) of populations and their distribution pattern among populations. Numerous studies have revealed the nonrandom distribution of genetic variation and emphasized the importance of understanding the genetic structure of a population (Ge *et al*, 1997; Ge and Hong, 1999).

Genetic structure is known to be due to a combination of various biologically and environmental important factors. In plants, life-history traits such as seed dormancy (Franceschinelli and Kesseli, 1999), pollen and seed dispersal ability (Ayres and Ryan, 1997; Chen and shong, 1997; Akimoto *et al*, 1998; Gagne *et al*, 1998; Franceschinelli and Kesseli, 1999; Fore and Guttman, 1999; Isagi *et al*, 2000; Levy and Neal, 1999; Wang *et al*, 2000a; 2000b), flowering phenology (Isagi *et al*, 2000), incompatibility mechanism (Boshier *et al*, 1995), mating system (Boshier *et al*, 1995; Li *et al*, 1995; Wang *et al*, 1996; Ayres and Ryan, 1997; Wang *et al*, 1997; Akimoto *et al*, 1998; Gagne *et al*, 1998; Yun *et al*, 1998b; Franceschinelli and Kesseli, 1999; Ge and Hong, 1999; Utelli *et al*, 1999; Hu and Wang, 2000; Wang *et al*, 2000a) and so on have been studied as factors that exert influence on the genetic structure of populations. For clonal species, the member, sizes and age of individuals all effect the genetic structure (Ayres and Ryan, 1997).

With allozymes and RAPD (random amplified polymorphic DNA), Sun (1999) studied dimorphic cleistogamous species, *Scutellania indica* in Hongkong. *S. indica* produced both chasmogamous (CH) and cleitogamous (CL) flowers on some plants, with some others only having CL flowers. The results indicated that effective CL self-fertilizing breeding system and genetic drift played the major role in determining the genetic structure of the species.

Forcioli *et al* (1998) used cpDNA (chloroplast DNA) to evaluate genetic structure of gynodioecious species of *Beta vulgaris* ssp. *maritima* (Chenopodiaceae), for which, hermaphrodites and female individuals can be found in natural populations. He found gynodioecy seemed to affect the distribution of cpDNA diversity: gynodioecious populations of *Beta vulgaris* ssp. *maritima* contained a great number of cpDNA types but were less differentiated among themselves than hermaphroditic ones. They thought these were mainly due to higher fertility of female plants and some other causes.

Because of the importance of biological characters, Hu and Wang (2000) further considered plant genetic structure was mainly determined by breeding system. Even so, ecological factors may influence plant breeding system and then genetic structure (Wei *et al*, 1999).

https://www.scienceinchina.com/doi/10.3724/CBB.j20-481

Many researches have also noticed the effects of ecological factors. These factors include such

as water condition (Zhong *et al*, 1995; Ren *et al*, 1999), anthropogenic interference (Yun *et al*, 1998b; Levy and Neal, 1999), soil fertility (Huff *et al*, 1998), soil type (Oline *et al*, 2000), forest community succession stage (Wang *et al*, 1996; Wang *et al*, 2000a; 2000b; Zhang *et al*, 2001), plant density (Chen and Song, 1997; Franceschinelli and Bawa, 2000), pollinator movements (Utelli *et al*, 1999; Franceschinelli and Bawa, 2000) and so on.

Using AFLP (amplified fragment length polymorphism) analysis, Wang *et al* (2000a) studied genetic structure of two species: *Schima superba*, *Castanopsis chinensis* across three communities: coniferous community, mixed coniferous-evergreen broadleaved community, evergreen broadleaved community in Dinghu Mountain, Guangdong Province, China. The results showed both species' biological characteristics and community microhabitat affected their genetic structure. Although *S. superba* had high gene flow due to easy seed dispersal, the evergreen broadleaved community was not suitable for its seedlings which required light, the shadows of canopy impeded their growth. Therefore, the population genetic variation of *S. superba* in this community was different significantly from that in the other two communities; In contrary, the seeds of *C. chinensis* were gravity-dispersed and confined themselves near their parents, so this species appeared high genetic divergence among populations in different communities than *S. superba*. Meanwhile, individuals of *C. chinensis* did not adapted to the coniferous community very well, therefore very low genetic variation was detected compared to the individuals in the other two communities.

One of typical experiments showing ecological factors influencing population genetic structure was done by Owuor *et al* (1997). In their study two opposite slope separated by approximate 100m were chosen. Despite sharing the same geology and macroclimate, the two sites differed sharply in microclimatic condition. The South-Facing Slope was ecologically more stressful and consisted mainly of an open park forest of *Ceratonia siliqua*, *Pistacia lentiscus* and savanna grassland, characteristic of the African savanna landscape. The North-Facing Slope, by contrast, mainly contains evergreen maquis of *Quercus caliprinos* and *Pistacia palaestina* representative of the European lush vegetation. Wild barley, *Hordeum spontaneum*, grew on both slopes. The RAPD analysis with this species revealed significant inter- and intra- slope genetic variation. Similar results were reported by Li *et al* (1999) in *Triticum dicoccoides*.

Although the efforts to combine genetic marker data with ecological information are being underway (Cruzan, 1998), because most of polymorphic DNA loci were caused by neutral and near-neutral mutations (Hu and Wang, 2000; 2001), they denied the methods of using genetic variation as a whole to study its correlation with environmental factors, and suggested examining the environmental adaptive genes and their mechanism responding to environment were meaningful.

Even so, many studies seem to overlook genetic structure from demographic perspective, which is also very important to study plant genetic variation influenced by ecological factors and changed with time.

To divide the individuals of Liaodong oak (*Quercus liaotungensis*), belonging to different populations, into three age classes (10 ~ 25 years old, 26 ~ 34 years old and 35 ~ 50 years old), Zhong *et al* (1995) and Yun *et al* (1998b) found the genetic structure of 26 ~ 34 years old individuals were different from the individuals of the other two classes. However, they did not carry out further analysis except considering that deforestation led to such result. Meanwhile, they did not analyze the demographic genetic structure of each population but put them together, therefore we can not find out how deforestation and/or other ecological factors influence each population genetic structure with time.

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The importance of demographic genetic structure study can be further demonstrated by some

studies in forest fragmentation.

The fragmentation of continuous forest broken into smaller patches is a world-wide phenomenon (Laurance and Bierregaard, 1997). Traditional theory predicted that forest fragmentation would be associated with genetic drift and inbreeding, and then reduced levels of genetic diversity (Turner, 1996), while such consequences did not occur in fragmented populations of *Swietenia humilis* (White *et al*, 1999) and *Acer saccharum* (Young *et al*, 1993). However, because the large proportion of *S. humilis* studied by White *et al* (1999) was prior to fragmentation, we do not know if the genetic erosion had happened in the progeny of this species. Young *et al* (1993) only studied the seedlings of *A. saccharum* in fragmented populations, and did not compare them with their adults, which might grow before fragmentation. Neither study showed how forest fragmentation might alter or reduce genetic diversity from one generation to the next, because only one generation was surveyed. Hence neither study provided a suitable test of whether genetic erosion was occurring. Genetic erosion would be demonstrated if the genetic structure of seedling population differed from that of adult populations.

Through a study of demographic genetic structure in *Carapa guianensis*, Dayanandan (1999) did not detect inbreeding within both sapling and adult cohorts of fragmented populations, but found that the allelic richness was lower in the sapling than adults in fragmented population, and the two cohorts were much more distinctive as genetic distance shown. Using demographic genetic structure study in *Symphonia globulifera* in Casta Rica, Aldrich *et al* (1998) found significant inbreeding in the seedlings of fragmented population, but not in saplings and adults which probably were produced prior to fragmentation. The subsequent study on the genotypes of seedlings of *S. globulifera* showed they were, in fact, dominated only by some "superadults" isolated out of fragmented population into pasture; this was therefore creating a genetic bottleneck and therefore rapid loss of genetic diversity (Aldrich and Hamrick, 1998).

Therefore, the available evidence indicates that loss of genetic diversity is likely to occur in fragmented population, but more studies on the demographic genetic structure in fragmented populations are urgently required.

2 Hybridization

The importance of hybridization in plants has been subject of intense scrutiny for most of the 20th century (Wolfe *et al*, 1998). Molecular studies have demonstrated that hybridization does play a significant role in the evolution of plants (O'hanlon *et al*, 1999; Hu and Wang, 2000). In forest trees, natural hybridization between closely related species has been recognized as a fairy common mechanism of exchange of genetic variation between distinctive gene pools (Bucci *et al*, 1998; Steinkellner *et al*, 1998; Yun *et al*, 1998a; Matos and Schaal, 2000). Weak reproductive barriers following short-term isolation of incipient species have been reported not to hamper hybridization and introgression (Bucci *et al*, 1998).

Documentation of hybridization initially depended on morphological characters. Hybrid indices based on morphological traits were used to demonstrate intermediary between parental types to infer that individuals under consideration either were or were not of hybrid origin. However, the plasticity of morphology often obscured the hybrid and their parents (Yun *et al*, 1998a).

Perron and Bousquet (1997) studied two closely related black spruce *Picea mariana* and red spruce *P. rubens* with RAPD analysis. Their results implicated that the real frequency of natural hybridization was much greater than generally observed under field conditions, from morphological characters alone (Perron and Bousquet, 1997). Other studies had also showed the inadequency of

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the morphological approach alone could not correctly detect natural hybridization (Klier *et al*, 1991; Kuehn *et al*, 1999), with problems arising from environmental and genetic effects superimposed under field conditions, and from character convergence and homoplasy. So it can be safely argued that, molecular phylogenies and DNA markers generally recover more numerous cases of natural hybridization or introgression than investigation based on phenotypic characters alone.

In some cases, morphological characters might reveal more occurrence of hybridization than molecular markers do (Hansen *et al*, 2000; Triest *et al*, 2000). The possible reasons are that we may not detect all the changes at molecular levels and the morphological characters are under complex genetic control.

Moreover, molecular methods, sometimes, may be helpless when the processes of hybridization are complex, as in the case of *Gilia achilleifolia* (Morrell and Rieseberg, 1998) and *Nuphar* × *rubrodisca* (Padgett *et al*, 1998).

For hybrids, to distinguish parent is valuable, and cpDNA variation is often used to assess the parentage of hybrids (Ferris *et al*, 1997; Bucci *et al*, 1998; Yang *et al*, 2000) because it is uniparental inherited (Dumolin-Lapègue *et al*, 1999; Vendramin *et al*, 2000; Matos and Schaal, 2000).

Spartina anglica originated from hybridization between *S. alterniflora* and *S. maritima*, but which of them was the maternal parent remained a mystery before. With cpDNA analysis, *S. alterniflora* was assured to be female parent (Ferris *et al*, 1997).

Bucci *et al* (1998) applied cpSSR to studied closely related species: *Pinus halepensis* and *P. brutia* and found that natural hybridization seemed to be successful only when *P. halepensis* was the pollen donor and *P. brutia* was the female parent, not reciprocally.

Such unilateral hybridization was also reported between *Dryopteris intermedia* and *D. Carthusiana* (Xiang *et al*, 2000). Interestingly, they found such hybridization was population-dependent with no constant maternal or paternal parent of hybrid in populations, but they did not propose clear interpretation.

Although hybridization is one of the main ways to produce new species, sometimes, we do not seem to hope it to happen. For more, see "Alien Species" in our next paper "Advances of Plant Molecular Ecology (II)" to be published.

3 Conclusion

Above, we introduce two research fields in current plant molecular ecology, and the other four fields: phylogeography, alien species, conversation genetic and contamination, will be discussed in another paper of us. These studies are not independent, but relevant, and embody the importance of combination between molecular biology and plant ecology.

参 考 文 献

Akimoto M, Shimamoto Y, Morishima H, 1998. Population genetic structure of wild rice *Oryza glumaepatula* distributed in the Amazon flood area influenced by its life-history traits. *Mol Ecol*, **7**: 1371 ~ 1381

Aldrich P R, Hamrick J L, 1998. Reproductive dominance of pasture trees in a fragmented tropical forest mosaic. *Science*, **281**: 103 ~ 105

Aldrich P R, Hamrick J L, Chavarriaga P, Kochert G, 1998. Microsatellite analysis of demographic genetic structure in fragmented populations of the tropical tree *Symphonia globulifera*. *Mol Ecol*, **7**: 933 ~ 944

Ayres D R, Ryan F J, 1997. The clonal and population structure of a rare endemic plant, *Wyethia reticulata* (Asteraceae): allozyme and RAPD analysis. *Mol Ecol*, **6**: 761 ~ 772

Boshier D H, Chase M R, Bawa K S, 1995. Population genetics of *Cordia alliodora* (Boraginaceae), a neotropical tree. 3. Gene flow, neighborhood, and population substructure. *Amer J Bot*, **82**(4): 484 ~ 490

Bucci G, Anzidei M, Madaghiele A, Vendramin G G, 1998. Detection of haplotypic variation and natural hybridization in *halepensis* – complex pine species using chloroplast simple sequence repeat (SSR) markers. *Mol Ecol*, **7**: 1633 ~ 1643

Chen X Y (**陈小勇**), Song Y C (**宋永昌**), 1997. Mating system and inferred inbreeding depression of a *Cyclobalanopsis clauca* population in Diaoqiao, Huangshan. *Acta Ecol Sin*, **17**(5): 462 ~ 468 (in Chinese)

Cruzan M B, 1998. Genetic markers in plant evolutionary ecology. *Ecology*, **79**(2): 400 ~ 412

Dayanandan S, Dole J, Bawa K, Kesseli R, 1999. Population structure delineated with microsatellite markers in fragmented populations of a tropical tree, *Carapa guianensis* (Meliaceae). *Mol Ecol*, **8**: 1585 ~ 1592

Dumolin-Lapègue S, Pemonge M H, Gielly L, Taberlet P, Petit R J, 1999. Amplification of oak DNA from ancient and modern wood. *Mol Ecol*, **8**: 2137 ~ 2140

Ferris C, King R A, Gray A J, 1997. Molecular evidence for the maternal parentage in the hybrid origin of *Sapartina anglica*. C.E. Hubbard. *Mol Ecol*, **6**: 185 ~ 187

Forcioli D, Saumitou-Laprade P, Valero M, Vernet P, Cuguen J, 1998. Distribution of chloroplast DNA Diversity within and among populations in gynodioecious *Beta vulgaris* ssp. *Maritima* (Chenopodiaceae). *Mol Ecol*, **7**: 1193 ~ 1204

Fore S A, Guttman S I, 1999. Genetic structure of *Helianthus occidentalis* (Asteraceae) in a preserve with fragmented habitat. *Amer J Bot*, **86**(7): 988 ~ 995

Franceschinelli E V, Bawa K S, 2000. The effect of ecological factors on the mating system of a South American shrub species (*Helicteres brevispira*). *Heredity*, **84**: 116 ~ 123

Franceschinelli E V, Kesseli R, 1999. Population structure and gene flow of the Brazilian shrub *Helicteres brevispira*. *Heretidy*, **82**: 355 ~ 363

Gagne G, Roeckel-Drevet P, Grezes-Besset B, Shindrova P, Ivanov P, Grand-Ravel C, Vear F, Tourvieille de Labrouhe D, Charmet G, Nicolas P, 1998. Study of the variability and evolution of *Orobanche cumana* populations infesting sunflower in different European countries. *Theor Appl Genet*, **96**: 1216 ~ 1222

Ge S (**葛颂**), Hong D Y (**洪德元**), 1999. Studies of morphological and allozyme variation of the endengered *Adenophora lobophylla* and its widespread congener *A. potaninii*. *Acta Genet Sin* (**遗传学报**), **24**(4): 410 ~ 417 (in Chinese)

Ge S (**葛颂**), Wang H Q (**王海群**), Zhang C M (**张灿明**), Hong D Y (**洪德元**), 1997. Genetic diversity and population differentiation of *Cathaya argyrophylla* in Bamian Mountain. *Acta Bot Sin* (**植物学报**), **39**(3): 266 ~ 271 (in Chinese)

Hansen K T, Elven R, Brochmann C, 2000. Molecules and morphology in concert: tests of some hypotheses in arctic *Potentilla* (Rosaceae). *Amer J Bot*, **87**(10): 1466 ~ 1479

Hu Z A (**胡志昂**), Wang H X (**王洪新**), 2000. Advances in plant molecular ecology. In: Lin Z P *et al* (**林忠平等**) eds. Green Gene for 21st Century. Beijing: Science Press, 89 ~ 104 (in Chinese)

Hu Z A (**胡志昂**), Wang H X (**王洪新**), 2001. Molecular mechanism of stress adaptation in plant natural populations. *Acta Bot Sin* (**植物学报**), **43**(2): 111 ~ 118 (in Chinese)

Huff D R, Quinn J A, Higgins B, Palazzo A J, 1998. Random amplified polymorphic DNA (RAPD) variation among native little bluestem [*Schizachyrium scoparium* (Michx.) Nash] populations from sites of high and low fertility in forest and grassland biomes. *Mol Ecol*, **7**: 1591 ~ 1597

Isagi Y I, Kanazashi T, Suzuki W, Tanaka H, Abe T, 2000. Microsatellite analysis of the regeneration process of *Magnolia obovata* Thunb. *Heredity*, **84**: 143 ~ 151

Klier K, Leoschke M J, Wendel J F, 1991. Hybridization and introgression in white and yellow ladyslipper orchids (*Cypripedium Candidum* and *C. pubescens*). *J Hered*, **82**: 305 ~ 318

Kolliker R, Stadelmann F J, Reidy B, Nosberger J, 1998. Fertilization and defoliation frequency affect genetic diversity of *Festuca pratensis* Huds in permanent grasslands. *Mol Ecol*, **7**: 1557 ~ 1567

Kuehn M M, Minor J E, White B N, 1999. An examination of hybridization between the cattail species *Typha latifolia* and *Typha angustifolia* using random amplified polymorphic DNA and chloroplast DNA markers. *Mol Ecol*, **8**: 1981 ~ 1990

Laurance W F, Bierregaard R O, 1997. Tropical Forest Remnants: Ecology, Management, and Conservation of Fragmented Communities. University of Chicago Press, Chicago

Levy F, Neal C L, 1999. Spatial and temporal genetic structure in chloroplast and allozyme markers in *Phacelia dubia* implicate genetic drift. *Heredity*, **82**: 422 ~ 431

Li J (**李军**), Tao Y (**陶芸**), Zheng S Z (**郑师章**), Zhou J L (**周纪纶**), 1995. Isozymatic differentiation in local population of *Glycine soja* Sieb. & Zucc. *Acta Bot Sin* (**植物学报**), **37**(9): 669 ~ 676 (in Chinese)

Li Y C, Fahima T, Beiles A, Korol A B, Nevo E, 1999. Microclimatic stress and adaptive DNA differentiation in wild emmer wheat, *Triticum dicoccoides*. *Theor Appl Genet*, **98**: 873 ~ 883

Matos J A, Schaal B A, 2000. Chloroplast evolution in the *Pinus montezumae* complex: a coalescent approach to hybridization. *Evolution*, **54**(4): 1218 ~ 1233

https://www.sciengine.com/doi/10.3724/CBB-t20-481

Meikle A, Paterson S, Finch R P, Marshall G, Waterhouse A, 1999. Genetic characterization of heather (*Calluna vulgaris* (L.) Hull) subject to different management regimes across Great Britain. *Mol Ecol*, **8**: 2037 ~ 2047

Morrell P L, Rieseberg L H, 1998. Molecular tests of the proposed diploid hybrid origin of *Gilia achilleifolia* (polemoniaceae). *Amer*

J Bot, **85**(10): 1439 ~ 1453

O'hanlon P C, Peakall R, Briese D T, 1999. Amplfied fragment length polymorphism (AFLP) reveals introgression in weedy *Onopordum* thistles: hybridization and invasion. *Mol Ecol*, **8**: 1239 ~ 1246

Oline D K, Mitton J B, Grant M C, 2000. Population and subspecific genetic differentiation in the foxtail pine (*Pinus balfouriana*). *Evolution*, **54**(5): 1813 ~ 1819

Owuor E D, Fahima T, Beiles A, Korol A, Nevo E, 1997. Population genetic response to microsite ecological stress in wild barley, *Hordeum spontaneum*. *Mol Ecol*, **6**: 1177 ~ 1187

Padgett D J, Les D H, Crow G E, 1998. Evidence for the hybrid origin of *Nuphar* × *Rubrodisca* (Nymphaeaceae). *Amer J Bot*, **85**(10): 1468 ~ 1476

Paul S, Wachira F N, Powell W, Waugh R, 1997. Diversity and genetic differentiation among populations of India and Kenyan tea (*Camellia sinensis* (L.) O. Kuntze) reveals by AFLP markers. *Theo Appl genet*, **94**: 255 ~ 263

Perron M, Bousquet J, 1997. Natural hybridization between black spruce and red spruce. *Mol Ecol*, **6**: 725 ~ 734

Ren W W (**任文伟**), Qian J (**钱吉**), Zheng S Z(**郑师章**), 1999. A comparative study on genetic differentiation of *Leymus chinensis* in different geographic populations. *Acta Ecol Sin*(**生态学报**), **19**(5): 689 ~ 696 (in Chinese)

Steinkellner H, Lexer C, Turetschek E, Glossl J, 1998. Conservation of $(GA)_n$ microsatellite loci between *Quercus* species. *Mol Ecol*, **6**: 1189 ~ 1194

Sun M, 1999. Cleistogamy in *Scutellaria indica* (Labiatae): effective mating system and population genetic structure. *Mol Ecol*, **8**: 1285 ~ 1295

Triest L, De Greef B, De Bondt R, Van Slycken J, 2000. RAPD of controlled crosses and clones from the field suggests that hybrids are rare in the *Salix alba-Salix fragilis* complex. *Heredity*, **84**: 555 ~ 563

Turner I M, 1996. Species loss in fragments of tropical rain forest: a review of the evidence. *J Appl Ecol*, **33**: 200 ~ 209

Utelli A B, Roy B A, Baltisberger M, 1999. History can be more important than 'pollination syndrome' in determining the genetic structure of plant populations: the case of *Aconitum lycoctonum* (Ranunculaceae). *Heredity*, **82**: 574 ~ 584

Valsecchi E, 1998. Tissue boiling: a short-cut in DNA extraction for large-scale population screenings. *Mol Ecol*, **7**: 1243 ~ 1245

Vendramin G G, Anzidei M, Madaghiele A, Sperisen C, Bucci G, 2000. Chloroplast microsatellite analysis reveals the presence of population subdivision in Norway spruce (*Picea abies* K.). *Genome*, **43**: 68 ~ 78

Wang H X (**王洪新**), Hu Z A (**胡志昂**), Zhong M (**钟敏**), Lu W J (**陆文静**), Wei W (**魏伟**), Yun R (**恽锐**), Qian Y Q (**钱迎倩**), 1997. Genetic differentiation and physiological adaptation of wild soybean (*Glycine soja*) populations under saline condition: isozymatic and random amplified polymorphic DNA study. *Acta Bot Sin* (**植物学报**), **39**(1): 34 ~ 42 (in Chinese)

Wang X Q (**汪小全**), Zou Y P (**邹喻苹**), Zhang D M (**张大明**), Hong D Y (**洪德元**), Liu Z Y (**刘正宇**), 1996. Genetic diversity of *Cathaya argyrophylla* with RAPD analysis. *Sci in China* (serial C) (**中国科学** (C **辑**)), **26**(5): 436 ~ 441 (in Chinese)

Wang Z F (**王峥峰**), Wang B S (**王伯荪**), Li M G (**李鸣光**), Zhang J L (**张军丽**), 2000a. Molecular ecology of lower subtropical species, *Schima superba* and *Castanopsis chinensis* in three succession series communities. *Acta Bot Sin* (**植物学报**), **42**(10): 1082 ~ 1088

Wang Z F (**王峥峰**), Zhang J L (**张军丽**), Wang B S (**王伯荪**), Li M G (**李鸣光**), 2000b. Molecular ecology of *Cryptocarya chinensis* populations in different communities. *Chin J Appl Ecol* (**应用生态学报**), **11**(3): 342 ~ 344 (in Chinese)

Wei W (**魏伟**), Wang H X (**王洪新**), Hu Z A (**胡志昂**), Zhong M (**钟敏**), Yun R (**恽锐**), Qian Y Q (**钱迎倩**), 1999. Primary studies on molecular ecology of *Caragana* spp. populations distributed over Maowusu sandy grassland: from RAPD data. *Acta Ecol Sin* (**生态学报**), **19**(1): 16 ~ 22 (in Chinese)

White G M, Boshier D H, Powell W, 1999. Genetic variation within a fragmented population of *Swietenia humilis* Zucc. *Mol Ecol*, **8**: 1899 ~ 1909

Wolfe A D, Xiang Q Y, Kephart S R, 1998. Assessing hybridization in natural populations of *Penstemon* (Scrophulariaceae) using hypervariable intersimple sequence repeat (ISSR) bands. *Mol Ecol*, **7**: 1107 ~ 1125

Xiang L, Werth C R, Emery S N, McCauley D E, 2000. Population-specific gender-biased hybridization between *Dryopteris intermedia* and *D. carthusiana*: evidence from chloroplast DNA. *Amer J Bot*, **87**(8): 1175 ~ 1180

Yang T W, Yang Y A, Xiong Z, 2000. Paternal inheritance of chloroplast DNA in interspecific hybrids in the genus *Larrea* (Zygophyllaceae). *Amer J Bot*, **87**(10): 1452 ~ 1458

Young A G, Merriam H G, Warwick S I, 1993. The effects of forest fragmentation on genetic variation in *Acer saccharum* Marsh. (sugar maple) populations. *Heredity*, **71**: 277 ~ 289

Yun R (**恽锐**), Wang H X (**王洪新**), Hu Z A (**胡志昂**), Zhong M (**钟敏**), Wei W (**魏伟**), Qian Y Q (**钱迎倩**), 1998a. Genetic differentiation of *Quercus mongolica* and *Q. liaotungensis* based on morphological observation, isozyme and DNA analysis. *Acta Bot Sin* (**植物学报**), **40**(11): 1040 ~ 1046 (in Chinese)

Yun R (**恽锐**), Zhong M (**钟敏**), Wang H X (**王洪新**), Wei W (**魏伟**), Hu Z A (**胡志昂**), Qian Y Q (**钱迎倩**), 1998b. Study on DNA diversity of Liaodong oak population at Dongling Mountain region, Beijing. *Acta Bot Sin* (**植物学报**), **40**(2): 169 ~ 175 (in Chinese)

https://www.scientiacta.com/cbb/cbb-t20-481/10.3724/CBB-t20-481

Zhang J L (张军丽), Wang Z F (王峥峰), Wang B S (王伯荪), Li M G (李鸣光), Zhang W Y (张炜银), 2001. AFLP analysis in *Crypotocarya concinna*, a dominant population in lower subtropical evergreen broad-leaved forests at Heishiding Natural Reserve. *Acta Ecol Sin* (生态学报), **21**(3): 391 ~ 398 (in Chinese)

Zhong M (钟敏), Wang H X (王洪新), Hu Z A (胡志昂), Qian Y Q (钱迎倩), 1995. A preliminary study on genetic structure of Liaodong oak (*Quercus liaotungensis*) populations in dry and moist habitats and its adaptive implications. *Acta Bot Sin* (植物学报), **37**(9): 661 ~ 668 (in Chinese)

(上接 743 页)

马 浩,1997.泡桐遗传值研究.博士学位论文,北京林业大学,北京

孙蒙祥,王灶安,1990.宜昌泡桐雌雄配子体发育及其生殖过程的研究.华中农业大学学报,**9**(2):107 ~ 111

佟永昌,杨自湘,韩一凡,1980. 一些树种染色体的观察.中国林科院林业研究所报告,**1**(1):83 ~ 88

陈志远,1981.湖北省泡桐资源调查研究文集.北京:中国林业出版社,11 ~ 15

陈志远,1986.泡桐属分类管见.华中农业大学学报,**5**(3):261 ~ 265

林 兵,林建兴,1990. RELP—遗传学研究的新领域.生物学通报,**7**(3):16 ~ 17

范国强,蒋建平,1997.泡桐叶片蛋白质提取方法的研究.植物学通报,**14**(3):61 ~ 64

舒寿兰,1985.四种泡桐染色体数目的初步研究.河南农业大学学报,**19**(1):48 ~ 51

胡惠蓉,陈志远,1995.泡桐属花粉的光学显微镜观察.见:泡桐研究进展,北京:中国林业出版社,239 ~ 243

龚 彤,1976.中国泡桐属植物的研究.植物分类学报,**14**(2):38 ~ 50

龚本海,郭燕舞,姚崇怀,1994.泡桐属植物 SOD 同工酶和可溶性蛋白质分析.华中农业大学学报,**13**(5):507 ~ 510

梁作椭 ,陈志远,1997.泡桐属细胞分类研究.华中农业大学学报,**16**(6):609 ~ 613

曹东威,陈受宜,1992. RAPD 技术及其应用.生物工程进展,**12**(6):1 ~ 5

蒋建平,1990.泡桐栽培学.北京:中国林业出版社

熊金桥,陈志远,1991.泡桐属花粉形态及分类的关系.河南农业大学学报,**25**(3):280 ~ 284

熊金桥,陈志远,1992.泡桐属的数量分类研究.植物研究,**12**(2):185 ~ 188

Darlington C D, Wylie A P, 1955. Chromosome atlas of flowering plants. George Allen and Nwin, London

Hames B D, Rickwood D P, 1990. Gel Electrophoresis of Proteins. Oxford Press, 217 ~ 220

Hu S Y(胡秀英), 1959, A monograph of the genus *Paulownia*. *TaiWan Museum*, **12**: 1 ~ 54

Mosseter A, 1992. Low levels of genetic diversity in red pine confirmed by random amplified polymorphic DNA markets. *Can J For Res*, **22**(3): 1332 ~ 1337

Palmer J D, 1987. Chloroplast DNA evolution and biosystematic use of chloroplast DNA variation. *Am Nat*, **130**(2): 56 ~ 59

Wang W Y, Pai R C, Lai C C, Lin T P, 1994. Molecular evidence for the hybrid of *Paulownia* based on RAPD markers and RFLP of chloroplant DNA. *The Appl Genet*, **89**(4): 271 ~ 275

我国选手获第 12 届国际生物奥林匹克竞赛团体总分第 4 名

第 12 届国际生物奥林匹克竞赛于 2001 年 7 月 8 日至 15 日在比利时首都布鲁塞尔举行,有 38 个国家和地区的 151 名选手参赛。经理论考试和实验考试,在 151 名选手中共评出金牌 17 枚,银牌 18 枚,铜牌 47 枚。我国代表队 4 名选手中有 3 名获得金牌,1 名获得铜牌,团体总分第四名。获奖选手是四川成都七中的童一(女)、金牌第 7 名,湖南师大附中的廖雅静(女)、金牌第 11 名,江苏海安高中的卢立(男)、金牌第 16 名,福建厦门一中的吴薇(女)、铜牌第 60 名。本次奥赛我国代表队由中国植物学会负责组织领导。据分析,我国代表队的优势逐渐下降的一个重要原因是学生在高中时生物学实验作得较少,实验水平较低,影响实验考试成绩。

https://www.sciengine.com/doi/10.3724/CBB-t20-481

(中国植物学会供稿)