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Distribution and Research Status of Sorbus Plants in China: A Postprint

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Abstract

Sorbus plants exhibit polymorphic crown forms, exquisite flower colors, vibrant fruits, and diverse leaf colors throughout the seasons, possessing high horticultural ornamental value. However, due to the presence of interspecific hybridization, polyploidization, and apomixis within the genus, Sorbus also represents a taxonomically challenging group. This study intends to systematically compile and analyze Sorbus specimen information from the National Specimen Resource Bank and global digitized plant specimen databases, map the collection distribution of Sorbus species in China, identify the distribution centers of wild Sorbus germplasm resources in China, construct a Sorbus specimen database for China, and provide references for the first national census and collection of forest and grassland germplasm resources. Based on clarifying the distribution locations and habitats of Sorbus plant resources, it was discovered that China harbors the richest Sorbus plant resources in the world and that Sorbus species are predominantly distributed in high-altitude regions. Particularly in the mountainous regions of southwestern China, where more than half of China's Sorbus species are distributed, multiple ploidy levels coexist and hybridization occurs frequently—could this be the key factor contributing to the rich species diversity within this genus? When Sorbus species distributed at high altitudes are introduced to low-altitude regions, can they adapt to the high summer temperatures at low altitudes? How do they adapt? Based on these questions, the author further reviewed the current research status of Sorbus plants within their professional field regarding morphological classification and phylogeny, adaptive evolution and conservation genetics, and plant resource utilization, identified unresolved issues in current Sorbus research, and further indicated directions that future research should prioritize. It is recommended that future research focus on the following issues: (1) Based on a solid phylogenetic framework, prioritize the issue of hybrid speciation. (2) Based on a comprehensive survey of wild Sorbus germplasm resources in China, select species with high horticultural ornamental value, and employ the latest molecular biology techniques and methods to study

the challenges of high summer temperatures encountered during their introduction and domestication processes, thereby providing a theoretical basis for the introduction and domestication of high-altitude species.

Full Text

Preamble

Distribution and Current Research Status of *Sorbus* L. in China

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Abstract

Plants of the genus *Sorbus* exhibit diverse crown forms, exquisite floral displays, vibrant fruits, and seasonally variable foliage, conferring exceptional horticultural and ornamental value. However, the genus also represents a taxonomically challenging group due to widespread interspecific hybridization, polyploidization, and apomixis. This study systematically compiled and analyzed herbarium specimen data from the National Plant Specimen Resource Center and the Global Plants database to map collection distributions of *Sorbus* species in China, identify distribution centers of wild germplasm resources, and construct a comprehensive specimen database to support the first national survey of forest and grassland germplasm resources. Our analysis reveals that China harbors the world' s richest *Sorbus* resources, with species predominantly distributed in high-altitude regions. More than half of Chinese *Sorbus* species occur in the mountainous areas of southwestern China, where multiple ploidy levels coexist and hybridization occurs frequently. We hypothesize that these factors may be key drivers of the genus' s exceptional species diversity. Furthermore, we examine whether high-altitude species can adapt to low-altitude environments, particularly regarding tolerance to summer high temperatures, and how such adaptation might occur. Based on our expertise, we conducted an extensive literature review covering morphological classification, phylogenetics, adaptive evolution, conservation genetics, and resource utilization. We identified unresolved research questions and propose future priorities: (1) investigating hybrid speciation processes within a robust phylogenetic framework, and (2) using advanced molecular techniques to study the mechanisms underlying high-temperature stress responses during introduction and domestication of high-altitude species, thereby providing theoretical foundations for their cultivation.

Keywords: *Sorbus*, type specimen, germplasm resources, introduction and acclimatization, development and utilization

Introduction

The genus *Sorbus* L., belonging to the subfamily Maloideae of Rosaceae, encompasses both broad and narrow taxonomic concepts. Broad-sense *Sorbus* (*Sorbus* L. sensu lato) comprises approximately 260 species, including both simple-leaved and pinnate-leaved groups widely distributed across temperate Asia, Europe, and North America (Aldasoro et al., 1998; Huntley, 1993; Phipps et al., 1990; Yu & Lu, 1974). Narrow-sense *Sorbus* (*Sorbus* L. sensu stricto) includes only pinnate-leaved groups (Watson & Manandhar, 2012; Zika & Bailleul, 2015), with about 88 species—1-2 broadly distributed in Europe, 7 in North America, and 60-70 in Asia (Li et al., 2017). According to Species 2000, China hosts approximately 123 broad-sense *Sorbus* species, making it the world' s richest reservoir of *Sorbus* germplasm. The mountainous regions of southwestern China and adjacent areas represent the diversity and distribution center for the genus (Zika & Bailleul, 2015).

Sorbus plants possess polymorphic crowns, elegant foliage, colorful fruits, and diverse seasonal leaf colors, rendering them valuable for ornamental horticulture and alpine native vegetation restoration (Li et al., 2019). Some species serve as important breeding stock and rootstocks for fruit trees, while others have medicinal, edible, and therapeutic value in their fruits and seeds, indicating substantial development potential. However, extensive phenotypic variation, combined with polyploidy and hybridization, has generated controversy regarding generic delimitation and infrageneric systematic positions. Furthermore, research on conservation biology, chemical constituents, and medicinal mechanisms remains limited for most species, and many wild taxa remain poorly known, constraining exploitation and utilization. For such a valuable yet taxonomically challenging group, herbarium-based studies are surprisingly scarce. Herbarium specimens serve as vouchers for taxonomic research, documenting spatiotemporal distribution patterns. Detailed compilation and analysis of collection data can elucidate specific distributions, research history, current status, and knowledge gaps. Our herbarium analysis reveals that China possesses remarkably rich *Sorbus* resources, with over half of Chinese species distributed in southwestern mountainous regions—both a modern diversity center and a critical zone for ongoing hybrid formation. The coexistence of multiple ploidy levels and persistent hybridization in this region may drive the genus' s rich species diversity. We also question whether triploid species in this region exhibit self-incompatibility, which species serve as pollen donors, and how hybridization processes unfold. Additionally, habitat analysis of herbarium specimens shows that *Sorbus* species predominantly inhabit high-altitude areas, raising questions about their adaptability and acclimation mechanisms when introduced to low-altitude regions with high summer temperatures.

Accordingly, this study aims to: (1) compile and analyze Chinese *Sorbus* herbarium specimen data to generate distribution maps, clarify resource distribution patterns, establish a comprehensive database, and provide baseline references for the national germplasm survey; and (2) review research progress in morphological classification, phylogenetics, adaptive evolution, conservation genetics, and resource utilization to identify unresolved questions and future research priorities.

1.1 Analysis of Herbarium Specimen Status and Distribution Mapping

We retrieved *Sorbus* species recorded in *Flora Reipublicae Popularis Sinicae*, *Flora of China* (FOC), and the Species 2000 database (http://www.sp2000.org.cn/), cross-referencing with the International Plant Names Index (IPNI, https://www.ipni.org/) and The Plant List (http://www.theplantlist.com/) to compile a preliminary checklist of Chinese *Sorbus* species. We then systematically searched the National Plant Specimen Resource Center (www.cvh.ac.cn) and Global Plants database (http://plants.jstor.org/) for Chinese *Sorbus* specimens, extracting detailed information including herbarium, accession number, collector, locality, collection date, and type specimen status. Using Excel 2010 and Visio 2017, we statistically analyzed these data and generated distribution maps. Specimens with detailed latitude and longitude records were mapped using QGIS to create collection distribution maps for Chinese *Sorbus* species.

1.2 Construction of the Chinese *Sorbus* Specimen Database

Based on our herbarium survey of Chinese *Sorbus* specimens (both type and non-type), we constructed a comprehensive database comprising scientific names, basionyms, coordinates, altitude, specimen type, herbarium, collection date, locality, collector, and habitat information.

1.3 Research Status of Chinese *Sorbus* Plants

We conducted literature searches in Web of Science, CNKI, VIP, and Wanfang databases using keywords including *Sorbus*, molecular phylogeny, hybridization, polyploidy, population structure, and apomixis. We screened literature focusing on morphological classification and phylogenetics, adaptive evolution and conservation genetics, and plant resource utilization to summarize current research and identify unresolved issues.

2.1 Basic Status of Chinese *Sorbus* Herbarium Specimens

Preliminary statistics indicate 13,331 *Sorbus* specimens are housed in Chinese herbaria, with 3,281 containing complete latitude and longitude data. After synonymization and removal of records outside China’ s administrative regions, we obtained 2,692 valid records (60 species, 7 varieties), including *Sorbus albopilosa*, *S. alnifolia*, *S. amabilis*, *S. arguta*, *S. aronioides*, *S. astateria*, *S. caloneura*, *S. caloneura* var. *kwangtungensis*, *S. coronata*, *S. corymbifera*, *S. cuspidata*, *S. discolor*, *S. dunnii*, *S. epidendron*, *S. esserteauiana*, *S. ferruginea*, *S. filipes*, *S. folgneri*, *S. foliolosa*, *S. globosa*, *S. glomerulata*, *S. helenae*, *S. hemsleyi*, *S. hupehensis*, *S. insignis*, *S. keissleri*, *S. koehneana*, *S. macrantha*, *S. megalocarpa*, *S. megalocarpa* var. *cuneata*, *S. meliosmifolia*, *S. microphylla*, *S. monbeigii*, *S. multijuga*, *S. obsoletidentata*, *S. ochracea*, *S. oligodonta*, *S. pallescens*, *S. pohuashanensis*, *S. poteriifolia*, *S. prattii*, *S. prattii* var. *aestivalis*, *S. pteridophylla*, *S. pteridophylla* var. *tephroclada*, *S. randaiensis*, *S. reducta*, *S. rehderiana*, *S. rehderiana* var. *cupreonitens*, *S. rehderiana* var. *grosseserrata*, *S. rhamnoides*, *S. rhombifolia*, *S. rufopilosa*, *S. sargentiana*, *S. scalaris*, *S. setschwanensis*, *S. tapashana*, *S. thibetica*, *S. thomsonii*, *S. tianschanica*, *S. tsinlingensis*, *S. vilmorinii*, *S. wilsoniana*, *S. yuana*, *S. zahlbruckneri*, *S. zayuensis*, *S. folgneri* var. *duplicatodentata*, and *S. pseudovilmorinii* (Figure 1). These specimens are distributed across 40 herbaria nationwide, with holdings ranging from 1 specimen (6 herbaria) to 491 specimens (Herbarium of Chengdu Institute of Biology, Chinese Academy of Sciences). The top 10 herbaria house 89% of all *Sorbus* specimens (Table 1). Provincial analysis shows that all Chinese provinces except Ningxia, Shanghai, Hong Kong, and Macao have *Sorbus* collection records. The top 10 provinces account for 88% of specimens, with Sichuan leading (910 specimens) followed by Hubei (346 specimens). Yunnan yielded the highest species diversity (44 species), followed by Sichuan (41 species) and Tibet (23 species) (Figure 2). Collectively, Sichuan, Yunnan, and Tibet account for 58 species (including 4 varieties), representing approximately 50% of Chinese *Sorbus* species, confirming southwestern China as the diversity center.

2.2 Status of Type Specimens of Chinese *Sorbus* Species

Among 123 *Sorbus* species, 38 species (including 3 varieties) lack type specimens, while the remaining 85 species (including 15 varieties) have 361 type specimens representing five categories (Figure 3). Isotypes are most numerous (111 specimens, 45 species, 7 varieties), followed by syntypes (87 specimens, 21 species, 3 varieties), holotypes (42 specimens, 31 species, 8 varieties), paratypes (40 specimens, 12 species, 2 varieties), and lectotypes (16 specimens, 10 species, 1 variety). An additional 65 type specimens (31 species, 2 varieties) were not categorized.

These 361 type specimens are housed in 17 herbaria worldwide, with only 81 specimens (22%) deposited in 4 Chinese herbaria, while 280 specimens (78%) are held in 14 foreign institutions (Figure 4). The top three herbaria are Harvard University Herbaria (A and GH, with 82 and 16 specimens respectively), Institute of Botany, Chinese Academy of Sciences (PE, 75 specimens), and Royal Botanic Garden Edinburgh (E, 73 specimens), collectively holding 66% of all type specimens.

Of the 361 type specimens, 303 have collection dates. The earliest specimen was collected in 1857, currently recognized as *Sorbus rhamnoides* (a syntype of *S. sikkimensis* var. *oblongifolia* from Sikkim, India, housed at Staatliche Naturwissenschaftliche Sammlungen Bayerns). The most productive decade was 1900-1909 (113 specimens, one-third of the total), followed by 1930–1939 (42 specimens). Among 361 specimens, 358 have collector information, predominantly foreign collectors (81% of specimens). Among domestic collectors, the Qinghai-

Tibet Expedition Team collected the most type specimens (17 specimens of 3 species and 2 varieties), followed by T. T. Yu (11 specimens of 3 species and 1 variety).

Of 361 type specimens, 356 have detailed locality data: 290 from China, 42 from India, and \$ \$5 from other countries. Among Chinese specimens, 285 have provincial data, with Yunnan (102 specimens, 27 species, 5 varieties) and Sichuan (95 specimens, 21 species, 4 varieties) being the most represented, followed by Hubei (32 specimens, 10 species) and Tibet (31 specimens, 11 species, 1 variety). Other provinces have <10 specimens each.

2.3 Database Construction and Specimen Information Analysis

We constructed a comprehensive Chinese *Sorbus* database comprising 2,692 non-type and 361 type specimens, including scientific names, basionyms, coordinates, altitude, collection year, and herbarium information. Analysis of 2,412 specimens (73 species, 15 varieties) with collection dates shows that 1,540 specimens were collected during 1950–1989 (half the database), with 262 specimens collected after 2010 (Figure 6). Monthly collection data show year-round activity, peaking during June–September (1,060 specimens). Habitat analysis reveals diverse ecological types, including coniferous-broadleaf mixed forests (dominated by *Abies*, *Picea*, *Betula*, *Quercus*), alpine rhododendron and willow shrublands, temperate deciduous broadleaf forests (dominated by *Quercus mongolica* and *Fagus*), and evergreen broadleaf forests (dominated by Theaceae). Following the Institute of Geography, Chinese Academy of Sciences (1959) classification using 1,000 m, 3,500 m, and 5,000 m as boundaries for low, medium, high, and extremely high mountains, 2,107 specimens (73 species, 12 varieties) contain altitude data. *Sorbus* species span a wide elevational range, with *S. folgneri* showing the greatest amplitude (104–5,000 m). Among 46 species (including 2 varieties) represented by >10 specimens (totaling 2,002 specimens), six species occur across low, medium, and high elevations (*S. folgneri*, *S. koehneana*, *S. caloneura*, *S. hupehensis*, *S. alnifolia*, *S. hemsleyi*), 19 species (including 1 variety) are restricted to high elevations (>3,500 m), and 21 species (including 1 variety) inhabit medium (1,000–3,500 m) and low (<1,000 m) elevations.

3. Research Progress on Chinese *Sorbus* Plants

Our detailed analysis of specimen collection data has illuminated the research history and distribution patterns of *Sorbus* in China, confirming China' s status as the global center of *Sorbus* diversity and the predominant high-altitude distribution of these species. We now review current research across multiple disciplines.

3.1 Morphological Classification and Phylogenetic Studies

Since Linnaeus established *Sorbus* L. in 1753, the genus has posed taxonomic challenges due to extensive hybridization and polyploidy, leading to both broad-and narrow-sense concepts (Lindley, 1822). Infrageneric classification and interspecific relationships remain unresolved through both morphological and molecular approaches (Campbell et al., 1997). Recent morphological studies show promise: pollen morphology can differentiate species (Yang et al., 2019), leaf stomatal traits vary significantly among species (Xi et al., 2020), and karyotype analysis reveals diploid chromosome numbers of 34 (Chen, 2014; Peng, 2016). Leaf venation characteristics can differentiate pinnate-leaved species (Xiong, 2019) but not simple-leaved groups at sectional level, though they aid species identification within simple-leaved taxa (Tian et al., 2022). These morphological traits provide important taxonomic evidence for molecular phylogenetic studies.

Molecular phylogenetic studies remain limited. Lo & Donoghue (2012) provided a preliminary framework dividing *Sorbus* into two major clades without resolving intraclade relationships. Wang & Zhang (2011) used nuclear ITS sequences to analyze 46 species across 6 subgenera, supporting *Sorbus* as a natural monophyletic group. Li et al. (2017) employed four nuclear and one chloroplast marker to study 54 narrow-sense *Sorbus* species (representing all traditional sections, series, and subgenera), supporting the traditional two-subgenus classification based on fruit characters (*Sorbus* and *Albo-carmesinae*) but revealing five major molecular clades that conflict with traditional morphological groupings.

In summary, despite progress from morphological, cytological, anatomical, and molecular evidence, controversies persist regarding generic delimitation and systematic positions of most species. Future phylogenetic studies should sample more representative species across different taxonomic groups and geographic regions, using transcriptome-derived single-copy nuclear genes to construct both nuclear and cytoplasmic gene trees for a robust phylogenetic framework.

3.2 Conservation Genetics Research

China exhibits both high *Sorbus* species diversity and endemism, with 43 endemic species recorded in *Flora of China* alone. Multiple species face endangerment from environmental change and human disturbance, including *S. amabilis*, *S. astateria*, *S. obsoletidentata*, *S. tsinlingensis*, and *S. yuana*. Conservation genetic studies remain limited to a few species. Qiu (2019) used SSR and chloroplast markers to study 18 populations of *S. alnifolia*, finding high genetic diversity, frequent gene flow, and moderate interpopulation differentiation, attributed to broad distribution, strong ecological adaptability, and diverse pollination and seed dispersal mechanisms, with environmental heterogeneity driving differentiation. Zheng (2008) studied eight populations of *S. pohuashanensis* across four provinces, finding higher genetic diversity than congeners and low interpopulation differentiation, linked to breeding system, broad distribution, and ecological habits, while expressing concern about island-like distribution patterns and potential genetic drift. Liu et al. (2003) used RAPD markers to assess 13 populations of endangered *S. amabilis*, revealing low genetic diversity, poor adaptive capacity, and geography-associated genetic variation, attributed to evolutionary history, logging, natural disasters, and genetic drift in small populations.

These studies involve few species with limited sampling and require methodological updates. Future research should employ population genetics using multiple single-copy nuclear and cytoplasmic gene markers to analyze genetic diversity, population structure, and demographic history of endangered species. Combined with distribution data and protected area networks, suitability modeling and Marxan analysis should identify priority and gap areas for targeted conservation.

3.3 Chemical Composition and Medicinal Value

Sorbus species are rich in flavonoids, phenolics, and cyanogenic glycosides (Turumtay et al., 2017), exhibiting anticancer (Yu et al., 2017; Park et al., 2017), hypoglycemic (Bailie et al., 2016), anti-inflammatory and antimicrobial (Matczak et al., 2018), and antioxidant properties (Mikulic-Petkovsek et al., 2017; Wang et al., 2019). International research has examined >10 species (e.g., *S. aucuparia*, *S. commixta*), while domestic studies focus on *S. tianschanica*, *S. pohuashanensis*, *S. discolor*, *S. koehneana*, *S. alnifolia*, and *S. keissleri* (Bai et al., 2009; Ma et al., 2015; Li et al., 2017; Wang et al., 2019; Xu et al., 2020), with most other species unstudied. Chemical and medicinal constituents vary among species and plant parts (Xu et al., 2020), warranting expanded research across the genus for new drug development. Current studies primarily focus on constituent identification, with few investigating molecular mechanisms of biosynthesis and activity (Liu et al., 2019). Beyond limited gene fragment studies (Wang & Zhang, 2011; Li et al., 2017), transcriptomic and genomic research remains lacking.

3.4 Resource Development and Utilization

Domestic research on ornamental *Sorbus* species remains limited, with studies on *S. pohuashanensis*, *S. alnifolia*, *S. amabilis*, and *S. tianschanica* yet to yield widespread horticultural application. The primary challenge involves adapting high-altitude species to low-altitude environments, particularly summer high-temperature stress (Pei et al., 2021). High temperature constrains seed germination, growth, reproduction, and causes leaf scorch (Zhao et al., 2021; Pei et al., 2021). Recent transcriptomic and genomic studies have begun elucidating molecular regulatory networks underlying high-temperature responses in *S. pohuashanensis*, identifying stress-related genes to support introduction of alpine species (Pei et al., 2021). Preliminary surveys indicate >10 ornamental species each in Sichuan and Tibet, but successful introduction to low-altitude areas remains the key constraint (Li et al., 2019). Building on molecular network studies (Pei et al., 2021), we must deepen investigations and combine traditional and molecular breeding to successfully introduce these valuable species into urban and landscape settings.

4. Summary and Outlook

Sorbus represents a taxonomically challenging genus characterized by widespread hybridization, polyploidy, and apomixis (Ďurkovič et al., 2011). Frequent hybridization and polyploidization drive ongoing evolution and speciation (Robertson et al., 2010) while complicating taxonomy. Based on herbarium analysis and literature review, we recommend prioritizing the following research areas.

4.1 Strengthening Specimen Collection Standards and Accelerating Type Specimen Digitization

We urge relevant authorities to establish field collection standards to ensure specimens are scientifically "valid" and usable. Only 24% of *Sorbus* specimens are "valid," a common issue across taxa, partly due to the lack of unified national collection standards. We also call for accelerated digitization of small-to-medium herbaria and 派遣 researchers to foreign institutions rich in Chinese type specimens to expedite digitization. Type specimens are crucial for scientific research (Shen et al., 2010; Yang, 2012; Lin et al., 2017), yet only 22% of Chinese *Sorbus* type specimens are housed domestically, a pattern common across plant groups that must be addressed through accelerated digitization.

4.2 Conducting Comprehensive Surveys of Wild *Sorbus* Resources

Most provinces lack systematic *Sorbus* surveys. Only Gansu (Yao & Yao, 2015), Qinghai (Sun & Sun, 2015), Sichuan (Li et al., 2019), and Tibet (Pan et al., 2007) have conducted partial surveys with insufficient coverage and content, lacking distribution, habitat, population, and community data critical for introduction and utilization. We propose comprehensive surveys prioritizing the diversity and endemism center (eastern Tibet, northwestern Yunnan, southwestern Sichuan), which harbors 50% of Chinese species, followed by Hubei, Hunan, Guangxi, and Shaanxi, then other provinces. Standardized protocols should document distribution patterns, habitat conditions, natural regeneration, phenotypic diversity, and variation.

4.3 Prioritizing Research on Hybrid Speciation and Resource Development

Persistent, frequent hybridization (Ludwig et al., 2013; Uhrinová et al., 2017) and polyploidization generate high species diversity, with many new taxa confirmed as hybrid derivatives (Robertson et al., 2004, 2010; Uhrinová et al., 2017). Understanding hybridization is key to plant evolution (Robertson et al., 2004), yet processes are complex, involving repeated backcrossing (Robertson et al., 2004). Research should address hybridization frequency, direction, parental identity, and environmental conditions. Complex ploidy levels create varied breeding systems: diploids are outcrossing and self-incompatible; triploids are apomictic and self-incompatible; tetraploids are apomictic and self-compatible

(Ludwig et al., 2013). Triploids' self-incompatibility necessitates interspecific pollen transfer, creating opportunities for new hybrids and serving as excellent material for studying self-incompatibility mechanisms. Southwestern China, with its coexisting ploidy levels and ongoing hybridization, is ideal for investigating these processes.

The key constraint for *Sorbus* utilization is the high-altitude distribution of most species. Introduction to low-altitude regions requires overcoming summer high-temperature stress, which affects reproduction, growth, and germination. Recent studies have begun exploring molecular mechanisms of high-temperature adaptation (Ding et al., 2003; Li et al., 2018). Pei et al. (2021) used RNA sequencing to characterize the molecular regulatory network of high-temperature response in *S. pohuashanensis*, providing a foundation for introducing alpine species. Rapid molecular biology advances offer unprecedented opportunities to elucidate mechanisms underlying high-temperature responses and adaptation, research that should be intensified.

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