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The wild relatives of grape in China: Diversity, conservation gaps and impact of climate change

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ABSTRACT

China is one of the major diversity centres of grape (*Vitis* spp.) and is therefore one of the most abundant sources of *Vitis* germplasm in the world. Grape wild relative species (GWRs) represent a potentially important source of valuable traits for the improvement of cultivated grape varieties and have significant characters for resistance to biotic and abiotic stress factors. We studied the ecogeographic diversity of GWRs, conservation gaps and impact of climate change on GWRs in China, based on a wide range of distribution data sourced from germplasm and herbarium specimens, field surveys and other literature. Results show that there are 39 species, 1 subspecies and 14 varieties of GWRs native to China and that 19 species and 9 varieties are the closest wild relatives to cultivated grape according to the Taxon Group Concept. GWRs are distributed in nearly all provinces in China except for Xinjiang, but they are particularly abundant in Jiangxi and Hunan provinces. The richest regions for GWRs are the Qinling, Daba, Wuling, Nanling and Wuyi mountains. Around 22% of GWR species are found in natural reserves (NRs) and are well protected, but 15 species are not found in NRs and require further strengthening of both protection and collection. The potential distribution of GWRs at the present and predicted future climate was compared using BIOCLIM. The results showed that simulated current distributions matched actual distribution ranges. Under the future climate scenario with doubled CO_2 concentration, suitable areas for continued survival of 21 GWRs could be reduced. Our results will therefore be extremely valuable for the development of a complementary conservation strategy for *Vitis* in China.

1. Introduction

Grapes are economically among the most important fruit in the world, there are 8000–10,000 grape cultivars existing worldwide today (Ramezani et al., 2009), and most production cultivars are derived from only one species *V. vinifera*, because of its high berry qualities. However, *V. vinifera* is highly susceptible to fungal diseases, which causes heavy losses in grape production (Wan et al., 2008a). On the other side, *V. vinifera* had narrow genetic background, grape breeders are making efforts to use wild germplasms to improve resistance of cultivars and to breed new resistant cultivars (Alleweldt and Possingham, 1988; Brown et al., 1999).

China is one of the major centres of diversity of grape (*Vitis* spp.) and is therefore one of the most abundant sources of *Vitis* germplasm in the world. Grape wild relative species (GWRs) are a potentially important source of valuable traits for the improvement of cultivated grape varieties and have significant characters for resistance to biotic and abiotic stresses such as cold, drought, pests and diseases. Grape breeding has proved that it is important to use wild germplasm resources carrying a range of resistance genes, to counter the shortage of the resistance genes within the cultivated species. Currently, many elite cultivars have been developed using GWRs such as *V. amurensis*, *V. heyneana*, *V. pseudoreticulata*, *V. davidii* and *V. bryoniaefolia*. In addition, GWRs and their hybrids have been used for wine production in China (Wan et al., 2008b).

With the environment pollution and ecoystem degradation of recent years, many wild animals and plants are endangered or faced with extinction and GWRs are no exception. The loss of a species means the loss of the genes that it carries. It is recorded in

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China Species Red List that *V. yunnanensis, V. wenchouensis* and *V. hui* are in serious danger with fewer than 5 remaining populations subjected to continuing decline. There is only one known remaining site for both *V. bashanica* and *V. mengziensis* and so their populations are under very serious threat (Wang and Xie, 2004).

Changes in climatic conditions on earth, including global warming, are no longer contested. According to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change (IPCC), global mean surface air temperature has increased approximately 0.8 °C since the start of 20th century, and will continue to rise between 1.1 and 6.4 °C by the end of this century (Betts and Hawkins, 2014), flooding and droughts will be more frequent and severe, some soils will degrade, and climatic extremes will be more likely to occur (Jones et al., 2007; Ainsworth et al., 2008). As some species have already responded to a temperature increase of 0.6 °C, it is clear that more substantial effects on species and ecosystems will occur in the future (Root et al., 2003), especially for those species with a restricted distribution pattern (Midgley et al., 2002) and also CWRs (Maxted et al., 2013).

Predicting the current or future distributions of species has principally been conducted using bioclimatic models that assume the climate ultimately restricts species distributions. These models summarise a number of climatic variables within the known range of a species, thus generating a 'bioclimatic envelope'. The models can then be used to: (a) identify the species current potential distribution, that is, all areas with climatic values within the species bioclimatic envelope and (b) assess whether these areas will remain climatically suitable under future climate scenarios (Pearson and Dawson, 2003).

In China, there are 3 national repositories for grapevine (Zhengzhou, Zuojia and Taigu), which specialize in grape germplasm collection, conservation, as well as identification and utilization. Nine species have been protected in national repositories, but they are all common species (Ren et al., 2012). Natural reserves play an important role in protecting wildlife including GWRs, but research on the distribution of GWRs has been restricted to certain regions with truly systematic studies absent in past years (Zuo and Yuan, 1981). The number of GWRs in China is unknown together with their geographical distribution. It is therefore not clear whether GWRs are receiving adequate protection. Knowledge is absent on which districts have the richest grape resources and which species are endangered. Furthermore, there is no reporting undertaken on the impact of future climate change on the GWR resources. Such information is crucial for research, protection and usage of the GWRs in China and indeed globally.

The present study aims to investigate (1) the number of GWRs in China and their relation with cultivars for priority utilization; (2) the distribution and conservation gaps of GWRs in China; (3) the impact of future climate change on GWRs in China.

2. Materials and methods

2.1. Data collection

2.1.1. Species data

We have set up a distribution database of the GWRs in China by surveying various sources of information: (1) 155 specimen records of wild grapes since 1990 from the major domestic specimen museums through the Chinese Virtual Herbarium (CVH, http://www.cvh.org.cn); (2) Flora of China (VITACEAE) (Ren and Wen 2007), as well as valid provincial and regional floras, such as Flora of Yunnan (Kunming institute of Botany, Chinese academy of science, 2000), Flora of Zhejiang (Flora of Zhejiang editorial board, 1993), A checklist of Vascular Plants of Guangxi (Zuo and Liu, 2010) and Dabieshan sylva (Zi and Zhang, 2006); (3) the scientific survey reports on natural reserves (NRs) in recent years, totaling 380 related reports on domestic NRs covering all mainland provinces in China except Hongkong, Macao and Taiwan areas; (4) the research summaries on wild *Vitis* published in various academic journals and the relevant literature of the wild *Vitis* records; and (5) recent field investigations in Henan, Hunan, Guangxi, Zhejiang, Jiangxi and Tibet.

Subsequently, we cross-checked, verified and where necessary corrected the species names and geographic references according to Chinese Ampelography (Kong, 2004). Controversial species are not included in the database.

Ultimately, we obtained 2675 unique localities for 38 species 1 subspecies and 13 varieties of GWRs that were then used for further analysis.

2.1.2. Climate data

The climate data used in this research are based on the gridded spatial database available from the World Climate website (http://www.worldclim.org/). The climate database, with 30 arc-second resolution (ca. 1 km at the equator), was developed using monthly mean temperature and monthly precipitation at climatic stations (ca. 7000 stations for temperature and 20,000 stations for precipitation) between 1950 and 2000 (Hijmans et al., 2005). This database is more accurate and precise, as it used altitude as one of parameters when interpolating the climatic variables, compared to the 2-dimensional interpolation used in previous estimations (Hijmans et al., 2005).

2.2. Diversity analysis

Taxonomical review was undertaken of all GWR species related to the cultivated grape, and analysis of their relationship to the domesticated species using the Taxon Group Concept established by Maxted et al. (2006).

2.3. Distribution, richness and gap analysis

The database in Section 2.1.1 mainly consists of species names, collection localities (with longitude and latitude), habitats and altitudes. For some specimens localities and published distributional data had only county names rather than detailed information of location such as geographic coordinates. Therefore it was necessary to determine each locality with latitude and longitude coordinates by referring to The Gazetteers of China (Department of Gazetteer, Institute of Topographic Science, National Survey and Drawing Bureau, 1983), which has been successfully used for analogous analyses (Lei et al., 2003; Xu et al., 2008; Wang and Ni, 2009; Wu and Zhou, 2012). There are 23 provinces, 5 autonomous regions and 4 municipalities in China. A province is equivalent to an autonomous region and municipality in terms of administrative level; thus we refer to all provinces and autonomous regions as "province" for the convenience of discussion (Huang et al., 2011). We have used ARC GIS 10.0 software (ESRI) to describe the geographical distribution of GWRs, and the number of GWRs distributed in each province in China.

Using DIVA-GIS 5.4 software (Hijmans et al., 2001), we produced a 1×1 decimal degree size grid map and statistic of the species richness in each grid. By using GIS overlap techniques we produced the distribution map in detail so as to show the regions where more species are distributed and hence the distribution centre of GWRs.

Based on the geographical distribution of GWRs, using ARC GIS 10.0 software (ESRI), we identified 'gaps' in *ex situ* conserved germplasm by comparing the layer of GWRs distribution with