

## Juan Wang

### ADDRESS:

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### EDUCATION:

2007-present Ph.D. in Molecular Ecology (expected in Jul.). State Key Laboratory of Grassland Farming System, School of Life Science, Lanzhou University

2003-2007 B.S. in Biological Science. School of Life Science, Northwest Normal University

### RESEARCH EXPERIENCE:

07-present Graduate Research

Advisor: Professor Jianquan Liu

1) Genetic variation within and between populations of a desert poplar (*Populus euphratica*) revealed by SSR markers

We investigated the within-population and long-distance separated population diversity *Populus euphratica* Oliv. in northwest China using eight pairs of simple sequence repeat markers. Our results reveal that this species has high overall genetic diversity. However, there was a high level of genetic diversity within the species and low genetic differentiation between populations. There was no distinct correlation between geographical distributions and genetic variation. The recent fragmentations of this species due to anthropologic and environmental effects resulted in its endangered status.

2) Genetic differentiation and delimitation between ecologically diverged *P. euphratica* and *P. pruinosa*

The fixed genetic differences between ecologically divergent species were found to change greatly depending on the markers examined. With such species it is difficult to differentiate between shared ancestral polymorphisms and past introgressions between the diverging species. In order to disentangle these possibilities and provide a further case for DNA barcoding of plants, we examine genetic differentiation between two ecologically divergent poplar species, *P. euphratica* Oliver and *P. pruinosa* Schrenk using three different types of genetic marker. We genotyped 290 individuals from 29 allopatric and sympatric populations, using chloroplast (cp) DNA, nuclear (nr) ITS sequences and eight simple sequence repeat (SSR) loci. Three major cpDNA haplotypes were widely shared between the two species and between-species cpDNA differentiation ( $F_{CT}$ ) was very low, even lower than among single species populations. The average SSR  $F_{CT}$  values were higher. Bayesian clustering analysis of all loci allowed a clear delineation of the two species. Gene

flow, determined by examining all SSR loci, was obvious but only slightly asymmetrical. However, the two species were almost fixed for two different nrITS genotypes that had the highest  $F_{CT}$ , although a few introgressed individuals were detected both in allopatric and sympatric populations. The two species shared numerous ancestral polymorphisms at cpDNA and a few SSR loci. Both ITS and a combination of nuclear SSR data could be used to differentiate between the two species. Introgressions and gene flow were obvious between the two species either during or after their divergence. Our findings underscore the complex genetic differentiations between ecologically diverged species and highlight the importance of nuclear DNA (especially ITS) differentiation for delimiting closely related plant species.

### 3) Population genetic evidence for ecological divergence between *P. euphratica* and *P. pruinosa*

Ecological speciation assumed that diverging species may differentiate depending on the selection pressure of the sampled loci. This assumption therefore indicates that interspecific differentiation may vary greatly between the sampled loci with different selection pressure. Here we test this hypothesis by population genetic analyses of the only two recently diverged species of *P. euphratica* and *P. pruinosa*. We sampled 12 populations of the two species across their geographic ranges and used a recently developed neutrality test based on the Maximum Frequency of Derived Mutations to examine the demographic and selective histories of individual species, and Isolation-with-Migration analyses to study the joint history of the species and detect gene flow between them. These findings highlight the importance of the natural selection in reducing gene flow of two species and accelerating interspecific differentiation at certain genomic loci associated with ecological adaptations and reproductive isolations.

Projects include:

1. National Nature Science Foundation of China (NSFC)
2. The National Key Project for Basic Research
3. The Program for New Century Excellent Talents in the Ministry of Education in China (NCET-09-0446)

## HONORS AND AWARDS:

### Graduate

- 2011-2012 Second-class Award of Academic Forum Thesis
- 2011-2012 Excellent Graduate Student of Lanzhou University
- 2011-2012 Special Grade School Scholarship
- 2010-2011 School First-class Scholarship
- 2009-2010 School Second-class Scholarship

### Undergraduate

- 2007 Outstanding Graduates of 2007
- 2006-2007 Excellence Award of English
- 2006-2007 Academic Excellence Award
- 2005-2006 First-class Academic Excellence Award
- 2003-2004 Study Winning Prize

**PUBLICATIONS:**

## REFERRED JOURNAL ARTICLES:

1. **Juan Wang**, Zhijun Li, Qihong Guo, Guangpeng Ren, Yuxia Wu. Genetic variation within and between populations of a desert poplar (*Populus euphratica*) revealed by SSR markers. *Annals of Forest Science* 2011, 6, 1143-1149. (IF=1.441)

2. **Juan Wang**, Yuxia Wu, Guangpeng Ren, Qihong Guo, Jianquan Liu\*, Martin Lascoux. Genetic Differentiation and Delimitation between Ecologically Diverged *Populus euphratica* and *P. pruinosa*. *Plos One* 2011, 6(10): e26530. (\* corresponding author; IF=4.411)

## OTHERS

1. Qiang Qiu, Tao Ma, Quanjun Hu, Bingbing Liu, Yuxia Wu, Haihong Zhou, Qian Wang, **Juan Wang** and Jianquan Liu. Genome-scale transcriptome analysis of the desert poplar, *Populus euphratica*. *Tree physiology* 2011, 00, 1-10. (IF=2.292)

2. Wuxia Wu, **Juan Wang**, and Jianquan Liu. Development and characterization of microsatellite markers in *Populus euphratica* (Populaceae). *Molecular Ecology Resources* 2008, 8, 1142-1144. (IF=1.631)

3. Haiyan Xu, Dachuan Shi, **Juan Wang**, Tingting Xu and Yuxia Wu. Isolation and characterization of polymorphic microsatellite markers in *Cupressus chenggiana* S. Y. Hu (Cupressaceae). *Conservation Genetics* 2008, 9, 1023-1026. (IF=1.254)

**REFERENCES:**

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