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Growth patterns and genetic structure of *Populus euphratica* Oliv. (Salicaceae) forests in NW China – Implications for conservation and management

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ABSTRACT

To investigate the influence of groundwater and river dynamics on genetic diversity and clonal growth of *Populus euphratica* forests along the Tarim river system (Xinjiang Prov., China), we genotyped nine old stands in three study areas of various distance to the main river. Using seven microsatellite loci, 850 genotypes were found among 1701 analyzed trees, with 204 of these comprising at least two trees. Population genetic analyses revealed a low degree of genetic differentiation (D_{est} = 0.014, G_{st} = 0.005), and no restriction to gene flow between stands. The forests can therefore be described by the infinite island model of gene flow. Stands in the three study areas differed strongly in clonality: in area I 82% of all trees grew from root suckers, clones averagely comprised 10.5 ± 2.0 trees; figures in area II were 45% and clones of 4.5 ± 1.0 trees, respectively. Area III had the largest trees, but was almost non-clonal (less than 3% of all trees were root suckers). By measuring current ground water depth and reconstructing river courses over more than one century, the varying ground water supply was identified as the most likely reason for the different degree of clonal growth. Neither survival nor lifespan of a stand depends on clonal growth. In the harsh environments inhabited by *P. euphratica*, the most important function of clonal growth may be the enhanced reproductive impact of large clones.

1. Introduction

In woody plants, clonality is often associated with harsh, resource-poor, or disturbed habitats. It is assumed to be an effective strategy to overcome environmental limitations by enhanced exploitation of resources or the ability to regenerate from damage (Peterson and Jones, 1997). The active zone of riparian lowlands with the frequent turnover of the floodplain area through river migration and meandering presents such a highly dynamic and frequently disturbed habitat (Amoros and Bornette, 2002; Hughes, 1997; Ward et al., 2002).

A lot of research has been directed at questions of succession and stand development of riparian forests in reaction to river dynamics (Dykaar and Wigington, 2000; Friedman and Lee, 2002; Kupfer and Malanson, 1993; Robertson, 2006; van Pelt et al., 2006, and others). The genetic structure within populations of both clonal and non-clonal forest trees in riparian environments also attracted a lot of attention (Arens et al., 1997; Chenault et al., 2011; Cole, 2005 and references therein, Comtois et al., 1986; Douhovnikoff et al., 2005; Legionnet et al., 1997; Rathmacher et al., 2010). However, only few studies address clonal growth patterns and the resulting genetic structure of populations in dependence of landscape history (Barsoum, 2002; Barsoum et al., 2004). In contrast to non-clonal species, spatial and genetic population structure of clonally propagating plants is not only a result of self thinning and succession, but also of the amount of clonal growth and therefore becomes more complex.

Using a set of seven SSR primers, we studied genetic structure and clonal growth patterns in *Populus euphratica* Oliv. (Euphrates poplar) in northwestern China. *P. euphratica* inhabits riparian ecosystems in arid regions from Morocco over North Africa to Central Asia, China, and India. In Asia, the species seems to be only locally distributed in the west (e.g., Peper et al., 2010) whereas it forms extensive woodlands called Tugai forests in the eastern part of its distribution range (Wang et al., 1996). This poplar is a typical pioneer species. In our study area, trees flower in mid-April. Seeds release starts at the end of July; usually the peak of seed release coincides with the annual high flood. Germination depends on wet and exposed sites found at river banks. Seedlings first develop long taproots to keep track with the declining ground water. Clonal growth by root suckering sets in when the plants reach an age of 11–15 years and root suckers bridge distances up to 40 m (Wiehle et al., 2009). As an obligate phreatophyte the plants need constant access to ground water (Gries et al., 2005). Stands die off when ground water drops below 10–13 m (Thevs, 2005). Despite being a pioneer species, *P. euphratica* is never replaced by later succes-

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sional species throughout its entire life cycle (Thevs et al., 2008a); the stands remain monospecific. Euphrates poplar forests are of great importance for plant and animal life, constitute a major natural resource for the local communities and provide ecosystem services such as landscape preservation, wind protection, and stabilization of moving sand, soil, and riverbanks. These services contribute to the prevention of desertification and the Chinese government therefore declared the conservation of *P. euphratica* forests along the Tarim river one of eighteen key projects in their implementation of the UN Convention to Combat Desertification (CCICCD, 1996). Despite of this, forests are under high pressure through habitat destruction, logging, grazing, and diversion of water for irrigation (Thevs et al., 2008b).

Our goals were (a) to determine the genetic structure of selected stands of *P. euphratica* within three regions displaying dramatically different structure regarding density and spatial distribution of trees, (b) to test whether these partially scattered and isolated stands are still reproductively connected and (c) to relate different patterns to environmental conditions. We discuss our findings with regards to conservation and management of the species.

2. Materials and methods

2.1. Study area and stand mapping

The study region is situated at the northern fringe of the Taklimakan desert, a large hyperarid basin in northwestern China (Xinjiang Province, see Thevs et al. (2008b) for detailed description). The main river, Tarim, and its tributaries are supplied with melt water from the mountains surrounding the Tarim basin (Tian-Shan in the North, Pamir in the West, Kunlun Mts. and Tibetan Plateau in the South). Due to the resulting annual floods, but also the high sediment load the river carries (up to 193 kg/m^3, Gentelle, 1992), the Tarim constantly moves its bed, or seeks a new one during the annual floods. These reach their maximum in late July to early September and make up for about 75% of the annual water runoff. With a long-term average below 50 mm per year, the contribution of precipitation is negligible.

Along the Tarim River and the Qayan River, a tributary to the Tarim, we mapped all trees in three areas (Table 1), all representing old-growth stands of *P. euphratica* but each with a different situation regarding ground water supply. All areas are situated in the Tarim Huyanglin Nature Reserve at the middle reaches of the river, southwest of Xinjiang's capital Urumqi (Bügür County, near Yengi Bazar, Fig. 1).

Within those areas nine plots for genotyping were established: area I (plots Ing5: 41°13′51″N, 84°12′18″E; Ing6: 41°14′01″N, 84°12′07″E and Ing11: 41°13′45″N, 84°11′57″E), area II (plots Ing8: 41°15′12″N, 84°13′03″E; Ing9: 41°15′43″N, 84°15′48″E and Ing10: 41°15′20″N, 84°13′53″E) and area III (plots YimB: 41°20′54″N, 84°24′42″E; YimE: 41°20′38″N, 84°24′40″E and YimF: 41°20′23″N, 84°25′18″E). Care was taken to choose only stands that did not show excessive logging or destruction through construction or agriculture.

All standing, dead and living trees and saplings reaching at least breast height were mapped with a Trimble R3 differential GPS system (horizontal precision 0.1–0.3 m) during flowering time (end of March to beginning of April) in the years 2005–2010. For all standing trees, diameter at breast height (dbh) was recorded. All flowering trees were sexed by visual examination of the inflorescences. Stands were checked twice within several days to meet the peak of bloom in most trees. Trees were revisited 2–4 weeks later to collect leaves for genetic analyses and classify vitality of all standing trees according to a six-part vitality scale: (1) at least 75% of crown volume with foliage, foliage dense; (2) 50–75% of crown volume alive, if above 75%, foliage scattered; (3) less than 50% of crown with leaves; (4) less than 25% of crown alive, trunk partially dead; (5) dead trunk, whole crown without leaves, only trunk sprout alive; (6) tree completely dead.

Ground water depth (GD) was recorded with a machine driven soil borer during baseflow (prior to the annual flood and therefore presenting the lowest ground water table) in July 2004 for each area. In addition, this figure was confirmed by comparing heights of the nearby Qayan river bed with ground height by differential GPS measurements (fixed mode). The closed capillary fringe above the ground water table was defined as ground water depth.

2.2. Genotyping

To reduce the amount and cost of laboratory work, we chose the grid-based approach proposed by Suzuki et al. (2004) designed to reveal a maximum number of genets with a minimum number of samples. In this approach, the stand is covered by a grid of variable size, and for each cross of grid lines the nearest tree is chosen for analysis. Grid size, i.e. distance between lines, was chosen to yield about half of all mapped trees. We genotyped 390–695 trees per site, resulting in a total of 1701 analyzed trees. In the field, leaf samples of all living trees were collected, air dried, and stored on silica. DNA was isolated using the Invisorb Spin Food Kit II (Invitek) following the manufacturer's protocol with the following modifica-

Table 1
Overview of the three investigated areas with nine genotyped stands of *Populus euphratica*.

Study area	I	II	III	Total
Plot	Ing5, Ing6, Ing11	Ing8, Ing9, Ing10	YimB, YimE, YimF	
Mapped area (ha)	22.0	6.4	82.0	110.4
Number of mapped trees	1400	899	721	3020
Trees alive	1219	776	444	2439
Trees flowering (% of living)	65.6	41.1	94.0	66.9
Density (living trees/ha)	52	139	4	
Mean dbh (cm, living trees)	43	23	72	
Trees ⩽ 10 cm dbh (%)	17.2	23.5	0. 8	
Trees ⩽ 1 cm dbh (%)	4.4	9.8	0.2	
Mean vitality (all trees)	4.04	4.21	4.51	
SD	1.04	0.96	1.37	
Number of genotyped trees	695	616	390	1701
Number of genotypes	126	339	385	850
Number of clones	94	98	12	204
Clonality C	0.87	0.46	0.04	
Clone size	10.5 ± 2.0	4.5 ± 1.0	2.5 ± 1.0	