

ISSN : 2347-503X

Research Chronicler

International Multidisciplinary Research Journal

Vol II Issue III : March 2014

Editor-In-Chief

Prof. K. N. Shelke

www.research-chronicler.com

Research Chronicler

A Peer-Reviewed Refereed and Indexed International Multidisciplinary Research Journal

Volume II Issue III: March – 2014

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An Analysis of Habitat Fragmentation and Recent Bottlenecks Influence**Mr. Chandan Bharti Mishra***Research Scholar, Department of Botany, University of Delhi (Delhi), India***Abstract**

The monoecious, animal-pollinated shrub *Brongniartia vazquezii* is an endemic and endangered species of the tropical dry forests of Central Mexico. Deforestation of the steamy dry forest has fragmented the habitat and resulted in the isolation of the only four extant populations of *B. vazquezii*. In this study, we assessed the genetic consequences of habitat fragmentation by comparing the genetic variability (allelic richness and expected mean heterozygosity, H_e), gene flow and population differentiation in both adult (before fragmentation) and seedling (after fragmentation) populations. As a study species we display that the genetic diversity (number of alleles per locus, expected heterozygosity) of populations living within floodplain water bodies is not severely impoverished compared to the genetic diversity within the main river channel. Central European salt habitats are mainly restricted to the maritime coast but scattered occurrences can also be found inland. In inland habitats, human activities have caused losses and reductions in the size of natural salt sites but have also created new anthropogenic habitats around potash mining dumps colonized by halophytic species in the last 30 yr. We aimed to investigate the effects of bottlenecks, isolation, and current habitat fragmentation on the genetic variation of a species commonly growing in these special habitats

Keywords: Deforestation, genetic, species

Rivers are multifarious ecological systems because of the diversity of aquatic habitats within the river itself and adjacent wetlands (Petts 1990; Mitsch and Gosselink 2000). These associated riparian ecosystems consist of a diverse mosaic of habitats and are considered hotspots of biodiversity (Toner and Keddy 1997; Bornette et al. 1998). Riparian ecosystems are characterized by floodplain water bodies of different size, age and isolation which are connected to the main river by seasonal floodings. Throughout the world, riparian ecosystems are under pressure from human activities

(Bravard et al. 1986).[1] In Europe riparian ecosystems have vanished completely or shrunk to a few scattered leftovers along the Danube, Elbe, Rhine, Rhone and Oder (Brookes 1988; Weigers et al. 1990). Recently, programs were launched to investigate the biodiversity and ecological function of these remnants and to develop action plans for long-term conservation of these endangered ecosystems (Maitland and Morgan 1997; Trockner and Schiemer 1997). [3]

Population genetics theory has provided the framework to explore the potential effects of

habitat fragmentation on the genetic structure of populations (Young *et al.*, 1996). Populations in fragmented habitats are expected to become differentiated due to founder effects, genetic drift and increased inbreeding, and a reduction in gene flow among populations (Templeton *et al.*, 1990).

Habitat inducement and epigenetic influences in genetic diversity

There is always a possibility of other biologically influenced dispersal factors to influence the enrichment of habitat fragmented clones. These could interfere with wind and pollinator movements (Li *et al.*, 2009) causing modernization of clones. This possibility was evidenced by an exceptionally low level of gene flow between two populations of *L. chinensis* (Zhang *et al.*, 2009). However, it was clear that physical and/or biological isolation were identified as the most significant factors in causing differentiation of these populations. It was interesting that although habitat heterogeneity like soil pH might not be correlated with genetic variation intrapopulation of the same ecotype, a dendrogram of between these populations constructed by the UPGMA method (Sneath and Sokal, 1973), [5] based on a similarity matrix of AFLP data and calculated according to the Jaccard index showed a close link between the clones grown in the same abiotic conditions (Zhang *et al.*, 2009). Therefore, the possibility of habitat inducement can not be ruled out in causing heterogeneity in stressful abiotic conditions of varied salinity/alkaline which have been known to cause heritable epigenetic variations in plants (Zhang *et al.*, 2010, Kimatu, 2010). Recent studies by Kimatu,

2011, suggested that narrowed genetic base due to inbreeding could contribute to morphological variations and ultimately lead to pathogenic attacks to plants. Such eventuality can more be amplified by habitat fragmentation and possible epigenetic variations leading to greater genetic diversity.

Does habitat fragmentation necessarily affect genetic diversity?

Habitat fragmentation has been found to alter the structure, distribution, and functioning of natural ecosystems (Saunders *et al.*, 1991). This has made many researchers to make the general conclusion that habitat fragmentation definitely affects the genetic diversity. Hence, many habitat fragmentation studies have been working with the hypothesis that it causes erosion of genetic variability and an increase and interpopulation genetic divergence in plant populations. This could be due to the increase in random genetic drift, inbreeding, and reductions in gene flow (e.g. Young *et al.*, 1996; Sork *et al.*, 1999; Lowe *et al.*, 2005).[12] Furthermore, the genetic diversity and variation of populations is expected to be reduced due to genetic bottlenecks which tend to lower the proportion of polymorphic loci and a reduction in the number of alleles per locus within habitat fragments (Nei *et al.*, 1975; Ellstrand & Elam 1993; Young *et al.*, 1996).

Methods

The study was conducted during 1997-98 at the Sierra de Huautla Natural Preserve (CEAMISH-UAEM), which is located in the State of Morelos (99_05_ to 99_08_W; 18_29_ to 18_32_N) in the central region of

Mexico. The vegetation is tropical dry forest (Rzedowski, 1978), highly fragmented as a result of recent human activities (roads, cultivated fields, ranching, etc.). The physiognomy of the forest is produced by a marked climatic seasonality. Most plants lose their leaves during 5–7 months of the dry season. The climate is warm subhumid (the driest of the sub-humid climates; García, 1988). The precipitation/hotness ratio is less than 43.2, and less than 5% of the rainfall occurs in winter. Mean annual temperature and precipitation for the study site are 24.5°C and 1039 mm, respectively (García, 1988).[15]

Sample Collection

Tissue sampling was done in the four extant populations of *B. vazquezii* in the Valle de Vázquez, Morelos, Mexico. Populations are separated by distances of 1.3–7.5 km. The sampled populations of *B. vazquezii* encompassed the total geographic range of the species (Table 1). Full-expanded young leaves were collected from 40 reproductive individuals in each population (adult populations). Simultaneously, seeds collected in the field were germinated in environmentally controlled conditions (humidity 50%, temperature 25°C and constant light) (seedling populations). Leaves of seedlings aimlessly chosen (*c.* 40 individuals per population) were used for electrophoretic analysis as in the case of adult individuals.

Discussion

In spite of the short geographic distances that separate the extant populations of *B. vazquezii*, low but significant genetic differentiation and high inbreeding were

detected. Although loss of genetic diversity and a reduction in gene flow are expected in fragmented or highly structured populations (Young *et al.*, 1996), our results do not support these expectations. Species with restricted geographical range, like *B. vazquezii*, do not necessarily have low genetic diversity. High gene diversity has been reported for the rare Hawaiian fern *Adenophorus periens* (Ranker, 1994), the endangered *Caesalpinia echinata* (Cardoso *et al.*, 1998), the narrow endemic fern *Polystichum otomasui* (Maki and Asada, 1998), an endangered pine (Delgado *et al.*, 1999), the rare Mexican pinyon pine (Ledig *et al.*, 1999), the endemic *Agave victoriae-reginae* (Martínez-Palacios *et al.*, 1999), in three endemics from Florida (*Eryngium cuneifolium*, *Hypericum cumulicola* and *Liatris ohlingerae*; Dolan *et al.*, 1999), in the annual endemic of Florida *Warea carteri* (Evans *et al.*, 2000) and in the endemics *Iris cristata* and *I. lacustris* (Hannan and Orick, 2000). In *B. vazquezii*, seedlings had higher heterozygosity than adult populations. Thus, despite being narrowly distributed and fragmented, *B. vazquezii* shows no signs of a reduction in genetic diversity, suggesting that gene flow may be mixing a formerly structured population (see Levin and Kerster, 1974; Young *et al.*, 1996) Gene flow amid populations is the only explanation for finding alleles in low frequencies at the seedling stage and their absence in the adult population (e.g. allele *c* of *Pgi* in population 2 can only derive from populations 1 or 3; Appendix). Accordingly, values of *Nm* suggest high gene flow among populations (cf. Table 4). However, this result is not unexpected given the short

distances that separate the populations. Furthermore, the reduction in gene flow among fragmented populations might be lower if the plant populations are wind-dispersed or animal-pollinated, as in the case of *B. vazquezii*. For instance, fragmented populations of *Acer saccharum* showed increased gene flow compared with intact or pre-fragmented populations (Foré *et al.*, 1992; Young *et al.*, 1993). As this result is counterintuitive, it may be a consequence of the breakdown of the former population structure, which, in turn, can produce negative effects by putting in contact two differentiated gene pools through outbreeding depression or hybridization between locally adapted populations (Young *et al.*, 1996; Holsinger *et al.*, 1999; Lande, 1999). Yet, positive effects of this phenomenon may occur if it enhances the

replenishment of heritable variation lost from some populations by drift. It is not possible to affirm to what extent these two possibilities apply to *B. vazquezii*, but these hypotheses should be addressed in future studies of the genetic consequences of habitat fragmentation.

Conclusion

Our results indicate that gene flow is restricted among populations from inland salt sites and the Baltic Sea coast, presumably due to their isolation, small sizes, genetic bottlenecks and/or founder events. Patterns of allele division indicate some occasional genetic exchange among habitat types in the past. Anthropogenic salt sites may facilitate gene flow among inland salt habitats preventing endangered inland halophyte populations from genetic erosion.

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