Biochemical Systematics and Ecology 59 (2015) 12–21

Contents lists available at ScienceDirect

Biochemical Systematics and Ecology

journal homepage: www.elsevier.com/locate/biochemsyseco

Molecular genetic diversity and differentiation of populations of ‘somnus’ passion fruit trees (*Passiflora setacea* DC): Implications for conservation and pre-breeding

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ARTICLE INFO

Article history:
Received 19 June 2014
Accepted 13 December 2014
Available online 22 January 2015

Keywords:
ISSR
RGA
Genetic diversity
‘somnus’ passion fruit
Natural population

ABSTRACT

The ‘somnus’ passion fruit tree (*Passiflora setacea*) is native to the ‘Cerrado’ and ‘Caatinga’ biomes in Brazil and possesses agrobiological and commercial traits of interest. Studies examining the nature of genetic variability in natural populations are important for the utilization of these traits in conservation and breeding programs. In this study, we analyzed 12 populations of *P. setacea* from different locations distributed in three agro-ecological zones within the Bahia state of Brazil. Eleven ISSR primers and four pairs of RGA primers were used to assay 109 and 49 unique and reproducible loci, of which 108 (99%) and 49 (100%) were polymorphic. Although the level of genetic diversity in ‘somnus’ passion fruit trees was greater than that observed for other species of the same genus, preferential collection of certain populations, such as those located in the cities of Vitória da Conquista and Licinio de Almeida, is important when considering the fact that ‘somnus’ passion fruit trees occur in areas that are highly disturbed. This disturbance is primarily due to the deployment of pasture, predatory extraction and accelerated urban expansion. An analysis of molecular variance revealed a balance between the estimated genetic variation within and among populations. These data may be useful for developing strategies for preservation of this species in the Cerrado.

1. Introduction

The Passifloraceae family consists of 630 species organized in 18 genera (Vanderplank, 1996), among which the genus *Passiflora* is remarkable due to the number of species it contains and due to its economic value. Approximately 120 species from the *Passiflora* genus are found in Brazil; consequently, the country is considered one of the major centers of diversity for this genus (Faleiro et al., 2005), along with Colombia, Ecuador and Peru. In the *Passiflora* genus, aside from the commercial ‘yellow’ species (*Passiflora edulis* Sims f. *flavicarpa*) and ‘sweet’ passion fruit (*Passiflora alata* Curtis), there are at least 50 other species with potential commercial value (Vieira and Carneiro, 2004). According to Mezzalira et al. (2009), the global

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http://dx.doi.org/10.1016/j.bse.2014.12.020

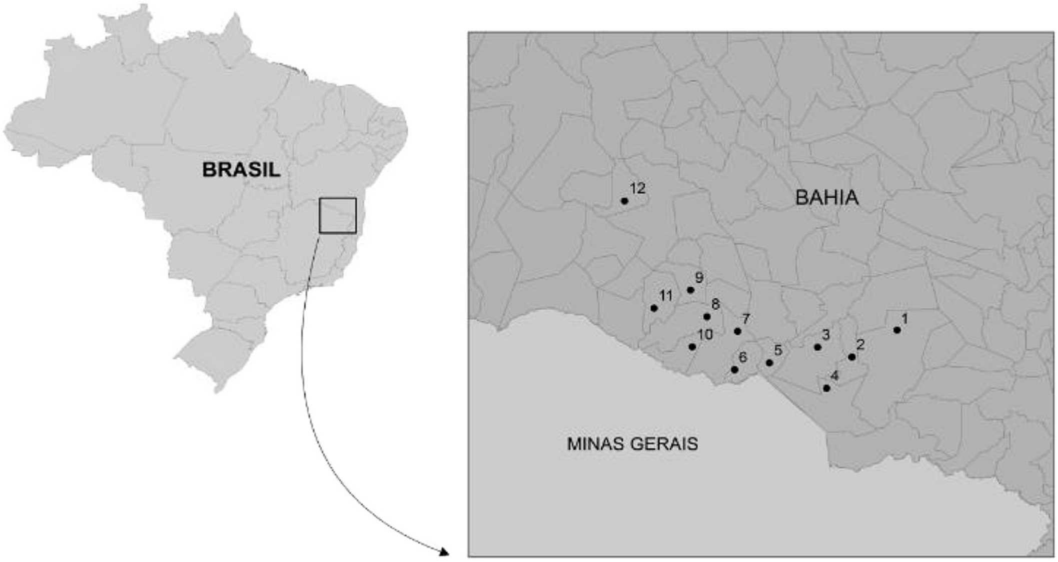

Fig. 1. *Passiflora setacea* sampling locations in the state of Bahia, Brazil. The circles indicate the sampled localities: 1(Vitória da Conquista = VC), 2(Belo Campo = BC), 3(Tremedal = TR), 4(Cândido Sales = CS), 5(Piripá = PP), 6 (Cordeiros = CO), 7(Condeúba = CD), 8(Jacaraci = JA), 9(Caculé = CA), 10(Mortugaba = MO), 11(Licinio de Almeida = LA), and 12(Igaporã = IG).

production of passion fruit in 2007 reached 664 thousand tons, with Brazil being the largest producer. According to IBGE (2009), approximately 400 thousand tons were produced on 47,000 ha. On the national scene, the state of Bahia had the highest production, producing 77 thousand tons over an area of 7800 acres (Roncatto et al., 2008).

Meletti et al. (2005) and Junqueira et al. (2005) have reported that some wild species of *Passiflora* have a significant potential to contribute to the genetic improvement of commercial passion fruit tree species, as they possess useful agro-biological characteristics, such as longevity, self-compatibility, better adaptation to adverse conditions, extended flowering periods, shorter androgynophores (which facilitate pollination by smaller insects), a higher concentration of chemical components that are of medicinal interest and resistance to diseases and pests.

With respect to the latter trait, ‘somnus’ passion fruit trees (also known as ‘sururuca’ [*Passiflora setacea* DC]), native to the Cerrado and Caatinga biomes in Brazil (Oliveira and Ruggiero, 2005), stand out because they show resistance to some diseases that affect the aerial parts of the plant, such as anthracnose, scab and septoria, and tolerance to passion fruit woodiness disease caused by the CABMV virus (Braga et al., 2006). As a result, this species constitutes an excellent source of genetic resistance to plant pathogens, allowing the incorporation of resistance genes into breeding programs through interspecific hybridization and the selection of ‘yellow’ or ‘sweet’ commercial passion fruit trees for introgression of resistance genes, as is already being performed in research programs developed by EMBRAPA Cerrado (Junqueira et al., 2008).

The accelerated devastation of native vegetation and habitat fragmentation has directly and indirectly caused the loss of genetic diversity due to environmental changes and/or extractive activities. According to Queiroz et al. (1992), in the case of *Passiflora* spp., the loss of the genetic diversity of wild species of the genus in semi-arid regions has been caused mainly by the formation of pastures, implementation of irrigation projects and production of energy for various activities; thus, the large, underexplored genetic diversity of the *Passiflora* genus is threatened by human actions.

Knowledge regarding the patterns of genetic diversity within a genus provides information for evaluating and using sources of wild germplasm. An understanding of the distribution of intrapopulation and interpopulation genetic variation can be an important factor not only for evolutionary biology but also for studies of conservation biology. As a result, reliable estimates of population differentiation may play a crucial role in understanding the connectivity between populations and may represent an important tool in the development of conservation strategies (Ballox and Lugon-Moulin, 2002).

Conservation of genetic diversity is a prerequisite for maintaining all levels of biodiversity and is a fundamental component of population sustainability (Namkoong et al., 2002). From this perspective, native species, such as ‘somnus’ passion fruit, deserve special attention because they possess a functional biodiversity with the potential for short-term use in breeding programs; however, their populations are unfortunately distributed in areas where they are not legally protected, and rapid population decline is occurring. The accurate analysis of genetic variation within and among remnant populations of this species is crucial for providing the basic information needed to establish conservation practices for specimens and/or populations that can be immediately used in breeding programs dedicated to Brazilian passion fruit cultivation.

In this work, polymorphisms of the ISSR and RGA loci were used to quantify genetic diversity and investigate its distribution in natural populations of ‘somnus’ passion fruit trees sampled from three agroecological zones located in the state of Bahia, Brazil. All the natural populations used in this study were located in anthropogenically affected areas. More specifically,