Chapter 5
The Genetic Diversity, Conservation, and Use of Passion Fruit (*Passiflora* spp.)

Carlos Bernard Moreno Cerqueira-Silva, Fábio Gelape Faleiro,
Onildo Nunes de Jesus, Elisa Susilene Lisboa dos Santos
and Anete Pereira de Souza

Abstract The characterization of genetic variability is important for conservation and biodiversity as well as the strategies and research techniques that contribute to such characterizations of flora, including the use of morpho-agronomic descriptors and molecular markers. In this chapter, we present and discuss the issues related to the genetic diversity of passion fruit (*Passiflora* spp.) to provide the reader with an updated view on the advances and challenges associated with the characterization, conservation and genetic diversity of the genus *Passiflora*. *Passiflora*, whose species are commonly known as passion fruits, stands out in the family Passifloraceae both for its number of species (approximately 520) and its ecological and economic importance. Passion fruits grow in various countries, and they are diversely represented in the Americas; in particular, Colombia and Brazil grow approximately 170 and 150 species of *Passiflora*, respectively. Despite increasing interest

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C.B.M. Cerqueira-Silva · E.S.L. dos Santos
Laboratório de Genética Molecular Aplicada, Departamento de Ciências Exatas e Naturais, Universidade Estadual do Sudoeste da Bahia (UESB), Itapetinga, Bahia, Brazil
e-mail: csilva@uesb.edu.br, cerqueirasilva1@yahoo.com.br

E.S.L. dos Santos
e-mail: elisalisboa@yahoo.com.br

F.G. Faleiro
Centro de Pesquisa Agropecuária do Cerrado, Empresa Brasileira de Pesquisa Agropecuária (Embrapa Cerrados), Brasília, Distrito Federal, Brazil
e-mail: fabio.faleiro@embrapa.br

O.N. de Jesus
Centro Nacional de Pesquisa em Mandioca e Fruticultura, Empresa Brasileira de Pesquisa Agropecuária (Embrapa Mandioca e Fruticultura), Cruz das Almas, Bahia, Brazil
e-mail: onildo.nunes@embrapa.br

A.P. de Souza (✉)
Centro de Biologia Molecular e Engenharia Genética, Departamento de Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas (UNICAMP), Campinas, São Paulo, Brazil
e-mail: anete@unicamp.br

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in this genus, genetic characterization, and breeding programs remain modest, especially considering the number of species not yet studied. Because almost all passion fruit diversity estimates derive from accessions maintained in germplasm banks using ex situ conservation to reduce the loss of species genetic variability, the scientific community must increase the number of these accessions. In addition, an urgent need exists for estimations of the diversity of natural populations and expanded analyses of passion fruit accessions present in germplasm banks, to provide more realistic estimates regarding the diversity of *Passiflora* and its representation in germplasm banks, both for conservation and biodiversity.

Keywords Conservation and management of biodiversity · Ex situ conservation · Genetic variability · Molecular markers · Passifloraceae

5.1 Introduction

5.1.1 The Characterization, Conservation, and Use of Biodiversity

Biodiversity is the assemblage of all genes, species, and ecosystems present in a specific area or on the planet, where diversity is the result of evolutionary processes (Nass 2011; Frankham et al. 2008). Studies devoted to characterizing the components of biodiversity are justified by the importance and ecological interest of their potential and immediate use by humans (Nass 2011), especially when certain specimens are known biological resources (or, more specifically, genetic resources).

Because the number and genetic variability of many species are rapidly declining as a direct or indirect consequence of human actions (Frankham et al. 2008), and the demand for food products and other derivatives (e.g., biofuels and new drugs) is growing rapidly (Lee et al. 2014), a notable need exists for research that helps establish conservation strategies as well as manage and make use of the variation in available genetic material. In this context, genetic resources are resources of natural raw material (genetic variability), both for breeding programs and conservation strategies.

Over recent decades, the use of molecular techniques in studies related to the characterization of genetic variability has grown exponentially, especially the use of molecular markers (Fig. 5.1). Of the major applications for molecular markers, Cerqueira-Silva et al. (2014a, b) and Faleiro (2007) highlighted the following: (i) the estimation of intraspecific and interspecific genetic diversity; (ii) the determination of evolutionary relationships and phylogenetic classifications; and (iii) the identification, characterization, and mapping of genes. All of these applications have contributed to the characterization, conservation, and use of biodiversity.

Rapid advances in molecular techniques and the consequent reductions in their costs have produced increasingly robust research, not only with regard to

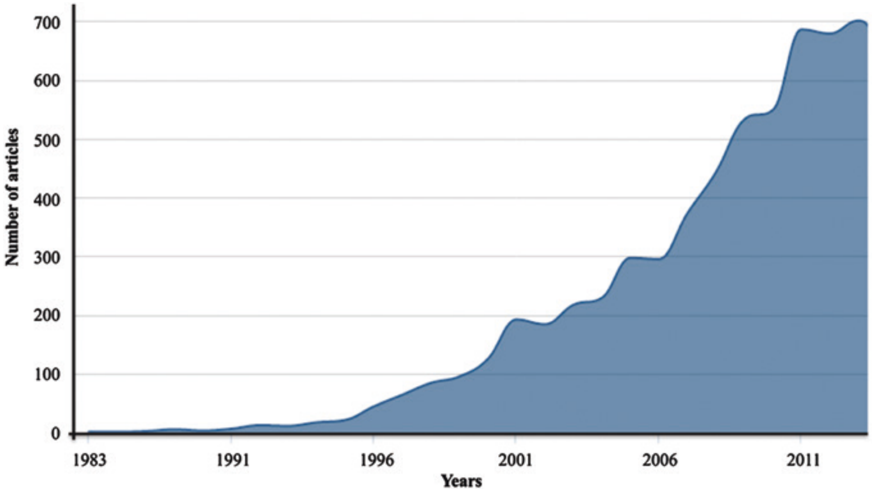

Fig. 5.1 The number of articles published using molecular markers to estimate the genetic diversity of passion fruit species

commercial species but also wild species with little or no direct/immediate economic effects (Phillips 2014; Ferreira and Rangel 2011). The quantitative and qualitative growth of information generated from molecular-genetic studies obtained using modern approaches, e.g., next-generation sequencing (NGS) and genotyping-by-sequencing (GBS), has greatly expanded the possibility of the associations between genotypic and phenotypic data.

The following sections present and discuss issues related to the genetic diversity of passion fruit (*Passiflora* spp.). This chapter seeks to provide the reader with an updated view of the advances and challenges associated with the characterization, conservation, and use of the genetic diversity present in the genus *Passiflora*.

5.1.2 The Diversity and Distribution of the Genus Passiflora

The family Passifloraceae Juss. ex DC. corresponds to a group of species with highly variable leaves and flowers (Ulmer and MacDougal 2004), which are often considered lianas or climbing plants with tendrils and occasionally trees or shrubs without tendrils (Cervi 1997). Estimates of the number of species in the Passifloraceae family vary between 520 (Bernacci 2003; MacDougal and Feuillet 2004) and 700 (Feuillet 2004), and the number of genera varies between 18 (Feuillet 2004) and 23 (Barroso 1978). These variations are the result of taxonomical uncertainties, the use of synonyms, and inconstant descriptions of new species (Wetzel et al. 2011). Despite the taxonomical uncertainties, within the family Passifloraceae the genus *Passiflora* is noted for its species diversity (approximately 520; MacDougal and Feuillet 2004). Species of this genus are commonly known as "passion fruits" and "passion flowers," In general, passion fruits are allogamous plants that exhibit self-incompatibility (Bruckner et al. 2005). However, certain species are self-compatible and can reproduce via self-fertilization, like some passion fruit species of the subgenus *Decaloba* (Varassin and Silva 1999).

With regard to their geographical distribution, approximately 96 % of passion fruit species are widely distributed across tropical and subtropical regions, especially in South America. In this context, countries such as Colombia and Brazil (with approximately 170 and 150 passion fruit species, respectively) are considered the diversity centers of the genus *Passiflora* (Bernacci et al. 2014; Ocampo et al. 2010; Fajardo et al. 1998). Although fewer passion fruit species are located outside the Americas, they have been observed in India, China, Southeastern Asia, Australia, and the Pacific islands (e.g., *Passiflora aurantia*, *P. cinnabarina*, *P. herbertiana*, *P. cupiformis*, *P. henryi*, *P. jugorum*, *P. moluccana,* and *P. siamica,* Cerqueira-Silva et al. 2014a).

Despite the species richness and wide distribution of the genus *Passiflora* across tropical regions, the lack of ecological and genetic research concerning most passion fruit species has become a risk factor for the conservation of their biodiversity. Various research groups have performed basic research devoted to advancing knowledge related to the geographic distribution of *Passiflora* (Scherer 2014; Ocampo et al. 2010; Ocampo-Perez et al. 2007), including the promotion and discussion of hypotheses related to patterns of distribution, ecological and evolutionary relationships, and the identification of the species at the greatest risk for extinction. Specific to the passion fruit species of Brazil, a recent study of 58 species indicated that most of the species were present in only two (12 species) or one (23 species) of the five biomes found in Brazilian forests (Scherer 2014).

Taking a macroecological approach in which both geographical distribution and climatic characteristics are considered, the occupation pattern of the climatic niches estimated for *Passiflora* shows that passion fruits restricted to homogeneous environments with high temperatures and significant rainfall are more susceptible to climate change (e.g., *P. vespertilio*, *P. micropetala*, *P. rubra*, *P. mansoi*, *P. ceratocarpa*, *P. candida*, *P. foetida*, *P. vitifolia*, *P. coccinea*, *P. nitida*, *P. riparia*, *P. ambigua,* and *P. quadrangularis*; Scherer 2014). The same author argued that more widely distributed *Passiflora* species in heterogeneous environments with rainfall concentrated during the warmer months (e.g., *P. setulosa*, *P. mendocaei*, *P. ishnoclada*, *P. caerulea*, *P. tenuifila*, *P. urubicensis*, *P. elegans,* and *P. actinia*) are at less risk for extinction and more likely to preserve the evolutionary history of the genus.

According to the information provided combined with the constant threat of genetic erosion or even extinction due to the fragmentation and reduction of forests via human activity, genetic estimates that provide information concerning variability and genetic structure are important for the conservation, management, and use of *Passiflora* (Faleiro et al. 2011a, b; Ocamp et al. 2010).

5.2 Genetic Variability and the Conservation of Passion Fruit

5.2.1 Diversity Studies Based on Morphological and Agronomic Descriptors

The wide morphological variability observed among passion fruits is one of its striking features, encompassing both interspecific and intraspecific variation. All of this variability is related to the wide geographical distribution of the genus and the evolutionary factors that resulted from the interactions between passion fruits and pollinators, seed dispersers, pests, and pathogens. The wide variation present in both the flowers and fruits of passion fruit emphasizes their beauty and potential influence on the ecological relationships of species (Fig. 5.2).

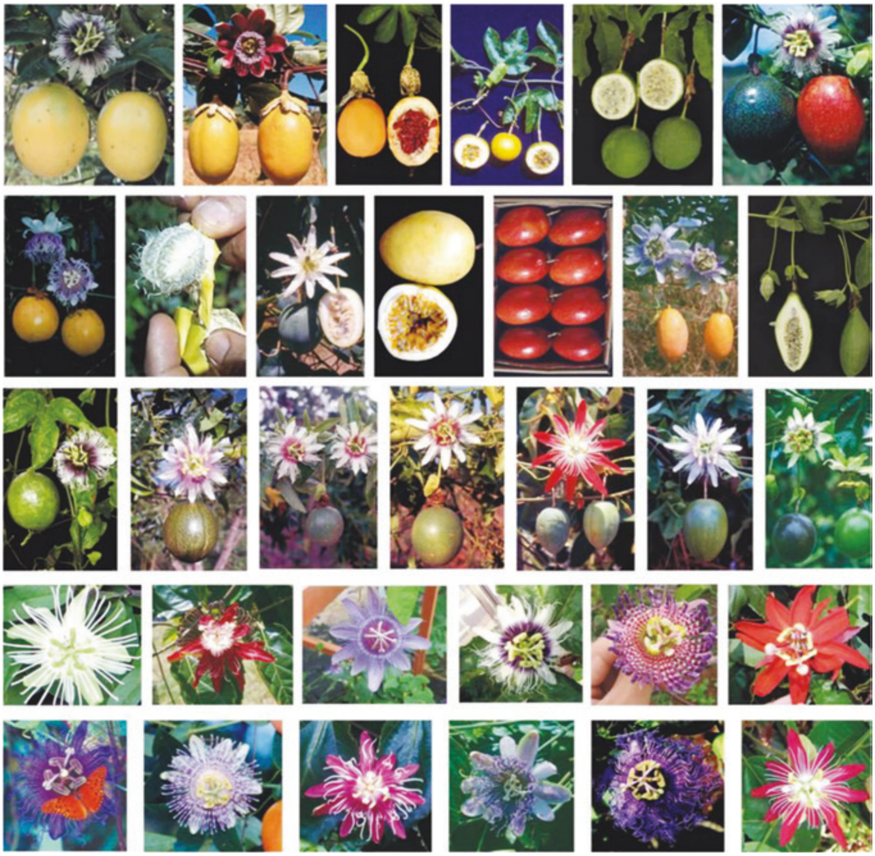

Fig. 5.2 The diversity of forms and colors in the fruits and flowers of passion fruits. Accessions conserved in the germplasm bank of Embrapa Cerrados. Credits: F.G. Faleiro and NTV Junqueira, researchers from Embrapa, Brazil

Most studies on the diversity of the genus *Passiflora* have been conducted to support pre-improvement actions, especially the pioneering studies of Oliveira (1980), Maluf et al. (1989), Oliveira et al. (2012), Ocampo and Coppens-d'eeckenbrugge (2009), Araujo et al. (2008), Castro et al. (2012), and Jesus et al. (2014), who proposed the establishment and use of morphological and agronomic descriptors to characterize passion fruit diversity. When characterizations of diversity primarily stem from the analysis of accessions held in germplasm banks and collections, the results from these studies contribute more to the advancement of breeding programs than to that of the population of *Passiflora* species.

Together, the variability estimates presented by various authors based on morphological and agronomic characteristics have indicated wide intraspecific variability among the *Passiflora* species (Ocampo et al. 2013; Faleiro et al. 2005, 2011a, b; Cerqueira-Silva et al. 2009). Studies have also observed preferred crosses, with the aim of enhancing the segregation or maintenance of characteristics of interest. Estimates of pathogen resistance, observed in various genotypes as reactions to anthracnose, woodiness virus, scab, fusarium, and bacterial blight, also support the genetic variability within and among *Passiflora* species (Batistti et al. 2013; Oliveira et al. 2013a; Cerqueira-Silva et al. 2008; Junqueira et al. 2003).

5.2.2 Genetic Variability Estimates Based on Molecular Markers

Estimates of genetic variability based on the polymorphisms of molecular markers are increasingly common among *Passiflora*. The first of these studies used isozyme markers (Segura et al. 1998) and randomly amplified polymorphic DNA (RAPD; Fajardo et al. 1998) to estimate the intraspecific and interspecific genetic diversity of passion fruit accessions. Since that first study, a variety of molecular markers have been used to (i) estimate the diversity of wild and cultivated accessions (Bernal-Parra et al. 2014; Cerqueira-Silva et al. 2014b, Oliveira et al. 2013, Ortiz et al. 2012, Santos et al. 2011); (ii) construct genetic maps (Pereira et al. 2013; Oliveira et al. 2008; Carneiro et al. 2002); (iii) characterize and confirm hybridizations (Santos et al. 2012; Conceição et al. 2011; Junqueira et al. 2008); and (iv) analyze either the recovery of recurrent genomes in plants obtained from backcrossing in a molecular marker-assisted program (Fonseca et al. 2009; Bellon et al. 2014) or the effect of selection on genetic variability (Costa et al. 2012). A recent compilation of publications regarding the use of molecular markers in *Passiflora* found that at least eight different types of markers have been used to characterize diversity, with the RAPD markers used most prevalently (approximately 50 % of all passion fruit diversity studies; Fig. 5.3; Cerqueira-Silva et al. 2014a). Although these markers are informative, they do not maximally exploit the available genetic information because it is impossible to distinguish heterozygote genotypes. In the last few years, however, the number of studies using other markers (e.g., microsatellites) has increased at the expense of studies using dominant markers (e.g., RAPD).

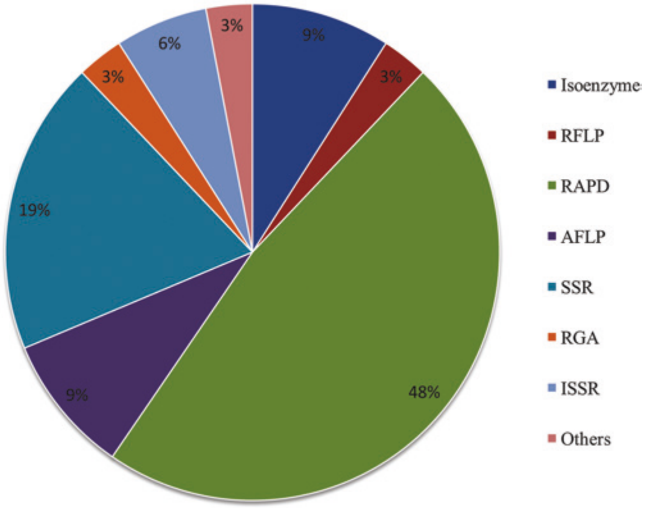

Fig. 5.3 The percentages of articles published using various molecular markers to estimate the genetic diversity of passion fruit

Although a growing number of studies have been devoted to characterizing the genetic diversity of passion fruits, estimates from primary scientific publication databases indicate that fewer than 15 % of passion fruit species have available genetic diversity data based on molecular markers (Cerqueira-Silva et al. 2014a). In addition, no population studies have been conducted that enable the evaluation of diversity patterns and the natural variability available within and among *Passiflora* species. In this context, the available knowledge, similar to that of morpho-agronomic evaluations, is the almost exclusively the result of the characterization of the accessions maintained in germplasm banks and collections.

Oliveira et al. (2005) and Padua et al. (2005) were the first research publications devoted to the development and characterization of microsatellite (or Simple Sequence Repeat, SSR) markers for *P. edulis* and *P. alata*, respectively. These publications marked an important step for population studies of *Passiflora*. However, new microsatellite markers for wild and commercial passion fruit species were not developed until 2012 (Cerqueira-Silva et al. 2012, 2014b, c; Penha et al. 2013; Cazé et al. 2012) when approximately 450 microsatellite markers were developed and characterized (Cerqueira-Silva et al. 2014a). Despite the morphological variability and high potential for polymorphisms observed in the microsatellite locus, the results obtained using these markers have mostly indicated the existence of low-to-moderate genetic variability in passion fruit species (Table 5.1).

Is also important to highlight that the SSR markers available for *Passiflora* were developed from the genomic DNA of only six species: *P. alata*, *P. edulis*, *P. cincinnata*, *P. contracta*, *P. pohlii,* and *P. setacea* (Cerqueira-Silva et al. 2012, 2014c; Penha et al. 2013; Cazé et al. 2012; Pádua et al. 2005; Oliveira et al. 2005, 2008).

Table 5.1 The average number of alleles (Na) and observed (H_O), and expected (H_E) heterozygosity values in the characterization of microsatellite loci from passion fruit species and studies of genetic diversity

Species	Microsatellite loci characteristics			References
	Na	H_O	H_E	
P. alata	3.1	0.26	0.53	Pádua et al. (2005)
P. edulis	7.6	0.58	0.62	Oliveira et al. (2005)
P. cincinnata	5.0	0.52	0.52	Cerqueira-Silva et al. (2012)
P. contracta	4.9	0.53	0.61	Cazé et al. (2012)
P. edulis	1.0	–*	–*	Ortiz et al. (2012)
P. cincinnata	3.3	0.26	0.36	Cerqueira-Silva et al. (2014c)
P. edulis	3.4	0.31	0.36	Cerqueira-Silva et al. (2014c)
P. setacea	2.8	0.34	0.41	Cerqueira-Silva et al. (2014c)
P. cincinnata	6.0	0.42	0.52	Cerqueira-Silva et al. (2014b)
P. edulis	6	0.43	0.50	Cerqueira-Silva et al. (2014b)
P. setacea	3	0.25	0.36	Cerqueira-Silva et al. (2014b)
P. alata	–*	–*	–*	Silva et al. (2014)
P. ligularis	12.2	0.98	0.96	Bernal-Parra et al. (2014)

*These studies did not observe polymorphic loci or analyze binary data (e.g., dominant markers); therefore, estimations of Na, H_O, and H_E were not possible

Therefore, efforts to increase the number of loci available for future genetic studies of *Passiflora* must be maintained.

Despite the economic importance of *Passiflora* (including alimentary, pharmaceutical, and ornamental uses), little is known about this genome. A better understanding of it is important to the efficient use of its genetic resources (Santos et al. 2014). Genomic information would enable the use of molecular markers, such as single nucleotide polymorphisms (SNPs), thereby expanding our knowledge of the genetic relationships between different species.

In addition to the identification of microsatellite markers and the development of new primer pairs, cross-amplification (which occurs when the DNA regions that flank the microsatellite loci are sufficiently conserved and enable the amplification of a microsatellite locus in different species with the use of the same primer pair) has been used to provide quick and cost-effective sets of microsatellite markers to genetically characterize passion fruit accessions and populations (Paiva et al. 2014; Cerqueira-Silva et al. 2014b, c; Silva et al. 2014; Oliveira et al. 2013b). Cerqueira-Silva et al.'s (2014b) recent experimental data and compilations of other results show that at least 20 *Passiflora* species have characterized microsatellite loci. Included among these species are the major commercial species in Brazil, *P. edulis* and *P. alata*, which have approximately 300 and 170 characterized loci, respectively. The same authors showed that 12 other passion fruits (*P. malacophylla*, *P. galbana*, *P. watsoniana*, *P. cincinnata*, *P. tenuifila*, *P. gibertii*, *P. setacea*, *P. foetida*, *P. morifolia*, *P. suberosa*, *P. rubra,* and *P. laurifolia*) have approximately 70 characterized microsatellite loci each. Cerqueira-Silva et al.'s (2014b) cross-amplification assay results showed that 23 microsatellite loci are conserved among 14 species, which confirms the potential use of these markers in intraspecific and interspecific genetic studies.

Because most diversity studies of *Passiflora* have been conducted using a few representative genotypes, we must highlight Bernal-Parra et al. (2014) who examined 41 accessions of *P. ligularis*; Cerqueira-Silva et al. (2014b) who examined a total of 116 accessions of *P. edulis*, *P. cincinnata,* and *P. setacea*; Ortiz et al. (2012) who examined 70 accessions of *P. edulis*; and Santos et al. (2011) who examined a total of 45 accessions of *P. edulis* and *P. alata*. Although these studies identified selectable genetic variability and the absence of genetic structures associated with the geographical origin of access, contrasting results regarding the magnitude of variability estimated for passion fruit species can be found in the literature. One such example is the absence of polymorphisms observed at 17 microsatellite loci used to evaluate *P. edulis* accessions (Ortiz et al. 2012) and the high variability observed at five microsatellite loci (mean = 12.2 alleles per locus; heterozygosity = 0.98) used to evaluate *P. ligularis* accessions (Bernal-Parra et al. 2014); both of these studies were performed in Colombia to support pre-breeding actions. Because of the lack of studies from natural populations, determining the representativeness of the group diversity of accessions available in germplasm banks is difficult.

5.2.3 Strategies and Actions for the Conservation and Use of Passion Fruit

The practical implementation of strategies and actions dedicated to conserve passion fruit remains incipient, and it is generally limited to the ex situ conservation of accessions in germplasm banks and collections. Approximately, 50 such collections are estimated to be spread across 32 countries; together, these collections represent at least 1200 passion fruit accessions (Faleiro et al. 2011a, b; Ferreira 2005). Approximately, 95 % of these accessions are located in germplasm banks in only nine countries: Brazil (32 %), Ecuador (30 %), Peru (14 %), Colombia (8 %), France (3 %), and USA, Costa Rica, Jamaica, and Kenya (2 % each; Cerqueira-Silva et al. 2014a; Ferreira 2005).

Embrapa, the Brazilian Agricultural Research Corporation (https://www.embrapa.br), has three passion fruit germplasm banks (BAG passion fruit; Fig. 5.4). These banks are located across three units: Embrapa Cerrado (the Cerrado Biome), Embrapa Cassava and Fruits (the Atlantic Forest Biome), and Embrapa Semi-Arid (Biome Caatinga). This distribution across different biomes is interesting with regard to the conservation of *Passiflora* genetic resources. In addition to the Embrapa BAGs, other important collections are located at universities and state/federal institutions in Brazil.

Despite the importance of these collections, accession loss during storage remains common. This loss includes problems with in vivo maintenance (including

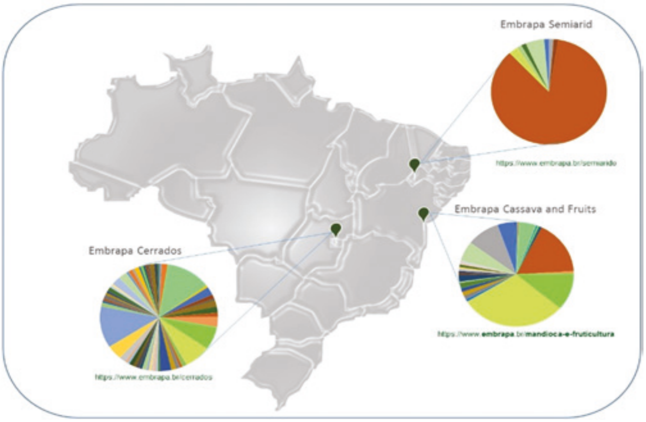

Fig. 5.4 Major germplasm banks of *Passiflora* from Embrapa. The *colors* in the pie charts represent the same species conserved in other germplasm banks. Within each graph, the *colors* represent the numbers of species preserved

improper species adaptation, and phytopathological problems) and difficulties with appropriate protocols to ensure the viability of stored seeds. These limitations can be overcome with a better understanding of the physiological ecology of the species, the type of seed (orthodox, recalcitrant or intermediate), the appropriate conditions for storage (ideal temperature and humidity), and new conservation strategies (e.g., in vitro tissue culture techniques and cryopreservation; Fig. 5.4). Cryopreservation has been used for long-term conservation at ultra-low temperatures (−196 °C) that suspend cell division, metabolic, and biochemical activities (Radha et al. 2012), thereby enabling the long-term storage of vegetative and reproductive structures (González-Benito et al. 1998; Solomon 2002) as well as species with recalcitrant or intermediate seeds (Santos 2000).

The first step to preserve the close relationship between conservation and biodiversity studies of *Passiflora* is research dedicated to identifying and prospecting species. The second step is the characterization of accessions in germplasm banks and collections. The first step is crucial to maintain more representative variability in germplasm banks and reduce the number of misidentified accessions. The second step is essential for their effective use to support pre-breeding actions (i.e., activities that involve identifying genes and traits in wild species as well as their potential incorporation into agronomically suitable materials) and breeding (i.e., the use of selection and recombination methods to obtain genetic gains; Fig. 5.5).

In this context, the contribution of genetic characterizations to estimate and understand the diversity of populations or groups of regional passion fruit accessions have enabled (i) the identification of converging and diverging crosses of commercial (e.g., *P. edulis*) and wild species (e.g., *P. setacea*, *P. cincinnata,* and *P. trintae*; Cerqueira-Silva et al. 2010, 2014c); (ii) the confirmation and characterization of interspecific hybrids (Santos et al. 2012; Conceição et al. 2011;

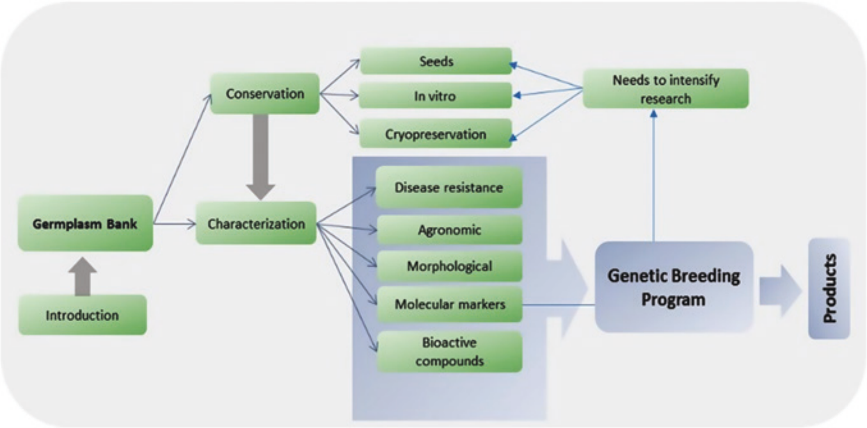

Fig. 5.5 A simplified flowchart of specific conservation strategies, including the characterization and use of accessions conserved in germplasm banks

Junqueira et al. 2008) that decrease loss and reduce costs via the restricted maintenance of seedlings; and (iii) the characterization and selection of specimens with a higher genomic contribution from the recurrent parent, which reduces the number of backcrossing cycles required to obtain the hybrid of interest (Fonseca et al. 2009; Bellon et al. 2014).

The use of wild germplasm is a major interest among passion fruit researchers (Faleiro and Junqueira 2009) because of the importance of introducing the characteristics found in several wild Brazilian *Passiflora* species into commercial species (Faleiro and Junqueira 2009; Faleiro et al. 2011a, b). Wild species are used intensively in passion fruit breeding programs; these species have been tested as rootstocks to obtain resistances to soil fungi and early death as well as to diversify production systems with new functional foods for *in natura* consumption and use as ornamental and medicinal plants (Faleiro et al. 2011a, b, 2012a, b).

Agronomical evaluations of wild *Passiflora* germplasm have indicated the potential of certain species for disease resistance, cold tolerance and improved physical, chemical, or flavor characteristics of passion fruit pulp, thereby enhancing its functional properties (Faleiro and Junqueira 2009). Self-pollinating species such as *P. tenuifila*, *P. elegans*, *P. capsularis*, *P. villosa*, *P. suberosa*, *P. morifolia,* and *P. foetida* have also been identified as well as those with shorter androgynophores that reduce stigma length in relation to the crown, thereby facilitating pollination due to smaller insects. These features increase productivity, decrease the labor costs entailed by manual pollination, and reduce the negative effects of African bees (Faleiro and Junqueira 2009).

Research performed at Embrapa on genetic compatibility, crossability rates, anthesis periods, pollen viability periods, and stigma receptivity have produced several fertile interspecific hybrids through artificial crossings (Junqueira et al. 2008).

Fig. 5.6 Different uses and cultivars of passion fruit. Credits: F.G. Faleiro, NTV Junqueira, researchers from the Embrapa, Brazil

Furthermore, DNA molecular marker-aided backcrossing has been used to recover commercial features while maintaining resistance and other genes of interest (Fonseca et al. 2007; Bellon et al. 2014). Hybrids involving three or more species have also been obtained to pyramid genes for disease resistance. Beyond genetic breeding, certain wild species, and released cultivars have ornamental potential and direct consumption uses (Fig. 5.6). The passion fruit breeding program at Embrapa has worked with regard to the population selection of wild species to increase fruit size for the fresh fruit market and produce ingredients for sweets and ice cream.

5.3 Perspectives and Challenges for the Conservation and Use of *Passiflora* spp.

Research involving the prospection, conservation, and characterization of commercial and wild passion fruit are strategically important for both conservation and breeding. Thus, the absence of phenotypic and molecular characterizations for most species and accessions of passion fruit is a challenge to introducing information from genetic diversity estimates into current breeding programs as well as to managing and conserving this biodiversity. In this context, we believe that the following research activities should be prioritized: (i) Population genetics should measured to understand the genetic diversity and structure of passion fruit; (ii) Phenotypic characterizations should be conducted to contribute to interspecific crosses and studies of the association between phenotypic and molecular data; and (iii) New accessions should be identified, especially wild species, to increase the representation within germplasm banks.

The identification of new microsatellite loci for *Passiflora* species and the use of cross-amplification strategies to popularize the use of these markers should increase the amount of passion fruit research. As Table 5.1 shows and recent studies

(Cerqueira-Silva et al. 2014a, b) have discussed, however, additional research should be performed to identify and characterize microsatellite loci because the current results indicate low allelic diversity among SSR loci from wild and commercial passion fruit. Recent research involving *Passiflora* species has used biotechnology (Faleiro et al. 2012a, b) and genomics; investigations of commercial passion fruit species have developed and characterized the first SNPs for *P. alata* (Pereira et al. 2013). Various research groups are providing information concerning the genomes of passion fruit species, and interesting results are already available from Santos et al. (2014), Cutri and Dornelas (2012) and Yotoko et al. (2011). These genomics studies have the potential to enhance the development of new markers [e.g., SSR markers, expressed sequence tags (ESTs), and SNPs] and expand discussions of the structure, organization, and evolution of the *Passiflora* genome.

Moreover, the development and use of large-scale genotyping should enable the use of genome-wide selection strategies, thereby enhancing the association of molecular diversity data with characteristics of agronomic interest.

5.4 Conclusions

Despite the advances observed over recent decades with regard to the characterization and use of the diversity within *Passiflora*, the scarcity of genetic and population information enables only a preliminary understanding of the distribution and magnitude of the genetic variability within passion fruit species. Given the increase of human interventions in the environment and the abiotic effects driven by climatic changes, population genetics remains open to studies regarding the conscientious management of *Passiflora* biodiversity.

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