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Seri biodiversity: An important approach for improving quality of life

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Abstract

The art of silk production is called sericulture that comprises cultivation of mulberry, silkworm rearing and post cocoon activities leading to production of silk yarn. Sericulture provides gainful employment, economic development and improvement in the quality of life to the people in a rural area and therefore it plays an important role in anti-poverty programme. India is a major centre of Seri biodiversity with diverse sericigenous fauna and flora. India represents a wide range of biodiversity due to its diverse climatic and cultural practices. Although mulberry silk dominates but non-mulberry silks have also an important role in global silk. The natural silk producing insects are broadly classified as mulberry and wild or non-mulberry. Non-mulberry sericulture is universally known as forest or wild sericulture that provides an important source of employment for the native population in forest areas. North east region of India is considered as the floral and faunal gate way for Asian main land to Indian Peninsula. The region is also considered as one of the 34 biodiversity hot spots of the world. Diversity of silkworm at the gene level is critical to success in any crop breeding as it serves a platform for specific breeding programmes. Genetic diversity is a particular concern because greater genetic uniformity in silkworm can increase vulnerability to pests and diseases. Hence, maintenance of genetic diversity is a fundamental component in long-term management strategies for genetic improvement of silkworm which is cultivated by millions of people around the globe for its lusture silk (Queen of textiles). The genetic diversity studies carried out in silkworm using divergent methods viz, quantitative traits, biochemical and molecular markers and in the present article the level of diversity and factors responsible for loss of diversity are reviewed.

Keywords: Cocoon, genetic diversity, molecular marker, silkworm

Introduction

The concept of biodiversity conservation and gene bank maintenance have gained greater momentum in the recent times and the biodiversity wealth are considered as common heritage of mankind and sovereign rights of the nations. Seri-biodiversity refers to the variability in sericigenous insects and their host plants, which are economically and ecologically important biodiversity. There are several wild sericigenous insects and their host plants, which are abundant in the north eastern and sub-Himalayan regions and other parts of the country (Kalita and Dutta, 2014) [8]. However, only 5 types of sericigenous insects are commercially exploited in India. Study on genetic diversity is critical to success in any crop breeding and it provides information about the quantum of genetic divergence and serves as a platform for specific breeding. Genetic diversity is usually thought of as the amount of genetic variability among individuals of a variety or a population of a species. It results from the many genetic differences between individuals and may be manifest in differences in DNA sequence, in biochemical characteristics (e.g., in protein structure or isoenzyme properties), in physiological properties (e.g., abiotic stress resistance or growth rate), or in morphological characters. Genetic diversity has been conventionally estimated on the basis of different biometrical techniques (Metroglyph, divergence analysis, and principal component analysis). The genetic diversity of *B. mori* is derived from hybridization of different geographical origins, mainly the Japanese, Chinese, European, and Indian strains, which have distinct traits (Bindroo and Moorthy, 2014) [2]. Among these four geographical strains, silkworm of temperate origin produces a higher quantity of good, finer, stronger silk fiber, whereas the tropical strains are hardy, tolerant to pathogen load, and resistant to diseases. However, the tropical strains produce low amounts of silk, which is coarser and weaker. To help the breeders in the process to identify the parents that nick better, several methods of divergence analysis based on

quantitative traits have been proposed to suit various objectives. As most of the desirable characters in silkworm are quantitative nature, multivariate statistical methods have been employed to measure the genetic diversity among the stocks. Jolly *et al.*, (1989) ^[6] subjected forty-nine silkworm breeds for this analysis and reported that these breeds were found to form three distinct clusters indicating the presence of distinct diversity among the breeds. Subba Rao *et al.*, (1991) ^[14] and Govindan *et al.*, (1996) ^[15] reported that breeds derived from the same parents were included in different clusters showing variation among the breeds derived from the same source. On the other hand, the breeds derived from the same source were included in the same cluster showing close affinity between advanced sister lines and those of differing genetic background occupied in a single cluster indicated uniformity in selection procedures. However, genotypes of temperate and tropical origin formed into separate clusters indicating environmental influence on the expression of characters. Though theoretically geographical diversity is an important factor, it is not the whole determining factor for genetic divergence. All these studies were aimed to identify suitable parents for breeding programme and recommended to cross the genotypes from different clusters for yield improvement. Though many characters in silkworm are subjected to divergence study, characters, namely, fecundity larval weight, single cocoon weight, cocoon shell weight, and filament length only, contributed about 97% to the total genetic divergence. Genetic diversity is most often characterized using data that depict variation in either discrete allelic states or continuously distributed (i.e. quantitative) characters, which lead to different possible metrics of genetic diversity. Genetic diversity can be assessed among different accessions/individuals within the same species (intraspecific), among species (interspecific) and between genus and families. It plays an important role in any breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of paramount importance in any kind of breeding programme; hence, the knowledge of genetic diversity and relatedness in the germplasm is a prerequisite for crop improvement programmes. Genetic diversity is also an essential aspect in conservation biology because a fundamental concept of natural selection states that the rate of evolutionary change in a population is proportional to the amount of genetic diversity present in it. Decreasing genetic diversity increases the extinction risk of populations due to a decline in fitness. Genetic diversity also has the potential to affect a wide range of population, community, and ecosystem processes both directly and indirectly. However, these effects are contingent upon genetic diversity being related to the magnitude of variation in phenotypic traits. In general, cocoon colour and cocoon shape, larval, marking, and quantitative traits have been used for differentiation of silkworm genotypes and, based on that, parents are being selected. However, recent advent of different molecular techniques led breeders to estimate genetic diversity on the basis of data generated by different molecular markers, which provided a means of rapid analysis of germplasm and estimates of genetic diversity, which were often found to corroborate phenotypic data. These molecular markers are broadly categorized as biochemical and molecular markers.

Silkworm germplasm conservation strategy

Realizing the pivotal role of sericultural germplasm resources for sustainable development of sericulture industry in India, the Government of India (GOI)/Central Silk Board (CSB)

established Central Sericultural Germplasm Resources Centre (CSGRC) at Hosur in 1991 to act as a trustee of sericultural germplasm for easy accessions by the breeders and other users of their research programme to utilize these valuable germplasm towards mulberry and silkworm crop improvement. The CSGRC, Hosur is mandated to function as the nodal centre for planning and coordinating all activities relating to sericultural germplasm viz. collection, characterization, evaluation, conservation, supply and exchange of mulberry and silkworm genetic resources in India. The centre has established a National silkworm gene bank for conservation and utilization of the genetic resources. Since 1991, the centre has collected mulberry and silkworm germplasm readily available in various sericultural research institutes and universities and also carried out exploration and survey mission particularly in the Himalayan ranges and Andaman Islands. As a result of concerted efforts, the centre has collected and conserved 357 silkworm germplasm resources of diverse origin in the field gene bank. The silkworm germplasm conserved at CSGRC, Hosur are maintained with a unique accession number allotted by the Centre for easy identification of the germplasm. The centre has also developed a system for registration of sericultural germplasm to protect the breeders rights/Intellectual Property Rights (I.P.R.).

Conservation of Seri biodiversity

The main aim of Seri-biodiversity conservation is to protect the available different ecotypes from extinction and use these in future breeding programmes. The extinction of traditional Indian silkworm races (Kashmir race, Chotopolu etc.) has only been due to lack of conservation/ management system. The scientifically maintained, characterized and evaluated germplasm is therefore, of utmost importance to have specific breeding plans for upgrading the productivity and production stability. This could be met by laying a strategy involving both conventional and genetic engineering/molecular biology techniques to alter the genetic make-up of breeds more quickly, efficiently and precisely to evolve productive and stress tolerant breeds. This will also enable cost effective and efficient gene bank management and reduce the number of duplicate accessions to a manageable size. Thus, germplasm collection needs to be identified, characterized and conserved, giving full attention to the conservation of local races also. Besides, characterization of silkworm germplasm is required to be documented properly so that information could be retrieved at any time for further use. Human society depends on biodiversity for its values, viz., food, fiber, fuel, shelter, medicines and several other day to day necessities without which sustenance of mankind on this earth is impossible. It is, therefore, important to enhance understanding, augmentation, conservation and sustainable use of biodiversity with appropriate human interventions. The importance of conservation of breeds is compulsory not only for initiating new breeding programmes but also for conserving the old races which have gone out of culture. Special emphasis needs to be given on saving the genetically important strains from extinction and exploring new strains for the development and progress of country's silk industry. Had there been the conservation programme of Seri-biodiversity earlier, we would not have lost some precious Seri biodiversity like Barapalu, Chatapalu and Kashmir Race. Kashmir Race had been the productive indigenous univoltine breed of Kashmir about 130 years back but has now become extinct due to outbreak of deadly Pebrine disease. Such has been the

production and productivity of this breed that in 1869 British managed to export from Kashmir (India) thousands of ounces of disease free seed of this Race to Europe in order to revive sericulture there. Characterization on the basis of morphological traits alone may not lead to sound judgment and discrimination of duplicate accessions. As such conservation of breeds is required to be based on more advanced reliable, quicker and unambiguous methods with high precision like DNA analysis, genomic analysis, biochemical markers, etc. In the present era of frontier sciences, there is need for identification and characterization of molecular/genetic attributes of different silkworm breeds, besides the use of conventional methods of breeding so as to have quicker and targeted improvement of silkworm breeds for their utilization in enhancing the production and productivity of cocoons with the ultimate objective of economic sustainability of farmers (Kamili *et al.*, 2003) [11].

Table 1: Types of silkworms present in India

Scientific name	Common name	Origin	Food plant
<i>B. mori</i>	Mulberry silkworm	China	<i>M.alba, M. indica, M. multicaulis, M. bombycis</i>
<i>A. mylitta</i>	Tropical tasar silkworm	India	<i>Shorea robusta, Terminalia tomentosa, T. arjuna</i>
<i>A. proylei</i>	Oak/temperate tasar silkworm	India	<i>Quercus incana, Q. serrata, Q. himalayana</i>
<i>A. assama</i>	Muga silkworm	India	<i>Litsaea polyantha, Machilus bombycine</i>
<i>P. ricini</i>	Eri silkworm	India	<i>Ricinus communis, Maninot utilisma, Evodea fragrance</i>

Loss of Seri biodiversity

The primary cause of loss of Seri biodiversity is deforestation in case of no mulberry silkworms. *B. mori* has undergone an intense process of domestication with frequent consanguineous crosses. As a result, the silkworm has accumulated a high level of homozygosity and, consequently, a low level of polymorphisms. This is probably because all cultivated silkworm strains originated from a common ancestor with a long history of inbreeding under consistently strong selective conditions for strain maintenance and improvement (Miao *et al.*, 2005) [12]. Nevertheless, RAPD analysis has proven to be an efficient technique to detect variability in different *B. mori* strains. These polymorphisms are useful in the genetic analysis of and discrimination between silkworm strains. Furthermore, RAPD molecular markers can be used to identify strains that are susceptible to the baculovirus Bm NPV. Plant diversity is the fundamental for agricultural production, maintains ecological niche. However in the present-day scenario plant genetic resources are associated with livelihood are being rapidly eroded and disappearing throughout the world due to various developmental changes. Moreover the loss of biodiversity in natural habitats occur with the expansion of agricultural production into new frontiers. In India because of habitat fragmentation, destruction, overexploitation, land use for agriculture and other purposes, a large number of species have already been lost and mulberry is one them (Tikadar and Dandin 2006) [15]. The other reasons for the loss of biodiversity is due to genetic erosion (monoculture, overexploitation and addition of improved variety).rare species. Natural calamities such as landslides in floods, cyclones have wiped out rare species of plants and animals in natural and protected habitats (Tikadar and Kamble 2008) [16].

Importance

Genetic and biological analyses of *B. mori* strains from germplasm banks are one of the most important steps in the maintenance, conservation, and use of these genetic resources (Chen, 2003) [3]. Based on the characterization of germplasm

The plan for conservation and improvement of the Seri-biodiversity therefore, should be based on the biotechnological interventions like biochemical markers, genes for disease resistance, identification of the rmtolerant breeds, Quantitative Trait Loci (QTL) based molecular characterization and Genome analysis using molecular markers. The other characters of interest in silkworm are breeds showing tendency of polyphagous behavior, breeds having different larval and cocoon colour as well as markings, breeds showing preference to artificial diet, breeds with high neatness, raw silk percentage and cocoon yield, breeds with high egg laying capacity. Conservation without effective utilization is useless. There is urgent need for increased utilization of Seri biodiversity both for commercial use and experimental use to increase the silk production and to evolve better yielding breeds.

data and the identification of resistant strains, it is possible to develop commercial and experimental silkworm hybrids for industrial and scientific research Srivastava *et al.*, (2005) [13]. Among 34 mega biodiversity countries in the world, India is home to many species of insects with a diverse silk moth fauna. In addition to the diverse silkworm races, there are vast genetic resources of mulberry, tasar, muga and eri host plants spread over diverse geographical locations. This offers a great opportunity for economic utilization of the natural flora and fauna. However, due to deforestation and destruction of habitats, there is a challenge to bring about development without disturbing the ecological balance. However, the present production of raw silk falls very much short of domestic demand. To meet this demand as well as to enhance the quantity and quality of silk export, silkworm germplasm has to play a pivotal role. The maintenance and sustainable use of all beneficial plants, animals, organisms, involves the development of a reservoir of gene assemblies or "Gene Library". The gene reservoir consists of geographically isolated races, genetic stocks, breeds evolved from exotic/indigenous crosses or hybrids besides the breeds/races collected from different centers/institutions. Sericulture is one of the important and viable economic activities in developing countries like India. In order to sustain and meet the future demands of this agro-based activity, it should efficiently be backed up by the directional improvement and conservation of silkworms and its host plant/s. Sher Kashmir University of Agricultural Sciences and Technology of Kashmir (SKUAST-K) is maintaining about 151 genotypes of bivoltine silkworms of diverse geographical origin. This includes the breeds numbering 25 developed at its T.S.R.I, in 1982 – 1999. Out of these 2 varieties, viz., SKAUR-1, SKAUR- 6 and their hybrid SKAU-HR-1 have been released during 1995 by the Ministry of Textiles, Govt. of India, for commercial exploitation in J&K State (Kamili, 1996) [10] an others like SKUAST-27, SKUAST-28, SKUAST-29, SKUAST-30, SKUAST-31, SKUAST-32, SKUAST-33 and SKUAST-34 are showing superiority in one or other characters (Kamili *et al.*, 2000) [9]. Dr. Tazima, a leading Japanese Seri culturist during his visit

to India in 1957 has expressed that Kashmir could be converted into silkworm gene bank for sustaining the sericulture of the whole World in view of its salubrious climatic conditions (Kamili and Masoodi, 2000)^[9].

China is the largest silk producing country with production of 170000 metric tons of raw silk followed by India with a production of 21390 metric tons of raw silk. In Jammu and Kashmir 30455 rearers are engaged with silkworm rearing with cocoon crop production of 1032.4 MT generating revenue of 1700 lakh rupees (Anonymous, 2015; CSB, 2016)^[1]. According to an estimate, one hectare of mulberry generates remunerative employment to 12-13 persons throughout the year (Jolly, 1987)^[7] with comparatively low investment and short gestation period. The industry is mainly concerned with leaf and cocoon production and does not involve any tedious technique, instead assures income to farmers in the quickest possible time. So sericulture has a great scope for employment creation. Since sericulture increases soil fertility, prevents soil erosion, helps in sustainable use of the forest, maintains forest ecosystem, preserves the wild flora and fauna, regulates precipitation, purifies air and prevent air pollution and economic exploitation of the forest directly or indirectly (Patra *et al.*, 2016). It is necessary to undertake necessary steps to promote sericultural activities so as to prevent the soil erosion and conserve the unique biodiversity of the Biosphere.

Conclusions

Genetic diversity is a particular concern because greater genetic uniformity in silkworm can increase vulnerability to pests and diseases. Hence, maintenance of genetic diversity is a fundamental component in long-term management strategies for genetic improvement of silkworm which is cultivated by millions of people around the globe for its lusture silk (Queen of textiles). The main aim of Seri-biodiversity conservation is to protect the available different ecotypes from extinction and use these in future breeding programmes for improvement in commercial characters of the silkworm. Further, it is necessary to undertake necessary steps to promote sericultural activities so as to prevent the soil erosion and conserve the unique biodiversity of the Biosphere.

Conflict of interest

There is no conflict of interest among the authors.

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