Evaluation of Bivoltine Silkworm (*Bombyx mori* L.) Hybrids for Disease Resistance and Suitability in Subtropical Conditions

Abstract:

The disease outbreak in silkworm generally hampers the silkworm larvae during the late larval period causing high mortality, formation of poor-quality cocoons or even the complete loss of entire crop, posing a significant challenge to sericulture industry. The current study was undertaken to screen the native silkworm hybrids for their resistance or susceptibility to flacherie (caused by bacterial infection) and grasserie (caused by a viral infection), particularly harmful to silkworm health and their yield potential in the subtropics of Jammu division. 12 hybrids namely U-8×PO1, ND3×PO1, PO1×U-8, U-3×U-1, JD6×U-6, U-4×U-6, PO3×ND5, U-6×ND3, ND3×NSP, ND2×NSP, SH6×NB4D2 and FC1×FC2 were selected and reared with proper rearing practices. The data was recorded for various parameters pertaining performance against disease outbreak and yield potential. The hybrids namely FC1×FC2 and U-4×U-6 demonstrated superior resistant hybrids and less susceptibility. Both the hybrids showed an incidence less than 2% for flacherie and 4% for grasserie respectively. The study found that the hybrids FC1×FC2 and U-4×U-6 can be utilized commercially to reduce disease-related losses and promote sericulture sustainability in subtropical regions. Incorporating such resistant hybrids into local practice would also provide more economic stability for farmers, reducing the hazards associated with silkworm rearing. Therefore, on the basis of current results, same two hybrids can be recommended for commercial exploitation at farmer level specifically for autumn rearing in subtropics of Jammu division. These resistant hybrids hold great promise for improving silkworm productivity thereby enhancing the sustainability of sericulture in the region.

Key words: diseases, flacherie, grasserie, hybrid, silkworm and susceptibility.

Introduction

In India, Sericulture occupies unique position in Indian economy and became most important agro-industry because of low investment, maximum employment generation potential as it is labour intensive and quick turn over. Due to domestication of mulberry silkworm from past 5000 years, silkworm has lost some of its wild characteristics such as resistance or tolerance towards certain microbial diseases which results in its susceptibility towards fungi, bacteria, virus and protozoan. Jammu and Kashmir hold unique position in

global silk market and well recognized for its quality bivoltine silk. Although the region is bestowed with most congenial environment suitable for sericulture, silkworm rearing is conducted for only two seasons namely spring and autumn rearing. More importantly only spring rearing is recorded to be the most fruitful from sericulture point of view as the disease incidence is most prevalent during autumn rearing resulting in considerable crop loss (Sharma *et al*., 2020). Only 10-15% farmers conduct silkworm rearing during autumn season which marks a huge gap in expected cocoon production (Shivkumar *et al.,* 2020). Development of region and season specific silkworm hybrids specifically for different agroclimatic conditions of country like India is a challenging task for the breeders. Silkworm breeders are trying hard to evolve resistant hybrids capable to yield good profit to the farmers. In this direction, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu has developed a series of potential bivoltine silkworm hybrids for fulfilling the need of sericultural farmers. Exploitation of the resistant of silkworm hybrids towards different diseases causing pathogens is a better option for managing the crop loss due to diseases. In view of the above, the present attempt has been made for screening and identification of resistance and susceptibility status of silkworm hybrids against various diseases.

Materials and Methods

The investigation was designed to evaluate potential bivoltine silkworm hybrids suitable for autumn rearing under subtropical conditions of Jammu Division of Jammu and Kashmir over disease susceptibility. Eleven indigenous bivoltine silkworm single hybrids evolved by Division of Sericulture, SKUAST-Jammu namely U-8×PO1, ND3×PO1, PO1×U-8, U-3×U-1, JD6×U-6, U-4×U-6, PO3×ND5, U-6×ND3, ND3×NSP, ND2×NSP, SH6×NB4D2 along with one check double hybrid namely FC1×FC2 from Regional Sericulture Research Station (RSRS), Dehradun were selected and reared as per standard rearing techniques by Krishnaswamy (1978) and Dandin *et al.,* 2003 under Completely Randomized Design (CRD). Screening of all the selected bivoltine silkworm hybrids was done for disease susceptibility and observations were recorded for each replication for given parameters:

Flacherie Incidence: The incidence of flacherie was observed by counting the number of flacherie infected worms and percentage was calculated by using the formula:

$$\text{Flacherie Incidence (\%)}: \frac{\text{Number of Iacherie infected worms}}{\text{Total no. of worm reared}} \times 100$$

Grasserie Incidence: The incidence of grasserie was done by counting the number of grasserie infected worms and percentage was calculated by using the formula:

$$\text{Grasserie Incidence (\%)}: \frac{\text{Number of grasserie infected worms}}{\text{Total no. of worm reared}} \times 100$$

The data thus generated was subjected to analysis of variance techniques by using statistical package (SPSS 16.0) and differences between means were tested by using Tukey's HSD ($P < 0.05$).

Results and Discussion:

Silkworm diseases pose significant challenges in Sericulture, as the vulnerability of silkworms to various pathogens can lead to substantial reductions in yield. This study assessed the susceptibility of different silkworm hybrids to flacherie and grasserie across multiple seasons. The data collected showed notable differences in disease incidence among the hybrids, revealing a clear seasonal pattern that supports earlier research (Selvakumar *et al*., 2002; Chandrasekaran and Nataraju, 2008; Babu *et al*., 2009; Reddy and Rao, 2009; Illahi and Nataraju, 2008; Balavenkatasubbaiah *et al*., 2015; Dar *et al*., 2017; Sharma *et al*., 2020). The prevalence of disease was significantly higher in the autumn season compared to the spring. Incidence of Flacherie Statistical analysis revealed a significant difference ($F = 10.962$; $df = 11$; $P = 0.000$) in flacherie incidence among the hybrids. The FC1×FC2 hybrid had the lowest disease incidence at 1.13 ± 0.01%, followed by U-3×U-1 (2.03 ± 0.32%) and U-4×U-6 (2.66 ± 0.19%). In contrast, the ND3×PO1 hybrid displayed the highest susceptibility, with an incidence rate of 7.88 ± 0.67%. These results are consistent with previous studies highlighting genetic variations in disease resistance among silkworm hybrids (Sharma *et al*., 2014; Balavenkatasubbaiah *et al*., 2014 and 2015; Sharma *et al*., 2019; Sharma *et al*., 2020).

The incidence of grasserie varied significantly among the hybrids ($F = 21.347$; $df = 11$; $P = 0.000$). The FC1×FC2 hybrid had the lowest incidence at 3.19 ± 0.42%, followed closely by U-4×U-6 at 3.33 ± 0.13% and U-3×U-1 at 3.44 ± 0.06%. On the other hand, ND3×PO1 showed the highest incidence of grasserie at 10.11 ± 0.16%, with SH6×NB4D2 and U-8×PO1 following at 8.91 ± 0.13% and 8.16 ± 0.16%, respectively. In terms of comparative susceptibility among hybrids, the FC1×FC2 hybrid consistently exhibited the lowest susceptibility to both flacherie (1.13%) and grasserie (3.19%), highlighting its potential as a strong candidate for sericulture. Conversely, ND3×PO1 was the most

vulnerable, with incidence rates of 7.88% for flacherie and 10.11% for grasserie. Other hybrids, including SH6×NB4D2 and U-8×PO1, also showed relatively high disease incidence. These findings are consistent with previous research (Balavenkatasubbaiah *et al*., 2014 and 2015; Sharma *et al*., 2019; Sharma *et al*., 2020), emphasizing the role of genetic resistance in influencing silkworm susceptibility to diseases. The results further confirm that disease prevalence is significantly affected by seasonal changes, with the highest incidences occurring in autumn and lower rates in spring. This seasonal pattern has been documented in earlier studies (Selvakumar *et al.*, 2002; Chandrasekaran and Nataraju, 2008; Babu *et al*., 2009; Reddy and Rao, 2009; Illahi and Nataraju, 2008). Silkworms, being cold-blooded organisms, are directly influenced by temperature, which significantly impacts their physiological processes (Polie, 2022). The environmental conditions in autumn, characterized by high humidity and temperature fluctuations, likely create an environment that favors pathogen growth, leading to increased disease outbreaks.

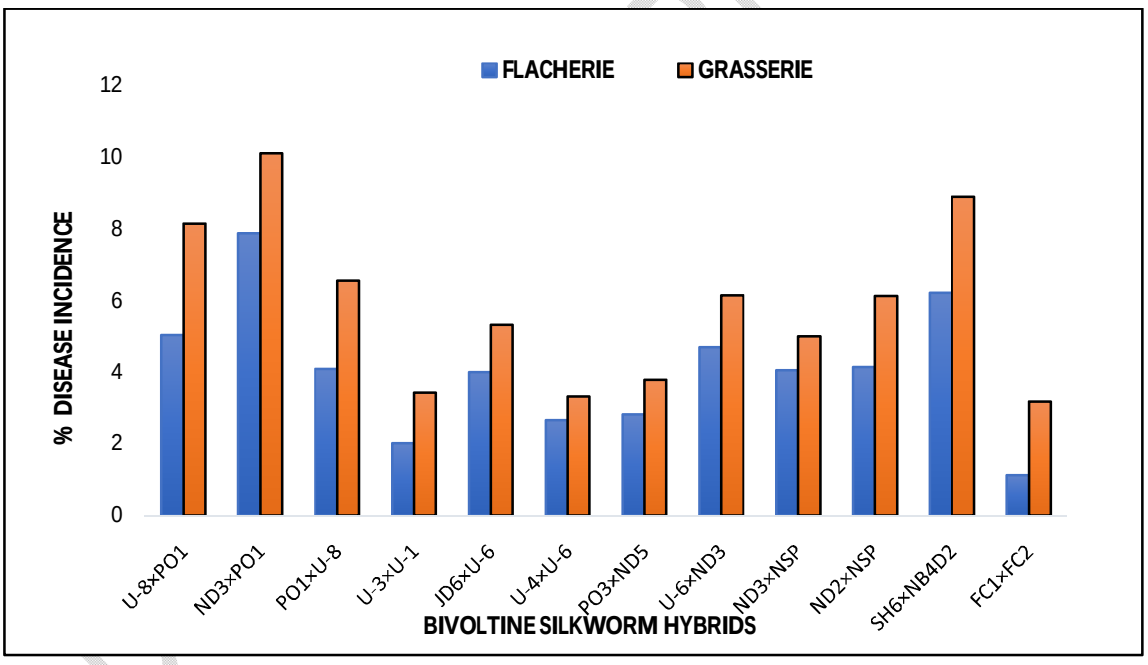

Figure-1: Incidence of silkworm diseases in different bivoltine silkworm hybrids.

Conclusion:

The present investigation was undertaken to generate information on suitability of selected hybrids for evaluation of potential hybrids suitable for autumn rearing under subtropical conditions of Jammu Division. Based on the results, among all the studied hybrids and the

control, three hybrids namely FC1×FC2, U-4×U-6, U-3×U-1 and PO3×ND5 were recorded to exhibit high resistance against flacherie and grasserie disease and the incidence of flacherie and grasserie diseases outbreak was recorded as low as 1% in case of flacherie, 3 % in case of grasserie. On the other hand, comparatively high incidence was recorded in ND3×PO1 (7.88%, 10.11%), followed by SH6×NB4D2 (6.22%, 8.91%) and U-8×PO1 (5.04% and 8.16%) for both the diseases respectively. As a result, using these resistant hybrids can greatly reduce losses caused by disease outbreaks, thereby increasing overall yield. This, in turn, would increase the profitability and sustainability of sericulture in the region, providing farmers with a consistent income and mitigating the economic risks caused by disease outbreaks. Such findings highlight the critical need of incorporating disease-resistant hybrids into local sericulture methods to ensure the long-term viability and expansion of Sericulture industry. Moreover, the study will provide an insight for future aspects of silkworm breeding for development of region and season specific hybrids.

Disclaimer (Artificial intelligence)

Option 1: Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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