

# ***In silico* Study of Post Translational Modifications in *Antheraea mylitta* Cocoonase from Different Ecoraces**

**Priya Porwal<sup>1\*</sup>, Sneha Prasad<sup>1</sup>, Jay Prakash Pandey<sup>2</sup> and Dev Mani Pandey<sup>1</sup>**

<sup>1</sup>Department of Bio-Engineering, Birla Institute of Technology, Mesra-835215, Ranchi, Jharkhand

<sup>2</sup>Central Tasar Research & Training Institute, Piska Nagari, Ranchi-835303, Jharkhand

Email: \*priyaporwal26@gmail.com

---

**Abstract**—*Antheraea mylitta*(Insecta: Lepidoptera: Saturniidae), the wild tasar silkmoth is widely distributed across several states in the southern, eastern and central region of India. The variation in climatic zones, food habits and habitat give rise to various ecorace system. According to available reports mainly 44 ecoraces have been enlisted. At last stage of metamorphosis silkmoth exude cocoonase which soften the cocoons by hydrolyzing sericin and allowing the moth to escape. Cocoonase is a proteolytic enzyme which proves to help in degumming process. Seeking its efficiency in degumming process we aimed to study cocoonase from different ecoraces and its post translation modifications (PTM) for finding one with high efficiency for degumming process. PTM such as myristoylation, glycosylation, phosphorylation, ubiquitination, SUMOylation may help in proper folding, stability and solubility of proteins. In silico study indicated the presence of multiple PTM which might help to improve the activity of this enzyme. *Antheraea mylitta* cocoonase sequences were retrieved from NCBI database, their PTM sites were predicted using online tools such as NetPhos, SUMOplot, and FindMod. Phosphorylation and SUMOylation are the two major PTM observed in enzyme sequences. The present study indicated that introduction of PTM might enhance the possible efficacy of the enzyme.

**Keywords:** *Antheraea mylitta*, cocoonase, degumming, post translational modifications.