"Genomic Innovations in Latrodectus Spiders: Advancing Sustainable Ecosystem Management"

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Abstract:

Sustainable ecosystem is huge topic for discussion in this era. It's a continuous process that comes from some biotic and abiotic factors such as; pollution of the atmosphere, waste production, toxic substance disposal, damaged aquatic ecosystems, deforestation, etc. To control the loss of biodiversity we must apply some innovative technologies of genome analysis and database management systems. Spiders (order Araneae) are the species which is broadly distributed in our diversity. Latrodectus is a genus of amazing spiders commonly known as a black widow have numerous attractive features and is a huge research topic, Because of its biological product and behavior. The literature review has been carried out by following reasoning methodology and is presented. The results of this study indicate that different researchers have taken different approaches to analyzing the genomic data with some broadly use methods like whole genome sequencing, genotyping, and different proteome analysis and management of data Overall, it is evident from the literature offers a meaningful option, especially for managing genomic data and provided new framework towards the sustainable ecosystem.

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Keywords: Sustainable ecosystem, *L. hesperus*, Whole genome sequencing, Genomic data.

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Introduction:

Ecology is the study of the relationship between living organisms and their environments. The ecology depends on some biotic and abiotic factors. A sustainable ecosystem is a biological environment and series of habitats that can increase and support itself without outside influence or assistance. In ideal sustainable ecosystems, everything is already provided within the ecosystem for life to survive. Nowadays there is a different branch of sociology that deals with the relations between human beings and their environment, and the balanced or harmonious relationship of living things to their environment. Which concentrate on issues of sustainable ecosystems including climate change; an emerging global crisis in water availability and water pollution; record loss of biodiversity and long-term damage to ecosystems, pollution of the atmosphere, waste production and disposal, impacts of chemical use, and toxic substance disposal, damaged aquatic ecosystems, deforestation, etc.

In the order of the above discussion previously researchers have drawn new methodology of species diversity, identification, and sequencing and also provide broadway analysis of bioproducts of the organism. In this study, we talk about broadly distributed species *Latrodactus* this genius of amazing spider commonly known as black widow member of the Theridiidae family. This genus contains 32 species, which include several North American "Black Widows" (Southern Black Widow *Latrodectus mactans*, Western Black Widow *Latrodectus hesperus*, and Northern Black Widow *Latrodectus variolus*) and has a much wider geographic distribution. Elsewhere, others include the European black widow (*Latrodectus tredecimguttatus*), the Australian Redback Black Widow (*Latrodectus hasseltii*), and several different species in Southern Africa that can be called Button spiders also identified.

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In most cases, the females are dark-colored, but some may have lighter bodies or even reddish. Many can have red, white, or brown markings on the upper side (dorsal) of the abdomen. Some can be readily identifiable by reddish markings on the central underside (ventral) abdomen, which are often hourglass-shaped.

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These small spiders have rare potent venom containing the neurotoxin latrotoxin, which causes the condition latrodectism, Female widow spiders have unusually large venom glands and their bite can be particularly harmful to large vertebrates, including humans. Despite their notoriety, *Latrodectus* bites rarely cause death or produce serious complications. It also produces silk fibers which are used in many forms like textile armor etc. The bioproduct of spiders, their behavior, evolution, and diversity is a broad topic of research.

Methodology

Against the backdrop of the aims and objectives of this study, the literature published in standard journals and from reputed sources was collected. The process of review was based on the standard method. For the review aspects like the research question being posed, theoretical background, methodology used, findings, conclusions, etc. were considered. The discussion is presented in chronological order so that it also indicates the underlying pattern of evolution of the innovative methods to find the new diversity and plan to propose the new technologies as a step towards a sustainable ecosystem. Bioinformatics is branched which helps to find better and less time-consuming technologies to conserve the essential biological information in the form of databases and provide numerous conclusions for human welfare.

Results and Discussion

It has been reported that many methodologies for ecosystem conservation and reformation are already applied. The need for this investigation is to discuss the sustainability of the ecosystem and the betterment of species diversity. For this, we reported some of the literature to draw a new framework with the help of bioinformatics. Whole genome sequencing and the identification of the species provide huge data on the organism. This means the information can be compared in many different ways. For example, a researcher might compare their results/findings of genomic data of one organism with that of other characteristics, which might be stored in a different database. Hence, to process genomic data researchers can analyze different sets of essential information and the methods. This branch of biology has a huge capacity for data analysis and storage capabilities which aims to discover new relationships between different organisms and data. Thus, because of the importance of *L. hesperus,* the literature has been specifically reviewed and the discussion is presented hereunder.

Kenneth Ross and Robert L Smith (1979) reported the interesting courtship and mating behavior of the black widow spider, they work on *Lactrodectushesperus*chamberlin and live and were studied to determine stimuli responsible for mate location and courtship initiation in this species. The researchers observed new courtship patterns which included a vigorous display performed by females. Male *L hesperus* also initiated courtship behavior on unoccupied female webs of another species. In addition to this Fleischmann RD(1995) discussed about the new approach for genome analysis based on sequencing and assembly of unselected pieces of DNA from the whole chromosome has been applied to obtain the complete nucleotide sequence (1,830,137 base pairs) of the genome from the bacterium *Haemophilus influenzae* Rd. His effort gave a new framework for microbial genomics. *H. influenza* Rd genome sequence was the first complete genome (Genome Sequence Database, accession number L42023) from a free-living organism.

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Lately in the order to the identification of the other different properties of *Latrodectus* Daly FF (2001)tested the effectiveness of *L. hasseltii* (redback spider) antivenom in neutralizing the lethal effects of *L. hesperus* and *L. mactans* (North American black widow) venoms. They used LD50 values for the *L. hesperus* and *L. mactans* venom preparations were determined. The investigation determined that to derive mouse LD50 values for *L. hesperus* and *L. mactans* venom obtained by electrical stimulation of live adult spiders. Redback spider antivenom is effective in neutralizing the lethal effects of *L. hesperus* and *L. mactans* venoms in a mouse envenomation model. Jessica E. Garb et al (2004) also reported the spider genus *Latrodectus* includes the widely known black widows, notorious because of the extreme potency of their neurotoxic venom. They suggested the monophyletic group with minimal amounts of genetic divergence, corroborating the hypothesis that human transport has recently expanded the range of this species.

To the new technologies the whole genome sequencing L hesperus was done by Ayoub et al. the group of researchers 1262MBp genome size, Length of sequence in 1,137,104,656, Number of scaffolds151,814 and for this, they use sequencing technology Illumina with 48.0x coverage also identified three related widow species evolutionary branching, gene annotation regulatory sequence identification and ortho/paralogy detection. It provides numerous data like several contigs and gaped scaffolds. Multiple bioinformatics analysis tools are used to find the actual systemic position of the *L. hespures* and other valuable information like mutagens.

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On the other hand, Yonghui Zhao et al.(2010) monitored incredible strength and toughness, spider dragline silk is widely lauded for its impressive material properties. Dragline silk is composed of two structural proteins, MaSp1 and MaSp2, which are encoded by members of the spidroin gene family. Further comparative mapping with taxa of increasing divergence from Latrodectus will pinpoint when the MaSp1 duplication events occurred and the phylogenetic distribution of silk gene linkage patterns.

In addition to the study, Heidebrecht A.et al(2013) found natural spider silk fibers combine extraordinary properties such as stability and flexibility which results in a toughness superseding that of all other fiber materials. As the spider’s aggressive territorial behavior renders their farming not feasible, the biotechnological production of spider silk proteins (spidroins) is essential to investigate and employ them for applications.

Later on, Amanda Kelly Lane et al (2013) stated that Orb-web and cob-web weaving spiders spin dragline silk fibers that are among the strongest materials known. Draglines are primarily composed of MaSp1 and MaSp2, two spidroins (spider fibrous proteins) expressed in the major ampullate (MA) silk glands. Prior genetic studies of dragline silk have focused mostly on determining the sequence of these spidroins, leaving other genetic aspects of silk synthesis largely uncharacterized. They also identified transcription of TuSp1 in MA glands.. Their results demonstrated previously unrecognized transcript complexity in spider silk glands.

Thomas H Clarke, et al.(2014) stated that Spiders (Order Araneae) are essential predators in every terrestrial ecosystem largely because they have evolved potent arsenals of silk and venom. They proposed a transcriptional program for the silk glands that involves regulating the gland-specific synthesis of silk fiber and glue components followed by protecting and processing these components into functional fibers and glues. Furthermore, our multi-tissue transcriptome facilitates evolutionary analysis of arachnid genomes and adaptive protein systems were proposed.

In addition, Sandra M Correa Garhwal et al, (2017) compared silk gene expression profiles of mature males to those of females from three cob-web weaving species (Theridiidae). They used de novo assembled species-specific male transcriptomes from *Latrodectushesperus*, *Latrodectusgeometricus*, and *Steatodagrossa* followed by differential gene expression analyses..

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Conclusion

Conservation of species diversity, a continual process that requires well-designed strategies and approaches that fulfill the desired goal, In view the above; literature published in the reputed journals has been reviewed in this study. We come from this conclusion the innovation in the techniques and methodology is the necessity of upcoming issues. And as we know form the above discussion it provide us bulk information and that can we can use in different researches to enhance the economical trades like textile, armor and medicine. Sandeep Pandey et.al. (2015) reported that new scientific tools and techniques have potentiality in reclamations of the wilderness but require an extensive testing. In this investigation the genomic analysis provides a less time consuming valuable information about the species identification and taxonomical information and also draws frame work to maintain the sustainable ecosystem through control the loss of biodiversity and endangered species records. These methodologies also carry us towards recombination technologies to improve the traditional quality and quantities of the species byproduct. But the challenges are large enough that require retrieving and reorganizing these techniques to enhance the sustainable ecosystem in the planate.

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