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BIODIVERSITY LOSS, EMERGING INFECTIOUS DISEASES AND IMPACT ON HUMAN AND CROPS

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Abstract

We are losing biodiversity through several factors ranging from global warming, climatic change, unsustainable use of natural resources, human settlements, demand for food, medicine etc. Consequently, the biodiversity losses are causing emergence of infectious diseases (EIDs) which are making them more virulent than the past. Both biodiversity loss and emergence of diseases significantly impact the human derived benefits in-terms of economy and food. Ecological stability, productivity and food-web interactions are indirectly correlated with biodiversity and any change in these will cause losses in biodiversity that would certainly influence the human derived benefits and crops. The current article reviews the biodiversity losses and emerging infectious diseases at various levels reported by recent literature which will help in current status of EIDs and future recommendations.

Introduction

Since the publication of *Species plantarum* by Linnaeus in 1753, several other famous taxonomists entered into the competition, and till date, we have several volumes of Flora and Fauna of various countries such as Pakistan, Iraq, Saudi Arabia, Russia, China, Turkey etc. and regions for example, Himalayan Region, Oceanic, Europe, Great Plains of North America etc with an estimated number of 960,000 described plant species (Crane, 2004). Similarly, the floral and faunal resources estimated approximately 1.727 million species (United Nations Environment Programme- World Conservation Monitoring Centre (http://www.unep-wcmc.org/about-biodiversity_133.html, February 2012). However, even now new floral and faunal species are being reported from the various regions, for example 50 new spider species from tropical forests of Papa New Guinea (http://news.nationalgeographic.com/news/2009/03/photogalleries/new-species-papua-new-guinea/photo4.html, February 2012) or several other species are reported in 2011 by the International Institute for Species Exploration (http://species.asu.edu/Top10, February 2012). Globally 10–100 million species have been estimated (http://www.unep-wcmc.org/about-biodiversity_133.html, February 2012). These estimated numbers of species shows that the earth is still un-explored completely despite remarkable advances in science, transportation and communications. On one side, the biodiversity is not fully discovered while on the other hand, the ever increasing pressure on natural resources, due to human interactions, diseases, global warming etc. is causing the loss in biodiversity. In 2010, it was estimated by UNEP-WCMC, that from the 1.7 million described species, 34% of them are threatened (http://www.unep-wcmc.org/about-biodiversity_133.html, June 2012).

Biodiversity is considered beneficial for human beings from several aspects right starting from food and shelter to daily commercial uses and medicines. These benefits have been classified by Giri *et al*., (2001) into three major categories i.e., ecosystem services, biological resources, and social benefits. The ecosystem services include water reservoirs, soil, micro and macro nutrients, ability to keep balance between clean environment and pollution by breaking down polluted materials into simple substances and absorbing it, and several kinds of disasters to be recovered from them (Giri *et al*., 2001). Biological resources include food, medicines, livestock, agriculture, forest products etc. while social, cultural, religious and traditional values along with education and research fall under social benefits (Giri *et al*., 2001).

Reasons for biodiversity loss: Biodiversity loss on larger or smaller scales and even extinction of species is caused by three major factors, Emerging Infectious Diseases (EIDs), global warming, and invasiveness of species (Lips, 2011). In addition, rapid shift of traditional polyculture system to monoculture (Perfecto & Vandermeer, 1996 and references therein). However, the below have also unavoidable effects on biodiversity losses:

- Habitat loss and degradation
- Fire suppression
- Rust diseases
- Introduction of alien species
- Overexploitation of vegetation and fauna
- Pollution and diseases
- Global warming of climate

Though in some cases, the increasing rate of urbanization and human settlements is responsible for the loss in biodiversity but in other cases, as reported for endangered frog (*Leiopelmahochstetteri*) of New Zealand, the populations of frogs were severely fragmented even before the human settlement (Fouquet *et al*., 2010).

Diversity losses and augmented threats: The losses in biodiversity have been estimated by several researchers indicating that the extinction rate is approximately 10 - 1000 times which might increase two fold in future (Keesing *et al*., 2010). As per estimate of IUCN Red List

(2010), 21% mammals, 12% birds, 28% reptiles, 30% amphibians, 26% fishes, 31% other invertebrates, 79% mosses, 61% ferns, 40% gymnosperms, 70% flowering plants and 16% algae are threatened to extinction while all lichens species and mushrooms are threatened to a level of 100% (http://www.unep-wcmc.org/about-biodiversity_133.html). These estimations predict a very serious picture of extinction of the taxa in coming future with alarming rates. Based on higher rates of threatened nature, they may be ranked from higher to lower percentages as lichens, mushrooms, velvet worms, flowering plants, ferns, arachnids, gymnosperms, brown algae, amphibians etc. However, the extinction rates at global, regional, and local levels are not studied yet completely, while special emphasis must be done on microbes and symbiotic organisms (Keesing *et al*., 2010).

The shortage of clean water, healthy food, fuel, fodder, timber wood, medicines, forest products, clean and healthy environment would be expected to decrease in near future as global warming and climate change are causing threats to the survival of biotic resources at all kinds of habitat levels. Several epidemics have been spread at higher virulence rates by losses of biodiversity and climate changes. These losses and their relations have been reviewed by several authors (Keesing *et al*., 2006, 2010) and factors and mechanisms behind the emergence of infectious diseases (EIDs). The loss of biodiversity is caused by several factors including disease spread by the species and excursion of EIDs. In present review, we aimed to elaborate the issues and studies highlighted after the year 2009 to envisage the current status of biodiversity losses and need for future research aspects.

Crops disease, food shortage and biodiversity losses: Generally, the plants pathogens complete their life cycles on vector and host species for example rust. The pathogens include bacteria, viruses, Oomycetes, fungi, nematodes, and parasitic plants. With the extinction of several species, the microbial strains, causing serious diseases in crops, are unable to find the vectors, as a result, they have evolved themselves and raised their capabilities to expand their infections to other species which were previously resistant or incompatible to those diseases. The socio-economic conditions at global level have brought the people to the poverty level that 1.3 billion people are spending their daily lives on an income of less than 1 US$, while due to food shortage, about 800 million people are suffering at global level (Strange and Scott, 2005). Devastating pathogen attacks cause mortalities in human populations. The historical examples of pathogen emergence, spread and killing of human populations includes (i) the “Great Famine” when millions of people died between 1845 to 1852, that was spread due to infection of the pathogen, *Phytophthora infestans* in Europe resulting the potato blight disease, (ii) Great Bengal Famine in 1943 resulted in the deaths of million due to lack sustainable yield and production of the agriculture system and (iii) southern corn leaf blight caused by the fungus *Cochliobolus miyabeanus* in 1973 at USA to corn fields resulted in food shortages (Strange, 2003; Strange & Scott, 2005). These famines were mostly caused by the reduced agriculture production and thus vigorously impacted the human derived economic and health benefits. The catastrophes further aggravated and marginalized the agricultural and soil ecosystem.

There are various levels of biodiversity which are categorized by Pongsiri *et al*., (2009) based on genetic, microbial, vector species, host species, community, and habitat structures. Changes in any of these will cause changes in gene frequencies both in host–pathogens, microbial communities composition within host, vectors, or outside environment, as well as structure, composition, and diversity of vegetations (Pongsiri *et al*., 2009).

Global warming and species loss: It has been estimated the current earth temperature would increase by 3°C by the 2025 due to global warming. This increase or decrease in temperature around the globe has led the way to endangered or near to extinct various species at different latitudes. It was argued that quarter of the biodiversity (floral and funal) will be lost under current regimes. Similarly, it has been suggested that the proportion of actual biodiversity loss will be more than 80 % of genetic diversity within species may disappear in certain groups of organisms by 2080 (Nature Climate Change, 2011*)*. Examples like the disappearance of polar bears, penguins, and ringed seals etc from artic regions are some of the re-knowned example.

Recently, comprehensive review on plants species diversity and sustainable crop pests management has been compiled by Ratnadass *et al*., (2012) with several case studies of emerging diseases of crop plants. They conclude that the pests and diseases incidence are not necessarily decreased by vegetation diversifications. Some of the pests have the capabilities to use wider ranges of hosts as well as several other mechanisms to reduce pests had also limitations which suggest further detailed studies on mechanisms.

Laurance *et al*., (2011) reviewed 249 data sets from the literature to see the pattern of upper zone, lower zone and presence or absence of thermally specialized species in tropical regions of American, African and Asia-Pacific continents. They observed that the American tropics had high abundance of species with upper (upper zone specialists) and lower limits (lower zone specialists) than other two continents. However, the islands showed scarcity of elevational specialized species (Laurance *et al*., 2011). On the other hand, the upper zone specialists were mostly ectothermic with few endothermic species both in plants, birds, and animals (Laurance *et al*., 2011). They suggested the pattern of the species in tropics would be helpful in determining correlation between global warming and biodiversity loss.

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Disease emergence and confrontation with human and derived benefits

Natural population die-offs: The sudden loss of individuals in populations within short interval of time periods are known as natural population die-offs, which lead to the fragmentation and consequently genetic drift and severe population bottlenecks. Recently, Juarez *et al*., (2011) defined population die-offs as “a 1-year decline in the number of individuals within a population derived from one or more extreme natural events, where individual losses increase by at least 25% in comparison to that expected from the annual average mortality rate reported for the species” for the purpose of assessing vulnerability. They had proposed the framework for assessing population die-offs in which they had presented terrestrial mammals as a model but suggested that other taxa may also be used for such a framework.

Emerging infectious diseases (EID): The data shows that 335 infectious diseases were emerged in last 64 years, among which 60.3% were borne by zoonotic pathogens i.e., through non-human animal sources (Jones *et al*., 2008). Daszak *et al*., (2000) has also classified some of the 18 most prevalent and virulent diseases according to their EID class, pathogens, hosts, geography, impact and factors associated with the emergence. Among these zoonotic pathogens, 71.8% were developed in wildlife envisaging spread at lower altitudes; most of them were bacterial or rickettsial infections suggesting that several new strains against antibiotics has been evolved (Jones *et al*., 2008). It was also revealed that socio-economic, environmental, and ecological factors played a key role in development and spread of EIDs (Jones *et al*., 2008). The factors causing spread of emerging diseases with reference to viruses have been reviewed in detail by Jones (2009) which has categorized them into three groups, i.e., major agricultural changes, altered biology, and molecular alterations:

Major agricultural changes include accelerated agricultural intensifications and extensifications; diversification through introducing new crops, vulnerable new cultivars, infected weeds, and plant breeding; decrease in genetic diversity in earlier introduced crops and severe fragmentation in wild plants populations, excessive use of chemicals, irrigation in arid zone, and protected cropping (Jones, 2009).

Altered biological category includes natural host range expansion, adaptation of introduced host and increased virulence, as well introduction of new virulent host-virus taxa (Jones, 2009).

Molecular alterations include selection, mutations, recombination, symbiosis, genetic drift, population bottleneck and founder effects, satellite viruses and nucleic acids, and integration of genome (Jones, 2009).

One of the comprehensive host-parasite continua is presented by Daszak *et al*., (2000) in which EIDs shows complex relations between domestic animals, human populations, and wildlife. The interrelated and some individual key factors that cause emergence of diseases are translocation, encroachment, introduction, spill-over and spill back, human encroachment, *ex-situ* contact, ecological and biomedical manipulations, agricultural intensifications (in domestic animals), technology and industry, global travel, and urbanization (Daszak *et al*., 2000).

Emerging infectious diseases, crops, and wild plants: Anderson *et al*., (2004) categorized 18 most virulent emerging infectious diseases of cultivated and wild plants into three major groups as EIDs from the four world staples; cash crops, secondary staples and non-food crops; and wild plants. They suggested that anthropogenic introduction of parasites were one of the most important factors that emerged diseases. Though there are enormous information on EIDs of crop plants but less information on wild plants which gives blurred picture for conservation measures which they recommended to study in detail in future (Anderson *et al*., 2004).

Lyme disease in fragmented forests: The density of White-footed mouse was significantly increased in fragmented forests in America where they caused potential risks to human being to transfer lyme disease caused by *Borrelia burgdorferi* bacterium because of the disappearance of predators and competitors (Nupp & Swihart, 1996, 1998; Krohne & Hoch, 1999; Allan *et al*., 2003). Small patches of fragmented populations with less than 2 ha area had higher densities of white-footed mice than larger patches with more than 2 ha area which may cause potential risks to human health (Allan *et al*., 2003).

Monoculture and ant diversity: One of the practical examples is the coffee plantations in Central America where the rapid shift of traditional mulitculture system towards monoculture has been observed in recent decade. This is causing loss of both the floral and faunal biodiversity and increase of ant diversity on the other hand (Perfecto & Vandermeer, 1996 and references therein). Traditional agroecosystem of coffee in Costa Rica consisted of 30 different species of ants, the numbers of species then decreased to six in modern unshadedagroecosystems (Perfecto & Vandermeer, 1996).

Blister rust and white pines: In western Canada and USA, among eight species of white pines, seven species are susceptible and infected by white pine blister rust pathogen (*Cronartium ribicola*) (Tomback & Achuff, 2010 and references therein). Currants and gooseberries i.e., *Ribes* are the main sources of spreading blister rust in pines (Tomback and Achuff, 2010). The populations of white pines have been decreased when the natural fires were eliminated which were causing watersheds in these regions but were helpful in regenerating and spreading pine populations. Either one way of the other, climatic changes have also been occurred rise in temperatures and consequently causing rapid increase in mountain pine beetles after rust (Tomback & Achuff, 2010 and references therein). All these factors are decreasing the white pine populations decreasing genetic diversity as well, or we can say that the decrease in pine populations have given the chances to rust disease to spread quickly when all kinds of favorable environment are available.

Western nile virus and abundance of birds: An Asian, African and European originated mosquito-borne virus i.e., Western Nile Virus, is spread through several birds species that causes severe illness and sometimes human fatalities (Allan *et al*., 2009). In North America, it was observed that high diversity in bird species was highly correlated with lesser spread of Western Nile Virus and reservoir competency in the area and vice versa for lower bird diversity (Allan *et al*., 2009). Specifically, the non-passerine birds played an important role in disease spread, where species richness was significantly negatively correlated with mosquito and human infection rates, while passerine birds show no such correlation (Ezenwa *et al*., 2006). However, Hamer *et al*., (2011) argue that as a vector-borne disease simply species-host species richness/diversity may not work when fine spatial scales of pathogens are considered into account. Rather, the vector host use and force of infection within a community of hosts determine local infection rates of West Nile virus (WNV) in mosquito vectors must be studied (Hamer *et al*., 2011). The study of Hamer *et al*., (2011) reported that there was significant positive correlation between host community force of infection i.e., mosquitoes (*Culexpipiens*) with avian diversity and WNV infection in American robin (*Turdus migratorius*) and the house sparrow (*Passer domesticus*).

Trichomonosis and avian species: Trichomonisis is caused by the protozoan parasite (*Trichomonasgallinae*) that causes necrotic ingluvitis in avian species worldwide. In British, the disease emerged in green finches and chaffinches, the epidemic caused higher rates of mortalities (Lawson *et al*., 2011). Sequencing ITS1/5.8S rRNA/ITS2 region, SSU rRNA gene, Fe-hydrogenase gene, and also RAPD analysis revealed especially by Fe-hydrogenase gene results that clonal strain of the parasite was responsible for spreading such a devastative epidemic in Britain (Lawson *et al*., 2011).

Amphibians, fungal diseases and warming of climate: Amphibians are considered as bio-indicators because they are more sensitive to any kind of environmental, geographical, climatic, or man-made changes. Estimated numbers of endangered amphibian species near to extinction are 1856 (Young *et al*., 2004; Stuart *et al*., 2008; Fouquet *et al*., 2010). Even, the species richness and biodiversity itself has been underestimated, as revealed by sequencing mitochondrial and genomic DNAs, morphological and bioacoustic data in two species of frogs, which revealed that there were more species in clades than the reported ones (Funk *et al*., 2011). Therefore, several studies have been made to study the relationship between biodiversity loss and mortalities or infectious diseases in amphibian species which also envisages the reasons for their extinctions, threatened or endangered nature.

*Batrachochytrium dendrobatidis*is one of pathogenic fungal species that is causing higher mortalities in amphibian species across the globe by spreading a disease, chytridiomycosis (Bosch *et al*., 2007). The detailed study based on observations since 1997 till 2007 on amphibian declination at Spain showed that rise in temperature as climate warming indicator was highly correlated with the disease, chytridiomycosis (Bosch *et al*., 2007). However, the hypothesis of drought correlation with chytridiomycosis in amphibians have been rejected by Kriger (2009) who emphasized that the extreme dry weather should favor the amphibians which helps them in decrease of disease virulence and spread.

On the other hand, the possibility also cannot be denied that these amphibians might have become less resistant as the temperature increased in area causing climatic changes too (Barbetti *et al*., 2012). In another study, DNA barcode analysis on 63 amphibian species and field data using transect method during 1998 to 2008 from the highlands of Central Panama revealed that diversity in taxonomy, lineage and phylogeny in amphibian species was decreased due to epidemic chytridiomycosis caused by the pathogen, *B. dendrobatidis* (Crawford *et al*., 2010). For the DNA barcode analysis, sequences of mitochondrial COI (cytochrome oxidase subunit I) and 16S rRNA genes were used for the analysis (Crawford *et al*., 2010).

In a recent studies, whole genome of *B. dendrobatidis* has also been sequenced which would provide valuable information about the virulence, mutations, disease spread, and other markers related information. Genome sequences of 24-Mb in populations of *B. dendrobatidis* using 20 global samples from Europe, North and Central America, South Africa, and Australia exhibited three lineages, i.e., global panzootic lineage (BdGPL) with two morphologically different i.e., Swiss lineage (BdCH) and Cape lineage (BdCAPE) (Farrer *et al*., 2011). From the genomic analysis, Farrer *et al*., (2011) reported that BdGPL was hypervirulent with genomic recombination, intergenomic phylogenetic conflict and heterozygosity. They postulated that the isolated allopatric Bd populations went under several recombination process that lead the BdGPL to spread worldwide and caused amphibian biodiversity losses consequently.

Leishmaniasis and forest fragmentation: The density of small mammals (marsupials, rodents, sloths etc.) as main reservoirs of leishmania increases with increasing forest fragmentation due to the loss of larger predators and consequently the disease itself spreads rapidly (Badaro, 1988; Ostfled &d Keesing, 2000; Terborgh *et al*., 2001; Yadon *et al*., 2003). However, in addition to climate change, environmental factors and forest fragmentations, social factors also had a role in disease spread (Chavez *et al*., 2008).

Habitat fragmentation and impact on indri health: To test the hypothesis that anthropogenic factors affecting habitat destruction causes forest fragmentation, environmental pollution, and degrades natural resources which affect health of wildlife at the end, Indri populations from the protected and disturbed forests (tourists' spots as well as degraded forests) were studied by Junge *et al*., (2011). The lemur population from disturbed forest zone showed poor health conditions as compared to those lived in undisturbed locations (Junge *et al*., 2011). Indri population from the disturbed locations had lesser weight per kg, lower pulse per minute as well as higher temperature and respirations per minute, high white blood cells, lymphocytes, segmented neutrophils, eosinophils, monocytes per µl, and higher percentage of hematocrit (Junge *et al*., 2011). In addition, significant differences in 12 trace minerals were also observed in both the populations (Junge *et al*., 2011). However, comparative mortality rates between populations could be the indicator which was not studied by Junge *et al*., (2011) which they recommended to observe in future to get clear picture of final impacts of habitat damages.

White-nose syndrome (WNS) and bats extinction: One of the emerging infectious diseases is white-nose syndrome (WNS), caused by the fungus, *Geomycesdestructans*, which is causing severe mortalities in hibernating bats in eastern North America (Frick *et al*., 2010). WNS is specifically causing extinction of common bat, *Myotislucifugus*, which will be extinct on regional basis within next 16 years (Frick *et al*., 2010).

Conclusion

Community stability, productivity and food-web interactions are indirectly correlated with biodiversity, any changes in these factors will cause losses in biodiversity at both the community and ecosystems levels (Worm and Duffy, 2003). Therefore, they concluded that the whole system is itself the complex and suggested to study the interaction between biodiversity and food-web in addition to the biodiversity conservation.

Community epidemiology must also be well studied once it passes through its early stages of research which will take time to be at its firm steps of advancement in next coming decade where there is also need a collaborative approach of working on complex systems by ecologists, epidemiologists, and evolutionary biologists (Roche & Guegan, 2011).

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