**FOREST GENETIC TOOLS TO IMPROVE FOREST RESILIENCE TO CLIMATE CHANGE AND FOREST HEALTH**

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Abstract:

Forest health parameters respond to climate change having a direct impact on forest resilience. Intensification of human impact on ecosystem within the last decades has led to unexpected disturbances in the resilience of forest ecosystem on a global level as well as the provisions made for ecosystem services. The current Anthropocene era has led us to reconsider the forest management approach and to device new management practices having flexible nature and better dealing with global climate changes. This review aims to focus on the contemporary forest genetic tools, their utility and limitations with respect to improvement of forest resilience, climate change and forest health. Potential implications of genetic tools in forest management, its goals and principles and its response reveal the role of genetically diverse and adapted seeds and stock to be the foundation of forest health and ecosystem in addition to major contribution of gene conservation in vulnerable species and population preservation for future generations. Adaptive implementation owing to climate change require new tools, methodologies, skilled workforce, better infrastructure, re – focused investments as well as refined and reliable research and management.

**Keywords: Forest Resilience, Forest Health, Climate change, Genetic tools, gene conservation.**

**INTRODUCTION**

Forest health has been the prime concern of forest pathologists including the symptom and causes as well as preventive measures to maintain forest health. There has been a shift in perspective pertaining to forest health towards tree disease and their important role in forest ecosystem mechanisms as well as the ecological health (Franklin et al., (1987), Teale and Castello, 2011). In lieu of this, it can be observed that the effect of native fungal diseases has been evident in maintenance of diversity in the forest as they facilitate the species to be more resilient towards other types of disturbances (Hansen 1999, Hansen and Goheen 2000). Exotic trees have high biodiversity and aesthetics but low commercial value due to their controlled and uniform plantation owing to native and exotic tree diseases, maintaining a controlled biodiversity (Carnuset al.,2006), Lombardero et al., 2012). On the contrary, the whole ecosystem can be threatened as a result of some tree species extinction owing to the act of some invasive exotic pathogens (Roberge et al., 2011, Cobb et al., 2013, Cahill et al., 2008, Davis et al., 2014).

**FOREST HEALTH RISKS**

Major contributors in forest change are lack of management, over exploitation, degradation, habitat fragmentation, species distribution shifts and ecological succession. In addition, there has been also a shift in forest development from traditionally sustainable timber production to its multipurpose role in recreation and as a source of clean air and water (MacDonald, 2003, Hepting and Cowling 1977, Petrokofsky et al., 2010). Along with that an increase in the trade of plant commodities to remote and faraway places globally and the effect of change in climate has further impacted retrogressively on the condition of forest health (Wingfield, 1990, Holdenrieder, 2000). Excessive trade and climate change can lead to greater risks of establishment, spread and influence of newer and dangerous pests and pathogens. Lack of taxonomical morphologic expertise recently due to retirement without replacement along with rapid updation of new molecular methodological advances are one of the major concerns in forest ecosystem disturbances (Gadoury et al., 2009, MacDonald et al., 2009, Hamelin, 2012, Wood and Gebhardt, 2013). Regional outbreak of exotic tree fungal pathogens can be better understood using landscape ecology tools and forest pathology perspectives (Holdenrieder et al., 2004, Hatala et al., 2011). Diversity studies of endophytes of tree species provide insights of tree health (Sieber, 2007, Witzell et al., 2014) in addition to implementation of conservational biology tools pertaining to tree disease (Orwig 2002; Holzmueller et al., 2010; Pautasso et al., 2013 ;Shearer et al., 2013). In this rapidly evolving ecological aspect, the major aim of the present study lies in the selective evaluation of forest health, climate change and its effects on forest resilience. Secondarily, this study attempts to map out bridges between forest health, climate change and forest resilience with other aspects. Keeping in mind the time and space constrains, the focus has been mainly concentrated on the different genetical tools used in these three regions and their overall effect.

Human forced global climate change superimposed many different anthropogenic impacts on forest ecosystem. Rate of photosynthesis and respiration are readily influenced by climate change (Friberg et al., 2011, Jiao et al 2015, Kueppers et al., 2004). Other factors include forest temperature, radiation, and moisture in addition to medium and long climate periods. Short term process like frequency of storm and wild fires, herbivory and species migration are also influenced by climate and weather conditions. Biophysical forest process rate along with species’ physiological tolerance are altered causing change in forest ecosystem owing to global climate changes (Olesen et al., 2007, Kellomaki et al., 2008, Malhi et al., 2008).

Forest is a self-organised and complex system which is equipped with multiple natural occurrences responding to the intrinsic and extrinsic factors. As in the height and density of tree canopy are dependent on the water availability revealing the echo physiological relationship between environmental controls and plant growth (Berry and Roderick, 2002). There will be evident change in the forest ecosystem and species composition in response to climate change and specifically reduction in water availability. Upon reaching a threshold the vegetation beyond this limit will be lacking the characteristic taxonomic composition like in extreme arid conditions forest may reduce to savannas or grasslands while in case of rainforest, the high temperature may show closed boreal canopy having sufficient moisture for an extended growing season (Price and Scott, 2006; Kellomaki et al., 2008).

Regional climates are also affected by the availability of forest as evident from the Amazon forests (Betts et al., 2008; Phillips et al., 2009). Large number of literatures is available with respect to climate change and forests (Bonan et al., 2003; Callaghan et al., 2004). Climatic changes like moisture change (Bonan et al., 2003), energy fluxes (Wilson and Agnew, 1992), forest fire and herbivory (Ayres and Lomardero, 2000), carbon cycle systems (Phillips et al., 2009) emphasize the importance of maintaining forest resilience in order to cope up with the climatic changes and to survive under such conditions.

Forest resilience or the ability of the ecosystem to regain its original state after perturbation and the maintenance of its characteristic composition, structure, function, and process rates (Holling, 1973). In other words, ability of the forest system to tackle with the disturbance and not being affected, retaining its own basic structure and function, is termed as forest resilience (Walker and Salt, 2012). Forest give different responses to different types of disturbances and climatic changes, and depending upon its capability to cope up, the forest may show variation in its characteristic taxonomy and ecological processes and may also be altered in certain conditions. The state of a forest ecosystem represents its most dominant species assemblage at that location in the ecosystem, their functional roles, characteristic morphology and features like height, layers etc. and these define the state of forest in a mature forest type. Many researchers have worked and differentiated engineering resilience and ecological resilience (Holling, 1973; Peterson et al., 1998; Gunderson, 2000; Walker et al., 2004). The former refers to the ability of the ecosystem to return to its exact state after a disturbance. It is characterised by only one steady state and is also known as equilibrium dynamics. On the contrary, ecological resilience is the ability to face the disturbance and bear with the adverse conditions before reaching a threshold after which the forest ecosystem changes completely to another state and is also known as the non-equilibrium dynamics.

Resilience is eminent property of ecosystem being conferred at different levels like genes, species, functional groups, and processes (Gunderson 2000; Drever et al., 2006) and is maintained as an important characteristic feature owing to societal adaptation to climate change as suggested by various researchers (Millar et al., 2007; Chapin et al., 2010). Forest shows the property of resistance towards little changes within bounds owing to non-catastrophic variations like chronic and dynamic insect herbivory, minor blowdown, or canopy gaps due to tree deaths individually or in groups. Forests are also resistant to environmental changes like weather patterns due to redundancy at functional species level. There has been evidence of high resilience in the ecosystem, but low resistance towards perturbation. However, contrary situation is seen in well-developed forests, especially primary forests, having both the properties of resilience and resistance towards changes (Drever et al., 2006). Resistance denotes stability, showing the capability of ecosystem to maintain a dynamic equilibrium by absorbing disturbances and being constant over longer periods of time.

**ISSUES OF SCALE AND RESILIENCE.**

 A theoretical method is dependent on its proper scaling. Majority of the studies based on resilience focus on the reason behind change or maintenance of a particular state, while scaling studies focus on the evaluation of phenomena responsible for steady state ecosystems (Holling, 1973). Species level beta diversity enhances ecosystem resilience to adapt for the large-scale climate change through redundancy level of regional species pool. Resilience needs a temporal component related to disturbance, frequency, and ecosystem recovery, which is considered over many decades to centuries (Thompson et al., 2009). The change in ecosystem is caused due to environmental change or disturbance which is having a high magnitude.

**GENETIC DIVERSITY AND RESILIENCE TO CLIMATE CHANGE.**

As resilience attributes different levels in the biodiversity, the genetic species composition becomes the most fundamental feature. Molecular variation among species within forest community, within ecosystem diversity, across a geographical area shows biological diversity. This genotypic variation among population is the basic expression of biological diversity. Individuals at population level contributing to each level of ecological hierarchy undergo natural selection adding to resilience of species and forest ecosystem (Muller-Starck et al., 2005). Diversity fosters natural regeneration and help in adaptation towards climatic changes occurring in the quaternary period and needs to be maintained in order to face the challenges posed by anthropogenic global warming. Genetic variation forms the basis of natural selection of genotypes within species in response to environmental fluctuations (Etterson 2004; Reusch et al., 2005; Schaberg et al., 2008). This largely depends on the in situ genetic variation among each population of species (Bradshaw 1991).

Exposure to environmental changes decides the rate of adaptation of that population, its dispersal, or its fate otherwise (Burger and Lynch 1995). Range of fundamental eco physiological tolerance of a species is the expression of its genetic diversity range. Interspecific competitive interactions, in addition to dispersal method, are the primary determinants of response to change in a particular species (Halpin, 1997). In addition to adaptation, migration also plays role in responding towards evident climatic change. Many researchers have suggested diversification as a best tool to adaptation towards unpredictable climatic conditions (Ledig and Kitzmiller 1992, Millar et al., 2007). The two main means of adaptation towards change as shown by a particular species, include the dispersal of seed or vegetative propagules towards favourable environmental condition for survival or through change in their gene frequency to encourage genotypes capable of adaptation to the climatic variation (Burdon and Thrall 2001; Reusch et al., 2005). Another method of adaptation includes phenotypic plasticity, if permitted by the genotype (Nussey et al., 2005). Gene flow is further enhanced by dispersal among fragmented trees species, resulting in maintenance of genetic diversity. Prevention of genetic drift and loss of genetic diversity caused due to inbreeding within small isolated community of tree species (Fuchs and Hamrick, 2010; Farwig et al., 2008).

In general, genetic diversity of a forest ecosystem is maintained through seed and pollen dispersal, affecting the silence over change in the long term with respect to space and time in addition to re-establishment on favourable grounds. However, this capacity may have been reduced owing to anthropogenic intervention in landscape and gene pool. Genetic and reproductive activity of populations is potentially affected by population fragmentation. This generates a concern regarding the idea of in situ resilience owing to potential genetic adaptation, there are both short and long term components with respect to adaptation at genetic level, which enables variability in gene frequencies promoting growth and reproduction in an altered environment. Higher degree of diversity within natural populations is responsible for population stability in different environments (Namkoong et al., 1996), potential pollutants (Kull et al., 2007; Cantin et al., 2020) and pest species (Thrall et al., 2001). These concerns exaggerate the need for genetically diverse species to overcome the predicted climate change (IPCC 2007), which is too quick for a species to be able to prepare itself for adaptation over the low diversity level species in the forest population.

Forests are generally undomesticated and exhibit a very high level of genetic diversity owing to effective population size, local adaptation, and neutrality in the evolution process among heterogeneous environment (Hamrick 1986). Operational programmes of tree reading and related infrastructure like seed and seedling production are active since mid-1900’s. Forest biologists have used proven trials for seed selection of important commercial species over in the last 200 years and to assess the seed distance without compromising local adaptation under suitable climate (Aitken and Bemmels 2015, Langlet 1971). Molecular biology techniques are being utilised in this area since 1990’s and early 2000s. Techniques like QTL mappings have facilitated the marker aided selection of growth, productivity, and other wood qualities. Since then, highly polygenic nature of economically and environmentally important traits have been evident (Manolio et al., 2009). Due to drop in cost of sequencing, the focus of forest genetics research has moved towards the search related to single genes with great impact in addition to testing small target set of genes in place of genome wide scan, in order to tackle the contemporary demand of climate change, forest health, adaptation, resistance and commercial issues pertaining to biotic and abiotic stress.

Forest genomics in insects and disease resistance and early detection.

Moving from economic trades like growth and wood quality are now replaced by pest resistance genes owing to non-native insects and disease impact in addition to some natives species of pest with increased range and impact pertaining to climate change. Genomic tools help to

a. Understanding genomic architecture of insects and disease resistance or tolerance. b. To Select tree species which can survive/ thrive under the presence of these pests.

c. To detect the invasive species of pests and pathogens.

This can be better understood by American chestnut example (Castanea dentata) (Westbrook et al., 2019). Chestnut blight fungus (Cryphonectria paresilica) in USA is a threat to American chestnut tree population. To overcome this problem, the American Chestnut Foundation, TACF has started a breeding programme between blight resistant Chinese chestnut (Castanea mollissima) and American chestnut (Castanea dentata). Only a few major loci bear blight resistance and thus between (blight resistant Chinese chestnut) Castanea mollissima X Castanea dentata (American chestnut) (F1 generation) upon backcross over 3 generations and then inter-crossed to Castanea dentata (American chestnut) progeny resulted in large production of BC3F2 trees between 2000 to 2018. Among these BC3F2 trees, about 1/3 were identified as potential parents for further generations (Westbrook et al. 2019) have developed genomic prediction models for blight resistance and have found it accurate as compared to pedigree analysis which makes it cost and time effective all alone. They also revealed blight resistance as well as the trade-off between the two species followed polygenic inheritance. TACF considered different options in development of resistant trees, namely inclusion of different chestnut sources of resistance via marker-assisted introgressive system and secondly the technique to establish transgenic method to be used to develop resistant Castanea dentata (New House et al., 2014).

Distribution and abundance of insect pests are equivocal to climate change, making it a serious factor. As evident in case of mountain pine beetle (MPB: Dendroctonus ponerosae) apparent in western North America. Warmer winter temperatures have caused its increased population exponentially (Safranyik et al., 2010). MBP has resulted in substantial mortality in Lodgepool pine (Pinus contorta) and Jack pine (Pinus banksiana) in Western Canada. Being one of the dominant parts of the forest ecosystem, these have caused profound ecological and economic complications, leading to demand of MPB resistant species to be breed in order to restore the areas. Cullingham et al., (2019) identified two important loci related to resistance using transcriptional profiling and selection tests. One of these two loci show consistent association with resistance in case of Lodgepool pine (Pinus contorta). This may facilitate in the development of genome wide marker-aided selection or genomic selection tools in breeding programmes.

**ADAPTATION TO CHANGING CLIMATE**

Population Genomic approaches lead to understanding of adaptive capacity in a tree population and challenges faced in warmer climates. Majorly high-level genetic diversity and considerable phenotypic plasticity among tree species has contributed in survival through past environmental variability. However, there is need of better knowledge regarding degree of adaptation at the local level towards the climate as well as new methods of tolerance capacity prediction and adaptation to new climates. Genomic approach provides rapid identification alternatives with respect to environmental factors showing phenotypic – genotypic and environmental associations (Alberto et al., 2013; Sork et al., 2013).

Performance of genomic data compare to phenotype measurement among short-term seedling common garden was evaluated by (Mahoney et al., 2019) in addition to long-term provenance trials. They determined the adaptive variance patterns and climate features of selection using factors like bud phenology, cold hardiness and growth. About >32,000 sample SNPs for genotypes and climatic data for 281 populations were utilized (Pinus contorta). The results showed seedling phenotype markers giving better explanation of adaptive variation as compared to genomic data set or climatic data alone. GEA (genotype environment association) analysis proved better in identification of climatic factors causing diversity in cases where phenotypic data was unavailable, thus making species management easier without long-term trials.

Applied ecological genomics can help to predict the potential of evolution apparent in the local population with respect to climate change. Allele frequency shifts for adaptive Loci pertaining to climate shifts were addressed by Ingvarsson and Bernhardsson (2019) using Populous tremula (European aspen). Populous tremula was used owing to its long history available regarding its genetics, genomics and phenotype. About 94 species across 10° latitude were sequenced for the whole genome in the areas of Sweden. The data so obtained was subjected to genotype environment analysis (LFMM) and GDM modelling was done for the estimation of genetic offsets (Fitzpatrick and Keller, 2015). This resulted in the mall adaptation description of an individual having specific allelic composition when environmental shift is subjected. Large genetic adjustments were required even in a short period of nearly 50 years for specifically northern population in order to cope with their local climatic conditions as compare to the southern populations which show smaller genetic offsets and convergence with the disproportionate effects among sub artics towards climatic change (IPCC 2018).

Apart from higher focus on economically important species, there has been also studies which evaluate the influence of population genomics to realize the neutral and adaptive processes related to non-commercial but ecologically valuable species. Mayol et al. (2019), provided the evidence of adaptive divergence among growth and phonology to be correlated with the variation in temperature among provenances. The study also emphasized on the demographic decline of some species to be more pronounced as compare to others. The novel aspect of use of pathway analysis to assess the collective effect of SNPs among biological categories revealed that flavonoid biosynthesis pathway has undergone differential selection, showing the functional relevance of oxidative stress or membrane stabilization required in cold temperatures (Schultz et al., 2016). Population genomics caters a wide span of genetic considerations owing to Forest health, forest resilience and climatic change including univariate SNP – environment and SNP – phenotype associations (Kremer and Le Corre, 2012) in addition to description of adaptation in terms of poly genic process, including various loci having distinctly small effects (Boyle et al., 2017). This clears the vision of genotypic mapping process of phenotypes and provides a better understanding.

Forest management addressing climate change in the contemporary scenario is considering implementation of assisted gene flow as an important genetic tool. This is made possible with its ability to apply or increase the pre-adaptive genotype frequency in new climate (Aitken and Whitlock, 2013). Genomic data has great contribution in enriching the conservation strategies by facilitating solid estimates, owing to population adaptive variations (Funk et al., 2019). Borrell et al. (2019), reported the potential of assisted gene flow framework and its limitations in a study on Betula nana (montane dwarf birch tree). They used genotype environment association (GEA) and environmental niche modelling in order to identify the maladaptive populations that is having allele frequency deviation in current and projected future environmental conditions (c – RONA, f - RONA). Vulnerability assessment through assessment of adaptive capacity of a particular species is a very challenging task. Godbout et al. (2019), reported genomic diversity to be the expression of its environment, including climate, soil, biotic interactions and many more and how it can be used to examine adaptive capacity .

Various species of tree show hybridization with cogeners, hence contributing towards local adaptation with respect to transitional environments (Bawa and Holliday, 2016). Many tree species have been hybridized to adaptive environment that is otherwise not typical to the species range like Populous Trichocarpa X Populous balsamifera (Suarez-Gonzalez et al., 2018), Pinus Strobiformis X Pinus Flexilis (Menon et al., 2019). Sequencing in this case was done using double digest RAD sequence and combination of individual based simulations and genetic cline analysis. The results showed northward integration due to non-concordance of morphological and genomic cline center estimates. Although appearing to be degrading the biodiversity, hybridization or introgression among tree species is a natural evolutionary trajectory characteristic which provides intermediate phenotypes among ectones and by directional transfer of adaptive variations.

**GENOMIC EVOLUTION AND GENOMIC TOOLS**

Attainment of high-quality reference genomes have been difficult due to size and complexity of tree genomes. The first tree genome was sequenced in 2006 of Populus trichocarpa (Tuskan et al., 2006) and Picea Abies in 2013 (Nystedt et al., 2013). About 52 out of 200 unique plant reference genomes belong to trees species (Wegrzyn et al., 2019). The situation has been improved with the application of new genomics, bioinformatics and precision phenotypic tools. Angiosperm genomes are much easier than conifer as the later bear a large size and high repetition in genome making and is difficult to understand and work on (De La Torre et al., 2014). DNA sequencing techniques have provided important breakthroughs in case of large genomes like gymnosperms. Whole genome duplication events have characterized the evolution of angiosperms (Lee beans Mack et al., 2019). They also have higher rates of chromosomal, rearrangement and mutation rates than that of gymnosperms (Pavy et al., 2017). Adaptive evolution rates are compare using coding regions among gymnosperms and angiosperms. Lower rates of neutral evolution but higher rate of non-synonymous substitutions have been reported among gymnosperms than that of angiosperms (De La Torre et al., 2017). Gymnosperms show higher gene family expansion which is related to defense responses, climatic tolerances as well as lignin and cellulose biosynthesis. In addition to genomics the phenomic tool like UAVs which use hyperspectral sensor to create leaf spectral indices helping in responding against drought stress or pest invasions are also very useful in forest resilience, climatic control and forest health (Calderon et al., 2015). Wegrzyn et al., 2019 reported a gap between the current state of data integration for non – model species and model species. Thus implementation of the data standards, ontologies, analytical work flows and integrated databases into cyberinfrastructures and inclusion in best practices is beneficial in this context.

**CONCLUSION**

Forest health and its long-term maintenance is imperative to functioning of global ecosystem in general and to fight against climate change in particular. Trees are architects of forest ecosystem and are under challenge throughout their life span owing to biotic and abiotic stresses. There has been a rapid improvement in knowledge, owing to genomics and genetic tools as to inform forest management and conservation decision in addition to accelerating breeding programs and to take up the climate change challenges. In order to get acceptance by various stakeholders from different public decisions making authorities, a genetic tool, economic and ecologically low at cost and high at benefits should be taken into account. Genomic tools are highly versatile and provide the insight of the plant’s history and this is one of the important criteria.

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