

Short Communication

Trees and Climate Change - The Search for Adaptation: Why Travel While I am Already There?

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Columbia, Vancouver, British Columbia, Canada**Received:** August 19, 2015; **Accepted:** September 21,
2015; **Published:** October 16, 2015**Abstract**

Assisted migration is a viable option to reducing the effect of the misalignment between forest trees migration rate and the speed of environmental changes caused by climate change. To ensure assisted migration success, several biological factors such as the contrasting thermal and photoperiod differences between plants original and new environments, novel Delphic conditions, and epigenetic factors require serious consideration for the safe moving of genotypes to new habitats. In situ selection in species' leading fronts offers great opportunities in identifying genotypes adapted to fluctuating environment and thus provide adapted material for pole ward movement with minimal risks. Available modern genomics-based quantitative genomics methods could offer an effective in situ selection approach for the delivery of greater gains of adapted stock faster than their counterpart conventional methods.

Keywords: Assisted migration; Adaptation; In situ selection; Peripheral populations; Modern quantitative genomics

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Most plant populations are locally adapted and genetically differentiated for adaptive traits. Global warming is threatening this adaptation. Assisted migration, the physical movement of genotypes to "favorable" new environments, is perceived as a viable option to ameliorate the misalignment between migration rate of plant populations and environmental alterations caused by climate change [1-3]. This process is critical for avoiding mal adaptation and requires perfect matching between the genotypes being moved and a constantly changing environment. While assisted migration seems sensible, it assumes perfect matching between the genotypes moved and their new environment in spite of the drastic changes caused by, for instance: a) contrasting thermal environments, b) substantial photoperiod shifts, c) novel and Delphic conditions and d) epigenetic after-effects associated with plants transfer (a.k.a., environmental preconditioning/imprinting) [4-9].

In forestry, assisted migration endeavors to accomplish two goals; namely, capturing the genetic gains achieved through long-term traditional tree breeding and moving the improved material to track the changing favorable environmental conditions created by the expansion of a species' climatic window across latitudes [10]. This is motivated by the time scale dedicated to, and the size of, finances invested in traditional programs. Tree breeding often involves repeated cycles of breeding, testing, and selection [11]. These programs are aimed at meeting the planting demands of specific breeding zones, and thus parents selection and offspring testing and reforestation are often restricted within these areas [12-14]. Substantial and unrestricted genetic movement is exercised within the confines of these specific breeding zones as offspring (new recombinations) are planted throughout these zones. Notwithstanding the man-made unrestricted genetic movement within breeding zones, these breeding programs are in essence, spatially static and might be slow in dealing

with the increased mobility required to cope with rapid climate change.

Populations at a species' leading latitudinal fronts harbor genotypes adapted to fluctuating, unstable environments, and there is thus an opportunity for their identification and use as planting sources for new sites with minimal latitude shift (Figure 1) [10,15-19]. In situ selection in these populations offers a unique partnership between nature and man where existing natural peripheral populations play a dual breeding (production of adapted offspring) and testing (exposure to fluctuating environment) role. To maximize survival of the selected individuals and their offspring, man-made in situ selection among these adapted genotypes should exclusively focus on adaptive traits rather than yield attributes. Most adaptive attribute, such as cold and drought tolerance and timing of growth initiation and cessation, are known to have high genetic control, and spatial and age effects differences will thus be minimal [20].

The extent of genetic diversity of species peripheral populations is often thought to be lower than that of their central counterparts; however, there is increased evidence supporting the role of gene flow as an important force replenishing genetic diversity [21], with some suggestions that gene flow will introduce genes that will be better adapted than local ones under future climate change scenarios [22-23]. Additionally, it is expected that the warming trend will increase growth and fecundity, improve survival, and promote germination and recruitment [24-23], thus chances for increased productivity in the new favorable environmental conditions.

Genetic evaluation and ranking of selected individuals at species' leading edge can easily be accomplished using modern genomics fingerprinting techniques [26]. Furthermore genomics-based quantitative genomics approaches that simultaneously utilize large amount of genomic information to explain the observed phenotypic variability of complex polygenic traits are available [27-29]. These

genetic analyses are perfectly suited to unstructured natural populations where prior knowledge of genealogy is often lacking. The selected individuals, in turn, would form the raw material for the production of adapted stocks for planting in new favorable environmental conditions that are located at the species' latitudinal front edge and beyond. This approach of natural breeding, testing and selection mimics traditional breeding and selection programs yet offers faster delivery of proven adapted stock.

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References

- McLachlan JS, Hellmann JJ, Schwartz MW. A framework for debate of assisted migration in an era of climate changes. *Conservation Biology*. 2007; 21: 297-302.
- Kremer A, Ronce O, Amancio RJJ, Guillaume F, Bohrer G, Nathan R. et al. Long-distance gene flow and adaptation of forest trees to rapid climate change. *Ecology Letters*. 2012; 15: 378-392.
- Pedlar JH, McKenney DW, Aubin I, Beardmore L, Beaulieu J, Iverson L. et al. Placing forestry in the assisted migration debate. *BioScience*. 2012; 62: 835-842.
- Skrøppa T, Tollefsrud MM, Sperisen C, Johnsen Ø. Rapid change in adaptive performance from one generation to the next in *Picea abies*- central European trees in a Nordic environment. *Tree Genetics and Genomes*. 2010; 6: 93-99.
- Vitt P, Havens K, Kramer AT, Sollenberger D, Yates E. Assisted migration of plants: Changes in latitudes, changes in attitudes. *Biological Conservation*. 2010; 143: 18-27.
- Frascaria-Lacoste NJ, Fernandez-Manjarres. Assisted colonization of foundation species: Lack of consideration of the extended phenotype concept - Response to Kreyling et al. *Restoration Ecology*. 2012; 20: 296-298.
- Kranabetter JM, Stoehr MU, Neill GA. Divergence in ectomycorrhizal communities with foreign Douglas-fir populations and implications for assisted migration. *Ecological Applications*. 2012; 22: 550-560.
- Saikkonen K, Taulavuori K, Hyvönen, Gundel TPE, Hamilton CE, Vänninen I. Climate change-driven species range shifts filtered by photoperiodism. *Nature Climate Change*. 2012; 2: 239-242.
- Bräutigam K, Vining KJ, Lafon-Placette C, Fossdal CG, Mirouze M, Marcos JG. et al. Epigenetic regulation of adaptive responses of forest tree species to the environment. *Ecology and Evolution*. 2013; 3: 399-415.
- Marris E. *Forestry: Planting the forest of the future*. 2009; 459: 906-908.
- Allard RW. *Principles of Plant Breeding*. 1999; Inc., N.Y.
- Ying CC, Yanchuk AD. The development of British Columbia's tree seed transfer guidelines: purpose, concept, methodology, and implementation. *Forest Ecology and Management*. 2006; 227: 1-13.
- Chaisurisri K, El-Kassaby. Genetic diversity in a seed production population vs natural population of Sitka spruce. *Biodiversity and Conservation*. 1981; 3: 512-523.
- El-Kassaby YA, Sziklai O. Genetic variation of allozyme and quantitative traits in a 29 selected Douglas-fir [*Pseudotsugamenziesii* (Mirb) Franco] population. *Forest Ecology and Management*. 1982; 4: 115-126.
- Lachmann M, Jablonka E. The inheritance of phenotypes: an adaptation to fluctuating environments. *Journal of Theoretical Biology*. 1996; 181: 1-9.
- Crawford RMM. *Plants at the Margin - Ecological Limits and Climate Change*. 2008; Cambridge Univ. Press.
- Bell G. Fluctuating selection: the perpetual renewal of adaptation in variable environments. *Philosophical Transactions of the Royal Society*. 2009; 365: 87-97.
- Hofmann AA, Sgro CM. Climate change and evolutionary adaptation. *Nature* 2011; 470: 470-485.
- Ketola T, Mikonranta L, Zhang J, Saarinen K, Örmälä A-M, Friman V-P. et al. Fluctuating temperature leads to evolution of thermal generalism and preadaptation to novel environments. *Evolution* 2013; 67: 2936-2944.
- McKown AD, Guy RD, Klápšte J, Gerales A, Friedmann M, Cronk QCB. et al. Geographical and environmental gradients shape phenotypic trait variation and genetic structure in *Populus trichocarpa*. *New Phytologist*. 2014; 201: 1263-1276.
- Yeaman S, Jarvis A. Regional heterogeneity and gene flow maintain variance in a quantitative trait within populations of lodge pole pine. *Proceedings of the Royal Society B: Biological Sciences*. 2006; 273:1587-1593.
- Alleaume-Benharira M, Pen IR, Ronce O. Geographical patterns of adaptation within a species range: interactions between drift and gene flow. *Journal of Evolutionary Biology*. 2006; 19: 203-215.
- Holliday JA, Suktan H, Aitken SN. Divergent selection and heterogeneous migration rates across the range of Sitka spruce (*Picea sitchensis*). *Proceedings of the Royal Society Series*. 2012; 279: 1675-1683.
- Savolainen O. The genomic basis of local climatic adaptation. *Science*. 2011; 334: 49-50.
- Alberto FJ, Aitken SN, Alía R, González-Martínez SC, Hänninen H, Kremer A. et al. Potential for evolutionary responses to climate change - evidence from tree populations. *Global Change Biology*. 2013; 19: 1645-1661.
- Chen C, Mitchell SE, Elshire RJ, Buckler ES, El-Kassaby YA. Mining conifers' mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. *Tree Genetics and Genomes*. 2013; 9: 1537-1544.
- Frentiu FD, Clegg SM, Chittock J, Burke T, Blows MW, Owens IPF. et al. Pedigree-free animal models: the relatedness matrix reloaded. *Proceedings of the Royal Society Series*. 2008; 275: 639-647.
- El-Kassaby YA, Klápšte J, Guy RD. Breeding without Breeding: selection using the genomic best linear unbiased predictor method (GBLUP). *New Forests*. 2012; 43: 631-637.
- Porth I, Klápšte J, Skyba O, Lai BSK, Gerales A, Muchero M. et al. *Populus trichocarpa* cell wall chemistry and ultra structure trait variation, genetic control and genetic correlations. *New Phytologist*. 2013; 197: 777-790.