

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, CanadaReceived: 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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