

The TransX project: A latitudinal network of provenance trials across eastern North America to test the climatic vulnerability of northeastern tree species and their potential for assisted migration

by Jacob Ravn^{1*}, Guillaume Moreau², Rafaella Mayrinck³, Malcolm Itter³, Cédric Albert^{1,4}, Lynsay Spafford¹, Dan Kneeshaw⁵, Alexis Achim², Marie-Pier Perron², Sébastien Dumont², Gabriel Rogers¹, Mackenzie Good¹, and Loïc D'Orangeville²

ABSTRACT

Adaptive silviculture hinges on our capacity to predict future changes in tree species demography (e.g. growth, mortality) in response to climate change. Experimental tree translocation studies across climate gradients can help anticipate such changes. The TransX experiment is a network of provenance trials, ranging from North Carolina (US) to Quebec (CA), where populations of ten boreal and temperate tree species, and genetically improved genotypes of four commercially important tree species have been planted simultaneously and will be monitored for their response to gradients of 14.5°C in mean annual temperature and 600 mm in precipitation. The objectives of this experiment are to: 1) quantify the effect of climate on trait variation and plasticity across selected tree populations and species, and 2) assess how such trait variation relates to growth and survival.

Here we outline the design of the experiment, and describe the research efforts to monitor annual survival, health, growth, leaf morphology and physiology, and track leaf phenology using time-lapse cameras. By exposing major tree species to a wide range of climate and site conditions, the TransX project will fill significant knowledge gaps on forest ecosystem responses to climate change and inform adaptive management strategies, such as forest assisted migration.

Keywords: climate change; common garden; leaf phenology; climate transfer distances; tree growth

RÉSUMÉ

La sylviculture adaptative repose sur notre capacité à prédire les changements futurs dans la démographie des espèces d'arbres (p. ex. croissance, mortalité) en réponse aux changements climatiques. Les études expérimentales sur la translocation d'arbres à travers différents gradients climatiques peuvent aider à anticiper ces changements. L'expérience TransX est un réseau d'essais de provenance, s'étendant de la Caroline du Nord (États-Unis) au Québec (Canada), où des populations de dix espèces d'arbres boréales et tempérées, ainsi que des génotypes génétiquement améliorés de quatre espèces d'arbres d'importance commerciale, ont été plantées simultanément et seront surveillées afin d'observer leur réponse à des gradients de 14,5 °C de température annuelle moyenne et de 600 mm de précipitations. Les objectifs de cette expérience sont les suivants : 1) quantifier l'effet du climat sur la variation et la plasticité des traits chez certaines populations et espèces d'arbres sélectionnées, et 2) évaluer comment cette variation des traits est liée à la croissance et à la survie.

Nous présentons ici la conception de l'expérience et décrivons les efforts de recherche visant à suivre la survie annuelle, la santé, la croissance, la morphologie et la physiologie des feuilles, ainsi que la phénologie des feuilles à l'aide de photos prises à intervalles réguliers. En exposant d'importantes espèces d'arbres à un large éventail de conditions climatiques et de sites, le projet TransX comblera d'importantes lacunes dans les connaissances sur la réponse des écosystèmes forestiers au changement climatique et éclairera les stratégies de gestion adaptative, telles que la migration assistée.

Mots clés : changement climatique ; jardin commun ; phénologie foliaire ; distances de transfert climatique ; croissance des arbres

¹Faculty of Forestry and Environmental Management, University of New Brunswick, 28 Dineen Drive, Fredericton, NB E3B 5A3, Canada

*corresponding author: Jacob Ravn at jravn@unb.ca

²Centre d'étude de la forêt, Département des sciences du bois et de la forêt, Université Laval, 2405 rue de la Terrasse, Québec, QC G1V 0A6, Canada

³University of Massachusetts Amherst, Department of Environmental Conservation, 160 Holdsworth Way, Amherst, MA 01003, USA

⁴École de Foresterie, Université de Moncton, Campus d'Edmundston, 165 Hébert boulevard, Edmundston, NB E3V 2S8, Canada

⁵Département des sciences biologiques, Université du Québec à Montréal, Montréal, QC H3C 3P8, Canada

Introduction

Large geographical shifts in the climate niche of most tree species are projected in the coming decades (Davis and Shaw 2001; McKenney *et al.* 2007), far outpacing species migration potential (Sittaro *et al.* 2017). The resulting changes in demographic rates (recruitment, mortality, growth) are expected to have significant impacts on the composition, structure, and function of forests (Allen *et al.* 2010; McDowell *et al.* 2020), threatening ecological and economic goods and services. Implementing adaptive management strategies to effectively address these challenges is essential, but doing so requires accurate predictions of species and forest responses to climate change.

Process-based stand simulation models can be used to predict forest demographic changes (Taylor *et al.* 2017), which can then be integrated into strategic forest management planning models (Ashraf *et al.* 2015; Metsaranta *et al.* 2024; Albert *et al.* 2025). However, these simulation models suffer from several limitations, including limited empirical knowledge of species climate response curves, i.e., how tree demographic rates will acclimate to the projected climate. The recent benchmarking of common models with empirical growth data from permanent sample plots across eastern North America shows that large uncertainties remain in how these models predict growth for different climates, challenging the potential reliability of predicted growth responses to climate change (Wang *et al.* 2025). These models can be informed through various observational data streams, including the dendroecological studies of mature trees (D’Orangeville *et al.* 2018), or continuous forest inventories under which the same set of plots are periodically remeasured (Searls *et al.* 2020; Wang *et al.* 2023). These approaches typically assume that a species response to climate variation is uniform across its geographic range and can be used to accurately predict population responses to differing climate conditions. However, the divergent responses among Ponderosa pine (*Pinus ponderosa* Dougl. ex P. & C. Laws.) populations to range-wide climate variation suggests that this approach can lead to inaccuracies in growth and demographic projections (Perret *et al.* 2024). Such findings highlight the importance of local population adaptation and respective acclimatization potential when predicting shifts in tree growth and forest dynamics under climate change.

Provenance trials have historically served to compare the growth and survival rates, and commercially desirable traits (e.g., form, volume growth rates, pest resistance) of tree populations (Mátyás 1996). These characteristics are ultimately the result of variation in functional traits among populations, including morphological variation (e.g., leaf thickness, stomatal density), physiological variation (e.g., hydraulic conductance, photosynthetic capacity), and phenological variation (e.g., leaf emergence, senescence). Understanding how functional traits compare between populations and species and how they vary along climatic gradients can help evaluate the vulnerability of tree species and populations to climate change, while also informing forest assisted migration (FAM), a promising silvicultural approach that involves planting warm-adapted trees in regions that will match historic local climate in the future to improve forest resilience to climate stress (Williams and Dumroese 2013; Park and Rodgers 2023). Selecting the optimal tree population for

FAM first requires a comparison of climatic sensitivity between populations of a candidate species. To do so, existing provenance trials can be assessed using population growth or survival responses to site climate, then using varying statistical methods to extrapolate such relationships to model population responses across wider climate spaces (Benito Garzon *et al.* 2011; Leites *et al.* 2012; O’Neill *et al.* 2014; Pedlar *et al.* 2021).

However, existing trials often have limited climate variation across sites, constraining the capacity to evaluate species responses to marginal or novel climate conditions (Leites *et al.* 2012; Park and Rodgers 2023). Further, these existing trial sites were not designed to assess how population translocation may be affected by novel site conditions, climate extremes, and photoperiod regimes (Leites *et al.* 2012; Pedlar *et al.* 2021; Park and Rodgers 2023). For instance, when selecting a population for FAM, planted populations may meet growth expectations, but phenological response mechanisms may be maladapted due to differing photoperiod, chilling, and warming dynamics between local and source environments, thus increasing spring frost risk due to early bud break for some provenances (Mura *et al.* 2022; Park and Rodgers 2023). The replication of provenance trials across large geographic areas can address these limitations, enabling comparisons of population-level responses to a large gradient in climate and site conditions (Aitken *et al.* 2008; O’Neill *et al.* 2014; Dalrymple *et al.* 2021; Sáenz-Romero *et al.* 2021).

The TransX experiment is a long-term network of provenance trials established in 2024, ranging from North Carolina (USA) to Quebec (Canada), where carefully selected natural populations of ten major boreal and temperate tree species, and improved genotypes of four commercially important northeastern coniferous tree species are planted simultaneously and monitored for their responses to gradients of 14.5°C in mean annual temperature gradient (Fig. 1) and 600 mm in precipitation. The experimental objectives are: 1) to quantify the effect of climate on trait variation and plasticity across species and populations and, 2) to assess how such trait variation relates to growth and survival.

In this paper, we introduce the experimental design of the study, describe the environmental conditions at each of the study sites, and the species and populations tested. We also outline the concurrent *ex-situ* TransX trial within climate-controlled phytotrons, research opportunities enabled by this initiative, describe the data collection program, and highlight avenues for future inquiry. This work seeks to offer a comprehensive and analytically grounded overview of this expansive research endeavour, with the aim of fostering interdisciplinary collaboration and promoting the transfer of technical expertise across scientific and forestry communities.

Methods

Study sites

We preferentially selected sites with well-drained soils and high productivity. Site harvesting and preparation prescriptions accounted for local site specifics and regional regulations. To enable comparison, each site was harvested with the objectives of minimizing: 1) soil disturbance, 2) residual slash, and 3) plant competition (Table 1). Site preparation was conducted between 2022–2024 during the winter and spring to avoid soil disturbance (Table 1). Nine out of 11 sites

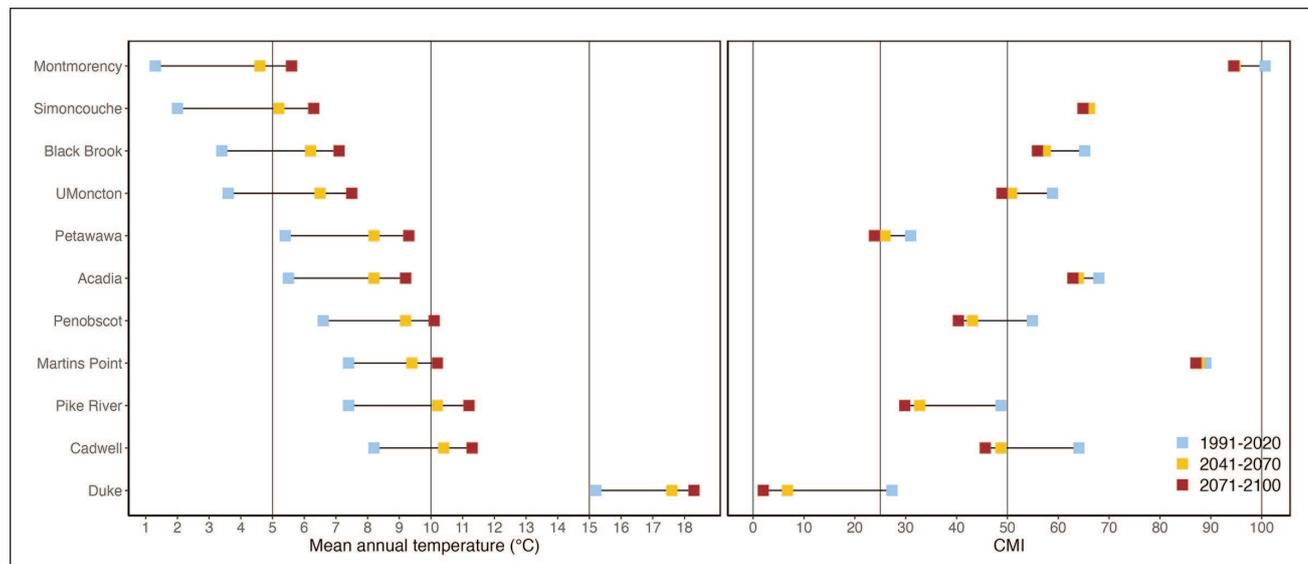


Fig 1. Historical and projected mean annual temperature and climate moisture index at each site for the intermediate climate scenario SSP 2-4.5, obtained from an ensemble of 13 general circulation models (Wang *et al.* 2016). Climate moisture index calculated by subtracting average annual precipitation (mm) from potential evapotranspiration (mm).

Table 1. Location and characteristics of study sites

Name	Location	Coordinates	Pre-harvest composition ^a	Site preparation ^b	Soil ^c
Montmorency	Réserve faunique des Laurentides, Quebec	47.2585, -71.1552	<i>Abies balsamea</i> , <i>Picea spp.</i>	Clearcut, Slash removal	Loamy sand [Moderately drained]
Simoncouche	Lac-Ministuk, Quebec	48.1892, -71.2179	<i>Picea mariana</i>	Clearcut, Scarification, Brushing	Sandy loam [Moderately drained]
Black Brook	Drummond Parish, New Brunswick	47.2513, -67.6743	Grass-dominated field	Chaining, Herbicide	Loam [Well drained]
UMoncton	Sainte-Anne Parish, New Brunswick	47.3445, -67.9744	<i>Acer saccharum</i> , <i>Betula alleghaniensis</i>	Clearcut (<i>Whole-tree removal</i>), Herbicide	Loam [Well drained]
Petawawa	Laurentian Hills, Ontario	46.0076, -77.4103	<i>Pinus banksiana</i>	Clearcut, Slash removal	Sand [Rapidly drained]
Acadia	Maugerville Parish, New Brunswick	46.0057, -66.3955	<i>Populus spp.</i> , <i>Acer rubrum</i> , <i>Picea spp.</i> , <i>Abies balsamea</i>	Clearcut, Slash removal, Herbicide	Sandy loam [Well drained]
Penobscot	Eddington, Maine	44.8194, -68.5914	<i>Fagus grandifolia</i> , <i>Populus spp.</i>	Clearcut, Herbicide, Slash removal	Sandy loam [Poorly drained]
Martins Point	Chester, Nova Scotia	44.5053, -64.3326	<i>Pinus resinosa</i> , <i>Quercus rubra</i> , <i>Acer rubrum</i>	Clearcut, Brushing, Herbicide	Silt loam [Well drained]
Pike River	Pike River, Quebec	45.0877, -73.0766	Grass-dominated field	Mowing	Clay loam [Poorly drained]
Cadwell	Pelham, Massachusetts	42.3582, -72.4212	<i>Tsuga canadensis</i>	Clearcut (<i>Whole-tree removal</i>)	Silt [Excessively drained]
Duke	Durham, North Carolina	36.0239, -78.9914	<i>Pinus taeda</i> , <i>Liquidambar styraciflua</i> , <i>Acer rubrum</i>	Clearcut, Prescribed burn, Herbicide	Sandy loam [Moderately drained]

^aPre-harvest composition species limited to dominant (approx. >= 25% density) tree species present immediately prior to harvest. ^bSite preparation activities are listed in chronological order. ^cSoil texture and drainage (indicated by values in brackets) values are derived from site managers, or provincial/state databases (New Brunswick Department of Energy and Resource Development 2015; Agriculture and Agri-Food Canada 2025; Institut de recherche et de développement en agroenvironnement 2025; Natural Resources Conservation Service, United States Department of Agriculture 2019)

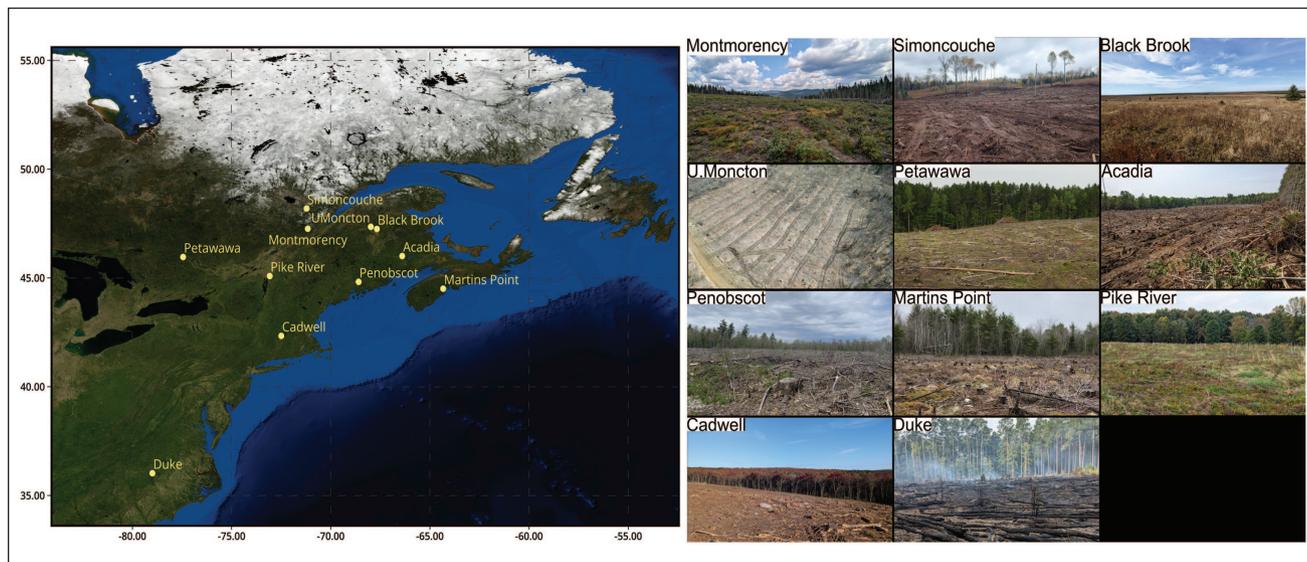


Fig 2. Location of the study sites and photos taken prior to tree plantation. Picture credit (left): NASA/Goddard Space Flight Center Scientific Visualization Studio The Blue Marble Next Generation data, courtesy of Reto Stockli (NASA/GSFC) and NASA's Earth Observatory; taken June 2004. Photo credits (right): Loïc D'Orangeville (Montmorency; Simoncouche; Black Brook; Acadia), Gabriel Rogers (Martins Point; Cadwell), Nicolas Girard (UMoncton), Sébastien Dumont (Petawawa), Jacob Ravn (Penobscot), Mathieu Lamarche (Pike River), Sarah Childs (Duke).

were on harvested stands, while two sites were established on cultivated fields (Fig. 2). Slash was removed when significant, and when competing vegetation was considered a risk for the experiment, herbicide and/or manual thinning interventions were applied post-harvest.

Experimental design

Each TransX trial site followed a completely randomized split-plot experimental design. At each site, natural populations (termed “wild trees” hereafter) and progenies bred for increased growth (referred to as ‘improved progenies’ hereafter) were separated into two different sections, each with its own replicated blocks. The wild section contained 16 blocks, each with ten tree species as main plots and six populations per species as subplots (Fig. 3). Each subplot contained six trees of the same populations, for a total of 360 trees per block (16 blocks = 5760 trees). The improved section contained 20 smaller blocks, each with four species as main plots, with 4–18 progenies as subplots within each plot (progeny counts varied by species due to seed availability). Each subplot contained two trees of the same progeny, for a total of 102 trees per block (20 blocks = 2040 trees; Fig. 3). All trees were planted at 2 x 2 m spacing. In a subset of sites (e.g., Duke and Pike River), some species or blocks were omitted due to space and logistical constraints. For all sites, plots and subplots were completely randomized within each block. However, a section of wild blocks was partially randomized to concentrate hardwood plots within a fenced area (due to a higher browsing risk than softwoods). Given budget constraints which only allowed for 408 m of fencing per site, it was decided to regroup hardwood species plots in 12 out of 16 wild blocks and fence that section of the experiment with temporary 2.4 m fencing. The four unfenced blocks will enable an assessment of browsing pressure at each site.

A consultation process in 2019 with forest industry, provincial governments of the Maritime provinces, and Mi'g-mawē'l Tplu'taqnn Inc. helped to inform the selection process of the wild tree species in the experiment. Five hardwood species are being evaluated: white birch (*Betula papyrifera* Marsh.), yellow birch (*Betula alleghaniensis* Britt.), red maple (*Acer rubrum* L.), sugar maple (*Acer saccharum* Marsh.), and red oak (*Quercus rubra* L.). Five softwood species are tested: red spruce (*Picea rubens* Sarg.), white spruce (*Picea glauca* (Moench) Voss), black spruce (*Picea mariana* (Mill.) B.S.P.), balsam fir (*Abies balsamea* (L.) Mill.), and eastern white pine (*Pinus strobus* L.). For each species, the aim was to include six populations that sourced across a wide temperature gradient within each species natural geographic range. Species from tree breeding programs included in our improved tree section are red spruce, black spruce, white spruce, and Norway spruce (*Picea abies* (L.) H. Karst.). These species were selected based on their economic importance in Atlantic Canada and their availability from the Atlantic Tree Improvement Council, and from J.D. Irving (JDI). Trees from the Atlantic Tree Improvement Council included 18 white spruce progeny, 10 black spruce progeny, and 17 red spruce progeny, with four Norway spruce progeny, and two red spruce progeny provided from JDI.

Seed sourcing

Acquiring seeds from wild populations of multiple species was challenging due to legal constraints when crossing borders, inconsistencies in seed production across species and regions (e.g., masting, climate extremes), costs associated with the collection itself, limitations in collector availability, and variation in seed quality (Clark *et al.* 2023; Wotherspoon *et al.* 2025). Despite these challenges, we aimed to select populations that best captured species-specific genetic variation

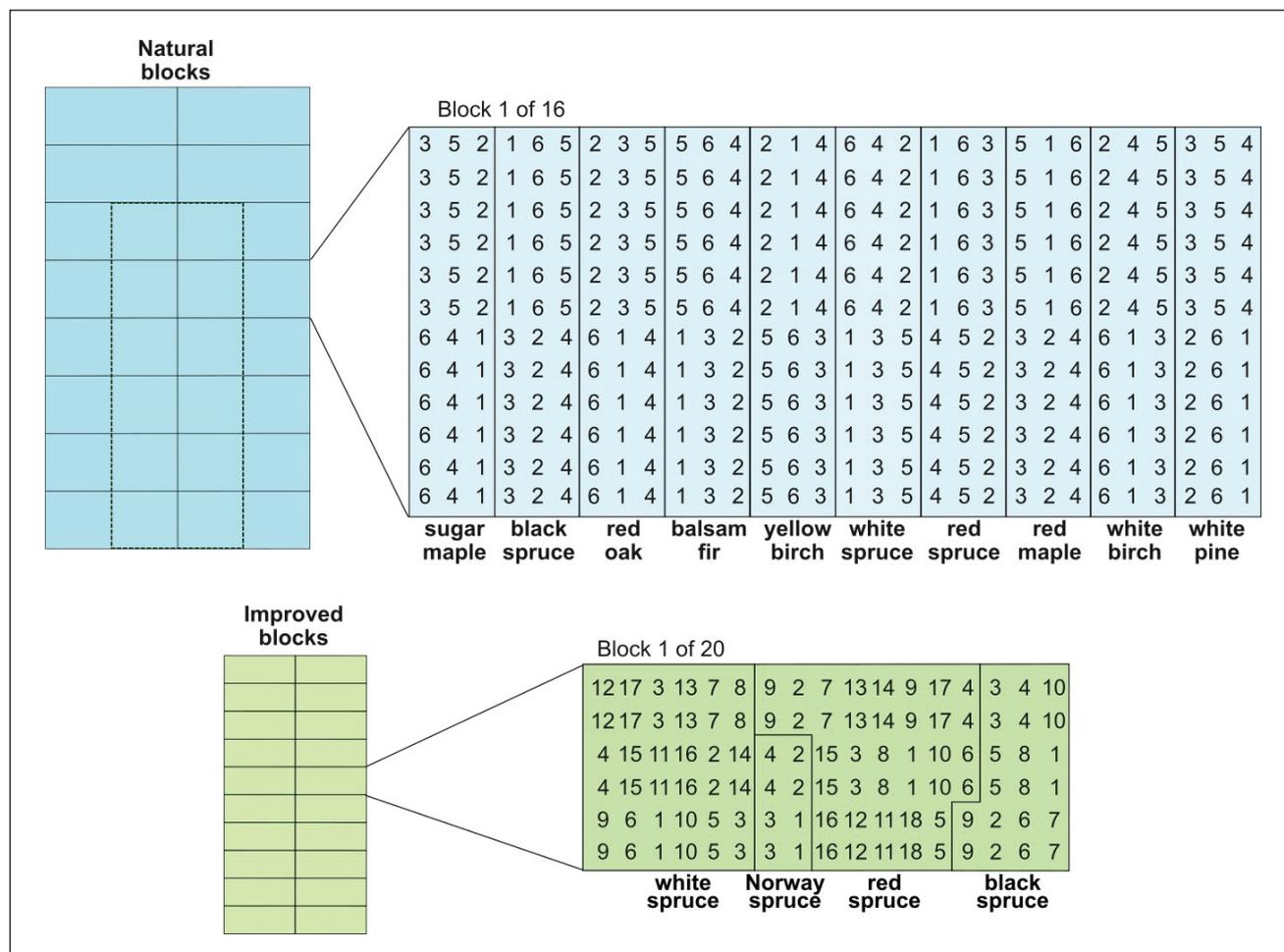


Fig 3. Experimental design of the TransX experiment. Within each site, wild and improved trees are tested separately with distinct experimental layouts, with a minimum area of 3.1 ha for a complete site. Wild trees are planted in 16 blocks (0.114 ha per block, 2.3 ha total), where each block (replicate) contains 10 species treatment plots, and each species plot contains 6 provenance subplots (6 trees per subplot). Improved trees are planted in 20 blocks (0.04 ha per block, 0.8 ha total), where each block contains 4 species treatment plots, and each species plot contains a varying number of progeny subplots (2 trees per subplot) ranging between 4 and 18. Plots and subplots are randomly distributed within each block. Polygon with dashed lines in the wild blocks represents the fenced section.

and climate ranges (Fig. 4). Bulk tree collections from multiple, mature, well-spaced trees were favoured to better represent local population-level genetic variation and responses. To minimize the effects of anthropogenic selection and genetic mixture with foreign, domesticated trees, every effort was made to obtain seed from isolated, relatively unmanaged stands. All wild-type project seeds were processed according to species requirements, subjected to a germination test, catalogued, and stored at the NTSC storage facilities in Fredericton, New Brunswick, Canada.

For the improved progeny, species breeding program objectives focused on increasing volume growth, improving tree form, and enhancing weevil resistance for host tree species (Thomas *et al.* 2024). Seed and scions of black spruce, white spruce, and red spruce trees deemed suitable for breeding objectives, referred to as plus trees, were collected throughout the Maritime provinces of Canada, as well as in Maine for black and white spruce. White spruce progeny included one wild control seedlot for performance compar-

ison, as well as first- and second-generation improvement progeny. The black spruce progeny included only second-generation progeny and one wild control seedlot. Red spruce progeny were all first generation, and Norway spruce progeny were first generation with some somatic embryogenesis³.

Seedling production and planting

Wild coniferous species and most of the improved progeny were grown at Kingsclear Tree Nursery in Fredericton, New Brunswick between 2022 and 2025.

Norway spruce and red spruce improved progeny provided by JDI were raised at the JDI Sussex Nursery in Sussex, New Brunswick in 2024.

The five hardwood species were grown at Strathlorne Forest Nursery in Strathlorne, Nova Scotia during 2024. In 2025, hardwood seedlings were raised at the Canadian Forest Service Atlantic Forestry Centre greenhouses in Fredericton, New Brunswick. Apart from the species grown at Strathlorne, all others were containerized to improve establishment suc-

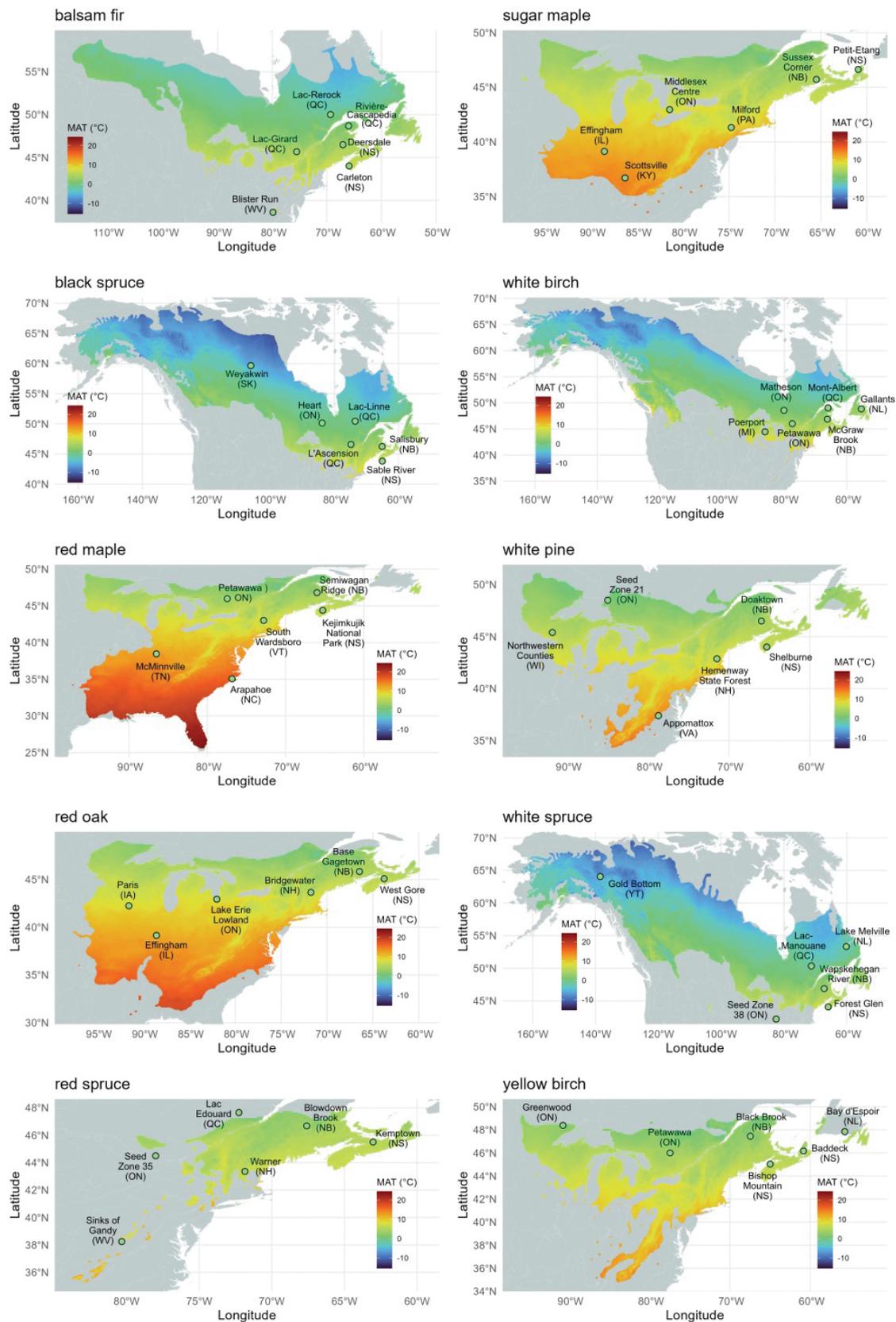


Fig 4. Location of origin for tested populations of each study species. The compositions of populations and species may evolve in the future based-on survival and performance. Coloured areas on the maps represent the mean annual temperature (1981–2010) across the species distribution range (Little 1971).

cess and to simulate standard nursery and plantation practices. Coniferous species were raised in a peat-perlite medium, yellow and white birch were grown in peat pellets at Strathlorne in 2024, and hardwoods raised in 2025 were grown in a lime-gypsum-peat. Nursery growing length was based on industry standards, i.e., all species were grown for one year with the exception of balsam fir and white pine which were raised for two years. Once nursery requirements were met, seedlings were bundled, organized per site, placed in plastic bags, stored at -2°C to maintain dormancy and to meet chilling requirements, and planted the following spring. During 2024 and 2025, extra seedlings of each species were raised for infilling at each site. Species planting year was determined by seedling development requirements, nursery capacity, and seed acquisition. Wild populations of white spruce, black spruce, red spruce, and balsam fir were planted with improved white spruce progenies in 2024. White pine, white birch, and yellow birch were planted alongside improved red spruce, black spruce, and Norway spruce in 2025. Planting of sugar maple, red maple, and red oaks will take place in 2026–2027 due to the germination failure of sugar maple at the Strathlorne Forest Nursery in 2024, and extreme field mortality rates of red maple and red oaks in 2025. Annual spring planting operations were conducted after the risk of frost subsided, and when sites were accessible by vehicle. Thus, planting timing ranged from February in Duke to June in Montmorency and UMoncton. Finally, annual thinning interventions and/or herbicide (around softwood species only) will be used to reduce plant competition until the growth of planted seedlings is unimpeded by non-planted vegetation.

Data collection

Precipitation, temperature, relative humidity, solar radiation, wind speed, and wind direction were monitored hourly with a WatchDog 3250 wireless ET station (Spectrum Technologies Inc. Aurora, IL, USA) at each site. Soil volumetric water content and soil water tension were monitored at two locations at each site using two Watchdog 1650 Microstation data logging stations each equipped with a WaterScout SM 100 sensor and a Watchdog Watermark Soil sensor. At each site, six 30 cm x 30 cm square soil pits will be dug following sampling procedures from Nelson *et al.* (2025) to be analyzed for texture and standard chemistry for site characterization.

Annual measurements of height and diameter alongside health assessments will be collected. In addition, phenological traits are monitored on a weekly to biweekly scale, with observers in the field on a subset of populations and sites, and automatically with multiple 6m-tall aluminum towers installed at each site supporting solar-powered time-lapse Flex-S cameras (Spypoint, Victoriaville, Québec) which take images of nearby trees every three hours. Analysis of regions of interest will then be delineated from these images to isolate individual seedlings. Since these cameras do not have a fixed white balance, grey non-reflective reference panels were installed in the field of view of all cameras to ensure that the color channel patterns observed across sites are true changes in leaf canopy characteristics and not color scaling artefacts; see Jacobs *et al.* (2009) and Delpierre *et al.* (2020). We previously validated the use of Spypoint cameras with reference panels in comparison to ground-based

and visual image-based phenology observations and found the level of agreement ($r = 0.74\text{--}0.78$) to align with previous phenocam studies; see Spafford *et al.* 2023b. The images are then processed to estimate tree health and the timing of phases such as leaf emergence based on the timing of points along annual relative greenness curves (e.g., 50% amplitude in the rising part of the greenness curve marks leaf emergence) (Spafford *et al.* 2023a). An *ex-situ* experiment using climate-controlled phytotrons is also being conducted to assess physiological trait responses within a subset of populations and species used within the TransX experiment. All five conifers along with red oak, sugar maple, and yellow birch were exposed to six temperature conditions with a mean summer temperature range of $14.5\text{--}24.1^{\circ}\text{C}$, and four water availability treatments, where seedlings were watered to field capacity at intervals between three to nine days. We selected temperature data from six TransX sites that spanned a wide, evenly spaced temperature gradient, and created weekly treatment schedules with 12-levels of daily temperature variation for each phytotron. Water availability treatments were designed with the objective of exposing seedlings to drought stress but also minimizing mortality and were selected based on existing knowledge of seedling water demand under similar phytotron temperature treatments (Vaughn *et al.* 2021). Phytotron photoperiod treatments were also adjusted weekly and designed to simulate annual photoperiod trends of each specific TransX site. Height growth, biomass allocation, gas exchange, and chlorophyll fluorescence will be measured to assess trait variation and phenotypic plasticity across populations and species, complimenting the *in-situ* experimental findings.

Research opportunities and management implications

Provenance trials spanning large climatic and latitudinal gradients can help address critical knowledge gaps on tree species and population responses to climate warming, drying, and translocation (Dalrymple *et al.* 2021). The additional costs, efforts, and international regulatory constraints (i.e., transporting seeds and seedlings across borders) required in such studies present considerable challenges to their establishment and their long-term maintenance and monitoring. Thus, the TransX experiment, with ten sites spanning over 11° in latitude, 600 mm in precipitation, and 14.5°C in MAT provides a unique opportunity for a wide range of research initiatives. The large temperature, moisture, and latitudinal gradients expose species to climate conditions and climate anomalies (e.g., early spring frost, drought, heatwaves), at/or beyond their existing climate envelopes, enabling the unique exploration of trait-environment variation for wild populations and improved progeny of key tree species. The long-term tracking of phenology data with phenocams can help refine species-specific phenology models (Spafford *et al.* 2023b) and will allow for the evaluation of ontological effects on phenology (Vitasse 2013). This information will complement the ongoing trait-environment assessments of factors such as leaf-level morphology (e.g., stomatal density, specific leaf area, leaf chemical composition), help to develop stronger species-specific climate response curves that incorporate population variation and ontogeny, thus enabling forest simulation models to generate estimates of climate change impacts on forests with greater accuracy.

While millions of commercially improved tree seedlings are planted annually, there is limited research on the relationship between climate adaptation and genetic selection for traits such as volume gain and form (O'Neill *et al.* 2014; Song *et al.* 2023). Therefore, the inclusion of improved seedlings within the experiment can be used to assess these critical relationships (i.e., potential trade-offs between growth and resistance to extreme weather, insects) and to inform climate-adapted tree breeding programs. These research outcomes can also be leveraged to enhance population and progeny selection success for FAM silvicultural approaches, and to reduce uncertainty when developing forest growth and yield models that account for climate change.

The TransX study will also provide numerous research opportunities in the long-term, such as high-resolution responses of reproduction, plasticity, growth, and transpiration to daily, monthly, and seasonal climate. Additionally, as the plantations mature, thinning experiments may be carried out to explore how density and competition influence climate resilience, and how this varies between species and populations. Finally, by exposing tree species to novel climate and site conditions beyond their current range, our northern and southern sites act as valuable sentinel sites, showing how pests, pathogens, novel weather extremes, and grazing intensity may interact with climate change and FAM. These sentinel sites can also be used to study how novel species and overstory assemblages influence soil properties, the soil microbiome, and understory plant and invertebrate communities.

The TransX experiment will contribute to our understanding of forest resilience to climate change. By developing a strong understanding of species trait variation, plasticity, growth, and survival, this experiment will enhance the accuracy of forest simulation models, and will support the development of strong species-specific FAM translocation guidelines, thus increasing the feasibility of operationalizing FAM. In turn, forest managers (government, industry, woodlot owners) will have increased confidence when managing for climate change risks, and for selecting species and populations that can both tolerate and benefit from climate translocation. Overall, this research will provide critical insights to guide climate adapted forest management.

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