POPLAR COUNCIL OF CANADA

DISCUSSION PAPER

POPLAR GENOMICS TO POPLAR PRODUCTION:

BRIDGING THE GAP FOR BEST USE OF OUR RESOURCES AND KNOWLEDGE

Prepared
for:

GENOME CANADA

by:

Barb Thomas, PhD
Jim Richardson, MScF

June 2006

EXECUTIVE SUMMARY

Canada has a tremendous poplar natural resource. Recent forest inventories estimate the scale of this resource at 4 billion m^3 on more than 160 million ha, of which about 28 million ha are stands with the genus *Populus* as the predominant species. Aspen (*Populus tremuloides* Michx.) is the most widely dispersed tree species in North America and is the cornerstone of many pulp and oriented strandboard mills in Canada. Yet, the forest industry in Canada is facing an economic crisis, with many mill closures. At the same time, the complete genome sequence of black cottonwood (*Populus trichocarpa* Torr. & A. Gray), a very important forest tree species, has been assembled by an international consortium, including Genome Canada supported Canadian scientists, making it only the third plant species in the world to achieve this status. Sequencing of the poplar genome has opened a wealth of opportunities. However, considerable resources will be required to pursue these possibilities and new and continuing financial, academic, and industrial collaborations across traditional partnership boundaries will need to be forged.

An enormous opportunity exists in bringing together two seemingly disparate groups represented by the forest industry and the genomics research community. With the help of government, an alignment of resources with the joint research needs of these communities at both the regional and national levels can be achieved. This collaborative approach will allow us to find new ways of doing business and thus ultimately in sustaining our forest industry. The size of the poplar resource, and the years of field trials and data enable us to benefit from the synergies of an integrated partnership between tree breeders, silviculture researchers, genomics experts and policy makers. Yet, despite the far-reaching benefits, there are fundamental differences between the key players that have made it very difficult to achieve the level of active exchange and collaboration that would allow synergies to develop and produce concrete solutions to fundamental industrial challenges.

The basic challenges involve communication and resources. To enhance the relationships, steps have been taken to assist each community to understand the other's 'culture', to develop joint goals and objectives and to build an ongoing interface mechanism. Discussions between the two communities hosted by the Poplar Council of Canada (PCC) have suggested that progress might be made by focusing on the needs of each community that can be met by the other, rather than focusing on the differences. Other scientific disciplines, including silviculture, pathology, physiology, biochemistry and ecology, also need to be integrated into this collaborative effort in order to meet the needs of industry, policy makers and society most effectively and efficiently.

Due to the long time-lines often encountered when working with trees, each party in this collaborative effort would benefit greatly from a long-term funding source with an effective user - researcher interface as discussed above. When new poplar material is available for deployment, or biotechnological tools are available to assist with screening of the material, funding must be readily available and the government and policy environment must also be in place to support and promote its use.

There are two main, ideally complementary, directions possible for genomics research in the context of poplar production and industrial utilization. The first is development of new tools with currently unknown practical applications. The second goes beyond scientific publication of the technology to integrated operational application. Current tools must be used to their best advantage today for selected traits and applied at the most appropriate phase in a breeding, testing and selection program. Where many of the new tools will eventually lead in terms of practical application is unknown, and while it is likely that their development will continue with or without the participation of the potential end-users, communication between basic researchers and potential end users during the development will aid use in application.

Integration of the communities may need to be facilitated by an effective organization which can help bring together the different elements. The PCC is well suited to provide such an organizational structure, particularly at the national level. Its members include most of the professional and academic agencies and companies in Canada involved in studying, breeding, growing and industrial utilization of poplar. By organizing widely-attended meetings and workshops aimed at linking its own traditional community of poplar breeders and growers with the poplar genomics community, PCC has demonstrated its commitment and ability to take on this organizational role. In doing so, PCC can work with its membership and partners to raise awareness of these opportunities and in return, gain support for both administrative and technical requirements.

A Genomics to Production workshop organized by the PCC with the aid of Genome Canada in Edmonton in April 2005 identified a number of specific steps to foster better cooperation between poplar genomics scientists, breeders, growers and potential funders. Some of these steps have already been undertaken. Others include working towards establishing a Canadian Poplar Consortium including all key stakeholders, and using the Internet as a communications vehicle to share and discuss priority topics for research and to invite researchers and partners to sign up with expressions of interest.

This paper provides another key step in highlighting and enhancing communication and understanding of the needs, drivers, logistical constraints, and enormous opportunities waiting to be taken advantage of by the industrial and government end-user communities and academic researchers.

POPLAR GENOMICS TO POPLAR PRODUCTION:
BRIDGING THE GAP
FOR BEST USE OF OUR RESOURCES AND KNOWLEDGE

Barb Thomas[1] and Jim Richardson[2]
Poplar Council of Canada

1. Introduction

The forest industry in Canada is facing a crisis in economic terms, with 56 pulp mills having closed since 1986, 13 of them in 2005 and six already scheduled for 2006. Seven major lumber mills have also closed. In order to remain competitive, the forest industry north of the 49th parallel will require something other than a 'business as usual' approach in the short to medium term.

At the same time as the forest industry has been facing enormous challenges, the genome sequence of a very important forest tree species in the Pacific Northwest, black cottonwood (*Populus trichocarpa* Torr. & A. Gray; the individual tree "Nisqually-1" selected from Washington State) has been completely sequenced, making it only the third plant species in the world (after rice and *Arabidopsis*) to achieve this status. Much of that work was done at the Joint Genome Institute within the US Department of Energy with substantial assistance from other research groups including Oak Ridge National Laboratory (US), the Treenomix program at UBC and the Genome Sciences Centre in Vancouver, Canada (Genome British Columbia), the Swedish *Populus* Genome Project located in Umeå, Sweden, and the Bioinformatics and Evolutionary Genomics Division, University of Ghent, Belgium.

With the help of government funding agencies, an enormous opportunity exists in Canada to bring together the forest industry and academic genomics researchers to align resources with need at both the regional and national levels. This collaboration will allow for the discovery of new ways of doing business and thus ultimately of sustaining our forest industry. Through this discussion paper, our intent is to outline the needs, challenges, and benefits of bringing these traditionally unconnected groups together, and also to provide ideas for overcoming these challenges, turning them into solutions. The paper aims to present these issues and opportunities to the two groups themselves and also to assist funding agencies and policy makers to support the realization of these opportunities.

Aspen (*Populus tremuloides* Michx.) is the most widely dispersed tree species in North America and is the cornerstone of many pulp and oriented strandboard mills in Canada. Many forest companies have employed the services of specialists or partnered with government organizations to enhance their fibre production through tree breeding and tree improvement programs. The size of the poplar resource, and the years of field trials and results, positions us well to benefit from the synergies that an integrated partnership between tree breeders, silviculture researchers and genomics experts would bring. Changes could be realized in development and design of tree improvement programs for more rapid and efficient selection and turnover of 'superior' trees to meet future needs for fibre and other products in a changing environment.

---

[1] Genstat Consulting, Box 45086, Lansdowne Postal Outlet, Edmonton, Alberta. Canada. T6H 5Y1.
Phone/Fax: (780) 432-4230, Email: genstat@shaw.ca

[2] J. Richardson Consulting, 1876 Saunderson Drive, Ottawa, Ontario. Canada. K1G 2C5.
Phone: (613) 521-1995 Fax: (613) 521-1997, E-mail: jrichardson@on.aibn.com

The Poplar Council of Canada (PCC) is a national non-profit organization of corporate and individual members who are directly involved in developing, nurturing, harvesting, converting and renewing the poplar (and willow) resource in Canada. Its members come from industry, woodlot owners, universities, research establishments and provincial and federal governments. PCC aims to develop, collect, maintain and disseminate information on the poplar resource and to promote its sound management and wise use for all Canadians.

An international meeting, primarily of poplar genomics researchers, was organized by Genome Canada and the UBC based Treenomix group, in Toronto in September of 2003. At this meeting and at a subsequent annual meeting of the PCC in Vancouver in 2004 it became clear that in order for the developing opportunities in poplar genomics research to be realized, a meeting focused solely on bringing these groups together was required to develop a new process to enhance communication.

The result was the ***Genomics to Production*** workshop, held in Edmonton April 8th and 9th, 2005 with 30 invited attendees from across the country. The event was hosted by PCC with support from Genome Canada and Canadian Forest Service. Those present included forest industry (5 companies), provincial (AB, QC, BC) and federal government (CFS, AAFC, Genome Canada) representatives, 10 academics from five universities, as well as participants from the Centre de Recherche en Biologie Forestière, Forintek, two forest nurseries, the Carnegie Institute and a Genome Canada representative. (A workshop summary is available on the PCC website.)

In December 2005, a steering committee of workshop participants met and determined that a critical next step was required. This group felt that the opportunities available to the forest sector from the newly-elaborated poplar genome and the associated scientific possibilities and challenges needed to be articulated so that the various players - research organizations, industry, and governments in their dual role as funders and policy makers - could understand and take advantage of the complex science surrounding completion of sequencing the poplar genome. This led to the preparation of the present discussion paper.

2. Industrial Needs

Based on the outcomes of the April 2005 workshop, a comprehensive list of industrial ‘needs’ in relation to traits of interest in poplar trees was developed. Tables 1 & 2 in Appendix A, provide this list grouped by two separate categories.

The needs identified in the tables cover traits from across the country and can be further separated out based on region, (e.g. drought in the prairies *versus* flooding resistance in northern Quebec), by industrial product (e.g. pulp *versus* oriented strandboard) and by the available resources of genetic material identified for particular traits, (e.g. clones that root well, *versus* clones that do not). Another important factor, which will be discussed below, is the time-line for developing production clones for any given trait.

3. The Poplar Natural Resource

Canada has an enormous poplar natural resource. Recent forest inventories estimate the scale of this resource at 4 billion m^3 on more than 160 million ha, of which about 28 million ha are stands with the genus *Populus* as the predominant species. Trembling aspen is the most widespread tree species in the country, and in the last 30 years the vast aspen resource in the boreal forest has been the focus of much industrial attention as the ‘last frontier’ of forest exploitation. Despite this attention, current estimated harvest levels are still less than annual allowable cut levels.

Other native *Populus* species of importance in Canada include bigtooth aspen (*P. grandidentata* Michx.), eastern and Plains cottonwood (*P. deltoides* Bartr. ex Marsh.) in parts of southern

Quebec, Ontario and the Prairies, balsam poplar (*P. balsamifera* L..) and black cottonwood (*P. trichocarpa*) in British Columbia and Alberta. In addition, hybrid poplars with genetic material from these and other non-native species, have been developed and planted widely as farm windbreaks for shelter and wood production. However, with only 4,900 ha of such plantations on forest land and 9,300 ha of short-rotation intensive-culture plantations on agricultural land, the scale is small compared to the natural resource. Nevertheless, there has long been strong interest in the potential of hybrid poplar plantations throughout Canada.

4. Past and Present Poplar Breeding in Canada

There is a long history of growing poplars in Canada, dating back from before the time of European settlement. People who came to Canada in the 17th and 18th centuries brought with them trees such as Lombardy poplar (*P. nigra* L. cv. Italica) and silver poplar (*P. alba* L.). They also took eastern cottonwood back with them to Europe where they hybridized spontaneously with the European black poplar (*P. nigra* L.) creating a hybrid that became known as ‘Canadian poplar’ (*P*. × *canadensis* Moench). Much later, in the early 20th century, this hybrid was introduced to Canada and gave rise to the very widely planted ‘Carolina poplar’ grown in Ontario, Quebec and the Lake States.

Selection and breeding of poplars for wood production in Canada began in the 1930s, largely stimulated by Carl Heimburger in Ontario. By the 1970s, there were active breeding programs in Ontario, Quebec and to a lesser extent in British Columbia. They followed classical breeding procedures, making numerous crosses of promising native and introduced clones, and testing and selecting the best progeny, showing the beneficial effects of heterosis, for further crossing and testing. The Ontario and Quebec programs had close associations with similar programs in the United States and Europe and there was considerable interchange of reproductive material (cuttings, pollen and seeds).

Meanwhile, similar strategies were followed at the Prairie Farm Rehabilitation Administration (PFRA) Shelterbelt Centre in Saskatchewan with breeding goals of improved suitability and vigour for windbreak plantings on the Prairies. The Shelterbelt Centre program has a history now more than 100 years old. The program has developed numerous poplar hybrids and has released several which have been widely planted across the prairies and have proved exceptionally well-suited for the purpose for which they were originally selected.

Although poplar breeding has been conducted in Canada for decades, significantly more activity has taken place in the last 10-years. This has occurred as forest companies look to secure fibre sources to meet future needs while recognizing that current fibre sources are coming from an ever-diminishing land-base. MacMillan Bloedel (now Weyerhaeuser) on Vancouver Island and Scott Paper in the Fraser Valley of BC both relied heavily on earlier breeding work of Drs. Reinhard Stettler and Paul Heilman for their sources of hybrid planting stock. More recently, Scott Paper has been looking at developing new hybrids for the Fraser delta region. New breeding efforts began on the Prairies when the PFRA Shelterbelt Centre reactivated their breeding program at the end of the 1990s after it had lain dormant for over a decade. A year later, a joint effort between Alberta-Pacific Forest Industries Inc. (Al-Pac) and PFRA also commenced with the mandate to complete 3-4 years of new hybrid breeding based primarily on crosses between Aigeiros (cottonwood poplars) and Tacamahaca (balsam poplars) and their associated hybrids. In addition, Al-Pac has conducted some hybrid aspen breeding on its own, and the Western Boreal Aspen Corporation has also been actively breeding aspen and hybrid aspen since the late 1990’s. PFRA is currently completing a range-wide collection of balsam poplar, and pure species programs for both aspen and balsam poplar have been undertaken by a number of companies in Alberta. In BC, a range-wide collection of black cottonwood has also been made by the BC Ministry of Forests. The most extensive long-term poplar breeding program in Canada is that of the Quebec Ministry of Natural Resources (MRNFP), aimed at producing hybrid poplars suited to each of the different regions throughout Quebec.

Canadian poplar breeding programs have specific mandates which range from producing shelterbelt trees for farm fields and riparian stabilization along stream edges, to intensive plantations of pure stands for deployment on private lands, to using in a mixed planting strategy with conifers on public lands. In addition, with the increase in interest in bioenergy, programs in the adjacent Pacific Northwest, e.g. Greenwood Resources, are working with the US Department of Energy to determine the energy values of different hybrid poplar clones and how best to develop breeding strategies to meet energy needs in the future.

For any breeding program, one of the major challenges is that of material availability since not all species of interest grow naturally in North America. In order to breed between different species of poplars, material must be available. Access to this breeding material however, can pose several challenges: 1) it is often difficult to obtain pollen from different species due to phytosanitary regulations and viability problems during shipping; 2) obtaining seed can also be difficult but is possible; 3) obtaining enough different seedlots is important if developing a pure species plantation for future breeding stock; 4) it often takes 5-10-years before the new trees flower; 5) exotic trees can be damaged by environmental conditions in their new location making healthy flowers difficult to obtain. Unless relatively large, healthy collections of pure species parents are available, it is not uncommon for only a few trees to contribute pollen or female breeding branches to programs year after year. Because some types of poplar hybrids are easily propagated from stem cuttings and further breeding is not required to produce more of them, there is a tendency to begin working with cuttings from only a few parents to produce a lot of offspring but ultimately only a few clones are deployed operationally.

Two other considerations are important to highlight. A new clone coming out of a breeding program may need to be tested for decades before it can be released for operational use. This is one of the fundamental challenges of tree breeding and one where molecular tools could play a significant role in ‘speeding up’ the cycle of testing and selecting of new material for different purposes. The second important consideration is that when individuals in a breeding program have been identified as having particular traits, such as being branchy or not branchy for example, most breeding program managers will discard the trees with ‘undesirable’ traits and only keep ones of the ‘type’ they are seeking. In order for the molecular tools to be developed to help in making new and future selections, ‘the GOOD, the BAD and the UGLY’ must be maintained for study material. Archiving of material with no immediate commercial use is very expensive and hard for operational managers to justify. Joint efforts must be used to maintain and care for this material with ‘known’ characteristics. Despite its lack of use in operational programs, this characterized material is fundamental to ensuring practical relevance of genomics tools.

5. Genomics Tools

Sequencing of the poplar genome has opened up a box full of opportunities, but significant resources are required to pursue such possibilities. As a result, any solution will require strong collaboration involving both the academic and industry communities. Determining which opportunities to pursue requires clear objectives and deliverables, from pure science to end-user applications. The tools and techniques currently available are expanding daily in this field and include, but are not limited to, the following:

a. It is possible to identify poplar genes with known functions based on extensive information from other plant species, e.g. the well studied model plant *Arabidopsis*, and to extrapolate cottonwood genomic information to a broad range of poplars and aspens, and to genetically similar *Salix* species.

b. Many poplar and aspen genotypes are easy to genetically manipulate (transform). Therefore, the functions of genes in specifying traits of interest can be monitored and explored quickly and efficiently. The speed at which genomics tools produce results contrasts markedly with the lengthy time-frames of tree breeding.

c. There are substantial genetic and genomic resources available within the Canadian and international research communities, including information on microsatellite markers, the annotated genome sequence anchored to the 19 poplar linkage groups (chromosomes), expressed sequence tag data-bases, pedigrees for mapping yield and disease resistance, and microarrays for whole genome gene expression profiling.

d. There are an increasing number of mutant populations of poplars available to study, including a population of activation tagged poplar lines developed by the Genome Canada/Genome Quebec Arborea project.

Utilization of these different tools and the information that can be obtained from them is fundamentally dependant on the plant material available and on how much is known about that material. For example, in order to identify trees resistant to drought (or disease etc.), the molecular geneticist first needs to have material that has already been characterized for these traits so that candidate genes of interest related to this trait can be identified within the genome. Once the molecular geneticist has identified genes of interest, then this can help with new selections in a breeding program using new seedlings or clones of unknown phenotype.

A great deal of work still lies ahead in identifying poplar genes in the poplar genome for traits of commercial importance, e.g. drought tolerance, insect resistance, disease resistance, wood density and pulp yield. If plant material is not available for these ‘retrospective’ studies, then it has to be located, characterized, and subsequently maintained and propagated. Maintenance of the material, even once it is identified, is an enormous challenge. In such a rapidly expanding field, the development of new tools may require a different expectation of the time involved and the opportunity for industrial application may be somewhat less tangible. However, by working together on projects today, end-users will be able not only to keep abreast of what is possible, but also to contribute to the discussion, providing insight into anticipated operational challenges of the future, such as climate change and reforestation.

6. Bringing the Players Together

The poplar genomics community (poplar researchers) and the poplar breeders and growers (research users) are two groups that would seem to have a lot to gain from working closely with each other. It would be an understatement to say that the two communities need each other. Two of the most profound benefits to Canada of bringing these groups together could be the long-term survival of a deciduous forest industry in Canada and support of a vibrant ‘biotechnology powerhouse’ in our academic research community, in which large investments have already been made. While the industry of the future will not necessarily look or behave in the same way as today, through innovation, policy incentives, and capacity-building we have the opportunity to realize greater value from our breeding programs and forests overall. While this paper and much of the genomics work has focused on poplars, the research conducted also serves as a stepping stone to gaining a better understanding of how traits are controlled at the gene level in the significantly larger conifer genome, thus providing broader scale benefit to Canadian forestry overall.

Yet, despite the far-reaching benefits, there are fundamental differences between the key players that have made it very difficult to achieve the level of active exchange and collaboration that would allow synergisms to develop. The basic challenges involve a lack of mutual understanding and resources (financial and people). These are not issues requiring research or technology, but rather arise from structural and institutional barriers involving human nature, policies and organizations.

The poplar genomics community is primarily academic (linked to high-technology and the information-technology industry), and involved in cutting-edge research in which publication in the peer-reviewed literature as well as intellectual curiosity are the key drivers. The level of activity is extremely intensive but goals are achieved in the relatively short time-frame of a few months or years. Financial resources needed for this high-profile research can be very significant, but these funds may be redirected by funding agencies to other target organisms very quickly. Poplar may have received significant funding in recent years but tomorrow it could be Eucalyptus or soy beans, or back to *Arabidopsis*.

The poplar breeding and nursery community is largely oriented towards practical applied research and operational production of improved planting stock. Academics are not common in this group. In the past, poplar breeding has been almost exclusively a government responsibility. More recently however, the forest industry in Canada has also developed significant poplar breeding/tree improvement programs. Some industry–government partnerships have also developed, resulting in some very useful synergies. The key drivers of industry are to meet goals of productivity and target production levels while dealing with the myriad of day-to-day challenges of field operations. In addition, the current time-frame is quite long for developing new poplar varieties. Typical breeding cycles for development of new selections are in the range of half a rotation for hybrid poplar crops with 10-20 year rotations or somewhat shorter with pure species forests with 60-80 year rotations. Financial resources for these programs are perennially limited by the struggling economic success of the forest industry. With an on-going shortage of university or college programs and training courses, and declining student intake by forestry programs, the number of active poplar breeders remains quite small.

Communication between the academic and industrial communities has been a challenge. The molecular biology language of genomics is poles apart from the field forestry language of tree breeding and growing. Glossaries can help improve mutual understanding, but the fundamentally different drivers of scientific research and publication *versus* field production and productivity noted above can be a basic disincentive to bridging this gap.

To enhance this relationship, some preliminary steps have been taken to assist each community to understand the other's 'culture', to develop joint goals and objectives and to build an ongoing interface mechanism. The opportunity to build 'capacity' in the delivery of research results at this interface and in the utilization of these outputs is challenging and will remain so without some form of joint collaboration and associated support. It is likely that a 'new-type' of individual will need to be recruited and trained to help bridge this unique gap between research producers and research users (government or industry). Their roles might also include establishing linkages to the social sciences to help gain information on public perceptions and develop and assess policy alternatives for enhancing the economic and environmental impacts of poplar-related forestry.

Discussions between the two communities hosted by the PCC have suggested that progress might be made by focusing on the needs of each community that can be met by the other, rather than on the differences. The needs of poplar genomics research that can be met, at least in part, by poplar breeders and growers include:

- material with a similar genetic background for replicated experiments (50 replicated specimens of clones with different phenotypes might be "nice to have", but at least ten might be essential);
- identification of highly contrasting phenotypes ('the good, the bad and the ugly') in genetically-characterized material, and access to many copies of each phenotype;
- pedigreed material with known, identified and available parents and progeny;
- gender-identified material; and
- provision of controlled environments (growth chambers, greenhouses, common gardens, ecological niches) where plant material can be grown to maximize expression of genetic differences across environmental gradients;
- access resources to take advantage of, and help develop, the range of genomics tools that can be targeted to specific, basic and applied research goals.

Similarly, the needs of poplar breeders and growers that can be met, at least in part, by poplar genomics research include:

- rapid development of poplars with traits which overcome problems such as disease susceptibility, drought sensitivity and cold sensitivity;
- help with rapid screening of multiple genotypes for specific traits; and
- indirectly, through cooperative arrangements, access to significant funding sources to assist in supporting long-term breeding and maintenance of material (e.g.: include funding requests for plant stock maintenance in grant applications).

An issue for poplar breeders and growers is that the genomics community, having completed the mapping of the poplar genome and propelled by the interests of major funding sources, may move on to other plant species before practical benefits of their work on poplar have been realized or even perhaps fully identified. This should also be considered by the genomics community in that the mapping of the poplar genome will benefit society in the final analysis, but only through end-user application. With the academic pressure to pursue continued scientific advances however, and the current methods used by Universities to judge the performance of their academics, this may not be recognized at the individual researcher level.

For both communities, long-term funding support, with an effective user-researcher interface as discussed above, will help ensure maximum benefit is derived from poplar genomics advances.

When new material is available for deployment, or biotechnological tools are available to assist with screening, selection and characterization of this new material, the social, government and policy environment must be in place to support and promote its use.

7. Natural Variation and Genomics Opportunities

The majority of forestry practices in Canada today take little advantage of the tremendous reservoir of genetic variation and potential already available in wild stands to enhance productivity. In part this may be due to a lack of understanding in the mills of what can be gained from this knowledge, or in many cases may be due to a mill being relatively old and unlikely to be able to take advantage of detailed information on the quality of forest stands, e.g. higher wood density in the trees found in one part of a forest management area *versus* another. The logistics of handling and identifying each truck-load of trees being brought into a log deck for processing is another challenge. A final challenge is the relatively limited information available about wood characteristics and genetic variation of wild stands.

Although it is well known, for example, that there is an enormous amount of natural variation in trembling aspen, this information is not well characterized for application. By using genomics tools to screen thousands of trees from a variety of site-types, stands and regions, we could gain important insights into the character of this natural variation. This could lead to better utilization and increasing mill efficiencies today, and possibly enhanced or new uses in the future. Another significant benefit would be to identify new parents to introduce into breeding programs where ‘specialty’ traits or resistant traits could be bred into deployment populations of trees.

8. New Tools

Given the costs associated with genomics work, it is clear that some level of trade-off is likely to occur between moving existing tools along the road to operational application and continued development of new tools with currently unknown applications. There appear to be two main, and ideally complementary, directions possible for genomics research: the first being tool development, and the second going beyond scientific publication of the technology and basic science findings to integrated applications.

There are today a host of ‘tools’ in the ‘toolbox’ that could have immediate applications. Integration of efforts must occur now to ensure that such applications are identified and brought to bear on commercial traits of interest and also to determine at what stage in a traditional tree breeding program the most information can be gleaned from such an application. For example, if a genomics tool is relatively expensive to use, and therefore only hundreds of trees can be screened *versus* thousands, then it would be better to focus on traits that are not easy to select on in initial screening or greenhouse trials. Wood quality traits are difficult or impossible to characterize in a seedling and can often take decades to fully understand. If the time it takes to identify better individuals could be cut in half or more, then huge benefits could be gained in time, testing-space, and cost. If diseases such as rust (*Melampsora* spp.) are easily identified in the nursery on 6-month-old seedlings, then initial screening can be done relatively quickly and cheaply without using expensive tools.

Although not necessarily considered tool development, developing ways to screen for multiple traits at one time would in the end be much more useful to the tree breeder than having to screen each tree many times to find out if it possesses the combination of characteristics that will make it overall a superior selection for deployment. Field testing, where many traits are being identified at once (winter hardiness, drought or flood tolerance, vigour, form etc.), is time consuming, but produces a richness of information that is currently unavailable by other means. Classic tree breeding tells us that a minimum of half a projected rotation age is needed to test material thoroughly, particularly trees with an exotic genetic background such as found in many hybrid poplars and aspens in Canada.

An early example of efficiencies that can be developed in the molecular technology field is the ‘multiplexing’ of microsatellite markers (used to track inheritance of genes or specific sections of the genome). Multiplexing involved moving from testing only a single marker each time in a sample to analyzing three or more markers at once. The time and cost to run these samples was reduced significantly and the amount of information gained from each analysis increased three-fold. New genotyping technologies allow this general approach to be used with increasing efficiency and information content.

Current tools must be used to their best advantage today for selected traits and applied at the most appropriate phase in a breeding, testing and selection program. Where new tools will eventually take us is unknown, but their development will likely continue whether the potential end-users participate or not. While we recognize that partnering is not an easy task, the potential advantages to be gained are great, providing synergies not otherwise possible.

9. Other Disciplines

Our analysis of how best to bridge the gap between poplar genomics and poplar production has centred on the two main communities of molecular geneticists on one hand and poplar breeders and growers on the other. A number of other scientific disciplines also need to be integrated into the joint efforts in order to meet the needs of industry, policy makers and society in general most effectively and efficiently. These scientific disciplines include silviculture, pathology, physiology, biochemistry and ecology.

Cultivation of poplars, especially hybrid poplars, is fraught with disease problems such as stem cankers, e.g. *Septoria musiva*, and leaf rusts, e.g. *Melampsora larici-populini*, which can cause significant loss of productivity and even mortality. Almost everywhere in the world where hybrid poplars have been grown, these diseases have appeared sooner or later. Many poplar growers consider *Septoria* stem canker the most serious problem faced by hybrid poplar cultivation. Susceptibility to these diseases is genetically controlled and clones with varying degrees of resistance to attack (or at least to significant damage) have been identified. Unfortunately, the disease organisms also evolve, forming new strains which may attack poplar clones which were previously resistant to the disease. Pathology and the genetics of disease organisms and of resistance must be closely integrated with the work of poplar genomics and production.

Genetics are only one part of the biology of poplars. Equally important is the physiology of how the trees grow, and the biochemical processes involved, since these provide information on traits controlled by genes for which there may be both natural and biotechnologically induced variation. These disciplines are particularly important in the study of such desirable traits as drought tolerance and cold hardiness, as well as more generally in relation to conditions of optimal growth and photosynthetic activity. Poplars are planted and grow in a more or less natural environment where they depend on physical elements such as light, soil, water and nutrients, and interact with other plants and animals. Thus the application of poplar genomics research results by poplar breeders and growers must also consider the science of ecology.

Efficiency and effectiveness in generating a sustainable and valuable industrial poplar resource requires that the integration extend beyond the scientific and technological disciplines to include practical experience, relational dynamics, organization, and management. The final product of a vigorous, healthy poplar stand with desirable characteristics requires, at a number of points in the process, the practical input of people ‘on the ground’ who know and understand first-hand the goals of the poplar users, the priorities in desirable traits of the material, and the problems of establishing and growing the trees. However, while important and necessary, scientific knowledge, technical skills and practical experience are not enough by themselves. Integration requires that these elements be embodied in people who can communicate effectively with each other, and who are willing to commit time and energy to a communal effort.

10. The Role of PCC

The integration effort will be facilitated by an effective organization which can help bring together the disparate elements. The PCC is well suited to provide the organizational structure to bridge the gap. Its members include most of the individuals, agencies and companies in Canada involved in studying, breeding, growing and industrial utilization of poplars. It is national in scope and not directly affiliated with any government organization. Although relatively few molecular geneticists are currently members of PCC, the Council recognizes the important role that this community can play. Perhaps most importantly, in recent years, through organizing widely-attended meetings and workshops aimed at linking its own traditional community of poplar breeders and growers with the poplar genomics community, PCC has demonstrated its commitment and ability to take on this organizational role. In addition, through PCC’s long association with the Canadian Forest Service (CFS) of Natural Resources Canada, it can help maintain communication between traditional forestry institutions and burgeoning new institutions. Beyond the meetings and workshops, the website, newsletter and working groups of PCC provide further tools to assist in integration. However, the current income generating activities of PCC limit the work it can undertake and efforts will need to be made to incorporate this administrative and technical role in any future funding applications.

11. Policy issues

The application of any technology, existing or new, requires that both the policy and societal environments promote and support their use to ensure the greatest economic and environmental benefits. With biotechnology tools, there are both provincial and federal policy regulations that cover their current use. An examination of those policies, primarily developed for annual crops, may be needed as the potential applications of new genomics tools become better understood. Provincial regulations in some regions of Canada do not promote or support the use of hybrid poplars on public lands, greatly limiting the economic opportunities for industrial competitiveness. Inviting government, and in particular the policy-makers, to the table at the beginning of any discussions linking genomics research outputs to operational production can only help to avoid political roadblocks when application of the technology is ready after years of research, investment and effort.

The public perception of biotechnology and its application has had limited study. Significantly more attention could be given to this, particularly for such long-lived species as trees. Some work in this area has been conducted in the Department of Rural Economy at the University of Alberta.

12. Next steps

The Genomics to Production workshop organized by PCC in Edmonton in April 2005 identified a number of specific follow-up steps that might be taken to foster better cooperation between poplar genomics scientists, breeders and growers. Some of these steps have already been taken, such as preparation and circulation of a workshop summary and glossary (available on the PCC website at http://www.poplar.ca/science.htm#G2P), and a follow-up meeting of the steering committee in Edmonton, December 15, 2005. Other actions became moot when a major research proposal (GENADAP), then being considered for funding, was not successful. Some steps identified still remain valid however, and are presented here as recommendations for further action.

a. Work towards establishing a Canadian poplar consortium including all key stakeholders. The nucleus of this could be formed from the Genetics and Breeding Working Group of PCC with a genomics dimension added, as a means of providing a continuing identity for the Edmonton workshop group and an on-going industry-academic interface.
b. Implementation of an exchange service using the PCC and its website as a communications vehicle to post priority topics for research and available sources of funding and to invite interested academic and industry partners to sign up with expressions of interest.
c. Establishment of links between PCC and provincial Genetics Councils across the country.
d. Creation of links to new developments such as:
    - the ‘Virtual Fibre Centre’ of CFS;
    - the new Life Sciences Strategy (which includes forestry) of the Alberta Department of Science and Innovation;
e. Building a list of potential projects with some short term deliverables that could be undertaken at a reasonable cost.
f. Participating in a possible new Genome Canada initiative aimed at identifying key areas for new investment in Genome Canada projects by the Federal Government.

Potential funding sources for helping to bridge the gap include:

a. National
    - NSERC - direct funding, industry collaborative programs, fellowships for individuals, research costs;
    - Genome Canada, depending on future funding;
    - Regional Genome Centres e.g., Genome Alberta, Genome BC, etc.;
    - Industry.

b. International
    - US Department of Energy;
    - International Collaborative Initiative (ICI) program (which was the basis of the original meeting of September 2003 – see page 5).

13. Acknowledgements

The authors of this paper express their sincere appreciation to the participants in the ***Genomics to Production*** workshop held in Edmonton in April 2005 for their willingness to recognize the gap and to start building bridges. We also thank the Steering Committee for continuing the process, and in particular to John Doornbos of the Poplar Council of Canada for his vision and perseverance in positioning PCC to meet the challenge. We also thank Dr. Carl Douglas for his careful editing of this document and last, but by no means least, to the Science and Industry Advisory Committee of the Board of Genome Canada for providing the all-important funding and support which has made much of this work possible.

Appendix A. List of industrial 'needs' in relation to traits of interest in poplar and aspen trees.

Table 1. Genetic and silvicultural traits of interest for early stage assessment in hybrid aspen/poplars.

A Genetic
1. Rootability of cuttings (clones with particular genetic backgrounds
2. Gender identity (pre-flowering and older non-flowering)
3. Resistance to herbivory (less tasty to moose, deer, voles)
4. Molecular determinants of hybrid vigour (+ sylleptic branching, branch angle)
5. Resistance to drought, flooding and salinity
6. Molecular determinants of wood density, pulp yields, secondary compounds, lignin levels etc.
7. Disease resistance in new hybrids
B Silvicultural
1. Nutrient use efficiency / fertilizer requirements
2. Tolerance to high-density greenhouse production (light use efficiency)
3. CO_2 impact on growth and root:shoot ratio in the greenhouse (genotype identification – hybrids versus pure species performance)

Table 2. General traits of interest in poplar biology

1. Transferability of genomics tools between poplar species.
2. Regulation of fall dormancy in poplars and its relationship to winter hardiness &/or drought tolerance.
3. Determination of wood stain susceptibility of native and hybrid stands
4. Understanding the change in trait expression in different environments (eg: *Septoria* disease resistance in balsam poplar in 'wild stands' with leaf spots only, to killing stem cankers in 'plantation stands'.
5. Regional identification of favourable wood characteristics
6. What is the spectrum of susceptibility of naturally occurring poplar hybrids to disease, pest and environmental stresses? Will this profile change with climate or management changes?
7. Development of molecular markers for parent identification in multi-hybrid crosses (e.g. *P. deltoides* x (*P. laurifolia x P. nigra*) either naturally or artificially produced.