

Economic comparison of traditional and genomics breeding for Douglas-fir

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EXECUTIVE SUMMARY

An economic analysis was undertaken to compare the value of the genomic and traditional breeding programmes for Douglas- fir in New Zealand. This report also attempts to demonstrate the value realised at different points in the value chain. The work was undertaken using NPV analysis for both the forest owners, and the end processors of the wood resource.

The analysis shows that there is the potential for substantial value gain from employing a genomic breeding programme compared with employing a traditional breeding programme for Douglas-fir. This value gain is present for both forest owners, and processors.

Assuming a 6% rate of return, a traditional breeding programme was shown to have the potential to deliver a benefit of \$36.2 million to both the forest growing and processing sectors. Results showed that a genomics programme delivers a potential additional \$11.6 million, representing an additional \$290 per ha over the predicted 40,000 ha of new plantings.

Genomics delivers a potential \$2.8 million **to forest growers alone**, with the traditional programme forecasting an overall negative NPV of \$4.5 million assuming a 6% rate of return. Genomics therefore presents an NPV gain on per ha basis of \$184, over the predicted 40,000 ha of new plantings. Traditional breeding with the current modelled genetic gains delivered a potential loss of NPV of \$4.5 million.

Genomics delivers a potential \$4.3 million (assuming a 6% rate of return) **to forest processors alone**, over and above the traditional breeding programme's potential delivery of \$40.7 million. Genomics therefore presents an additional NPV gain on per ha basis of \$106, over the predicted 40,000 ha of new plantings.

The greatest challenge for Douglas-fir is the very long time frames, both overall and until the programs reach positive cash flow, 60 years and 40 years respectively, due to the long rotation cycle of Douglas- fir. This means the modelling takes into account 60 years of planting and management costs, including 40 years without harvesting, and only 20 years of harvest income.

INTRODUCTION

Forest tree breeding has delivered significant gains over the last 60 years, e.g. radiata pine (Kimberley et al. 2015). Douglas-fir breeding in New Zealand has stopped and started, with the result that less genetic gain has been delivered (Dungey et al. 2012). The New Zealand breeding programme was stalled for some considerable time when Swiss needle cast first came into the country, and has recently been re-invigorated.

In the meantime, genomics science has accelerated massively, with DNA-based technologies now being applied in poplars, and in pines (e.g. Mousavi et al. 2016, Bartholomé et al. 2016). Considerable debate on the value of these technologies to New Zealand breeding has stimulated the need to investigate the possible financial benefit of application to New Zealand Douglas-fir.

An economic analysis was undertaken to compare the value of the genomic and traditional breeding programmes for Douglas- fir in New Zealand to share with the Specialty Wood Partnership Programme. In addition, in order to determine where value is realised at different points in the value chain, an NPV analysis was undertaken separately for both the forest growers and wood processors.

METHODS

Assumptions

The percentage genetic gains for density and volume were provided from work done by Heidi Dungey and Mari Suontama. Genetic gains were derived from the genetic response formula as described e.g. Falconer & Mackay (1996) and based on population parameters for Douglas-fir in New Zealand (Dungey et al. 2012). Selection proportion for both traits was 20%, equivalent to selection intensity of 1.4 (Falconer & Mackay 1996).

All gains described on a per generation basis:

Traditional breeding

- 8% wood stiffness 12%, DBH (diameter at breast height).

Genomic breeding

- 20% wood stiffness, 20% DBH (diameter at breast height).

These values were the projected gain for the first generation of improved trees, subsequent generations are expected to have a 15% increase in both volume and density.

Research and implementation costs were also provided by Mari Suontama and Heidi Dungey. The timeline of these costs are found in Appendix 1. Genotyping and the costs of progeny trials were included in these costs.

The effect of the volume gain translates directly into increased harvestable volume, assuming an 85% harvest recovery rate. This is the sole factor in the value gain to the forest owner, no consideration was made to an increase in log prices due to increased stiffness as there is little segregation on actual wood stiffness currently undertaken operationally in forests.

The report does not consider any analysis on vegetative propagation. Considerable gains would be made per generation if the time to deployment was reduced – i.e. moving from seed orchard to vegetative propagation. This is highlighted throughout the literature (Harfouche et al. 2012).

Management and harvest costs were extracted from consultation with industry players for ballpark figures. The harvest and transport rates are from Allan Laurie Consulting's guide, assumed medium-steep terrain and 100km haul, for a total harvest cost of \$58/tonne.

The modelling was based on the assumption that planted area of Douglas-fir in New Zealand would increase by 40,000 ha over 35 years, as outlined in the 'Outcome benefits to New Zealand' document, submitted as part of the business case in the initial SWP proposal. This analysis did not factor in the replanting of existing Douglas-fir areas with the improved cultivars.

Log price was assumed at \$130/m³, again based on consultation with industry. Confidential conversations with log traders placed the premium for Douglas-fir logs at \$US 5-10/tonne over radiata pine.

The volume to weight conversion was adjusted for each generation to take into account the increases in wood stiffness and volume (DBH), this had the effect of increasing harvest and transport costs on a per m³ basis, and the effect is more pronounced for the genomics programme.

These results do not consider the de-risking for investors that may arise from other aspects of traditional or genomic breeding, notably selection for disease resistance, i.e. Swiss Needle Cast, nor do they include any value derived from carbon sequestration.

RESULTS

Forest owners

NPV comparison, taking into account all forest management, harvesting, and transport costs has the genomics programme delivering a potential \$2.8 million, with the traditional programme forecasting an overall negative NPV of \$4.5 million assuming a 6% rate of return. Genomics therefore presents a NPV gain on per ha basis of \$184, over the predicted 40,000 ha of new plantings. There are a number of factors behind these low NPV's, chiefly the very long time frames, both overall and until the programs reach positive cash flow, 60 years and 40 years respectively, due to the long rotation cycle of Douglas- fir. This means the modelling takes into account 60 years of planting and management costs, including 40 years without harvesting, and only 20 years of harvest income.

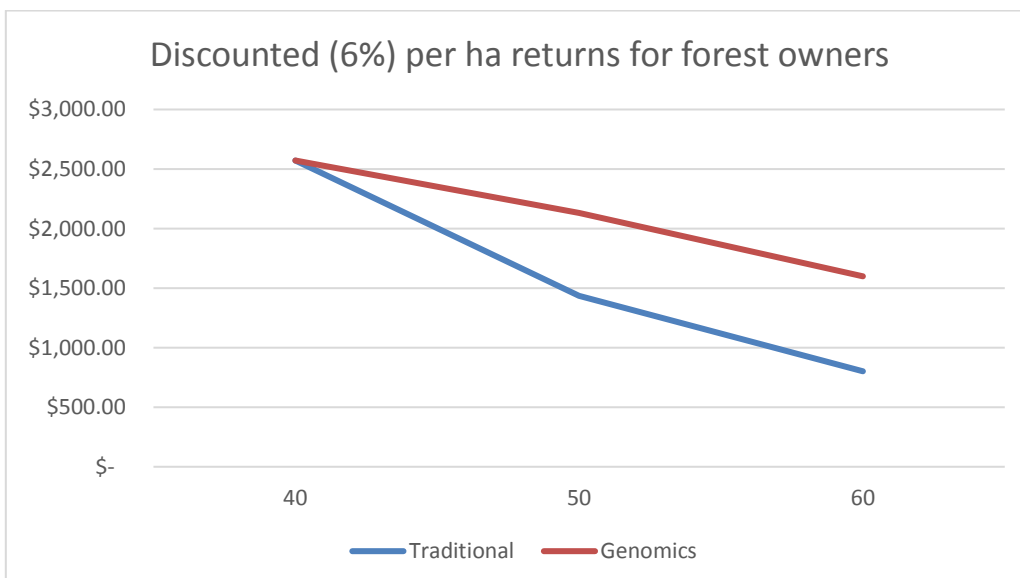
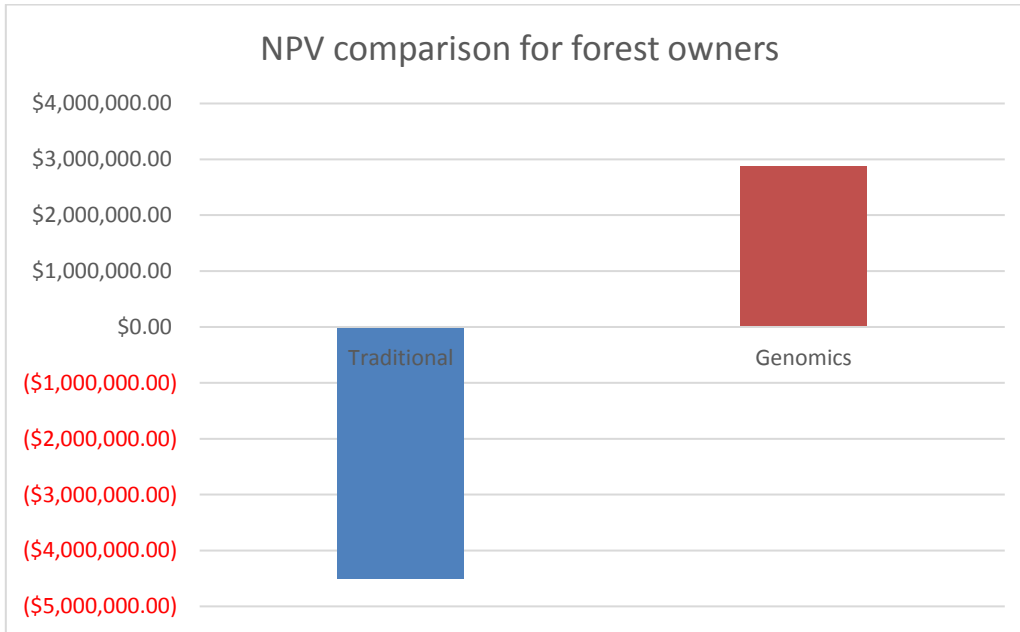


Figure 1 and 2. Discounting the per ha returns to present value, after all costs accounted for, shows that the genomics programme presents a clear value gain as the additional volume from the genetic gain starts to come on stream.

Processors

The value gain to processors is assumed to come from two areas. Firstly, the increased volume able to be produced due to the increased available wood resource, secondly, there will be an increase in the proportion of wood meeting the MGP10 structural standard due to the increased stiffness of the wood, therefore increasing the amount of wood being able to be sold at the higher structural timber price point. Raw material costs were assumed to account for 50%-58% of end product total costs, depending if it is structural or industrial sawmilling, based on the WoodScape project.

This analysis assumed that the processing of Douglas-fir would be limited to structural and industrial sawmilling, as this the predominant current use. It did not factor in a move to processing into higher value wood products such as LVL and plywood, or additional value adding steps such as use in CLT or OEL, both of which have been investigated and show promise as a use for Douglas-fir. Also to note, is that this analysis does not consider the production of high value chemicals, e.g. Taxifol, which are known to be present in Douglas-fir, which may dramatically change the economics of the programmes.

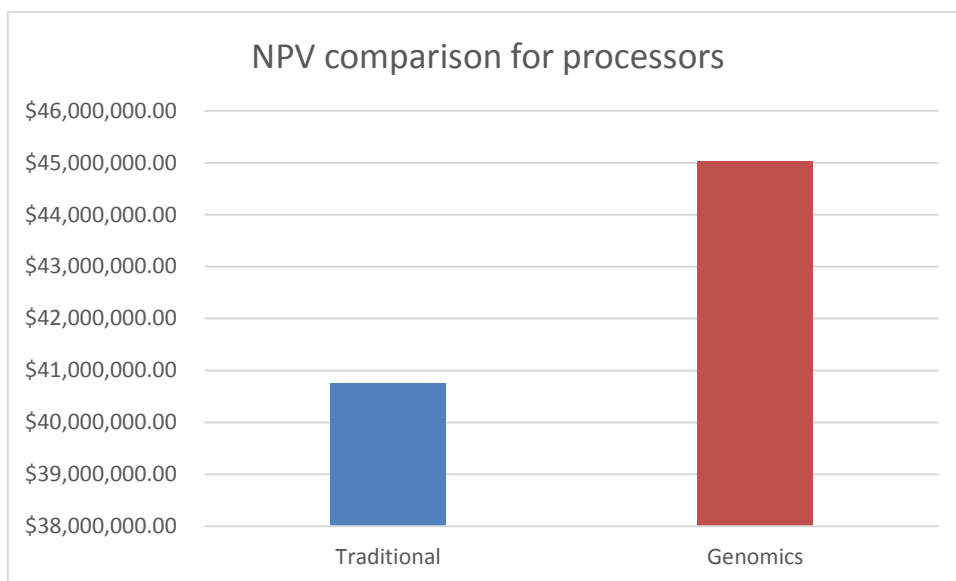


Figure 3. The genomics programme returns an NPV of \$45 million, compared with the traditional programme's \$40.7 million, a gain of \$4.3 million, at 6% rate of return.

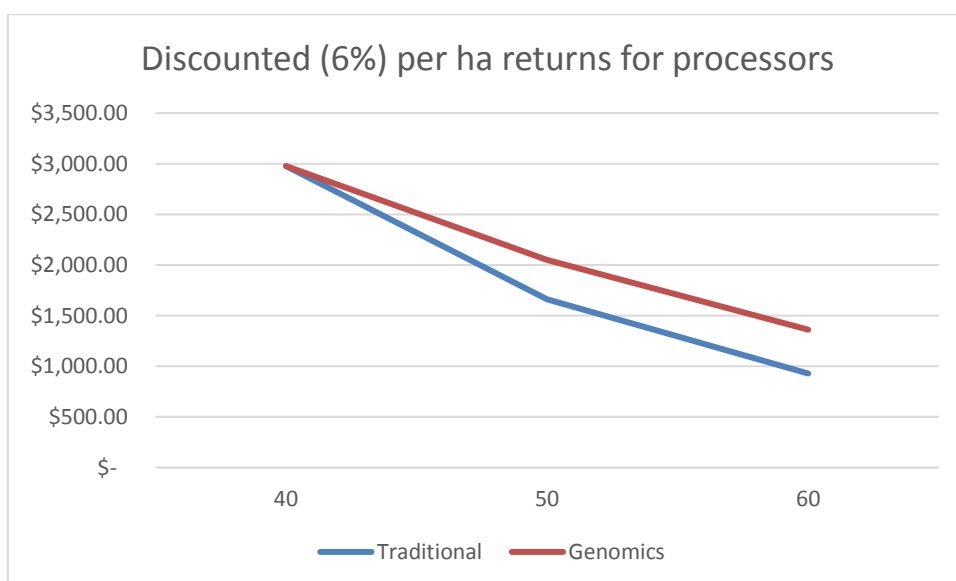


Figure 4. Like with the returns to the forest owners, there is a clear value gain from the genomics program as the enhanced selected genotypes start to come on stream.

CONCLUSION

The analysis shows that there is the potential for substantial value gain from employing a genomic breeding programme compared with employing a traditional breeding programme for Douglas-fir. This value gain is present for both forest owners, and processors.

Further work into how that value gain translates into different processed end products would be recommended to provide information about alternative potential processing scenarios. This work would also best be done in conjunction with identifying how genomic selection can target and improve specific traits in Douglas-fir such as chemical composition which may increase the variety of potential processing options and open up higher value markets far removed from today's traditional processed wood markets.

REFERENCES

- Bartholomé, J., Van Heerwaarden, J., Isik, F., Boury, C., Vidal, M., Plomion, C., & Bouffier, L. (2016). Performance of genomic prediction within and across generations in maritime pine. *BMC Genomics*, 17(1), 604. <http://doi.org/10.1186/s12864-016-2879-8>
- Dungey, HS, Low, CB, Lee, J, Miller, MA, Fleet, K, Yanchuk, AD. (2012). Developing breeding and deployment options for Douglas-fir in New Zealand: breeding for future forest conditions. *Silvae Genetica*, 61:3, 104-115.
- Dungey, H. S., Low, C. B., Lee, J., Miller, J. T., Fleet, K., & Yanchuk, A. D. (2012). Developing breeding and deployment options for Douglas-fir in New Zealand: breeding for future forest conditions. *Silvae Genetica*, 61(3), 104–115.
- Falconer DS, Mackay TFC (1996). Introduction to quantitative genetics. Fourth Edition. Longman Group Ltd. Pearson Education Limited. Harlow, Essex, England.
- Harfouche, A., et al., (2012). *Accelerating the domestication of forest trees in a changing world*. *Trends in Plant Science*, 2012. 17(2): p. 64-72.
- Kimberley, M. O., Moore, J. R., & Dungey, H. S. (2015). Quantification of realised genetic gain in radiata pine and its incorporation into growth and yield modelling systems, 1687(May), 1676–1687.
- Mousavi, M., Tong, C., Liu, F., Tao, S., Wu, J., Li, H., & Shi, J. (2016). De novo SNP discovery and genetic linkage mapping in poplar using restriction site associated DNA and whole-genome sequencing technologies. *BMC Genomics*, 17, 1–12. <http://doi.org/10.1186/s12864-016-3003-9>
- Porth, I., Bull, G., Ahmed, S., El-Kassaby, Y. A., & Boyland, M. (2015). Forest genomics research and development in Canada: Priorities for developing an economic framework. *Forestry Chronicle*, 91(1), 60–70. <http://doi.org/10.5558/tfc2015-011>

APPENDICES

Appendix 1: Timelines, rotation ages and assumptions in the economic analysis.

Douglas-fir breeding scenarios for traditional breeding and genomic selection														Genetics up to here...		
Year -10	Year 0	Year 10	Year 12	Year 22	Year 24	Year 34	Year 36	Year 40	Year 46	Year 48	Year 58	Year 60	Year 64	Year 70	Year 72	Year 88
Seed orchard 1 seed used for commercial seed and for progeny trial	Progeny trial 1 initiated	Phenotypic assessment 1 & BLUP selection for grafting	Seed orchard 2 established	Seed from orchard 2 available	Progeny trial 2 established	Phenotypic assessment of Progeny trial 2 BLUP and selection for grafting	Seed orchard 3 established		Seed from orchard 3 available	Progeny trial 3 established	Phenotypic assessment of Progeny trial 3 BLUP and selection for grafting	Seed orchard 4 established		Seed from orchard 3 available		
\$45k			\$70k	\$150k	\$45k		\$70k	\$150k	\$45k	\$70k		\$150k	\$45k			
Establish commercial stand 1					Establish commercial stand 2			Harvest Commercial stand 1	Establish commercial stand 3			Harvest Commercial stand 2			Harvest Commercial stand 3	
seed by year 10	2/0 crop + grow for 8 years = 14 years (rotation age 40 yrs)	grafting 2 years Genetic gain stiffness 8% Genetic gain DBH	10 years until seed production	2/0 growing of seedlings	2/0 crop + grow for 8 years	grafting 2 years Genetic gain stiffness 8% Genetic gain DBH 12%	10 years until seed production		2/0 growing of seedlings	2/0 crop + grow for 8 years	grafting 2 years Genetic gain stiffness 8% Genetic gain DBH	10 years until seed production				
Genomic selection without clonal																
Year -10	Year 0	Year 10	Year 12	Year 22	Year 24	Year 26	Year 36	Year 38	Year 40	Year 50	Year 52	Year 54	Year 62	Year 64	Year 76	Year 90
Seed orchard 1	Progeny trial 1 established	Phenotypic assessment 1 & GeBV's selection for Genomic selection	Seed orchard 2 established	Seed from orchard 2 available	Raise families, rogue in nursery using genomics.	Establish Seed Orchard 3 directly from seedlings	Seed from orchard 3 available	Raise families, rogue in nursery using genomics.	Establish Seed Orchard 4 directly from seedlings	Seed from orchard 4 available	Raise families, rogue in nursery using genomics.	Establish Seed Orchard 5 directly from seedlings		Seed from orchard 5 available		
\$45k			\$70k	\$350k	\$45k	\$200k	\$45k	\$200k	\$45k	\$200k	\$45k	\$200k	\$45k			
Establish commercial stand 1				Establish commercial stand 2			Establish commercial stand 3		Harvest Commercial stand 1	Establish commercial stand 4		Harvest Commercial stand 2	Establish commercial stand 5	Harvest Commercial stand 3	Harvest Commercial stand 4	
	2/0 crop + grow for 8 years = 14 years (rotation age 40 yrs)	grafting 2 years		Genetic gain stiffness 20% Genetic gain DBH			Genetic gain additional 15%			Genetic gain additional 15%						