

The 2025 MWP Award – Full motivation

Citation

The 2025 Marcus Wallenberg Prize is awarded to Dr Gerald Tuskan for his pioneering work in sequencing and analysis of the first tree genome.

His leadership in sequencing this genome and the associated scientific breakthroughs have been instrumental in revolutionizing research on tree and forest genomics. These have paved the way for genome-based breeding of commercially important trees and have enabled many substantial downstream impacts on the global forest bioeconomy.

Background and Prize Motivation

The American forest geneticist Gerald Tuskan led a project to sequence the genome of the black cottonwood tree *Populus trichocarpa*. The full genome sequence was published in 2006 (Tuskan et al. 2006) and was the third plant genome after the model plant *Arabidopsis* and rice to have complete genomes sequenced. The genome of *Populus trichocarpa* was found to be rather compact with just over 500 megabases (500 million letters of genetic code), being four times larger than the genome of *Arabidopsis*.

Tuskan's work has enabled the establishment of the black cottonwood as a model tree genus to be used in a wide range of molecular genetics studies including those relating to wood biology, flowering and tree phenology. This project provided foundational understanding of the genomic information of trees. The sequencing of the *Populus trichocarpa* genome, and the methods and tools developed during this project, paved the way for numerous other tree genome sequencing projects including various conifers such as the Norway Spruce (Nystedt et al., 2013), and the loblolly pine *Pinus taeda* (Neale et al., 2014) as well as the important plantation tree genus *Eucalyptus* (Myburg et al., 2013). These genome sequencing and related studies have impacted positively on breeding programmes of trees important to the forest bioeconomy of many countries.

The leading role that Gerald Tuskan played in sequencing and analysing the poplar genome significantly advanced the field of forest genomics providing valuable insights to improve the growth, productivity and resilience of forest species. It has provided the basis for genome-based selection of tree varieties in traditional breeding as well as in breeding using modern genetic technologies, for enhanced traits such as improved growth, resistance to diseases and better wood quality.

In a world challenged by the impacts of climate change, tree resilience to changes in the environment has become increasingly important. In this regard, Gerald Tuskan's research has generated tools to develop trees adapted to environmental stresses, including drought, extreme temperatures, soil conditions and the often associated growing threats of insect pests and pathogens. All these factors are crucial for maintaining forest ecosystems in the face of climate change.

Almost exactly twenty years has passed since the publication of this first tree genome sequence by Tuskan et al. (2006). This milestone work provided the foundation for many similar projects such as sequencing and studying the important tree symbiotic mycorrhizal fungi (Tisserant et al., 2013). Gerald Tuskan has participated in many of these research initiatives, which continue to grow in their impact and importance (Jansson, et al., 2010; Sannigrahi et al., 2010; Cregger et al., 2018; Harfouche et al. 2019). For example, he has been at the forefront of applying new genetic engineering tools including the Nobel Prize winning CRISPR-Cas9 technology (Doudna and Charpentier, 2014) to improve specific traits such as disease resistance, drought tolerance and growth rate. There is no question that the impact of this work will grow substantially in relevance in coming years and that it will continue to dramatically change the face of forest science globally.

Other than his specific research skills and accomplishments, Gerald Tuskan has had a great influence in promoting collaborative research efforts, working across disciplines such as molecular biology, ecology and environmental science. His collaborative approach has helped to build a global network of researchers focussed on improving tree genetics and sustainability. He is widely recognised as a skilled leader that has helped to foster partnerships between academia, industry, and government agencies to push forward the boundaries of tree genomics and bioenergy research. He has also mentored numerous graduate students and early-career scientists, helping to train the next generation of experts in forest biology, genomics and bioenergy.

Gerald Tuskan



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The center includes seventeen institutions focussed on accelerating the domestication of non-model plants and microbes to enable high-impact innovation across the bioenergy sector. He has published

more than 350 papers, many of which are highly cited including those related to his leading role in sequencing the first tree genome, that of the black cottonwood, *Populus trichocarpa* in 2006.

Gerald Tuskan is one of the world's best known forest scientists, having initiated many collaborative studies relating to tree growth and biology, acknowledged for numerous years in the top 1% of cited scientists worldwide in plant biology, receiving many important awards for his work including being recognised as a Battelle Distinguished Inventor at the Oak Ridge National Laboratory and as a Distinguished Scientist Fellow of the DOE Office of Science.

References

- Cregger, M.A et al. 2018. The *Populus* holobiont: dissecting the effects of plant niches and genotype on the microbiome. *Microbiome* 6: 31. [Doi.org/10/1186-018-0413-8](https://doi.org/10.1186-018-0413-8).
- Doudna, J. and Charpentier, E. 2014. The new frontier of genome engineering with CRISPR-Cas9. *Science* 346, DOI 10.1126/science.1258096
- Harfouche et al., 2019. Accelerating climate resilient plant breeding by applying next generation artificial intelligence. *Trends in Biotechnology* 37: 1217-1235.
- Jansson et al., 2010. Phytosequestration: Carbon biosequestration by plants and the prospects of genetic engineering. *Bioscience* 60: 685-696.
- Myburg et al., 2014. The genome of *Eucalyptus grandis*. *Nature* 510: 356-362.
- Neale D. et al. 2014. Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. *Genome Biology* 15: R59.
- Nystedt, B. et al. 2013. The Norway spruce genome sequence and conifer genome evolution. *Nature* 497: 579-584.
- Sannigrahi et al., 2010. Poplar as a feedstock for biofuels: A review of compositional characteristics. *Biofuels, Bioprod. Bioref.* 4: 209-226.
- Tuskan, G.A. et al. 2006. The genome of the black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science* 313, 1596-1604.
- Tisserant, E. et al. 2013. Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. *PNAS* 110: doi.org/10.1073/pnas.1313452110