

1. Record Nr.	UNINA990003249230403321
Autore	Morris, John w.
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2. Record Nr.	UNINA9910416103303321
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Introduction -- The White spruce genome -- Targeted and whole genome re-sequencing for population and evolutionary genomic inferences in Norway spruce -- Transposable elements in Spruce -- An intact, but dormant LTR retrotransposon defines a moderately-sized family in white spruce (*Picea glauca*) -- The DNA methylome of Norway spruce -- Epigenomics in Norway spruce -- Comparative Genomics of Spruce -- Comparative genomics with the comparisons of BACs between loblolly pine and white spruce -- Wood formation and genomic selection in white spruce, data imputation strategies -- Ecotypes in Norway spruce ("Genomics of adaptation to drought across the Central European range of Norway spruce") -- Local adaptation in the interior spruce hybrid complex -- Genomics of secondary metabolism - Terpenoids in spruce (Evolutionary dynamics of TPS gene family in Chinese spruce) -- Lignin biosynthesis in Norway spruce as an anti-fungal defense -- Future prospects.

Sommario/riassunto

This book offers comprehensive information on the genomics of spruces (*Picea* spp.), naturally abundant conifer tree species that are widely distributed in the Northern Hemisphere. Due to their tremendous ecological and economic importance, the management of forest genetic resources has chiefly focused on conservation and tree improvement. A draft genome sequence of the 20-gigabase Norway spruce genome was published in the journal *Nature* in 2013. Continuous efforts to improve the spruce genome assembly are underway, but are hindered by the inherent characteristics of conifer genomes: high amounts of repetitive sequences (introns and transposable elements) in the genome and large gene family expansions with regards to abiotic stress, secondary metabolism and spruces' defense responses to pathogens and herbivory. This book presents the latest information on the status of genome assemblies, provides detailed insights into transposable elements and methylation patterns, and highlights the extensive genomic resources available for inferring population genomics and climate adaptation, as well as emerging genomics tools for tree improvement programs. In addition, this volume features whole-genome comparisons among conifer species, and demonstrates how functional genomics can be used to improve gene function annotations. The book closes with an outlook on emerging fields of research in spruce genomics.