Genomic Resources for the Study of Loblolly Pine and Other Conifers

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Genomic techniques and technologies are poised to revolutionize many of our approaches to forest biology, as well as forest management. Rapid advancement in the genomic sciences and their infiltration into so many aspects of biology has been facilitated by the rapid release of large datasets to the public via the Internet. Such openness with data release is a relatively new phenomenon, and is predicated on the expectation that important and useful information will be gleaned more efficiently when multiple groups of researchers are allowed to apply a wide variety of bioinformatics tools independently to the analysis of the enormous datasets produced by genomic techniques. One of the challenges facing all biologists is how to keep up with the growing array of databases and bioinformatic tool sets to identify those most useful for addressing particular sets of problems.

Although the development of genomic datasets for conifers has lagged the torrent of information being made available for various model systems, as with other organisms, conifer resources are growing rapidly, and with them come great opportunities to mine the data for new research hypotheses. This presentation will summarize the current content of conifer information available at major public repositories for genomic data, such as GenBank and EMBL. Conifer data housed at smaller online sites, such as Dendrome and Fungen, will also be reviewed. Both structural, as well as functional genomics resources will be covered. A variety of bioinformatic tools available to online users for mining these datasets will also be discussed. As loblolly pine is the conifer species for which the most data is available online, most of the examples to be presented will focus on this species, but examples for other species, particularly the spruces, will also be examined.

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