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Southern Pine Beetle Prevention Program: One Million Acres Protected

John Nowak[a,b]

Southern Pine beetle (SPB) severely impacts the South's tourism and wood-based industries, and also negatively impacts watersheds and wildlife habitat, most notably that of the red-cockaded woodpecker. The SPB Prevention Program is a cornerstone piece to the USDA Forest Service's efforts to institute a comprehensive approach for preventing and reducing the impacts of SPB on federal, state, and private forests through silvicultural means, such as thinning. In 2011, the program reached the milestone of one million acres treated using an all-lands approach to reach across boundaries and federal and state borders working with 12 national forests, 13 states and more than 13,000 landowners. Since the SPB Prevention Program started in 2003, there has not been a major SPB outbreak, which has allowed for a single focus on prevention work instead of suppression activities. The SPB Prevention Program is a successful model upon which to develop future proactive forest health strategies that can be applied across large geographic areas and among many different cooperators and stakeholders. The SPB Prevention Program won the 2009 Regional Forester's Award for "Natural Resources" and the 2011 Chief's Award for "Sustaining National Forests."

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Application of Molecular Genetic Tools for Forest Pathology

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In recent years, advances in molecular genetics have provided powerful tools to address critical issues in forest pathology to help promote resilient forests. Although molecular genetic tools are initially applied to understand individual components of forest pathosystems, forest pathosystems involve dynamic interactions among biotic and abiotic components of the environment. More sophisticated and holistic molecular genetic approaches are now available to better understand dynamic interactions of forest pathosystems. This presentation will describe how advanced molecular genetic technologies can improve our understanding of ecosystem interactions to promote resilient forests. These molecular genetic tools include (1) molecular diagnostics for detecting, identifying, and monitoring forest pathogens and other organisms; (2) phylogenetics for determining evolutionary relationships and global distributions of forest hosts, pathogens and associated organisms; (3) population genetics for assessing population structure of forest organisms; (4) genomics for evaluating gene structure and function; and (5) metagenomics for analyzing forest communities, ecological functions, and interactions among the abiotic and biotic environment.

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Assisted Resilience in Western Larch

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The resiliency of western larch (*Larix occidentalis* Nutt.) was called into question when the larch casebearer (*Coleophora laricella* Hubner), a non-native insect, was discovered in Idaho in 1957. However, the impacts were historically mitigated through a biological control program that released 7 species of parasitoid wasps in the 1960s and 1970s. The most effective were *Agathis pumila* (Ratzeburg) (Hymenoptera: Braconidae) and *Chrysocharis laricinellae* (Ratzeburg) (Hymenoptera: Eulophidae). Studies in NE Oregon have shown that they reduced populations of larch casebearer and the biological control program is considered a major success. Flare-ups of larch casebearer continue to occur across the range of western larch, but don't persist for long periods. Scientists with Oregon State University have recently documented the persistence of the introduced parasitioid wasps in Oregon, Washington, Idaho, and Montana but inference regarding population regulation is not possible without long-term studies. It appears that western larch has maintained its resiliency due to the assistance of forest entomologists.

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Armillaria Root Disease in the Western USA

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Armillaria species display diverse ecological behaviors from beneficial saprobe to virulent pathogen. *Armillaria solidipes*, a causal agent of Armillaria root disease (ARD), is a virulent primary pathogen with a broad host range. ARD is responsible for reduced forest productivity as a result of direct tree mortality and non-lethal cryptic infections that impact growth. It is typically more severe in intensively managed forests and in maladapted trees. Armillaria isolates collected from more than 500 climatically diverse, georeferenced plots established throughout the western USA were identified using DNA-based diagnostics. Survey data and associated climatic data were used to develop bioclimatic models to predict current and future distributions and disease activity of *A. solidipes*. Future host distribution models were coupled with Armillaria models to forecast areas in which hosts will be maladapted and thus more susceptible to ARD. Preliminary prediction maps indicate that although the distribution changes, suitable climate space for *A. solidipes* will remain available across the western landscape under various climate-change scenarios. Moreover, ARD is expected to intensify as hosts become increasingly stressed.

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