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RESEARCH COLLOQUIUM SERIES

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Mountain Pine Beetle System Genomics:
Spatial genetic structure of the mountain pine beetle outbreak in western Canada

Friday
Nov. 26, 2010

3:30 - 4:30

LECTURE THEATRE
7 - 150

The mountain pine beetle, (*Dendroctonus ponderosae*), is currently causing an epidemic of record size in Western Canada. Tree mortality, mostly lodgepole pine (*Pinus contorta*), has occurred over 15 million hectares of forest through the combined action of the beetle and its fungal associates (primarily, *Grosmannia clavigera*). The Tria Project, Mountain Pine Beetle Systems Genomics, is a multidisciplinary investigation of these three primary organisms in the outbreak – beetle, fungus, and the host pine. A major goal of the project is to develop an integrated landscape map containing information on the genomic variation of each organism. This information can be used to infer current dispersal patterns, long-term phylogeographic processes and to study adaptive changes associated with a shift into new environments. This talk will highlight some of the key research achievements of the Tria project and discuss recent developments in the analysis of the spatial genetic structure of the mountain pine beetle. Information on "neutral" microsatellite variation in beetles from 49 sampling locations throughout BC and AB shows a North-South population structure that is supported by Bayesian structure analysis, North-South genetic relationships and diversity gradients, and the lack of isolation by distance in the northernmost cluster. Our findings are consistent with spatiotemporal analyses of the current epidemic that supports a multi-center hypothesis. Northern outbreaks are consistent with an expansion out of the Chilcotin plateau while southern outbreaks are consistent with multiple centers of origin.

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