Getting at the Root of the Mountain Pine Beetle’s Rapid Habitat Expansion and Forest Devastation

The mountain pine beetle has wreaked havoc in North America, across forests from the American Southwest to British Columbia and Alberta, with the potential to spread all the way to the Atlantic coast. Millions of acres of forest have been lost, with severe economic and ecological impacts from a beetle outbreak ten times larger than previous outbreaks.

Because of its importance and impact on forestry, the mountain pine beetle’s genome has been recently sequenced. Using this new resource, authors Janes et al. (2014) examined how the pine beetle could undergo such rapid habitat range expansion and whether population genetics and the cataloguing of genome wide mutations could shed any light on possible molecular causes of the outbreak. From beetles collected at 27 sites in Alberta and British Columbia, they looked for any patterns among their catalog of 1,536 mutations (single-nucleotide polymorphisms).

They found several candidate genetic markers and conclude that the mountain pine beetle may have been able to spread by adjusting its cellular and metabolic functions to better withstand cooler climates and facilitate a larger geographic dispersal area. Such information could give important new clues for the forestry industry to help curb the current devastation of North American forests from this pest.

Reference

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New Analysis of Seven Ant Genomes Reveals Clues to Longer Life Spans Associated with Sociality

Roux et al. (2014) tried to uncover which genes could be involved in ant-specific adaptations, notably in relation to the evolution of complex social systems and division of labor.

Using a combination of state-of-the-art evolutionary tools, the article examines the signatures of positive selection on a phylogeny of seven ants and compares these signatures with those detected in other insect data sets composed of 12 species of flies and 10 species of bees. This design allowed the authors to identify molecular patterns unique to ants, compared with flies and bees.

Overall, they identified 24 functional categories of genes that experienced strong positive selection in the ant lineage. Among the significant categories, some were related to nervous system development, behavior, immunity, metabolism, protein translation, and degradation, but similar patterns were observed in flies and bees.

Strikingly, they also found ant-specific signals of positive selection on genes with mitochondrial activity that accounted for 11 out of the 24 significant categories. Additional analyses suggested that this could be an important molecular clue that may be responsible for increased life span of queens in the ant lineage—ant queens can live up to 30 years in some species. Mitochondria are cellular power plants whose by-products are thought to be toxic and responsible for aging. “The improvement of mitochondrial activity by positive selection on ant genes might have been an important step toward the evolution of extreme lifespan that is a hallmark of this lineage,” said author Julien Roux.

Reference

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