

Assembling the transcriptome of a noxious weed: New resources for studying how plants invade

March 5 2013

In order to build and maintain cells, DNA is copied into ribonucleic acid (RNA) molecules, also called transcripts. Transcripts are often like a recipe for making proteins, and a collection of all the transcripts in a cell is called a transcriptome.

Pankaj Jaiswal, Assistant Professor of Botany and [Plant Pathology](#) at Oregon State University, Samuel Fox, a Postdoctoral Associate in Jaiswal's laboratory, and colleagues assembled transcriptomes of a [noxious weed](#), *Brachypodium sylvaticum*, or slender false brome. The [transcriptome](#) provides an extensive [genetic tool](#) for studying how invasive species, like slender false brome, successfully spread into novel ranges. In addition, the genome is available for a closely related species, *Brachypodium distachyon*. Together, the transcriptome and genome can be used as a reference for pinpointing differences in slender false brome genes and [gene activity](#) that may contribute to its invasive capabilities.

Slender false brome is an invasive grass that is native to Europe, Asia, and North Africa. It was introduced into the United States about 100 years ago and is listed as a noxious weed along the West Coast of the United States. "It is aggressively invasive within its current range—near monocultures of this grass occupy thousands of hectares of mixed coniferous understory and grassland habitats in Oregon," says Mitch Cruzan, coauthor and Associate Professor of Biology at Portland State University.

Slender false brome is ideal as a model for invasive [plant evolution](#). "False brome is in the process of active range expansion and is wildly successful despite experiencing colder, wet winters and drier summers than plants in the native range," explains Cruzan, "so it is a great system for studying ecological and evolutionary aspects of invasion."

Fox and colleagues have assembled the transcriptomes for two slender false brome populations from its native range (Greece, Spain) and one population from its invasive range (Oregon). Comparing transcriptomes across ranges will reveal new changes in gene expression in the highly successful invasive population. "This system has great potential as a comparative framework for studying adaptation to new environments and invasion," comments Jaiswal.

To allow future studies to identify the functions of slender false brome genes, the authors also compared the false brome transcriptome to those of well-studied agricultural species, including rice and sorghum. If false brome possesses a gene that has already been studied in an agricultural species, it will be easier to identify the gene's supposed function. The teams from Jaiswal's and Cruzan's laboratories are exploring these newly developed genetic resources, which may provide insights into how slender false brome has adapted to Oregon's different environmental conditions.

The authors published their results, including details on data retrieval, in the March issue of *Applications in Plant Sciences* (available for free viewing at <http://www.bioone.org/doi/pdf/10.3732/apps.1200011>). Fox and Cruzan note, "The seed and genomic resources are publicly available, so it would be relatively easy for any research group to establish a research program focused on slender false brome."

Provided by American Journal of Botany

Citation: Assembling the transcriptome of a noxious weed: New resources for studying how plants invade (2013, March 5) retrieved 20 September 2024 from <https://phys.org/news/2013-03-transcriptome-noxious-weed-resources-invade.html>

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