Markers Point the Way to New Oat Traits

America's oat production has decreased since the 1950s, but consumer demand remains as strong as ever, especially with mounting scientific evidence that oats are good for us.

Their soluble fiber, beta-glucan, for example, appears to reduce blood-cholesterol levels and has been formulated for use in food and beverage products. The grain has nonfood applications, too, including use of oat flour in skin- and hair-care products.

Now, a concerted effort to furnish oat breeders with the latest tools in molecular genetics could make even better use of such versatility, broadening the cereal grain's commercial horizons and increasing its production.

"Genomically, oat has lagged behind other cereal crops, like corn and barley," says molecular biologist Eric Jackson, who is in the Agricultural Research Service's Small Grains and Potato Germplasm Research Unit at Aberdeen, Idaho. But an oat-genomics project he and ARS geneticist Don Obert (Aberdeen) proposed in late 2008 to address the deficit has quickly gained momentum, thanks to the participation of 2 ARS Regional Molecular Genotyping Laboratories, 5 other ARS locations, 10 U.S. universities, 9 foreign laboratories, and support from General Mills, Inc., members of the North American Millers' Association (NAMA), and the USDA-Agriculture and Food Research Initiative's Plant Breeding, Genetics, and Genomics program.

"NAMA has long supported efforts to bring new tools to oat researchers," says Jane DeMarchi, the association's director of government relations. "We believe this project will help ensure that oats remain a viable crop."

A key objective is to provide oat breeders with a fast, accurate means of identifying valued traits in elite commercial cultivars and germplasm sources. To that end, the group is scouring the oat genome for DNA marker regions associated with the expression of these traits. Of particular interest are increased dietary fiber content, elevated levels of grain beta-glucan and tocopherol, and improved disease resistance.

The markers—small pieces of DNA—are like molecular signposts pointing out a desired trait's genomic whereabouts. Several different kinds can be used, but the type the oat genomics group seeks is the SNP (single nucleotide polymorphism). The aim is to find and describe (through sequencing thousands of expressed genes in important North American oat varieties) 3,000-plus SNP markers.

ARS plant geneticist Gina Brown-Guedira (Raleigh, North Carolina) and ARS molecular biologist Joe Anderson (West Lafayette, Indiana) will develop diagnostic assays from the newly discovered marker-trait associations. This, in turn, will enable use of marker-assisted selection (MAS) to accelerate the development of new oat varieties with enhanced benefits to human health. Brown-Guedira's genotyping lab will

then use the assays to quickly inform breeders which offspring plants inherited an intended trait—say, for crown rust resistance. Normally, determining this trait would necessitate growing the plants to maturity, inoculating them with the pathogen, waiting for disease symptoms to appear, and evaluating the plants' response. But with MAS, resistant plants could be identified in about 3 days based on high-throughput DNA analyses using diagnostic markers.

Another goal, pursued by ARS geneticist Jean-Luc Jannink (Ithaca, New York), is to develop a predictive computer model oat breeders can use to forecast which candidate varieties will perform best, whether it be for food, feed, or industrial uses.—By **Jan Suszkiw,** ARS.