

RU:

Forage and Range Research Laboratory

Location:

Logan, UT

Primary Contact for Bioenergy:

Steve Larson

Current research projects and objectives:

Comparison of seasonal accumulated growth among grass species adapted to western U.S. – the objective identify large-stature perennial grass species that may be suitable as low-maintenance forage and bioenergy feedstocks. Seasonal accumulated growth of basin wildrye (*Leymus cinereus*), mammoth wildrye (*L. racemosus*), interspecific hybrids of *L. cinereus* x *L. triticoides*, tall wheatgrass (*Thinopyrum ponticum*), intermediate wheatgrass (*Thinopyrum intermedium*), switchgrass (*Panicum virgatum*), tall fescue (*Festuca arundinacea*), robust needlegrass (*Acnatherum robustum*), meadow brome (*Bromus riparius*), and reed canarygrass (*Phalaris arundinacea*) will be compared in replicated field evaluations near Tetonia, ID and Logan, UT.

DNA Sequencing and genetic mapping of lignin biosynthesis genes from Leymus wildryes – the objective is to identify genetic markers and develop transformation constructs to improve forage digestibility and bioenergy conversion characteristics of *Leymus* wildryes.

Identification of QTLs controlling biomass accumulation, plant height, regrowth potential, growth habit, fiber and lignin content, mineral content, and other traits in basin x creeping wildrye hybrids –Caespitose basin wildrye grows over 2 m tall and is the largest perennial grass native to western North America. Basin wildrye was once abundant on sites where soil and water and water accumulate, such as alluvial fans and river floodplains, where modern agricultural operations are now focused. Although basin wildrye has considerable biomass accumulation potential, it is susceptible to grazing and repeated clipping. Creeping wildrye is a strongly rhizomatous grass, usually less than 1.5 m tall, and is one of the few native Great Basin grasses resistant to grazing, trampling, or repeated clipping. Interspecific hybrids of basin wildrye and creeping wildrye display a heterotic combination of plant height, biomass production, regrowth, and other potentially useful traits. The objective of this project is to identify DNA markers that could be used to combine these heterotic traits and develop hybrid varieties suitable as dedicated forage and bioenergy feedstocks adapted to the high-elevations, cold-growing seasons, and hot-dry summers of the western U.S.

Lead Scientists:

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Key Accomplishments:

Constructed high-density molecular genetic maps for the 164-sib TTC1 and 170-sib TTC2 full-sib families derived from crosses of the *L. triticoides* x *L. cinereus* TC1 and TC2 hybrids crossed to a *L. triticoides* tester genotype (T-tester). Identified QTLs controlling growth habit (rhizome proliferation), plant height, flowering, mineral content, and fiber (ADF and NDF) content, seed shattering, seed dormancy, and salt-tolerance in the TTC1 and TTC2 families. Evaluation and

fine-genetic mapping of LG3a growth habit QTL in four advanced backcross populations. Constructed and sequenced EST (15,000 clones forward and reverse) and BAC (384,000 clones with average size of 150 kilobase totaling 5.3X genome equivalents) DNA libraries for the allotetraploid *Leymus* TC1 and TC2 hybrids, aligned *Leymus* ESTs to the rice genome, and tested more than 1800 EST derived microsatellite markers. Isolated and genetically mapped one or more ESTs for nine of the ten known lignin biosynthesis genes including phenylalanine ammonia-lyase (PAL), cinnamate 4-hydroxylase (C4H), 4-hydroxycinnamyl coA ligase, hydroxycinnamoyl CoA:shikimate hydroxycinnamoyltransferase (HCT), p-coumarate 3-hydroxylase, caffeoyl CoA O-methyltransferase (CCoAOMT), cinnamoyl CoA reductase (CCR), ferulate 5-hydroxylase (F5H), caffeic acid/5-hydroxyferulic acid O-methyltransferase (COMT), and cinnamyl alcohol dehydrogenase (CAD). Developed cDNA subtraction libraries from subterranean branch meristems of caespitose basin wildrye and rhizomatous creeping wildrye.

Other scientific expertise or capabilities already available to the RU that could be applied to bioenergy research:

The USDA-ARS Forage and Range Research Laboratory has eight Research Geneticists and twelve research support staff focused on evaluation and development of native and introduced perennial grass species used for agriculture, landscaping, and other conservation uses in the western U.S. The Forage and Range Research Laboratory has extensive capabilities for multi-year and multi-location perennial grass field evaluations in diverse irrigated and dryland growing environments of the Great Basin and Intermountain regions. The Forage and Range Research Laboratory also has wet-lab and NIR equipment dedicated to analysis of grass lignin, fiber, and soluble carbohydrate content. The Forage and Range Research Laboratory also has equipment and expertise for cytological and genomic analysis GISH and FISH microscopy, six dual-96 or dual-384 well thermocyclers, quantitative RT-PCR thermocycler, two Partec flow cytometers, two ABI3730 instruments, and an Affymetrix GeneChip system.