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Selection for forage quality in tall fescue using a dihaploid generation approach

Bryan Kindiger
United States Department of Agriculture-Agricultural Research Service, USA

Within the *Festuca-Lolium* genome complex there is a need for modern breeding approaches that can facilitate the rapid development of improved germplasm or cultivars. Traditional recurrent or mass selection methods for population or synthetic development are labor intensive and time consuming. The recent development of annual ryegrass *Lolium multiflorum* Lam. subsp. *multiflorum* lines, that when hybridized by tall fescue (*Festuca arundinacea* Schreb. (syn.=*Lolium arundinaceum* (Schreb.) Darbysh.), generate F1 hybrids capable of exhibiting genome loss of either the ryegrass tall fescue genome resulting in the recovery of both ryegrass and tall fescue dihaploid (DH) lines. Gamete selection performed at the F1 generation was found to be effective and may have application toward the selection of additional quantitative forage quality or agronomic attributes in tall fescue germplasm. The described gamete selection strategy is applicable to tall fescue (*L. arundinaceum*) and may have applications across the *Lolium/Festuca* genus.

Biography

Bryan Kindiger has completed his PhD from the University of Missouri, Columbia and has been employed with the USDA-ARS for 23 years. He is the lead Researcher for the development of cool-season grass forages at the Grazinglands Research Laboratory. He is presently working on a dihaploid inducement approach for representatives of the *Lolium* and Festuca *genus*.

bryan.kindiger@ars.usda.gov

Notes:

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