

Mapping of diploid bluebunch wheatgrass genome using EST-SSR and GBS markers

Richard R.-C. Wang¹, Xingfeng Li², Steve R. Larson¹, Kevin Dorn³, Jesse Poland³,
Lee R. DeHaan⁴, Matthew D. Robbins¹, Shaun B. Bushman¹,

¹ USDA-ARS Forage & Range Research Laboratory, Logan, UT 84322-6300

² Shandong Agricultural University, Taian, 271018, P.R. China

³ Kansas State University, Manhattan, KS 66506

⁴ The Land Institute, 2440 E. Water Well Road, Salina, KS 67401

Abstract:

Bluebunch wheatgrass [*Pseudoroegneria spicata* (Pursh) A. Löve] is an important North American forage grass belonging to the tribe Triticeae. It has the basic **St** genome; variants of it constituted a component maternal genome, in combination with other basic genomes, in polyploid species of the genera *Australoroegneria*, *Campeiostrachys*, *Douglasdeweya*, *Elymus*, *Kengyilia*, *Roegneria*, *Thinopyrum*, and *Pascopyrum*. Previously, only the **St** genome in tetraploid *Elymus wawawensis* (**StStHH**) had been mapped with expressed sequence tag derived simple sequence repeat (EST-SSR) markers. To date, **St** genome in diploid *Pseudoroegneria* species has not been mapped. Using a mapping population of diploid bluebunch wheatgrass derived from (Anatone × Atomic) × (Goldar × P-7), we mapped 230 EST-SSR and 3468 genotype by sequencing (GBS) markers to 14 linkage groups (7 each from each parent). Based on sequence homology of GBS markers between **St** genome of bluebunch wheatgrass and that in intermediate wheatgrass [*Thinopyrum intermedium* (Host) Barkworth & D. Dewey] (**J^{vs}JSt**), the 14 linkage groups were assigned to 7 **St**-genome chromosomes. Total number of mapped molecular markers ranged from 344 (**6St**) to 679 (**2St**) averaging 528 markers per chromosome. The molecular map of **St** genome will be useful in whole genome sequencing of this pivotal genome in Triticeae.

Reference:

Mott, I.W., S.R. Larson, T.A. Jones, J.G. Robins, K.B. Jensen, M. Peel. 2011. A molecular genetic linkage map identifying the **St** and **H** sub-genomes of *Elymus* wheatgrass (Poaceae: Triticeae). *Genome*. 54:819-828.

Wang, R.R.-C., S.R. Larson, K.B. Jensen, B.S. Bushman, L.R. DeHaan, S.W. Wang, X.B. Yan. 2015. Genome evolution of intermediate wheatgrass revealed by newly developed EST-SSR markers of its three progenitor diploid species. *Genome* 58: 63-70.