BGS 254, Orange lemma 1, rob1

Stock number: BGS 254  
Locus name: Orange lemma 1  
Locus symbol: rob1

Previous nomenclature and gene symbolization:

Orange lemma = pl (18).  
Orange lemma = br (1, 3).  
Orange lemma = o (19).  
Robiginosum-o = rob-o (9).

Inheritance:

Monofactorial recessive (1,3, 18, 19).  
Located in chromosome 6HS (6, 7, 21, 22); rob1.a is about 10.8 cM proximal from the msg36 (Male sterile genetic 36) locus (7, 13); rob1.a about 2.2 cM distal from the cul2 (uniculm 2) locus (7, 10, 13); rob1.a is near RFLP marker HVM031 in 6H bin 06 (4); rob1.a is associated with SNP markers 1_0462 to 1_0185 (positions 73.90 to 134.55 cM) in 6H bins 06 to 08 of the Bowman backcross-derived line BW666 (5); rob1.a and cul2.b (Uniculm 2) are associated with SNP markers 2_0600 to 1_0185 (positions 90.99 to 134.55 cM) in 6H bins 06 to 08 of the Bowman backcross-derived line BW206 (5); rob1.a and gsh4.l (Glossy sheath 4) are associated with SNP markers 1_0462 to 2_0118 (positions 73.90 to 156.09 cM) in 6H bins 06 to 09 of the Bowman backcross-derived line BW407 (5), likely in 6H bin 06.

Description:

The lemma, palea, and rachis have an orange pigmentation that is present in immature spikes, can be observed at heading, and is retained in mature grain and spikes (3, 19). The orange pigmentation is visible at the base of sheath of seedlings and in exposed nodes after jointing. Internodes have a layer of orange tissue and stems have an orange color as the straw dries. The mutant stock for rob1.f (OUM189) has a lighter orange lemma color than that in other mutants at the rob1 locus (14). The Bowman backcross-derived line with the rob1 gene, BW666, had slightly lower acid-detergent lignin (ADL) content than Bowman (17), but it was also more susceptible to common root rot, caused by Bipolaris sorokiniana (15). Compared to Bowman, BW666 had slightly lower grain yields (8). The rob1 mutants have a sequence change in the gene encoding cinnamyl alcohol dehydrogenase (CAD) (2, 23). Cattle have shown a grazing performance for orange lemma barley (8), as has been reported for low lignin mutants in other crops (12).

Origin of mutant:

A spontaneous mutant in CIho 5649 (15).

Mutational events:

rob1.a in CIho 5649 (GBC340, GSHO 707) (11, 19); rob1.b (OUM185), rob1.c (OUM186), rob1.d (OUM187), rob1.e (OUM188), rob1.f (OUM189) in Akashinriki (OUJ659, PI 467400) (14); rob1.1 (NGB 115071), rob1.2 (NGB 115072) in Bonus (NGB14657, PI 189763), rob1.3 (NGB 115073), rob1.4 (NGB 115074), rob1.5 (NGB 115075), rob1.6 (NGB 115076) in Foma (NGB 14659, Clho 11333), rob1.7 (NGB 115077) in Kristina (NGB 14661, NGB 1500) (16); rob1.g (200A12/8/2) from Emir (Clho 11790) isolated following a cross to Hordeum bulbosum (20).
Mutant used for description and seed stocks:

rob1.a (GSHO 707) in CIho 5649; rob1.a in Bowman (PI 483237)*8 (GSHO 2069, BW666, NGB 20752); rob1.a with cul2.b in Bowman*8 (GSHO 2075, BW206, NGB 22034); rob1.a with gsh4.l in Bowman*7 (GSHO 2072, BW407, NGB 20640).

References:


Prepared:


Revised:

Orange lemma 1 (rob1.a) spike with orange pigmentation on the lemma to the left compared with normal Bowman
Orange lemma 1 (rob1.a) spike rachis internodes with orange pigmentation to the left compared with normal Bowman
Orange lemma 1 (rob1.a) culm with orange pigmentation to the left compared with normal Bowman
Orange lemma 1 (rob1.a) grain compared with normal Bowman grain; rob1.a grain on lemma side to the left, normal Bowman in the middle, rob1.a grain on palea side with lateral spikelets to the right.