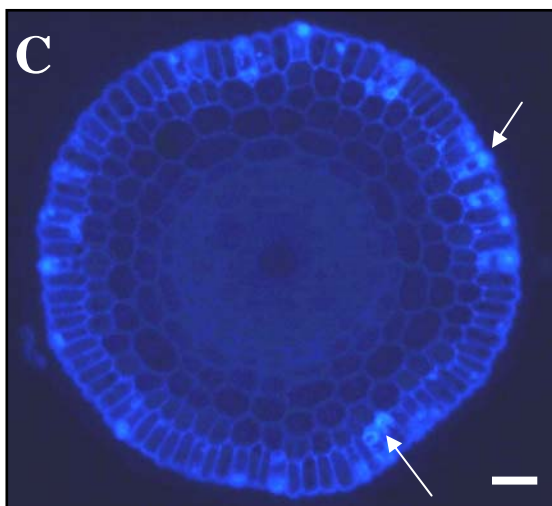
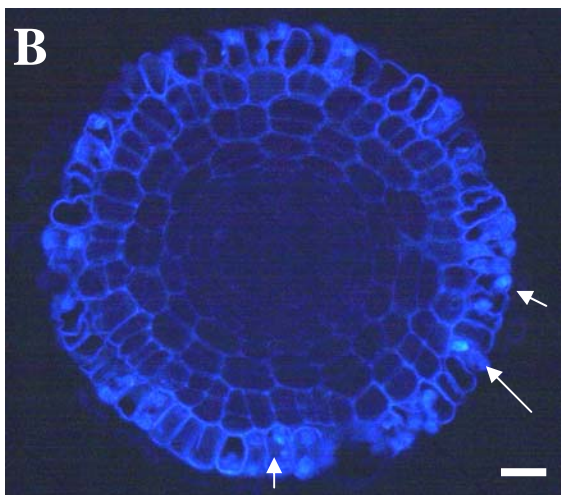
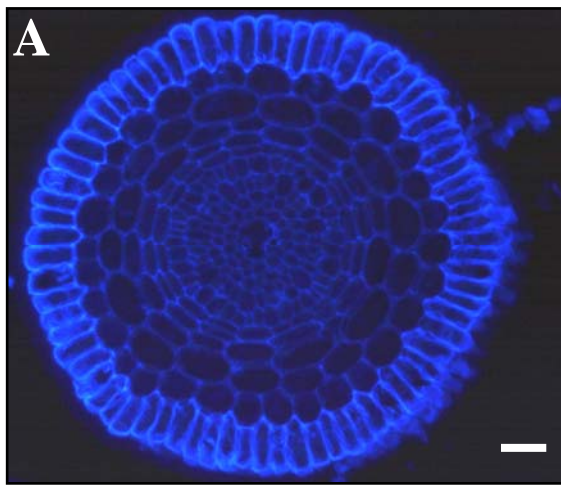


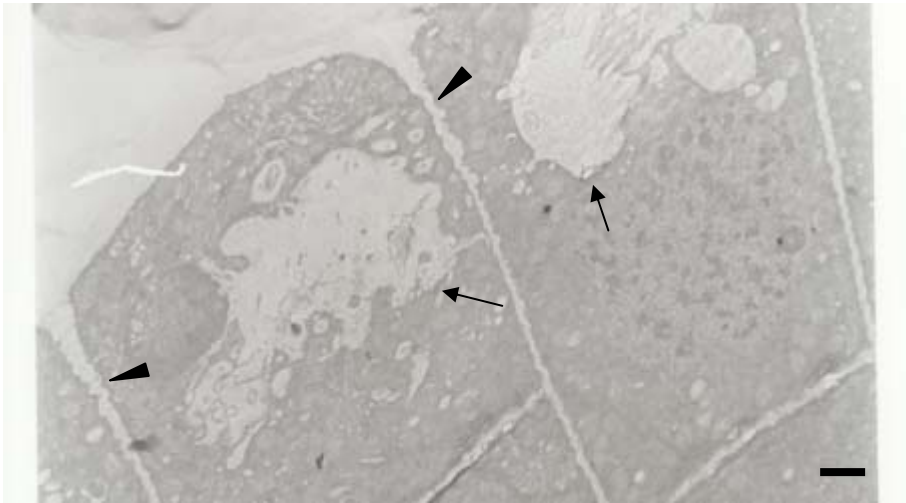
**Supplemental Figure 1. *sad3* and *sad4* mutants have root cap defects.**

Roots of three day old *A. strigosa* seedlings showing the appearance of the root cap and root epidermis in the region of the root tips of wild type and mutant lines under bright field (A, C, E) and UV (B, D, F) illumination. WT, wild type (A, B); *sad3*, mutant #1139 (C, D); *sad4*, mutant #9 (E, F). Scale bar 600  $\mu$ m.



**Supplemental Figure 2. Aniline blue staining of *sad3* and *sad4* mutants.**

Cross-sections of roots of two day-old wild type (A), *sad3* (B) and *sad4* (C) seedlings stained with aniline blue showing the accumulation of callose (arrowed) in the epidermal cells. Scale bars, 50  $\mu\text{m}$ .



### **Supplemental Figure 3. Epidermal defects in *sad4* mutants**

Transmission electron micrograph of a cross-section of the epidermis of a root of a two day-old seedling of *sad4* mutant #9 in the meristematic zone. Arrows indicate sac-like structures; arrowheads indicate wavy/thickened appearance of cell margins. Scale bar 2  $\mu$ M.

**Supplemental Table 1.** Sugar linkage analysis of monodeglucosyl avenacin A-1 intermediates accumulating in *sad3* and *sad4* mutants

	Glycosyl residue	Mol percentage present
<i>sad3</i> (#1139):	Terminal glucopyranosyl residue (t-Glc)	57
	2-Linked arabinopyranosyl residue (2-Ara p)	30
	4-Linked arabinopyranosyl residue (4-Ara p)	<5
<i>sad4</i> (#9):	Terminal glucopyranosyl residue (t-Glc)	43
	2-Linked arabinopyranosyl residue (2-Ara p)	34
	4-Linked arabinopyranosyl residue (4-Ara p)	<5

Methylation analysis was carried out following standard methods (Anumula K.R., 1992). The error limit for GC detection was ~5%.

**Supplemental Table 2.** Reduced growth rate of roots of *sad3* and *sad4* mutants

	Root growth (cm/day) <sup>a</sup>	
	1-2 days after germination	2-3 days after germination
<i>sad3</i> :		
M	1.2	0.8
WT	1.2	1.8
<i>sad4</i> :		
M	1.1	0.8
WT	1.3	2

<sup>a</sup> Values are means calculated from 169 to 209 plants; maximum s.e.d 0.1 cm/day.

M: mutant, WT: wild type, F4 homozygous mutant and wt seed derived from backcrosses with the S75 parent (Papadopoulou et al., 1999).

**Supplemental Table 3.** Analysis of F<sub>2</sub> progeny derived by selfing an oat plant with the genotype *Sad1/sad1 sad3/sad3*.

<i>Sad1</i> genotype (SNP analysis)	Chemotype		Deduced genotype	No. of progeny <sup>c</sup>
	A-1 <sup>a</sup>	MDG A-1 <sup>b</sup>		
<i>Sad1Sad1</i>	-	+++	<i>Sad1Sad1sad3sad3</i>	9
<i>Sad1sad1</i>	-	+++	<i>Sad1sad1sad3sad3</i>	20
<i>sad1sad1</i>	-	-	<i>sad1sad1sad3sad3</i>	11
Total				40

<sup>a</sup>A-1, avenacin A-1

<sup>b</sup>MDG A-1, monodeglucosyl avenacin A-1

<sup>c</sup>Segregation is consistent with a 1:2:1 ratio ( $P > 0.9$ )

**Supplemental Table 4.** Analysis of F<sub>2</sub> progeny derived from a cross between *sad1* mutant #109 and *sad4* mutant #9

Chemotype A-1 <sup>a</sup>	MDG A-1 <sup>b</sup>	Expected genotype	No. of progeny <sup>c</sup>	Root morphology	<i>Sad1</i> genotype (SNP analysis)
+	-	<i>Sad1_Sad4_</i>	68	WT	n.t.
+	+	<i>Sad1_sad4sad4</i>	20	<i>sad4</i> (6)	
		<i>(Sad1Sad1sad4sad4)</i>		WT* (14)	
		<i>(Sad1sad1sad4sad4)</i>			
-	-	<i>sad1sad1_ _</i>	30	WT	n.t.
Total			118		

<sup>a</sup>A-1, avenacin A-1

<sup>b</sup>MDG A-1, monodeglucosyl avenacin A-1

<sup>c</sup>Segregation is consistent with a 9:3:4 ratio as expected for two unlinked loci ( $P > 0.9$ )

n.t. – Not tested