## Supplement 1 Published markers for *Agrostis* species

<table>
<thead>
<tr>
<th>Marker Type</th>
<th>Application</th>
<th>Citations</th>
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<tbody>
<tr>
<td>Isozymes</td>
<td>Differentiation of 19 <em>A. palustris</em> Huds. Cultivars</td>
<td>Warnke et al., 1997</td>
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<tr>
<td>&quot;</td>
<td>Allotetraploid inheritance of alleles in <em>A. palustris</em> Huds</td>
<td>Warnke et al., 1998</td>
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<tr>
<td>RAPD</td>
<td>Differentiation of 110 plants from 17 old putting greens in Wisconsin</td>
<td>Casler et al., 2003</td>
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<tr>
<td>RAPD-SCAR</td>
<td>Differentiation of <em>A. stolonifera</em> and <em>A. capillaris</em></td>
<td>Scheef et al., 2003</td>
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<tr>
<td>AFLP</td>
<td>Differentiation of 13 <em>Agrostis</em> species/40 accession from around the world</td>
<td>Vergara and Bughrara, 2003</td>
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<tr>
<td>&quot;</td>
<td>Analysis of <em>A. stolonifera</em> and <em>A. gigantea</em> cultivar genotypes</td>
<td>Vergara and Bughrara, 2004</td>
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<tr>
<td>AFLP</td>
<td>Differentiation of 5 <em>A. stolonifera</em> cultivars</td>
<td>Caceres, 2000</td>
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<td>RFLP</td>
<td><em>A. stolonifera</em> linkage map</td>
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<td>RAPD &amp; AFLP</td>
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<td>ITS and matK</td>
<td>Species-level ID of wild collected <em>Agrostis</em> plants and interspecific hybrids</td>
<td>Reichman et al., 2006</td>
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<td>Chloroplast SSRs</td>
<td>Species-level ID of <em>Agrostis &amp; Polypogon</em> recipient of transgenic pollen</td>
<td>Zapiola et al., 2010</td>
</tr>
</tbody>
</table>
Supplement 2 Figure

A. transcaspica GRIN-19
A. transcaspica GRIN-11
A. transcaspica GRIN-12

A. capillaris Game-3
A. capillaris Game-9
A. capillaris Game-15
A. capillaris Exeter-5

A. capillaris Exeter-11
A. capillaris Exeter-13
A. gigantea Reton-14
A. gigantea Reton-2
A. gigantea Reton-11
A. gigantea Major-13
A. gigantea Major-2
A. gigantea Major-10

A. canina Novobent-3
A. canina Novobent-8
A. canina Novobent-14

A. canina Vesper-2
A. canina Vesper-5
A. canina Vesper-11

A. stolonifera Crenshaw 311-6
A. stolonifera Crenshaw 324-5
A. stolonifera Crenshaw 45-10
A. stolonifera Penn A-4-16
A. stolonifera Penn A-4-9
A. stolonifera Penn A-4-11
A. stolonifera Baskett-14
A. stolonifera Baskett-5
A. stolonifera Baskett-6
A. stolonifera Ona-10
A. stolonifera Ona-6
A. stolonifera Ona-8
A. stolonifera Rainbow-12
A. stolonifera Rainbow-2
A. stolonifera Rainbow-5
A. stolonifera CBG1-351
A. stolonifera CBG1-346
A. stolonifera CBG1-349

— 0.5 Changes
Supplement 2 Figure Caption

Supplement 2. Molecular confirmation of species identification for Agrostis samples used in this study. A randomly chosen Most Parsimonious Tree (MPT) is shown for the matK data matrix. Indels were coded as present or absent within the data matrix (Simmons and Ochoterena, 2000). Heuristic parsimony tree searches and bootstrap support for the matK data matrix were evaluated in PAUP* v4.03b10 (Swofford, 2003). Four heuristic searches of 1000 replicates were run with stepwise random addition of sequences and tree bisection and reconnection (TBR). Five hundred bootstrap replicates were generated using 10 stepwise random additions of sequences per replicate also run under TBR. The matK MPTs were based on 46 informative characters and had Tree length = 51, Consistency Index = 0.922, Homoplasy index = 0.078, Retention Index = 0.992, Rescaled consistency index = 0.914. Branch lengths in number of changes and bootstrap values ≥ 80% are shown for the branches. The sequences for wild collected creeping bentgrass were strictly placed within the clade containing A. stolonifera cultivars. The relative positions of other taxa are in agreement with the finding of Rotter et al. (2010).
Supplement References


