Milling energy requirement of the aneuploid stocks of common wheat, including alien addition lines

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Summary. Aneuploid stocks, which included Triticum aestivum/alien, disomic, chromosome addition lines, wheat/alien, ditelosomic, chromosome addition lines, and the available aneuploids of 'Chinese Spring' wheat, were used to locate genes that influence milling energy requirement (ME). Genes that affected ME were found on all seven homoeologous chromosome groups. The addition of complete wheat chromosomes 1B, 1D, 2A, 2D, 5B, 6B, 7B and 7D increased ME. Positive effects were also found in specific chromosome arms: 1BS, 2DS, 5AS, 5BS and 6BL. Wheat chromosome 3B conditioned low ME and the gene(s) responsible was located on the short arm. Other negative effects were attributed to wheat chromosome arms 4BL, 4DL, 5DS and 6DS. Alien chromosome additions that conferred high ME included 2H, 5H, 6H of barley, Hordeum vulgare and 2R, 2Rz, 4R, 4RL, 5R, 6RL and 7RL of rye, Secale cereale. Those that conferred a low ME included 1H Ch of H. chilense, and 6U and 7U of Aegilops umbellulata, 5R and 5RS of S. cereale and 5Rm and 5R'S of S. montanum. Although the control of ME is polygenic, there is a major effect of genes located on the short arms of homoeologous group 5 chromosomes.

Key words: Milling energy (ME) – Common wheat – Aneuploid analysis – Alien chromosome – Triticeae

Introduction

The aneuploid stocks of wheat (Triticum aestivum) and related species have been used routinely for the past 30 years to located genes to specific chromosomes, as can be easily confirmed by consulting the catalogue of gene symbols (McIntosh 1988). Allison et al. (1976) described the use of milling energy (ME) to assay barley genotypes with good malting potential. This technique has since been developed and used in the barley breeding and research programmes of the Scottish Crop Research Institute (Swanston 1987; Ellis et al. 1989; Swanston and Taylor 1990). Essentially, low milling energy indicates the potential for good malting quality, but only if high enzyme levels are developed during malting. High milling energy can be more certainly associated with poor malting performance.

In this paper, we aim to determine the genetic basis of ME by identifying chromosomes that influence the character. The effects of individual chromosomes of seven distinct genomes were assessed, using the wheat aneuploid stocks that contain or lack specific chromosomes or chromosome arms. Chromosome nomenclature is based on chromosome homoeology.

Materials and methods

The species used included: wheat, Triticum aestivum cultivars 'Chinese Spring' (CS) and 'Holdfast' (Hold) (AABBDD, 2n=6x=42); barley, Hordeum vulgare cultivars 'Betz'es and 'Natasha' (HH, 2n=2x=14) and rye, Secale cereale cultivars 'King II' and 'Imperial' (RR, 2n=2x=14). The aneuploid stocks included: CS tetrasomics (2n=44), except for chromosomes 4A and 4D; 29 available CS ditelosomics (2n=40 + 2t); 18 compensating nullisomic/tetrasomic combinations (2n=42). The available wheat/alien addition lines for both complete and telosomic chromosomes included: CS/H. vulgare cv 'Betz'es (AABBDDHH, 2n=44), H. chilense (AABBDDHH 114, 2n=44, or 42+2t); CS/S. cereale cultivars 'King II' and 'Imperial' (AABBDDDR, 2n=44, or 2n=42+2t); CS/S. montanum (AABBDDDR'R', 2n=44, or 42+2t) and CS/Aegilops umbellulata (AABBDDDU', 2n=44). The 'Hold/King II' complete and telosomic additions were also included (2n=44 or 42 + 2t). Caryopses of the above genotypes were germinated, and cytological checks were made in root-tip squashes to ensure
plants carried the correct chromosome complement. Five plants of each checked line and parents were grown to maturity under glasshouse conditions from March to September, 1989. Mature grains were threshed from harvested, ripe plants and samples were taken for the measurement of milling energy.

Milling energy requirement (ME) was measured by the use of the Comparamill (Allison et al. 1979). The sample size was reduced to 1 g, and variation was assessed relative to the least significant difference calculated after replicated milling of parent cultivars. Mean ME values for parental lines were: 'Chinese Spring', 70 J; 'King II,' 77.5 J; and 'Betzes', 125 J. The pooled standard deviation was 2.2 J and the LSD 95% was 4.5 J.

Results

The ME requirements of the genotypes tested are given in Tables 1 to 3. These are summarised below according to species.

Triticum aestivum

Tetrasomic lines with significantly higher ME values than the control CS include 1B, 1D, 2A, 2D, 5B, 6B, 7B and 7D. Interestingly, the positive effects of 1B are also seen when 1B is present as a tetrasomic in nulli-1D/tetra-1B (1D/1B), and this is converted to a negative effect in nulli-1B/tetra-1D (1B/1D). Since 1BL also has a negative effect, the short arm of 1B, which is absent in the ditelosomic 1BL line, must carry genes with a positive effect. Tetrasomy of 6B also confers a high ME in 6A/6B, but 6D/6B shows no significant effect. The absence of 7A increased ME in both 7A/7B and 7A/7D. However, 7D/7A and tetra-7D showed a significant decrease in ME. The ditelo-7AL showed a significant increase in ME, indicating that genes influencing the expression of this character are located predominantly on the short arm. Similarly, chromosome arms 3BS, 4BL, 4DL, 5DS and 6DS are also implicated as carrying genes with negative effects. This is verified in the case of 3B, with positive results when 3B is absent (both 3B/3A and 3B/3D) and a negative value when 3B is present in extra dosage (tetra-3B). In the case of group 5 wheat aneuploids, the conclusions are supported by the results of the various 5R addition lines (see below).

Aegilops umbellulata

Addition of 6U and 7U significantly lowered ME relative to CS wheat. Effects of other chromosomes were not significant.

Hordeum vulgare

ME values greater than the euploid CS were found in addition lines for chromosomes 2H, 5H, 6H and 7H.

Hordeum chilense

The addition line with a short 1HF telosome showed low ME, but none of the other H. chilense addition lines were significantly different from CS.

Table 1. Milling energy requirement of the aneuploid stocks of ‘Chinese Spring’ wheat

<table>
<thead>
<tr>
<th>Homoeologous group</th>
<th>Tetrasomic nulli-tetrasomic (nulli/tetra)</th>
<th>Ditelosomic</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1A/1B NS</td>
<td>1A/1B NS</td>
</tr>
<tr>
<td>2</td>
<td>2A/2B NS</td>
<td>2A/2B NS</td>
</tr>
<tr>
<td>3</td>
<td>3A/3D +5.1</td>
<td>3A/3D +5.1</td>
</tr>
<tr>
<td>4</td>
<td>4A/4B +5.6</td>
<td>4A/4B +5.6</td>
</tr>
<tr>
<td>5</td>
<td>5A/5D -5.2</td>
<td>5A/5D -5.2</td>
</tr>
<tr>
<td>6</td>
<td>6A/6B +13.0</td>
<td>6A/6B +13.0</td>
</tr>
<tr>
<td>7</td>
<td>7A/7B +7.7</td>
<td>7A/7B +7.7</td>
</tr>
<tr>
<td></td>
<td></td>
<td>7A/7B +7.7</td>
</tr>
</tbody>
</table>

* The effect of a particular chromosome is given as the deviation from the wheat parent. The mean value of Chinese Spring was 70.0 J

\(^{b}\) S and L – Telosomic for short and long arm, respectively

\(^{c}\) Trisomic for chromosome 4A

NS – Not significant

Secale cereale

Secale cereale cv ‘King II’ chromosomes were present as addition lines in two wheat genetic backgrounds: Chinese Spring and Holdfast. In both sets of additions the intact chromosome 5R had a negative effect. The telosome addition of 5RS conferred significant lowering of the ME of the respective wheats. High ME values were produced by addition of 6RS (CS/KII) and 6R and 6R (Hold/KII), with the long arm having the greatest effect. Genes affecting ME on 6RL are probably in the same homoallelic series as those on 6DL of wheat. Addition of 2R and 2R also conferred significantly high ME values.