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Gene expression analysis of starch metabolism using mRNAseq and the potato genome sequence

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Introduction

Crops such as potatoes that have storage organs (tubers) placed in the soil produce twice the amount of energy per area unit compared to cereals. This makes these kinds of crops well suited as a starting point for future crops for biofuel production. In order to develop a potato crop with higher starch yield, presently not available, detailed knowledge about starch metabolism is crucial. Accumulation of carbohydrates in the form of starch in potato tubers is the result of both anabolic and catabolic processes. These processes are highly redundant in terms of gene isoforms and multiple metabolic pathways. Synthesis of starch can take place by direct incorporation of glucose-1-phosphate into starch catalysed by starch phosphorylase [1] or via ADP-glucose catalysed by ADP-glucose pyrophosphorylase [2,3,4] and starch synthase [5], while starch breakdown can occur via phosphorylolytic or hydrolytic reactions [6,7,8]. In potato, starch synthesis takes place not only in tubers but also in leaves in the form of transient starch during the day, which is consumed in the absence of photosynthesis during the night.

Gene Model Curation

Table 1: Manual curation of 1569 gene models participating in carbon metabolism.

<table>
<thead>
<tr>
<th>Gene model types</th>
<th>No</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene models with correct transcript model</td>
<td>129</td>
<td>76.3 %</td>
</tr>
<tr>
<td>Gene models where the transcript having the longest CDS is correct</td>
<td>124</td>
<td>73.3 %</td>
</tr>
<tr>
<td>Gene models not validated due to low coverage and/or non unique matches</td>
<td>16</td>
<td>9.4 %</td>
</tr>
<tr>
<td>Gene models manually corrected based on mRNAseq</td>
<td>15</td>
<td>8.8 %</td>
</tr>
<tr>
<td>Gene models with more than 1 gene (fusion)</td>
<td>13</td>
<td>7.6 %</td>
</tr>
<tr>
<td>Correct gene model is annotated as multiple genes (split gene)</td>
<td>4</td>
<td>2.3 %</td>
</tr>
</tbody>
</table>

Methods

The present transcriptome analysis of the genes involved in potato carbon metabolism reveals large isoform plasticity both in regards to expression levels and tissue- and cultivar specificity (Figure 2). Starch synthesis occurs both in leaves and tubers and for the majority of the enzymatic steps involved, it is possible to identify gene loci showing either leaf- or tuber specific expression, reflecting a genetic compartmentation of the synthesis. This can be exemplified by starch phosphorylase where two loci (PGSC0003DMG100000000 and PGSC0003DMG190000000) show opposite expression pattern. Another clear example of tissue specificity is also Fructose bisphosphate aldolase where 4 loci (PGSC0003DMG100000000, PGSC0003DMG190000000 and PGSC0003DMG100000000) are highly expressed in both stolons and tubers. This indicate that the regulatory effect of this enzyme on e.g. carbon partitioning [12] is controlled by expression of tissue specific isoforms. Although several isoforms of a gene exist in a genome, their expression level, and hence their importance for the pathway they are a part of can differ widely. This can be illustrated with starch synthesis, where one loci (12111) is 5–20 times higher expressed than the other 6.

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