**Figure S1 - Cluster heat map of transcription data.**
The hierarchical clustering was generated using Spearman correlation coefficients of expression values. Three biological replicates (I, II and III) were included for each of the following conditions:
–Fe: Fe deficient; -Fe/Fe-WEHS: 1 h of supply with Fe-WEHS; -Fe/Fe-PS: 1 h of supply with Fe-PS; -Fe/Fe-CIT: 1 h of supply with Fe-citrate. The color scale indicates the degree of correlation (white, high correlation; red, low correlation).
Table S1 - Results of Real-time RT-PCR experiments performed for a set of transcripts differentially expressed in the different comparison of microarray analysis.

Probe ID, description, microarray fold change value and RT-PCR data (means±SE of three biological replicates) were reported.

Transcripts affected by Fe-WEHS supply

<table>
<thead>
<tr>
<th>Probe_ID</th>
<th>Description</th>
<th>Microarray</th>
<th>Real-time RT-PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC194872_1016_38_S</td>
<td>Amino acid transporter, putative</td>
<td>-3.34</td>
<td>-1.09 ± 0.54</td>
</tr>
</tbody>
</table>

Transcripts similarly affected by Fe-citrate, Fe-PS supply and Fe-WEHS

<table>
<thead>
<tr>
<th>Probe_ID</th>
<th>Description</th>
<th>Fe-citrate vs -Fe</th>
<th>Fe-PS vs -Fe</th>
<th>Fe-WEHS vs -Fe</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC215712_723_40_S</td>
<td>R2r3-myb transcription factor</td>
<td>4.60</td>
<td>2.49 ± 0.23</td>
<td>4.41</td>
</tr>
</tbody>
</table>

Transcripts similarly affected by Fe-citrate and Fe-PS supply

<table>
<thead>
<tr>
<th>Probe_ID</th>
<th>Description</th>
<th>Microarray</th>
<th>Real-time RT-PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC203581_620_40_S</td>
<td>BEL1-related homeotic protein 11</td>
<td>-3.61</td>
<td>-2.29 ± 0.17</td>
</tr>
</tbody>
</table>

Transcripts specifically affected by Fe-WEHS supply

<table>
<thead>
<tr>
<th>Probe_ID</th>
<th>Description</th>
<th>Microarray</th>
<th>Real-time RT-PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>NP000616_1157_38_S</td>
<td>Polygalacturonase 7</td>
<td>2.57</td>
<td>2.36 ± 0.33</td>
</tr>
<tr>
<td>TC196187_747_39_X</td>
<td>Sucrose synthase</td>
<td>-2.89</td>
<td>-9.97 ± 0.01</td>
</tr>
<tr>
<td>TC199665_1578_35_S</td>
<td>Putative urease accessory protein F</td>
<td>2.64</td>
<td>1.45 ± 0.08</td>
</tr>
<tr>
<td>TC208334_1863_38_S</td>
<td>N-acetyl-glutamate synthase</td>
<td>2.01</td>
<td>1.92 ± 0.03</td>
</tr>
<tr>
<td>TC211460_599_40_S</td>
<td>BHLH transcription factor JAF13</td>
<td>-2.01</td>
<td>-2.60 ± 0.16</td>
</tr>
<tr>
<td>TC216298_625_39_S</td>
<td>Metalloproteinase m41 fis1, putative</td>
<td>2.16</td>
<td>1.70 ± 0.02</td>
</tr>
</tbody>
</table>

Transcripts similarly affected by Fe-citrate supply

<table>
<thead>
<tr>
<th>Probe_ID</th>
<th>Description</th>
<th>Microarray</th>
<th>Real-time RT-PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC216298_625_39_S</td>
<td>Metalloproteinase m41 fis1, putative</td>
<td>2.16</td>
<td>1.70 ± 0.02</td>
</tr>
</tbody>
</table>

Transcripts specifically affected by Fe-PS supply

<table>
<thead>
<tr>
<th>Probe_ID</th>
<th>Description</th>
<th>Microarray</th>
<th>Real-time RT-PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC196187_747_39_X</td>
<td>Sucrose synthase</td>
<td>-2.89</td>
<td>-9.97 ± 0.01</td>
</tr>
<tr>
<td>TC199665_1578_35_S</td>
<td>Putative urease accessory protein F</td>
<td>2.64</td>
<td>1.45 ± 0.08</td>
</tr>
</tbody>
</table>
Table S2 - Number of differentially expressed transcripts resulted by root transcriptional profile comparisons of plant supplied for 1 h with the three natural sources of Fe and Fe-sufficient plants using LIMMA analysis.

Differentially expressed transcripts were identified by each transcriptional profile comparison through LIMMA analysis (adjusted p-value ≤ 0.05; |Log2(R)| ≥ 1); -Fe/Fe plants supplied for 1 h with Fe citrate, Fe-PS or Fe-WEHS; +Fe: Fe-sufficient.

<table>
<thead>
<tr>
<th>Comparison</th>
<th>Upregulated transcript</th>
<th>Downregulated transcripts</th>
</tr>
</thead>
<tbody>
<tr>
<td>-Fe/Fe-citrate vs +Fe</td>
<td>542</td>
<td>576</td>
</tr>
<tr>
<td>-Fe/Fe-PS vs +Fe</td>
<td>337</td>
<td>437</td>
</tr>
<tr>
<td>-Fe/Fe-WEHS vs +Fe</td>
<td>68</td>
<td>22</td>
</tr>
</tbody>
</table>
Figure S2- Shared transcripts modulated in Fe-deficient plants after 1 h in response to supply with the three natural Fe sources relative to Fe-sufficient plants.

Fe-deficient plants were supplied for 1 h with Fe-WEHS (-Fe/Fe-WEHS) or with Fe-PS (-Fe/Fe-PS) or with Fe-citrate (-Fe/Fe-citrate). As control, Fe-sufficient plants were used (+Fe).
Table S5 - Sequence of forward and reverse primers used in Real-time RT-PCR experiments.

TC_ID (Tentative Consensus ID), description, 5’-3’ sequence of forward and reverse primers and efficiency (%) were reported.

<table>
<thead>
<tr>
<th>TC_ID</th>
<th>Description</th>
<th>Forward primer (5’-3’)</th>
<th>Reverse primer (5’-3’)</th>
<th>Efficiency</th>
</tr>
</thead>
<tbody>
<tr>
<td>TC192148</td>
<td>Histone protein, LelH</td>
<td>CAAAAGGCCAAAAGCTGCTACC</td>
<td>AGGCTTACAGGCTGTTCCGAG</td>
<td>89.16%</td>
</tr>
<tr>
<td>TC196208</td>
<td>Ubqupin protein, Lel/hb3</td>
<td>AGCCAAAGAAGATCAAGACA</td>
<td>GGCTCTGAAACCTTTCATAGG</td>
<td>87.25%</td>
</tr>
<tr>
<td>TC203463</td>
<td>1-Alpha elongation factor, Lel/F1a</td>
<td>TGGAATAGCTCGAGTTGCTG</td>
<td>TTCTCTACCTGAAGGCCCTG</td>
<td>99.15%</td>
</tr>
<tr>
<td>NP000616</td>
<td>Polygalacturonase 7</td>
<td>GAGCTTAAAGTGGGAGATGC</td>
<td>GGCTAGCCCATGTTGACTG</td>
<td>93.15%</td>
</tr>
<tr>
<td>NP0287571</td>
<td>TCP protein</td>
<td>GTCTATGCGCGATATGATTT</td>
<td>TGCGGTGCTGTTCTAAATT</td>
<td>60.00%</td>
</tr>
<tr>
<td>TC194872</td>
<td>Amino acid transporter, putative</td>
<td>GTCCCTGGTCATCCCTATT</td>
<td>CGAAACACTAATTAGCAGA</td>
<td>90.20%</td>
</tr>
<tr>
<td>TC196187</td>
<td>Sucrose synthase</td>
<td>CTGCTTGTCGAGCTGTTGCTG</td>
<td>TTGAAGATCCCTTTCGGCGATG</td>
<td>93.05%</td>
</tr>
<tr>
<td>TC199965</td>
<td>Putative urease accessory protein F</td>
<td>GGACAGCAGCTTTTGAATG</td>
<td>CAGTCAAGCAAAGACCCAGAG</td>
<td>95.02%</td>
</tr>
<tr>
<td>TC203581</td>
<td>BEL1.1-related homoeotic protein 11</td>
<td>GAATGCAATTCTGGGCAAAT</td>
<td>TTGCGTAAATGAGTACAA</td>
<td>99.00%</td>
</tr>
<tr>
<td>TC208234</td>
<td>N-acetyl-glutamate synthase</td>
<td>CGAAGGAAGGACATCAGCC</td>
<td>TGAGCTGTTACAGGTCGAAT</td>
<td>96.40%</td>
</tr>
<tr>
<td>TC211460</td>
<td>MLH transcription factor JAF13</td>
<td>TCACCAAGGAGAGATGGCTGC</td>
<td>CTGCGGATCGAAATGACAGG</td>
<td>86.00%</td>
</tr>
<tr>
<td>TC215512</td>
<td>R263-myb transcription factor, putative</td>
<td>AGGCTACTGAGAGGAGGAAAA</td>
<td>TAGCGTGAAATCCACACTCA</td>
<td>88.60%</td>
</tr>
<tr>
<td>TC216298</td>
<td>Metalloprotease m41 fish, putative</td>
<td>AATGCAACCTCTTCTCACCC</td>
<td>ACTTTGCTTCTCCATGAGGAGA</td>
<td>96.35%</td>
</tr>
</tbody>
</table>