**Ash Dieback**

The pathogen *Hymenoscyphus pseudoalbidus* causes a fungal infection of the leaves and stem of ash trees (*Fraxinus excelsior*).

It has already caused massive damage to forests throughout Europe and was recently discovered in the UK (2012). The majority (~90%) of trees are highly susceptible, thus huge selection pressure is being placed on European populations to increase resistance. We wish ultimately to identify genetic or epigenetic variants that confer resistance, enabling the conservation of ash trees in Europe.

**Assembly Results**

<table>
<thead>
<tr>
<th>Statistic</th>
<th>CLC contigs</th>
<th>CLC + SSPACE scaffold</th>
<th>CLC + SOAP scaffold</th>
<th>SOAPdenovo</th>
</tr>
</thead>
<tbody>
<tr>
<td>N50</td>
<td>48,135</td>
<td>98,766</td>
<td>66,181</td>
<td>43,259</td>
</tr>
<tr>
<td>N90</td>
<td>93,223</td>
<td>97,397</td>
<td>66,891</td>
<td>61,415</td>
</tr>
<tr>
<td>Assembly size</td>
<td>2,927 Mb</td>
<td>87.5 Mb</td>
<td>88.1 Mb</td>
<td>1,210 Mb</td>
</tr>
<tr>
<td>No. scaffolds</td>
<td>203,780</td>
<td>89,285</td>
<td>87,476</td>
<td>141,991</td>
</tr>
<tr>
<td>Max. length</td>
<td>412,238</td>
<td>696,341</td>
<td>488,806</td>
<td>920,639</td>
</tr>
</tbody>
</table>

**CEGMA® score**

- Partial: 97.2%
- Complete: 88.7%

**Annotation Results**

- Total no. genes: ~36,000
- Mother leaf: 1,567 unique
- Mother cambium: 1,038 unique

94% with BLASTN hits <1E^-5 (87% with <1E^-20)

Transcriptome CEGMA scores: 98.8% partial, 93.6% complete

**Methods**

- **Low heterozygosity** 'mother' tree
- **Sibbed to produce** 'progeny' tree
- **DNA extracted from cambium** and sequenced on Illumina HiSeq 2500 and Roche 454 FLX++
- **Contigs assembled de novo using** CLC Genomics Workbench® Scaffolder produced using SSPACE®, compared to SOAP scaffold and SOAPdenovo®
- **Gene and transcript detection using** CLC Transcript Discovery pipelines and MAKER® annotation pipeline
- **Functional annotation using** BLAST and MAKER

**Conclusion**

By making the reference genome publicly available on our website (www.ashgenome.org) we are encouraging other groups to use this foundational resource for evolutionary and ecological genetics studies. These could include the discovery of markers for a low-susceptibility genotype, which could be used to aid the breeding of resistant ash tree populations.

**Future Studies**

Using bisulphite sequencing data from a range of high and low susceptibility individuals, we aim to compare DNA methylation patterns between these groups. We will also continue our work on transcriptome annotation.

**Acknowledgments**

We thank the following people for helpful input: Martin Simonsen, Mahesh Parichha, and Richard Nichols. The project is funded by an emergency grant from NERC, Elizabeth Sollars and Jasmin Zohren are funded by INTERCROSSING, an EU-funded Marie Curie Initial Training Network.

**Further information**

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**References**

2. *Evolutionary Applications*, 5, 219-238.
3. CLC de novo assembly white paper, www.clcbio.com