

## Plant research

From food to medicine, plants are essential to our everyday lives but are under increasing pressure...



**30%**

population increase by 2050<sup>1</sup>  
Placing greater demand on crop yields.

Only...



...plant species occupy

**90% of the arable land<sup>2</sup>**

Vulnerable to impacts of climate change and disease.



**21%**

of plant species at risk of extinction<sup>3</sup>

Decreasing diversity & loss of potentially valuable traits.

Genome sequencing is imperative to preservation and improvement efforts but...

**225**  
Plant genomes sequenced<sup>4</sup>

**VS**

**160,000**  
Microbial genomes sequenced<sup>5</sup>

Why so few sequenced plant genomes?

Because plant genomes are...

Human **3 Gb**

Wheat **15 Gb**

Tulip **34 Gb**

Paris japonica **152 Gb**

...large

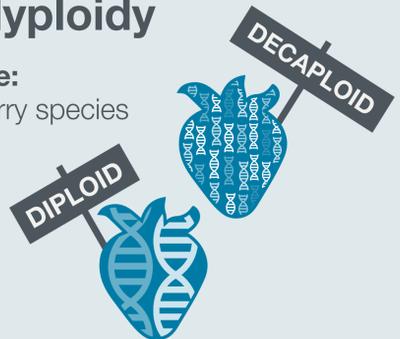
...highly repetitive

Example:  
Maize over 80% repetitive DNA<sup>6</sup>



...polyploidy

Example:  
Strawberry species



Nanopore sequencing

Closing the gap in plant genomes



**Long reads**

Simplify *de novo* assembly, improve reference genomes, resolve structural variations and repetitive regions with up to 2 Mb reads.



**Scalable**

From portable MinION™ to high-yield, high-throughput PromethION™



**Easy, rapid prep**

Streamlined library prep in just 10 minutes



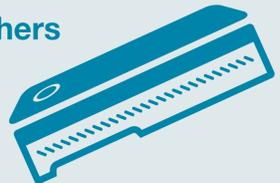
**Direct**

Detect modified bases alongside nucleotide sequence without bisulfite conversion

“  
Using this [PromethION] platform, we sequenced the 2.56 Gb lettuce genome at >100x coverage using just a few flow cells.

Dr. Alexander Wittenberg, KeyGene

In just 4 days, at the cost of \$1000, researchers achieved a more contiguous assembly of the *Arabidopsis thaliana* genome than the existing gold standard<sup>7</sup>.



PromethION

**Flexible, on-demand sequencing**

Designed to run up to 48 independently addressable flow cells

**High yield, high throughput**

Up to 9,600 Gb data (all 48 flow cells sequencing)\*

**Long reads**

Read length equal to fragment length

**Cost-effective**

No CapEx required



The PromethION is needed. It generates such a lot of data in such a consistent way that we can more easily access any genome.

Dr. Hans Jansen – CTO, Future Genomics Technologies

Download the white paper at [nanoporetech.com](http://nanoporetech.com)

1. United Nations. 2017. Available at: <https://www.un.org/development/desa/en/news/population/worldpopulation-prospects-2017.html>

2. Finkers, R. 2018. Available at: <https://nanoporetech.com/resource-centre/knowyour-onion-impact-long-reads-large-genomes>

3. Royal Botanic Gardens Kew. 2016. Available at: [https://stateoftheworldsplants.com/2016/report/sotwp\\_2016.pdf](https://stateoftheworldsplants.com/2016/report/sotwp_2016.pdf)

4. NCBI. Available at: <https://www.ncbi.nlm.nih.gov/genome/browse#/eukaryotes/>

5. Royal Botanic Gardens Kew. 2017. Available at: [https://stateoftheworldsplants.com/2017/report/SOTWP\\_2017.pdf](https://stateoftheworldsplants.com/2017/report/SOTWP_2017.pdf)

6. Schnable, P.S. et al. 2009. Science. 326:1112–1115.

7. Michael, T.P. et al. 2018. Nat Commun. 9(1):541.

\* Based on current internal flow cell performance of 200 Gb (October 2018). Theoretical PromethION performance of up to 15 Tb.

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