Kaka: Towards a Distributed Genotype Database

Helge Dzierzon and Samantha Baldwin

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TOC

- ► Why?
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- Conclusions and Outview

Genotype Data in PFR

- ▶ Many species: Kiwifruit, Apple, Pear, Potato, Grape, . . .
- ▶ Divers: Genotype data: GBS, QTL. . . .
- The data is semi structured

PFR Wetware Distribution

- ▶ 14 PFR sites in NZ
- Data exchange across sites challenging
- Analysts distributed as well



Current way of "Sharing"

- ▶ The K-Drive
- Excel Sheets



Database Initiatives in PFR

- ► EBrida (commercial breeder's DB)
- Kea (inhouse sample tracking)
- Ensembl (Genome Browsing)
- Kaka (Genotypes concentrates on samples)
- Kakapo (Locations)
- **.** . . .

Kaka

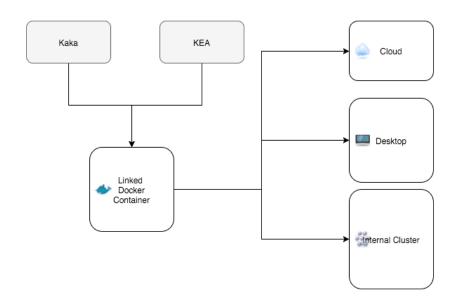
- Supplement to Kea
- ▶ Python Django
- PGSQL and JSON (NoSQL)
- Continuous integration
- Containerisation
- Needs location (Chr, location on Chromosome)





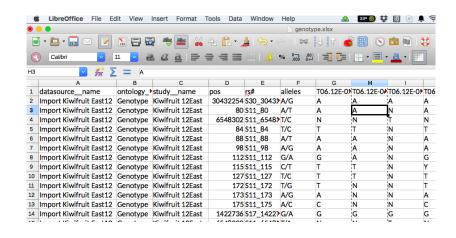


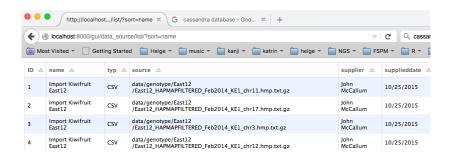
Distributed DB

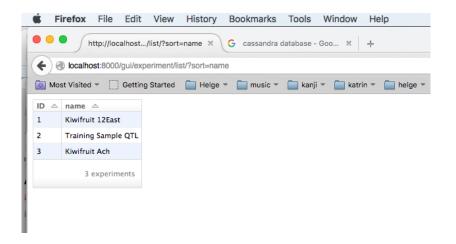


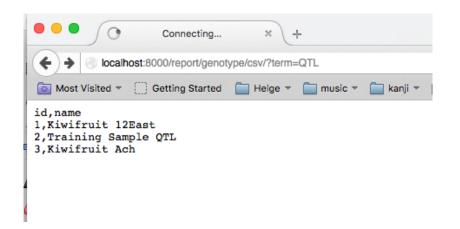
Querying via API

```
http://localhost/report/genotype/xlsx/?experiment=12East
http://localhost/report/genotype/csv/?experiment=12East
http://localhost/gui/genotype/list/
```









Conclusions

- Genotype and phenotype information in one database
- ▶ It is a great tool already but needs a nerd
- ▶ It needs some input from the research community
- Kea needs to be attached as a docker container
- The data input is very manual
- ▶ It needs an interface to Ensembl

Thank you! Questions?

