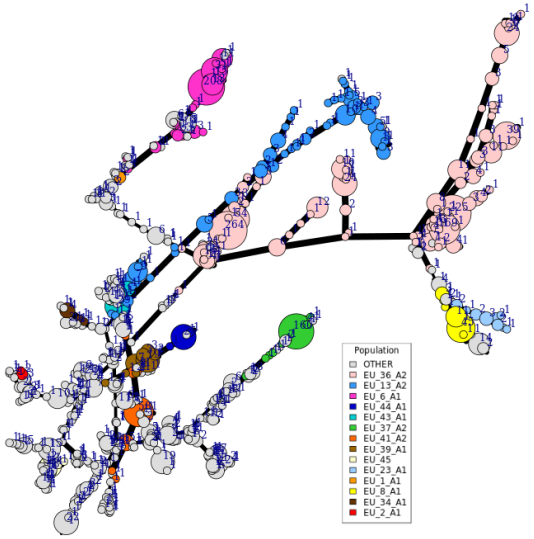
EuroBlight

A potato late blight network for Europe

Global early warning for new and emerging *P. infestans* genotypes

Step 1. The *P. infestans* global genetic landscape initiative (*Pi*GGL)

Jens G. Hansen & David Cooke



How can we as a global network contribute?

Late blight early Warning – new genotype/s appears!

Short term

Alerts and transboundary warnings

Farmers adapt IPM strategy accordingly

Effective system for disease surveillance and sampling of isolates (Hunting the new and the rare)

Fast and reliable characterization of the pathogen

Effective and coordinated communication and dissemination of results (SMS, SoMe, maps & charts, newsletters)

Long term

National list of varieties updated

Breeding programs adapted

Dissemination of results

Assessment of the epidemic potential of new emerging races

Accelerated breeding for resistance

Adaptation of IPM based prevention and control strategies

Global early warning for new and emerging *P. infestans* genotypes

Super goal: Improved preparedness for new and emerging genotypes or races of *Phytophthora infestans*

Step 1. Activity: "The *P. infestans* global genetic landscape initiative (*Pi*GGL)"

Goal: Generating the *P. infestans* global genetic landscape – to be prepared for new and emerging genotypes of *P. infestans* on a global scale.

- 2022: Preparation, alignment studies, establishing protocols etc.
- 2023: sampling and analysis of 1000-2000 isolates per network (EuroBlight, USABlight, Tizon Latino, AfricaBlight and AsiaBlight).

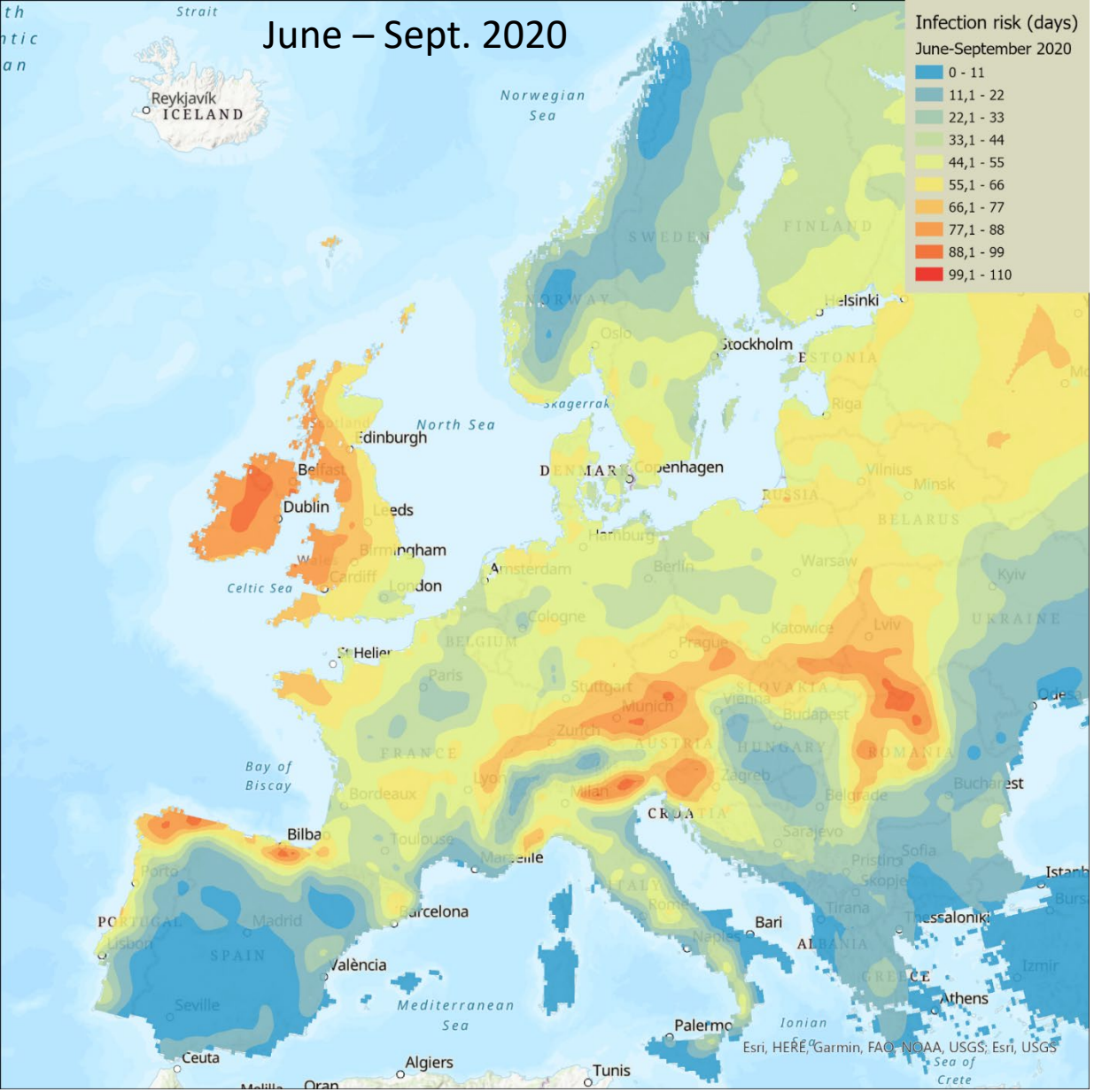
Target activities

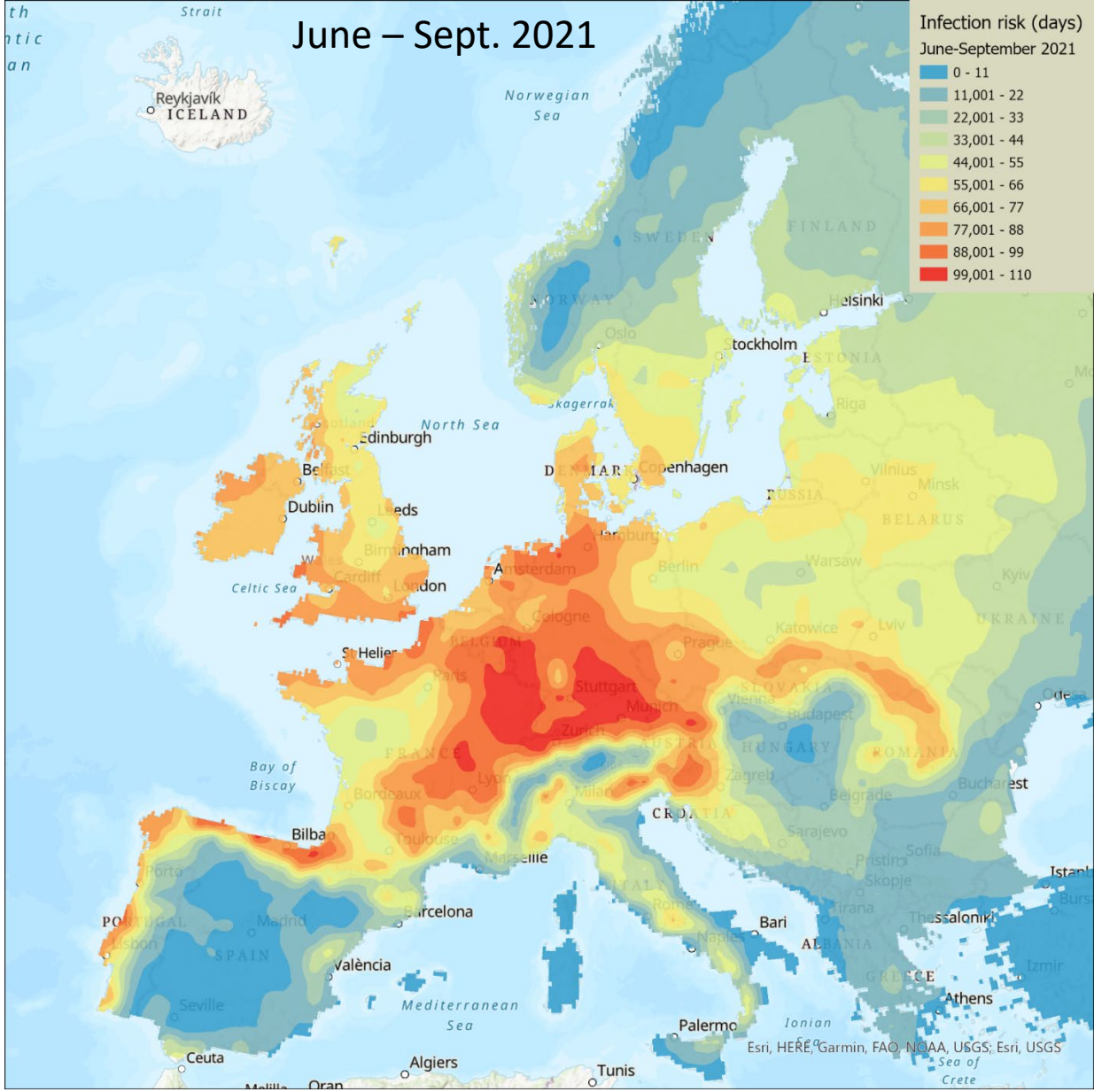
Need to have

- Establish and document a global network of dedicated labs covering all 5 PLB continental networks. Labs participate in 2022 in alignment studies and preparation of protocols for sampling and analysis of sampled data. This is ongoing
- In 2023 sample up to 2000 isolates per network, analyse the data with SSR/SNP/Amplicon sequencing or any molecular method agreed upon in the Lab technical group and upload the results into the EuroBlight database
- Publish a scientific paper about the initiative and the results

Nice to have

- Global phenotyping strategy / Platforms - to characterise / phenotype the new genotypes
- Global network of Trap & Field Nurseries - for monitoring resistance in time and space





Identify Late blight disease development hot spots and centres of diversities

GENOTYPE

Genotype map | Genotype frequency map | Genotype frequency chart | Frequency rank | World map

Continent

Europe

Year

All
2021 2020
2019 2018
2017 2016
2015 2014
2013 2012
2011 2010
2009 2008
2007 2006
2005 2004

Host

All
N/A Other
Potato Tomato

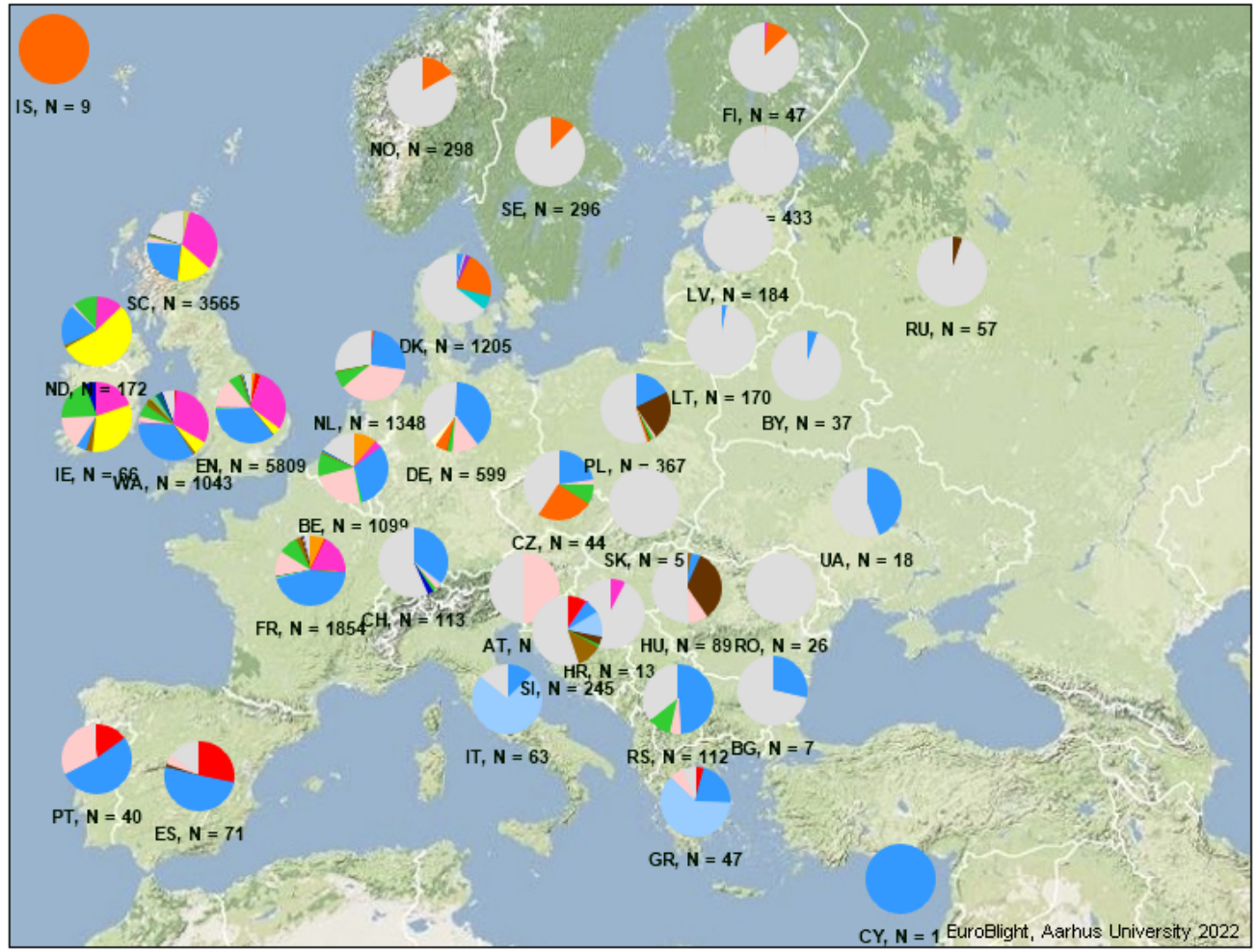
Show

Genotype legend

EU_1_A1	EU_2_A1
EU_5_A1	EU_6_A1
EU_8_A1	EU_12_A1
EU_13_A2	EU_23_A1
EU_33_A2	EU_34_A1
EU_35_A2	EU_36_A2
EU_37_A2	SIB_1_A1
EU_39_A1	EU_38_A2
EU_40_A2	EU_41_A2
EU_10_A2	EU_22_A2
EU_3_A2	EU_43_A1
EU_42_A2	EU_45
EU_44_A1	Other

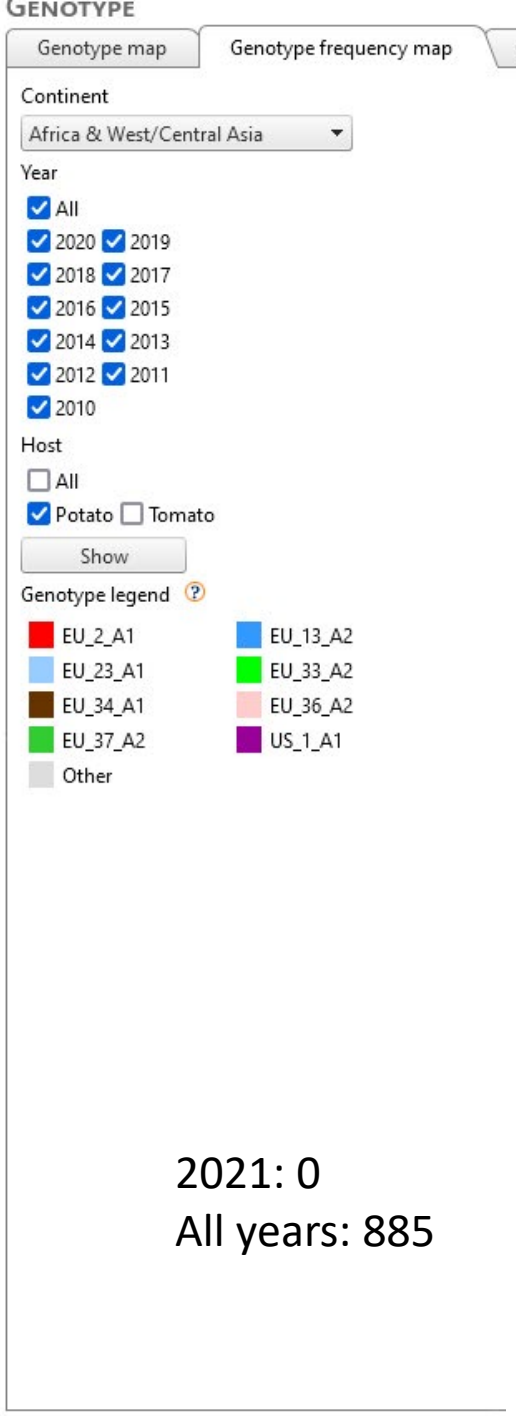
Genotype frequency distribution

Help



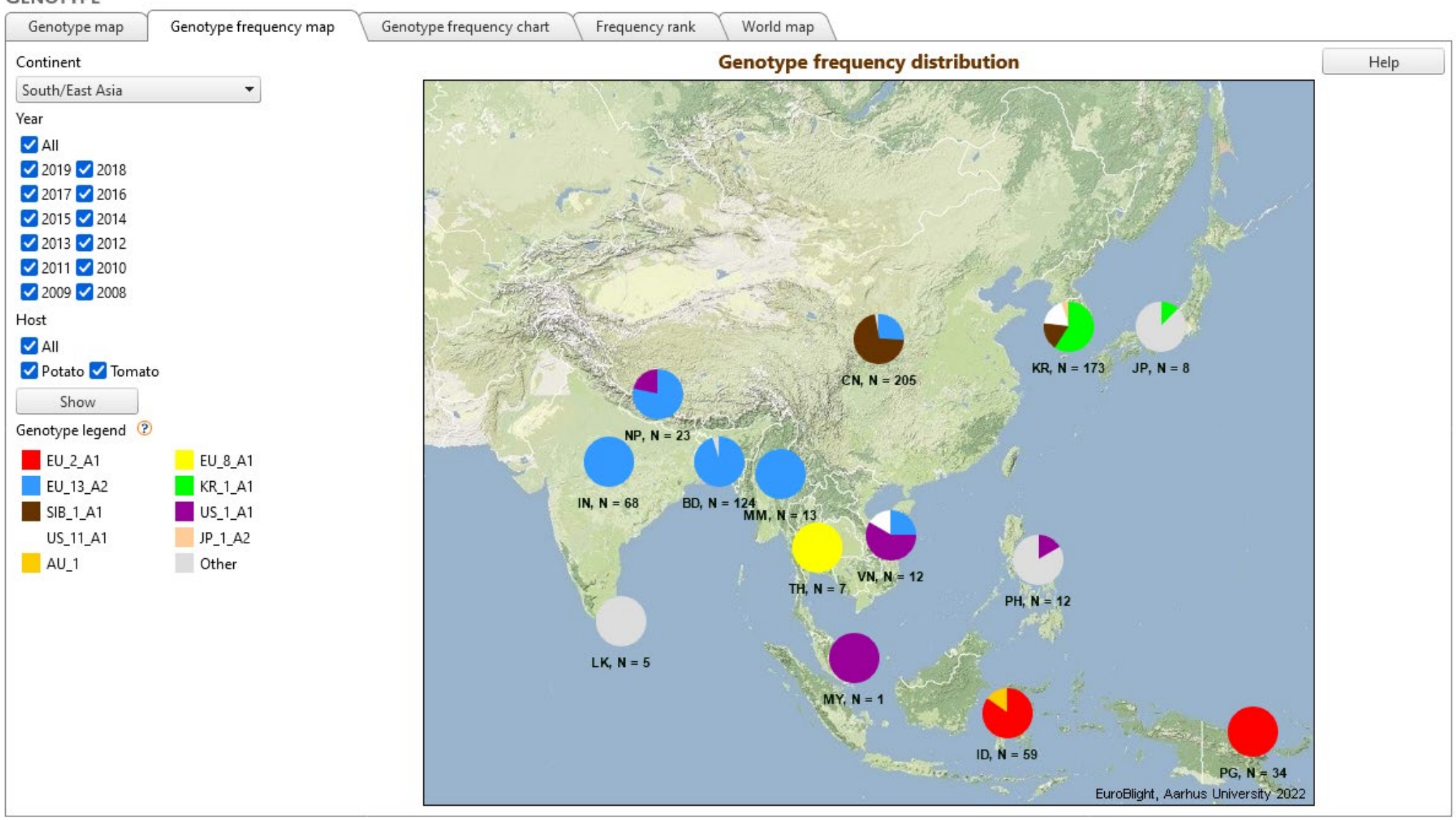
2021: 2495

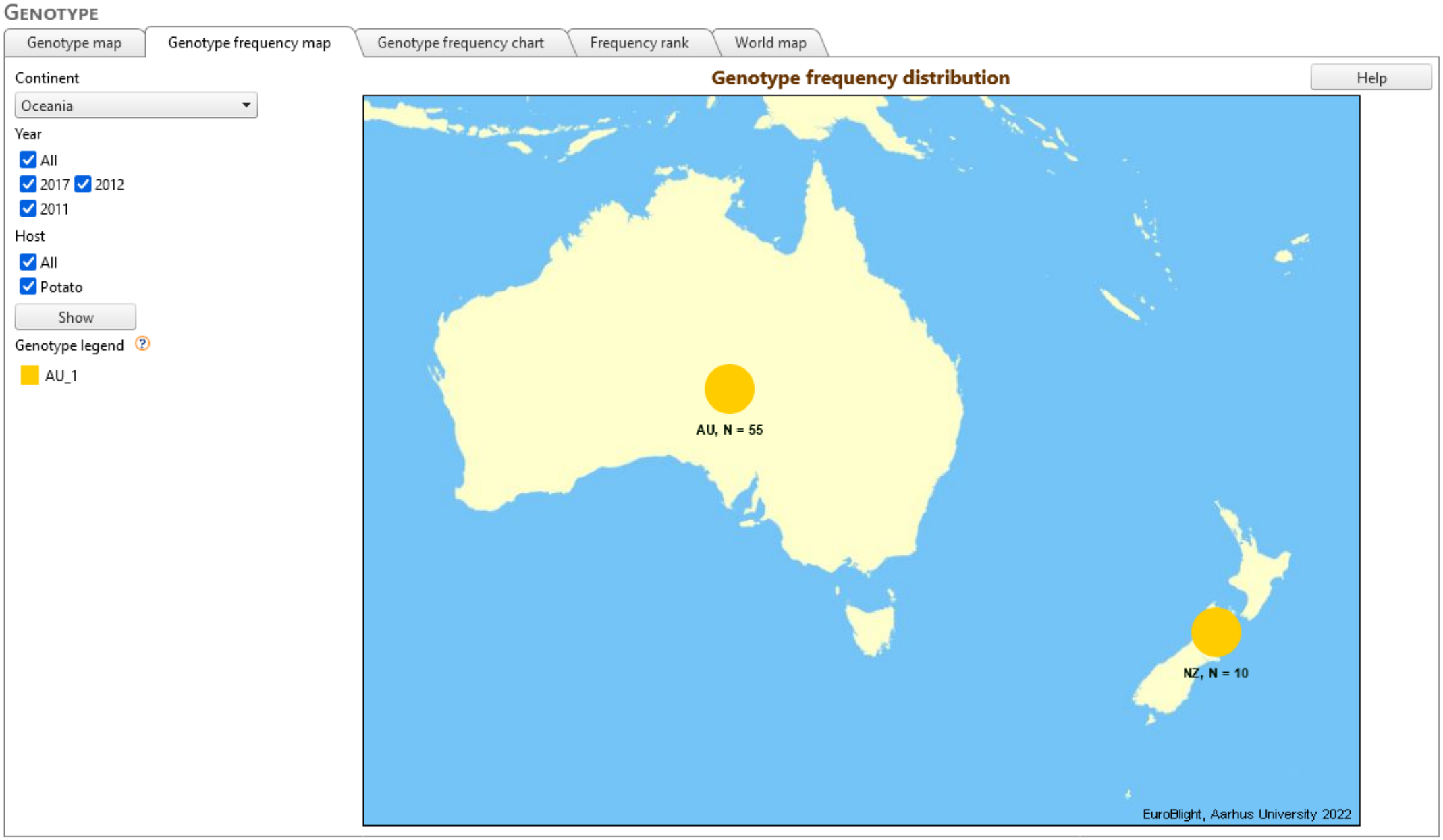
All years: 42446



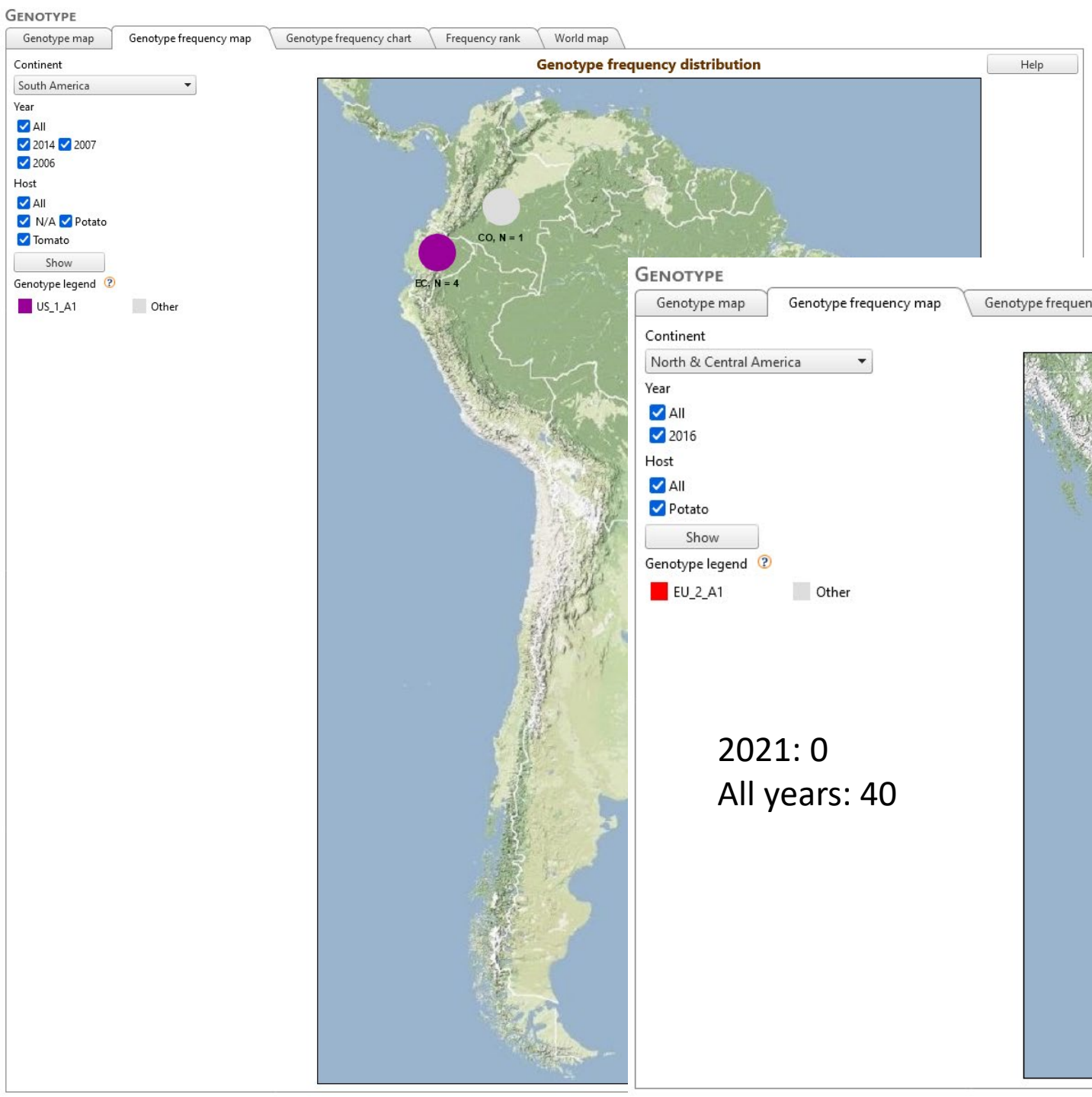
2021: 0
All years: 727

2021: 0
All years: 885

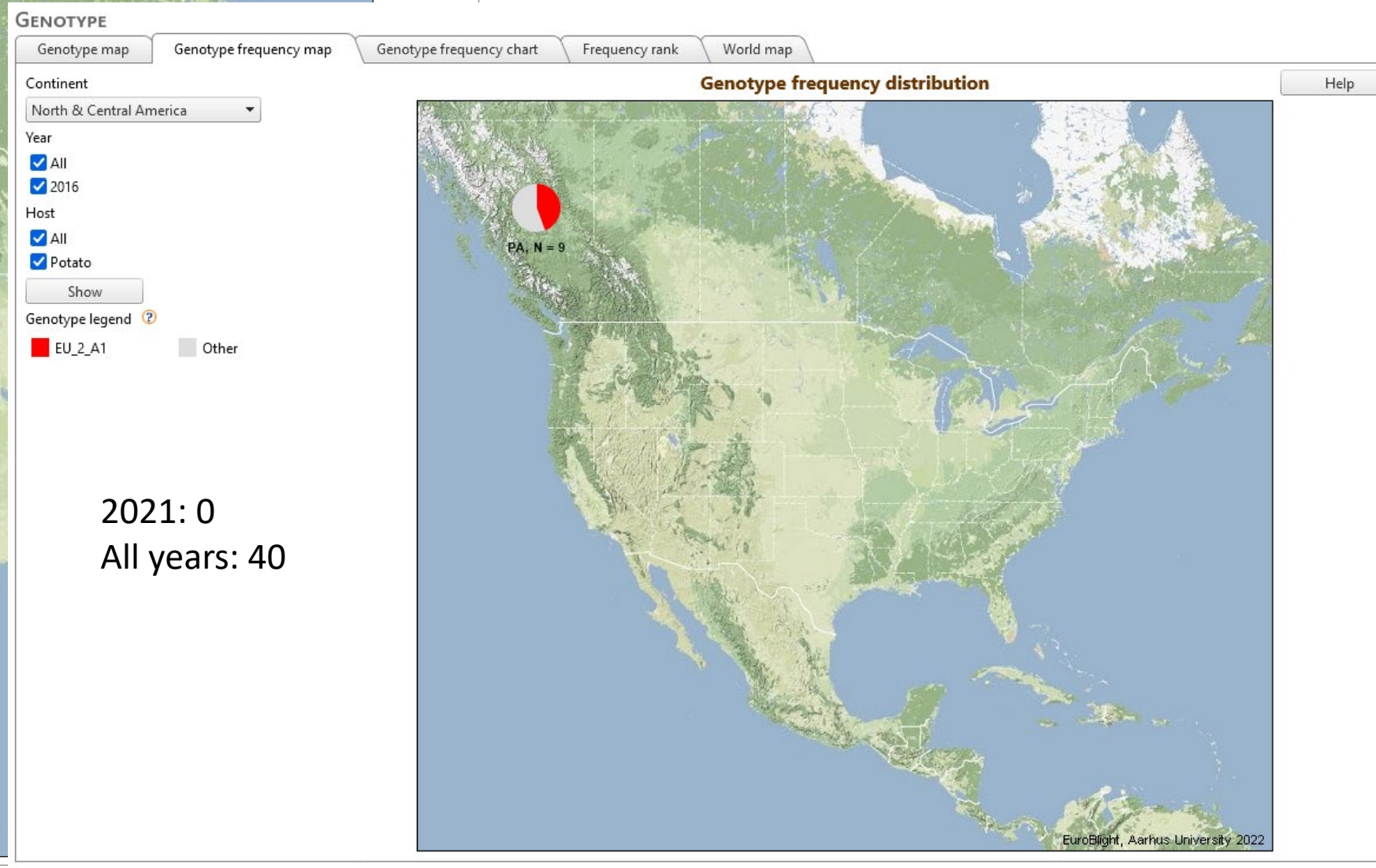




2021: 0
All years: 85



2021: 0
All years: 183



2021: 0
All years: 40

Region	Number of Isolates in the EuroBlight database	Period
Europe	42446	1995-2021
Africa & West & Central Asia	727	2008-2020
South/East Asia	885	2005-2019
Oceania	85	2020-12 & 2017
South America	183	2014-2019
North and Central America	40	2016 & 2019

Genotype

Genotype map | Genotype frequency map | Genotype frequency chart | Frequency rank | World map

Continent

Europe

Country

All countries selected

Host

All

N/A Other Potato

Tomato

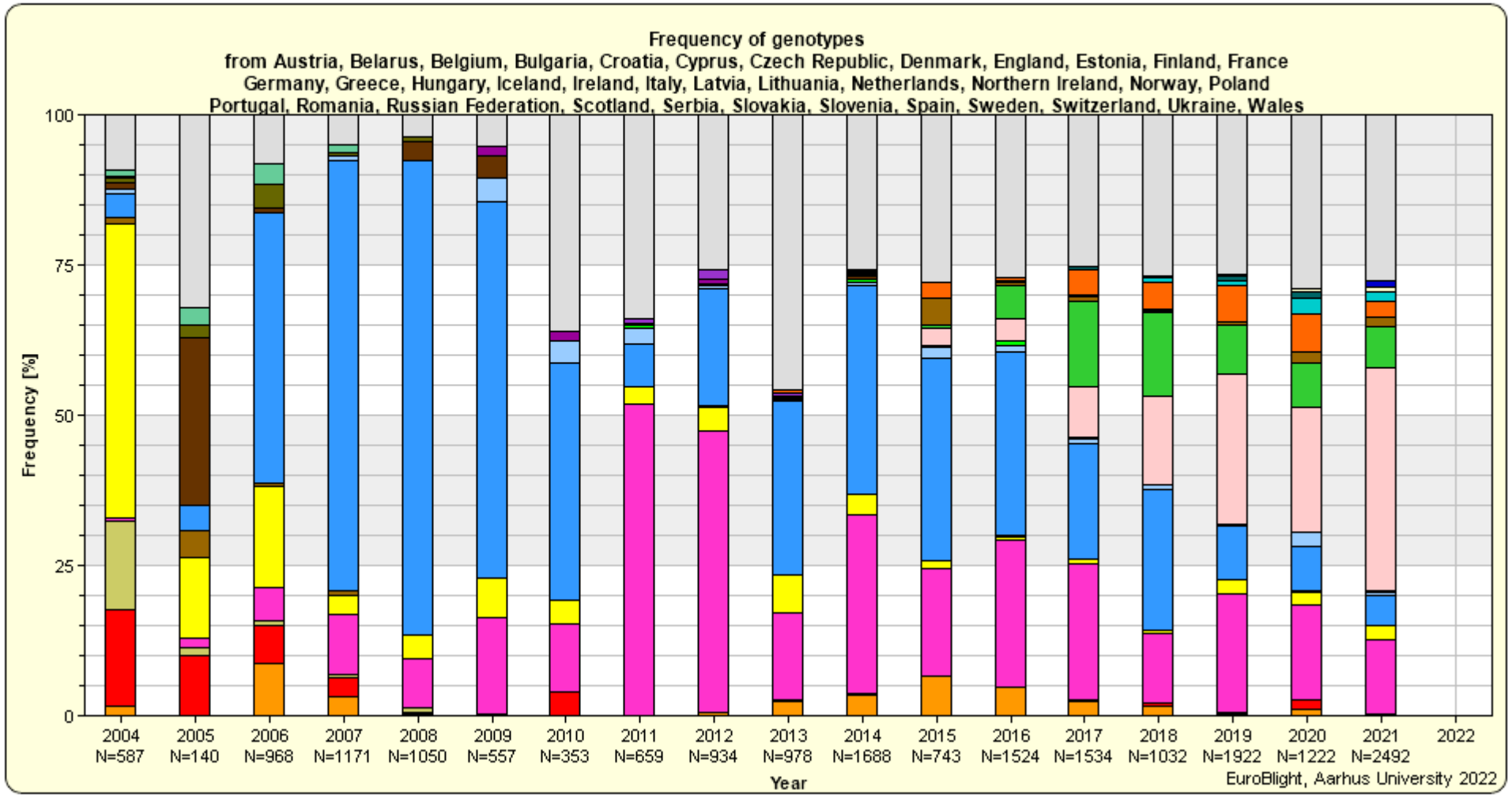
Show

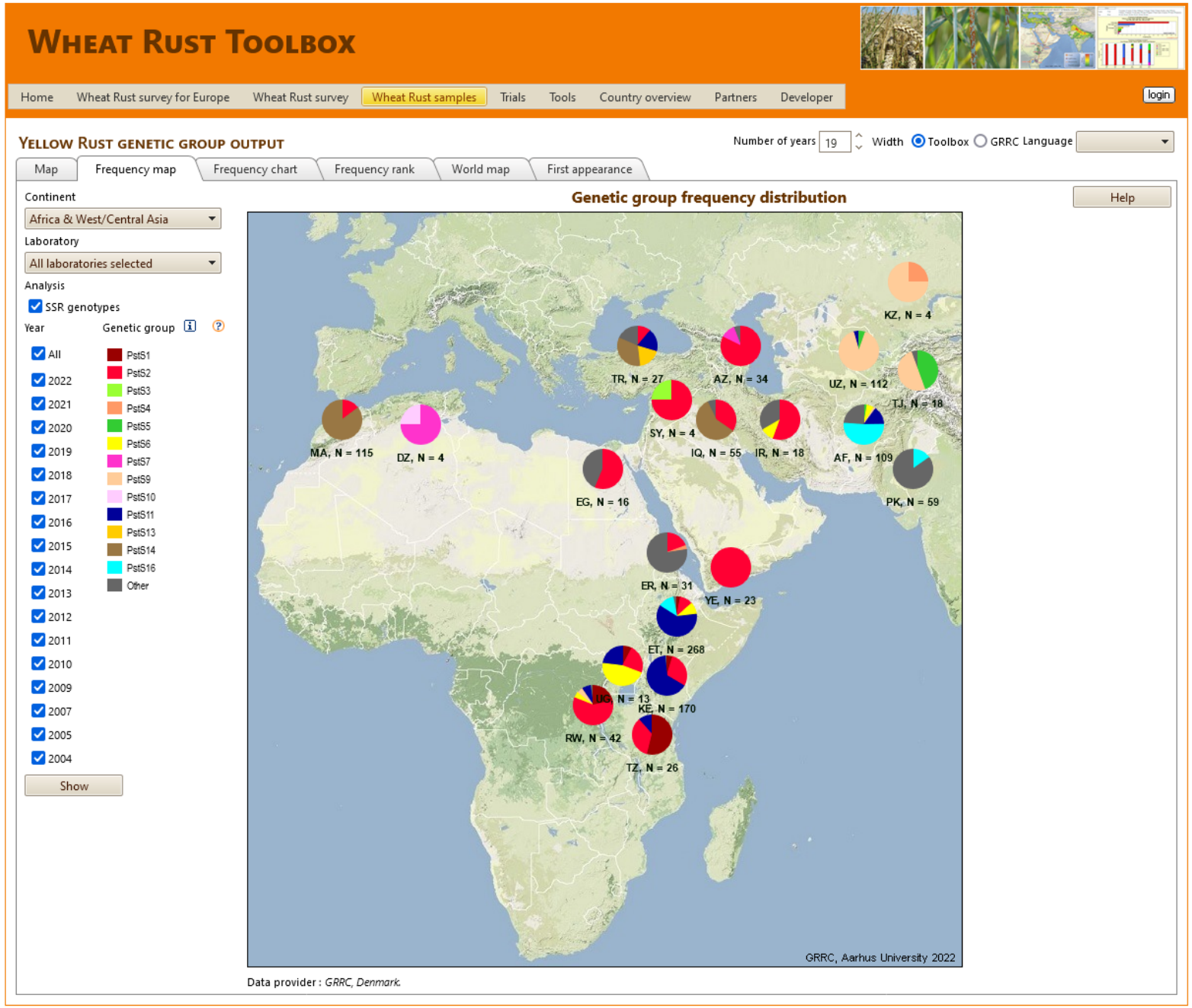
Genotype legend

EU_1_A1, EU_2_A1, EU_5_A1, EU_6_A1, EU_8_A1, EU_12_A1, EU_13_A2, EU_23_A1, EU_33_A2, EU_34_A1, EU_35_A2, EU_36_A2, EU_37_A2, SIB_1_A1, EU_39_A1, EU_38_A2, EU_40_A2, EU_41_A2, EU_10_A2, EU_22_A2, EU_3_A2, EU_43_A1, EU_42_A2, EU_45, EU_44_A1, Other

Genotype frequency distribution

Help





Bill and Melinda Gates Foundations has funded global wheat rust early warning since 2008

Since 2010 uses the same global database at AU as for *P. infestans*!

The BMGF Foundation has far not supported research and development in Potato

We can change that – if we come up with good arguments!!

Collaborate with the USAID innovation lab Coordinated by David Hughes, Pen state University (CIP included also)

New BMGF proposal on “global infrastructure for transboundary diseases”

P. Infestans will be proposed as a use-case in 2023

Technologies for higher resolution genotyping *P. infestans*

Goal: Extending SSR fingerprinting to sequence-based analyses

WHAT and WHY?

- Harness power of high-throughput and affordable sequencing
- Analysis of more loci in genome than 12 SSRs
- Provide raw data to understand the way genome is evolving in response to selection pressure
    - Mutation rate across different parts of genome
    - Ploidy advantage and destabilisation of genome over time – LOH
- A closer link to phenotype than current neutral SSR markers
    - Effectors – links to R-gene stability
    - Fungicide resistance genes – some targets known and others could be discovered
- Harness network to understand phylogeography and pathogen evolution over time and in space

HOW?

- Baseline SSR typing to identify populations/samples to target
- Whole Genome – 250 Mbases of highly repetitive sequence – very difficult to assemble and process
- Targeted
    - PENSEQ – enrichment of genes of choice followed by Illumina sequence - Aman poster
    - Multiplex effector PCR followed by Illumina sequence Kurt Lamour Uni Tennessee
    - Oxford NanoPore – real-time selective sequencing of key targets (portable?)
- Discussions underway on a phase of pilot studies to compare methods and develop pipelines for data analysis


Thank you for your attention