

BioDT use case 4.1.2.1

Genetically detected biodiversity: crop wild relatives

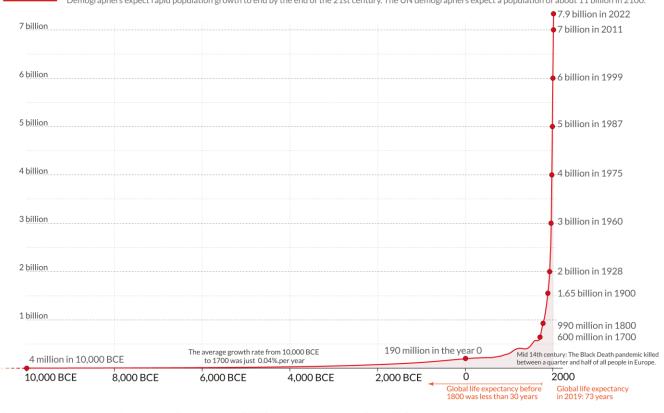




Introduction

- There are two factors that are mainly challenging food security:
 - Population growth and
 - Climate change
- Human population has increased from one to seven billion just over the past 200 years
 - About 700% increment
- Expected to reach 11 billion by the end of this century





Based on estimates by the History Database of the Global Environment (HYDE) and the United Nations. On OurWorldinData.org you can download the annual data.

This is a visualization from OurWorldinData.org.

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Introduction

Population density, 2022

The number of people per km² of land area.

200 500 1,000 100

Source: FAO via World Bank (2021); Gapminder (v6); HYDE (v3.2); UN (2022)

OurWorldInData.org/world-population-growth • CC BY

Our World in Data

This is specially so in developing countries

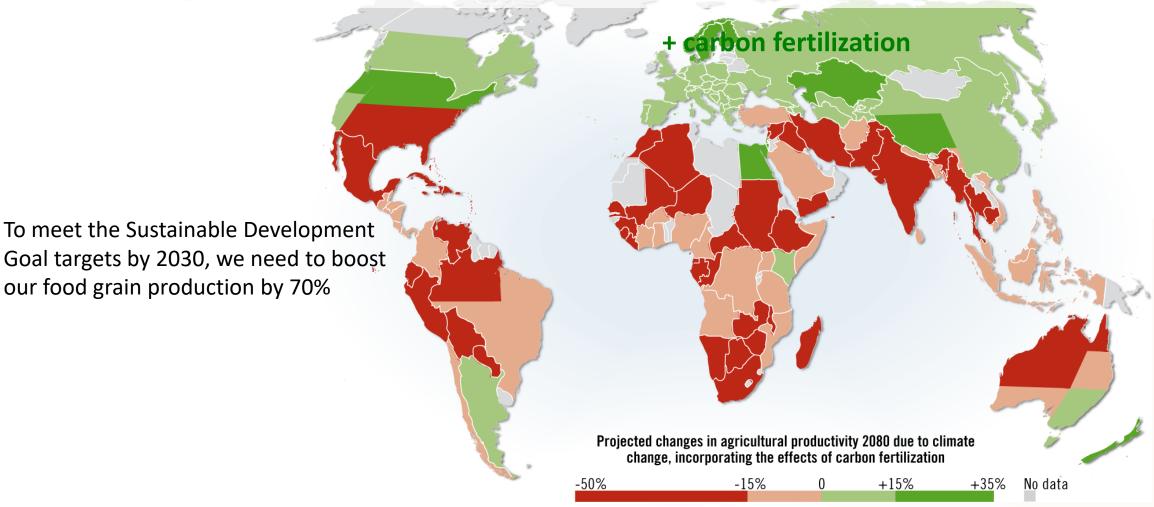






Introduction

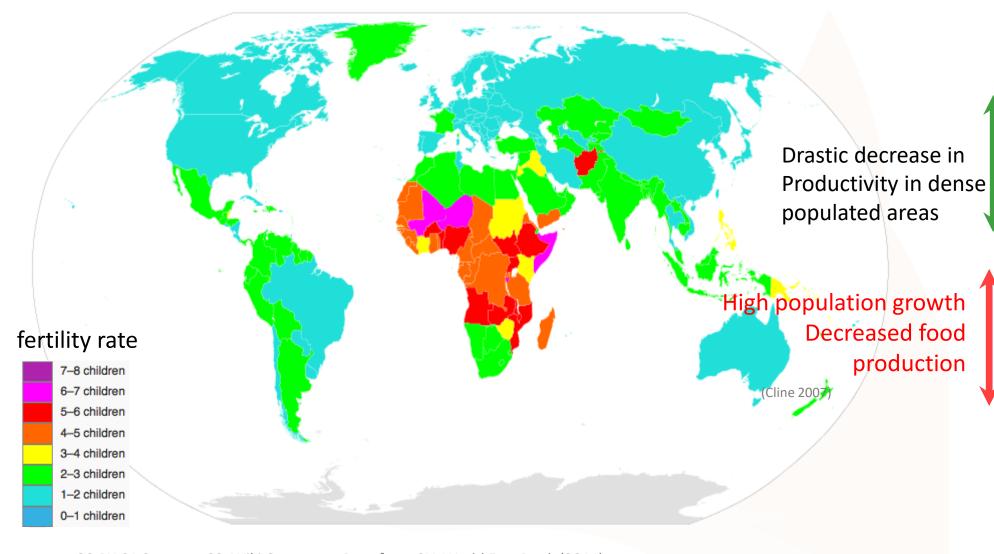
Agricultural production will decrease by 2% each decade (IPCC AR5 WGII, 2014).



Map by Hugo Ahlenius, GRID-Arendal (2008). Source: Cline W. (2007, 2008). Global Warming and Agriculture.



Quite contrary patterns of productivity and population growth



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There is a critical need to fill the gap

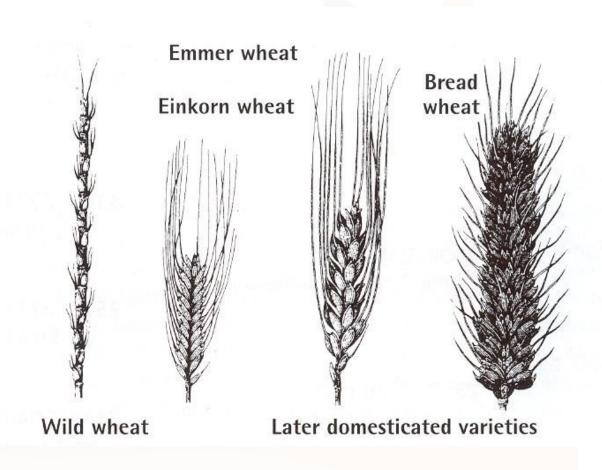


WE NEED CROPS:

- with higher yields
- with higher nutritional values
- adapted to degraded lands
- adapted to changing environments
- Untapped genetic diversity can be found in:
 - Traditional cultivars
 - Landraces
 - Crop Wild Relatives

Human induced pressure on domestic crops

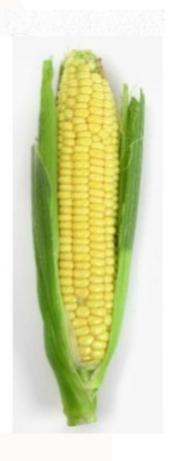
- We were selecting the traits of our interest
 - Genetic homogenization
 - Loss of genetic diversity and some adaptive traits
 - To diseases and
 - Extreme conditions



Human induced pressure on domestic crops

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Human induced pressure pressure on domestic crops

- We were selecting the traits of our interest
 - Genetic homogenization
 - Loss of genetic diversity and some adaptive traits
 - For resistance to diseases and
 - Extreme conditions
- The domesticated gene pool (genetic diversity in crops and breeding lines) is limited by the "domestication bottleneck"







Why crop wild relatives?

- A larger genetic diversity (gene pool) is required to tackle current challenges and large changes
- Crop wild relatives provides an untapped resource for genetic diversity
- They have been through selective pressure as they have to go through several environmental conditions
- Some are adapted to:
 - Drought conditions
 - Water logged areas
 - Warmer temperature
 - Colder temperature
 - Saline soil
- Some are resistant to insect and fungal pests as well as other diseases
- They have important genetic resources that are needed to cope with the changing globe and to feed the ever growing population

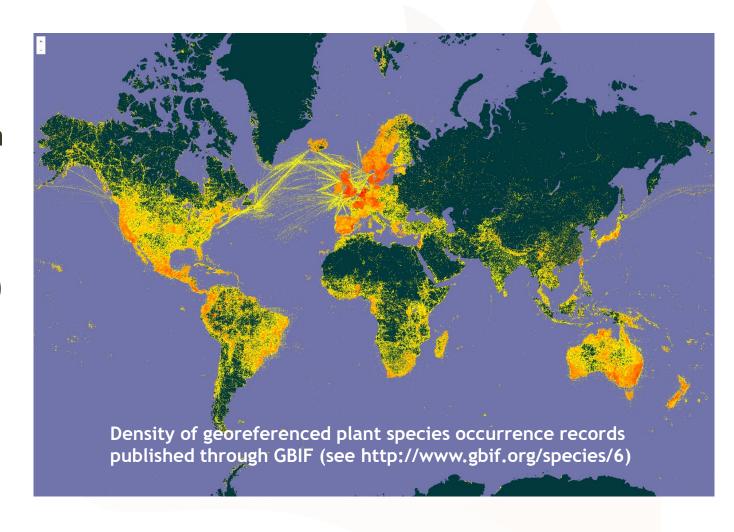




- Crop wild relatives are wild plant species closely related to crops.
- By broad definition it refers to all taxa within the same genus as a crop (Maxted et al. 2006)
- They account for around 21% of the world flora (MAXTED AND KELL 2009)



Last updated: 2017-06-08

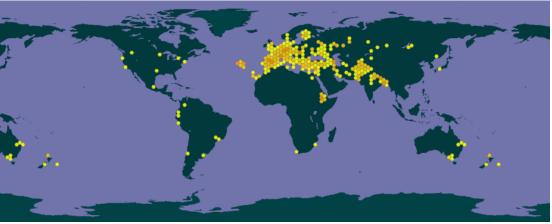






- Belongs the family Fabaceae
- It can withstand extreme environments from drought to flooding
- Cropped after the main cropping season
- If crops fail, the same farm lands can be covered by it
 - This makes it a climate smart species
- Thus grasspea is often the only alternative to starvation when other crops fail





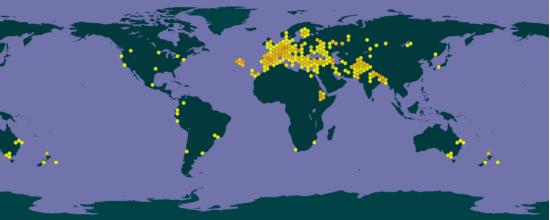






- It fixes nitrogen and serve as a natural nitrogen fertilizer
- It is very rich in protein
- It also serves as a fodder
- Considered as a super crop to beat protein malnutrition in the future











- presents a fascinating paradox it is not only a life saver but also a destroyer as well
- It has a neurotoxin chemical
- when eaten as a large part of the diet over a long period, it can cause
 - Permanently paralyze of the lower limbs in adults - lathyrism
 - Brain damage in children
- This is often the case during famine periods



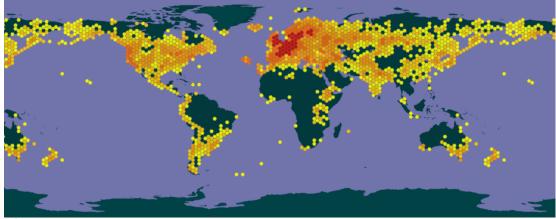






- Quite widely distributed
 - Diverse land races and farmers' varieties
- More than 180 herbaceous species belonging to the same genus
 - Diverse wild relatives
 - Easy to experiment with them
- Huge genetic resources
 - Certain varieties from western Asia have a low level of neurotoxin



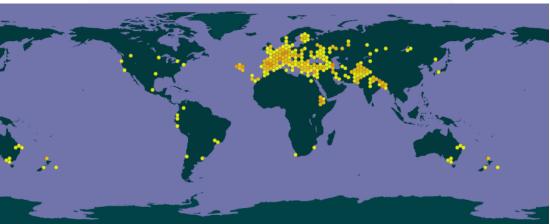






- Searching for variety or a wild relative with low neurotoxin content
- This will allow to raise a grasspea with reasonable neurotoxin content through breeding

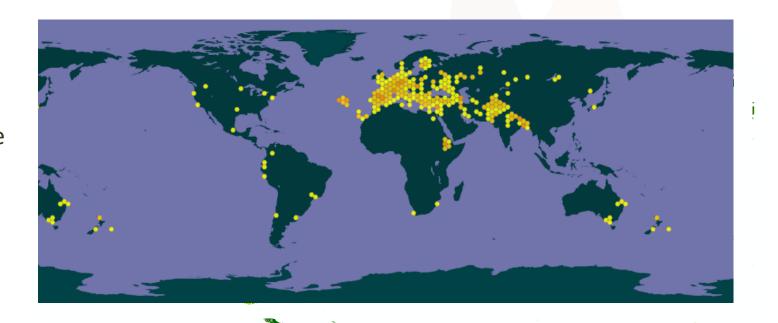






Ecotype mapping

- Varieties growing in similar ecotypes most likely have similar characteristics and genetic resources
- Modelling ecotypes for both farmers' varieties as well as the other species in the genus (wild relatives) can present huge information for plant breeders
- Ecotypes can be mapped by linking environmental variables with occurrence points
- To work with large and high resolution data, super computers are needed





- Linking
 - The ecotypes, online available occurrence and genetic data bases with digital twin
- Building the digital twin model in the way it can make a report whenever new occurrence data and genetic resources are put online from the potential ecotypes/areas
 - Data poor areas/poorly known habitats
 - Marginal environments



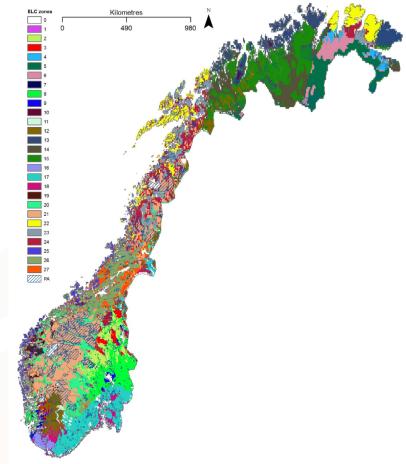


Figure 3 The ELC map for Norway composed of 27 ELC zones each representing a unique combination of environmental variables. See Table S8 for average values in each zone. Zone 0 refers to those areas where information for some of the components making up the map is missing. Variables used to create map: altitude, northness, eastness, slope, precipitation seasonality, isothermality, topsoil organic content and topsoil pH. Created in CAPHTOGEN using the ELC mapas tool. Cell size is equivalent to 10 km² at the equator. Map drawn to Geographic Coordinate System: WGS 1984.



- We can use the Digital Twin service for:
 - Automation of data flow (data fusion from distributed data sources)
 - Dynamic model updating (e.g. feeding in updated environmental data, followed by new model iteration)
 - Automated model uncertainty analysis (comparisons with real-life data)
 - Automated alert for new genetic diversity with predicted interesting target genetic properties (desired alleles)





- This facilitates provision of vital information to plant breeders, conservation scientists, researchers and police makers about potential genetic resources from
 - potential ecotypes
 - data poor areas
 - marginal habitats
 - Highly saline, acidic, dry, wet, warm, cold etc. areas
- This can serve as a prototype for other crops as well
 - Similar method and platform can be applied





- Obtaining traits of interest through breeding is time taking
- Availability of whole genome is important
- I don't think the gene responsible for biosynthesis path way of the toxin is mapped and known
- We don't have a lot of information on the inheritance properties of the gene of interest





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Crop wild relatives 27/09/2022



- @BiodiversityDT
- (in) BioDT

