Climate change and Hevea species

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For development of plants with high yield and resistant to environmental stresses.

● The effects of global warming and climate change have brought worldwide concern about decreases in crop yields for staple grains and biomass resources.

● Development of plants with important added characteristics will contribute to vital global issues such as securing a steady supply of food/resources and climate change.

Contribution to SDGs

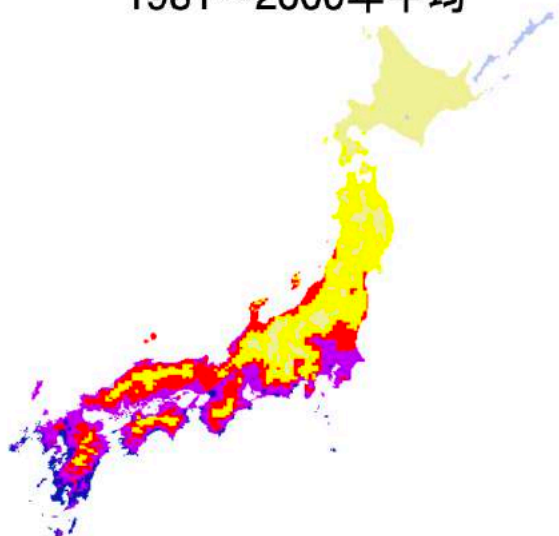Global warming
Weather changes
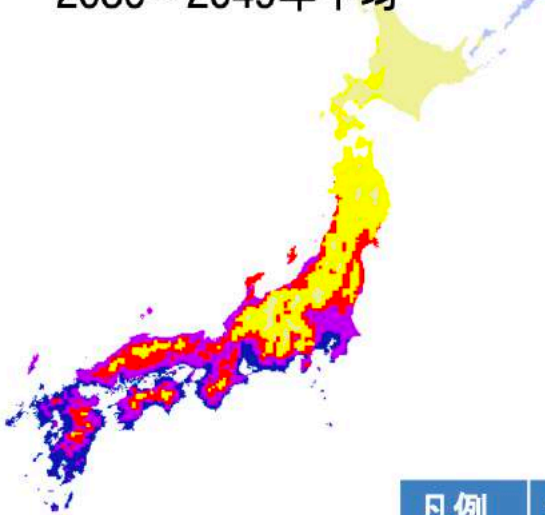
Increase of population Food crisis
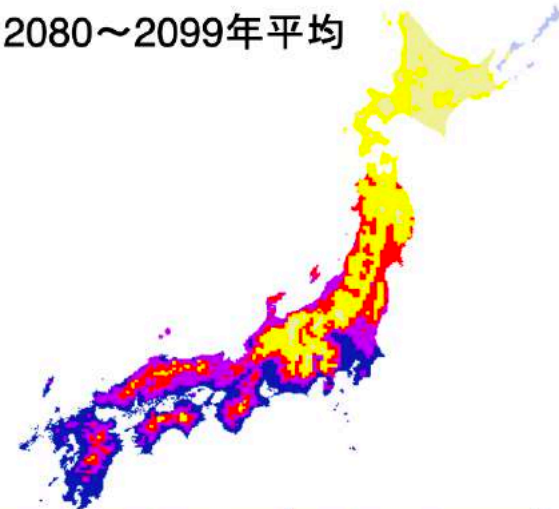
気候変動への対応

NARO 資料より

1981〜2000年平均　　　2030〜2049年平均　　　2080〜2099年平均

今後予想される年平均気温の変化
（IPCC第5次報告書における気候変動シナリオのうち
RCP4.5（温度上昇が中庸なシナリオ）に基づいて解析し
た今後の年平均気温の変化。）

凡例	年平均気温(℃)	地帯区分
	8℃以下	寒地
	8〜12℃	寒冷地
	12〜14℃	温暖地
	14〜16℃	暖地
	16℃以上	亜熱帯
	予測データ無し	

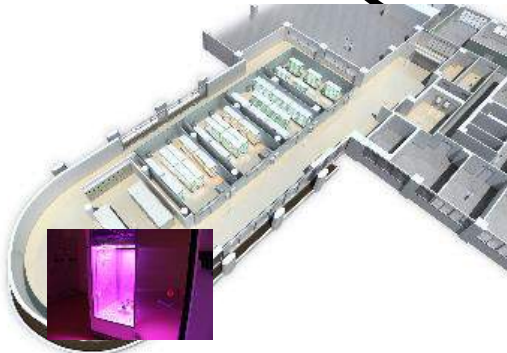# Effect of global warming in JPN

Observation

2030～2049年平均
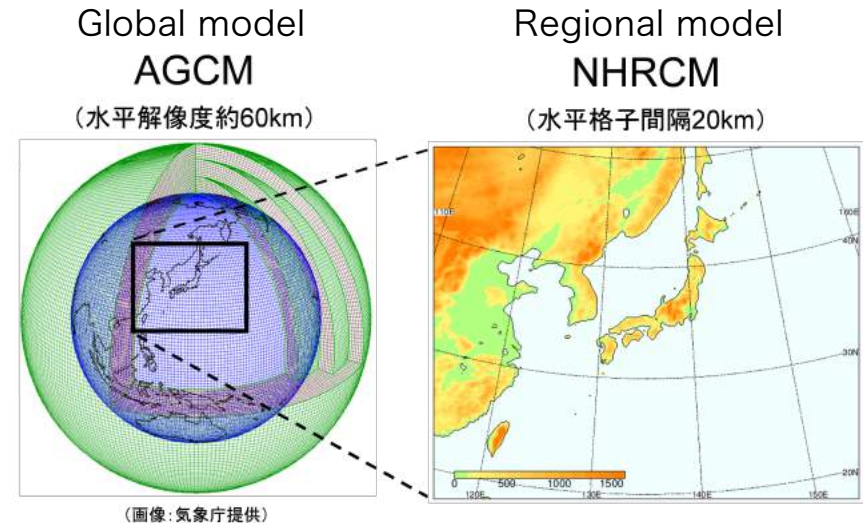
Data collection

Prediction

Experiment

d4PDF is an ensemble climate prediction database

database for Policy Decision making for Future climate change

- Data base for climate prediction (Total data ca. 3PB)
- Compare effects on future climate change by 3 kinds of Scenario
- Evaluate effects stochastically from various ensemble data
- Use for
  climate, hydrological, affairs, electricity, agriculture etc.
- Calculation areas
- Globe：resolution 60km
- Near JPN：resolution 20km

Global model
AGCM
（水平解像度約60km）

Regional model
NHRCM
（水平格子間隔20km）

（画像：気象庁提供）

http://www.miroc-gcm.jp/~pub/d4PDF

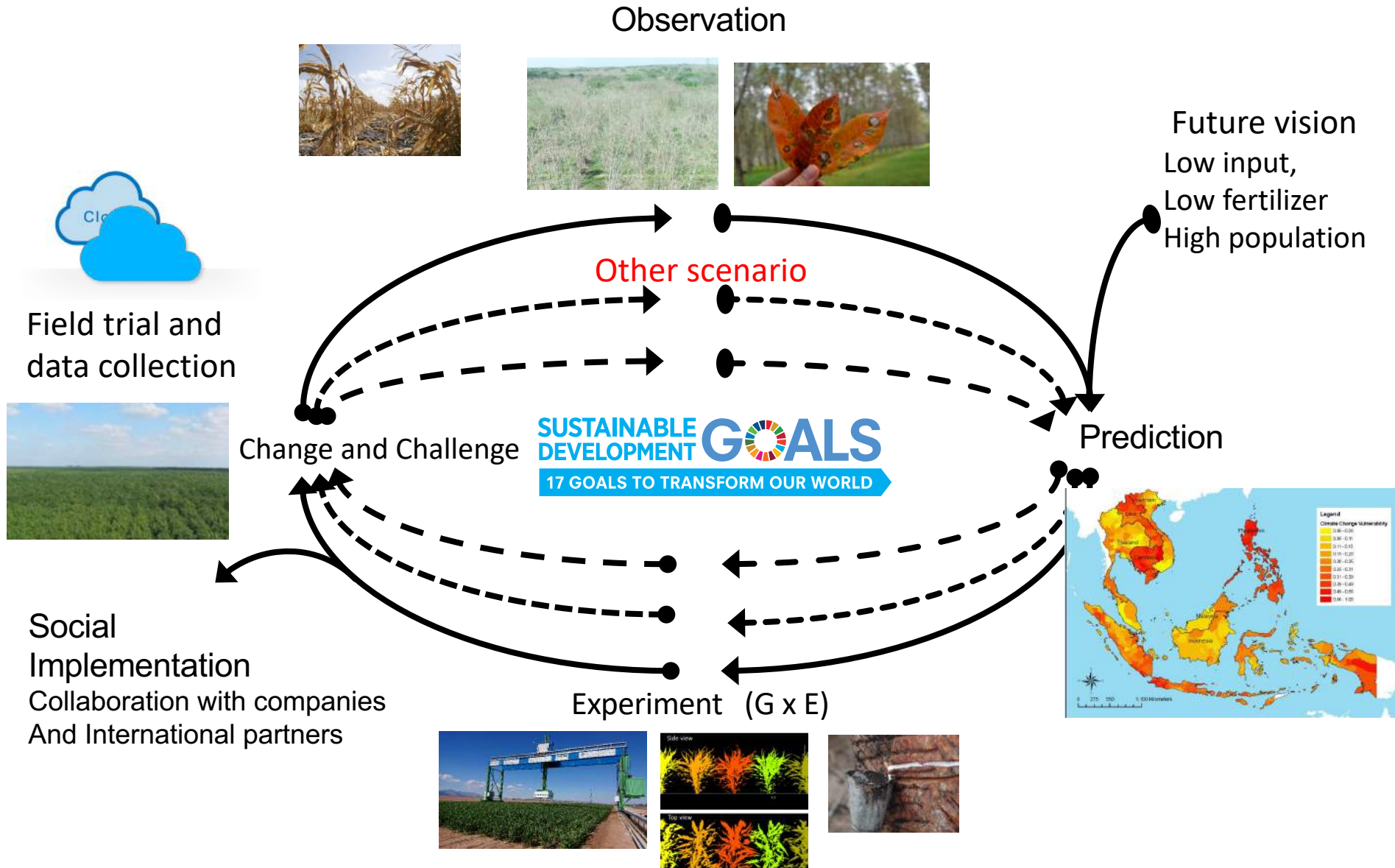| Scenario	Calculated span	members
Past experiment	61 yrs.(1951〜2011)	100
Non-Global warming experiment	61 years	100
2°C increase	61 years	54
4°C increase	61 years	90

Large scale climate control against climate change

Example
・Control of solar-irradiation by applying aerosol in atmosphere.
・Positive removal of GHG
Needs social and ethical discussion for realization but actively discussed using several models.

Disease resistant clone to uptake more Green House Gas.

Cycle for Sustainable Development
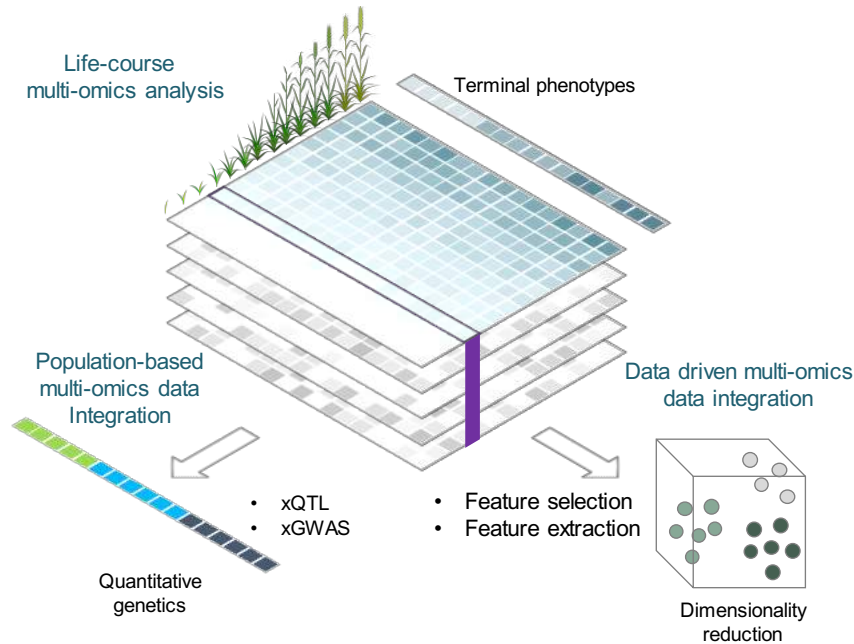## Observation—Prediction—Experiment—Change and Challenge

Observation

Future vision
Low input,
Low fertilizer
High population

Other scenario

Field trial and
data collection

Change and Challenge

SUSTAINABLE
DEVELOPMENT G❍ALS
17 GOALS TO TRANSFORM OUR WORLD

Prediction

Social
Implementation
Collaboration with companies
And International partners

Experiment   (G x E)

Genome x Environment

Genome: Each accession, cultivar, clone has different characteristics.
Environment: They behave differently against various environmental conditions.

SV274: a diverse panel of 274 barley accessions worldwide

Population-scale genotype datasets

- Pan-genome sequencing
- Whole-genome re-sequencing
- Exome-sequencing
- Random amplicon sequencing

Life-course multi-omics analysis

Terminal phenotypes

Population-based multi-omics data Integration

- xQTL
- xGWAS

Quantitative genetics

Data driven multi-omics data integration

- Feature selection
- Feature extraction

Dimensionality reduction

Formulation of G2P relationship based on genetic and environmental factors

Mochida et al., PCP accepted

Deep learning technology is required for data collection and elucidation of optimal condition.

As for "Genome" we are paying special attention on Hevea species.
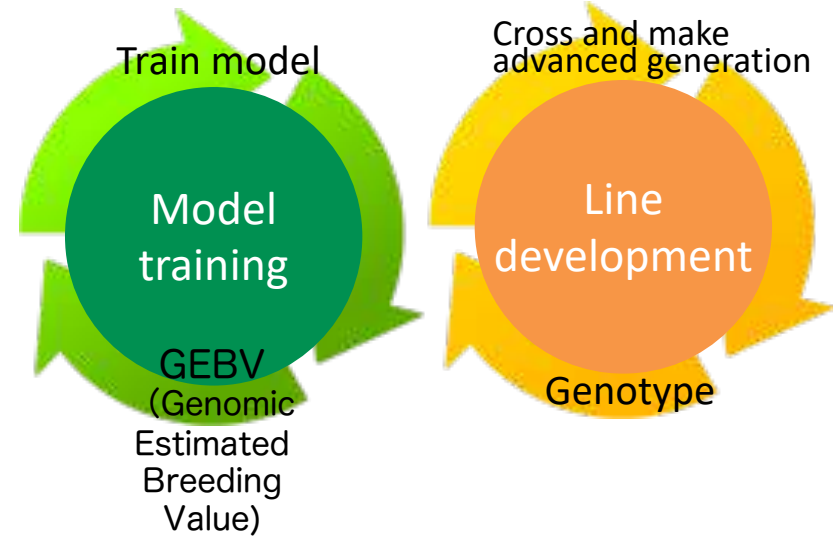
Toward: Genome x Environment

GWAS (Genome Wide Accession Study) and GS (genomic selection) are powerful methods to overcome environmental challenges

GWAS
(Genome Wide Accession Study)
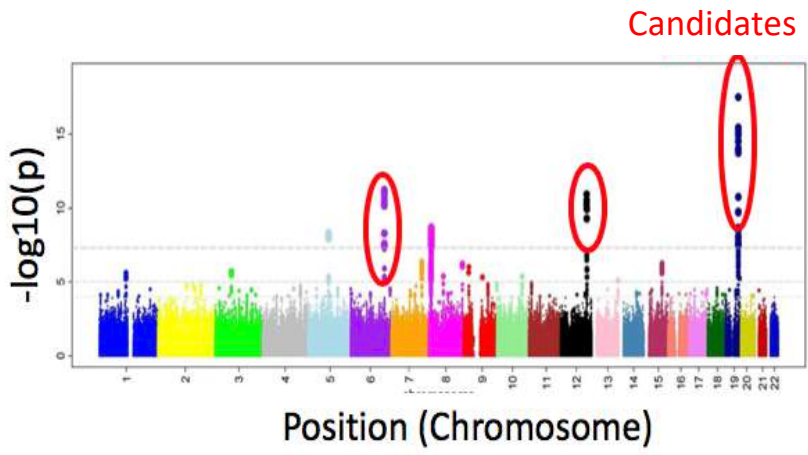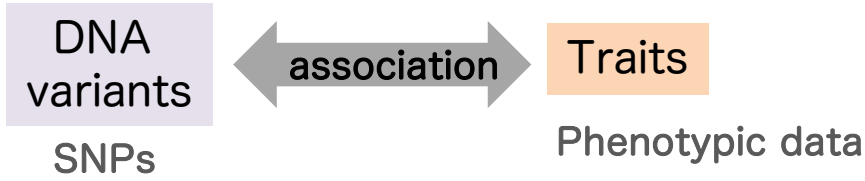
GS (Genomic Selection)

Performing these analysis with high accuracy, the quality of the original genome data is also important.

Hevea species

1. : Euphobiaseae
   1. : Hevea
      1. ***Hevea brasiliensis***
      2. *Hevea benthamiana*
      3. *Hevea camporum*
      4. *Hevea guianensis*
      5. *Hevea microphylla*
      6. ***Hevea nitida***
      7. *Hevea pauciflora*
      8. *Hevea rigidiflora*
      9. ***Hevea spruceana***
      10. *Hevea camargoana*

Drawing of the leaves and flowers
Photograph by: Martius, C., Eichler, A.G., Urban, I.,
Flora Brasiliensis, vol. 11(2): fasicle 64, p. 299, t. 44 (1874)

For latex productivity and disease resistance

H. brasiliensis   *H. spruceana*   *H. nitida*
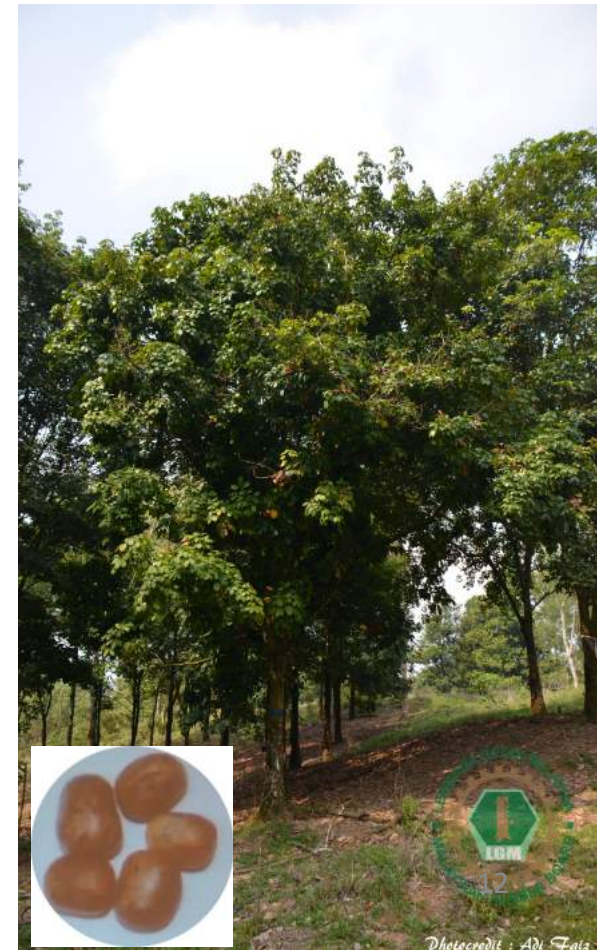
Genus *Hevea* and *Hevea guianensis* including var. *lutea*
Hevea benthamiana — — —
Hevea brasiliensis
Hevea camargoana   ○
Hevea camporum   ☆
Hevea microphylla   ✪
Hevea nitida
Hevea nitida var. *toxicodendroides* ★
Hevea pauciflora including var. *coriacea* — ·· —
Hevea rigidifolia   ●
Hevea spruceana
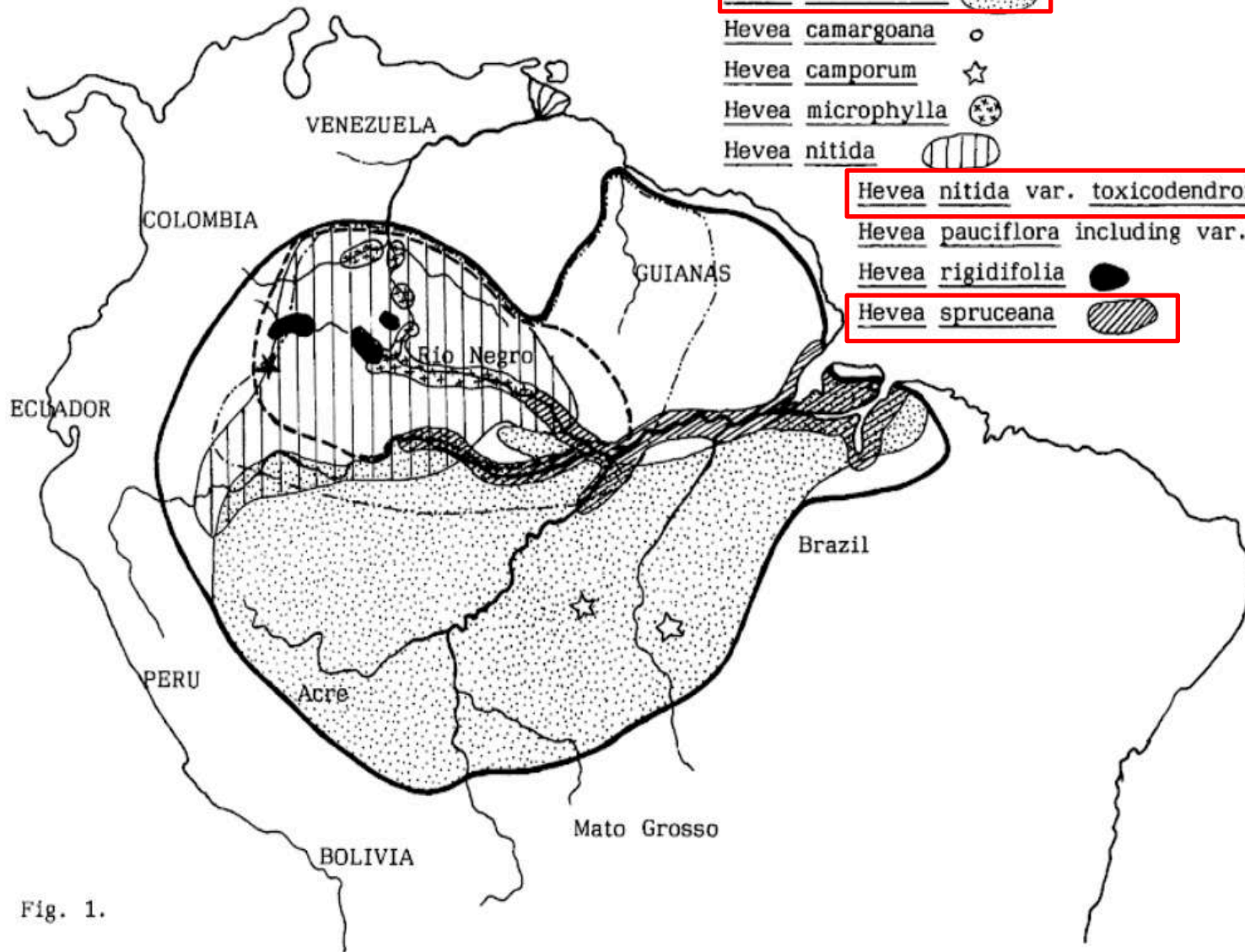
Fig. 1.

Hevea species distribution

	Latex	SALB (M. ulei)
H. brasiliensis	Main commercial source	Susceptible
H. nitida	Anti-coagulant latex	Not infected naturally
H. spruceana	Watery and Low quality (high proportion of resin)	Susceptible (It is used in breeding programmes to improve the disease resistance of H. brasiliensis))
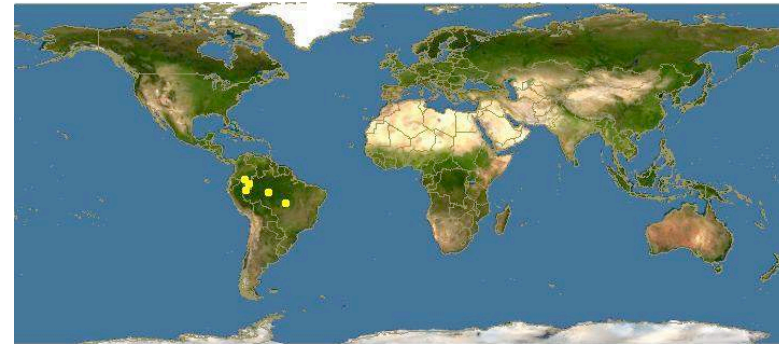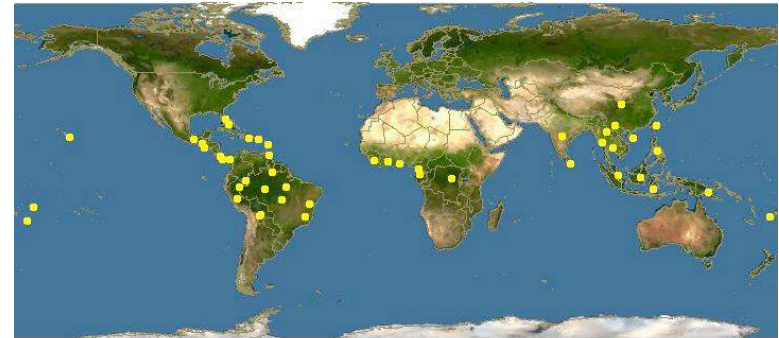
Toward: Genome x Environment

GWAS (Genome Wide Accession Study) is a powerful method to elucidate the strong correlation between SNPs with traits
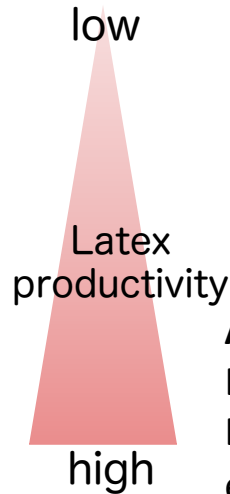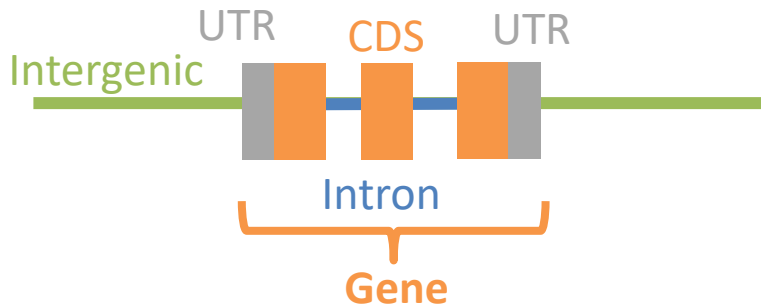

Aim:

Identifying multiple causative genes
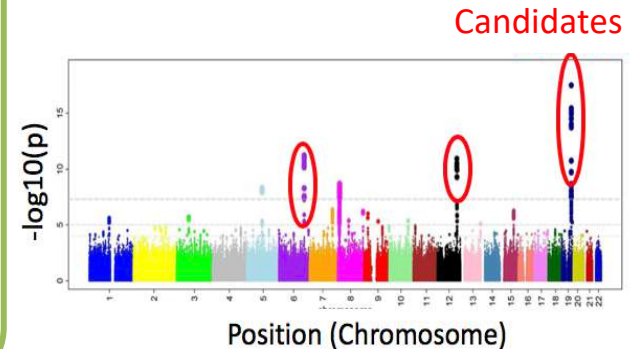
GWAS identify SNPs and other variants in DNA associated with a trait. We try to establish the specific SNPs as a breeding marker. It is possible to identify the causative gene.
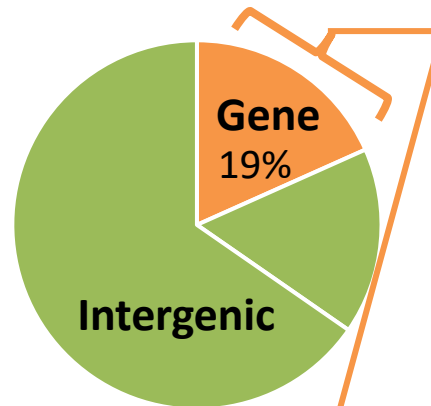
Number of SNPs in the three Heveas

	Latex
H. brasiliensis	Main commercial source
H. nitida	Anti-coagulant latex
H. spruceana	Low quality (high proportion of resin)

H. nitida

105.0 M bp
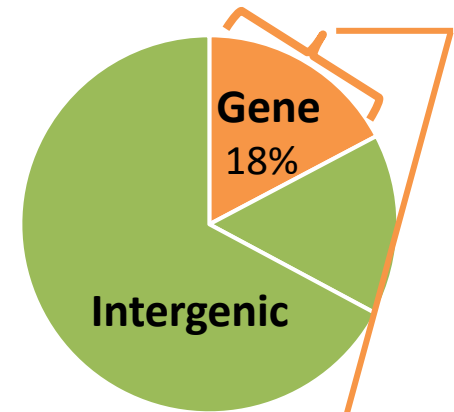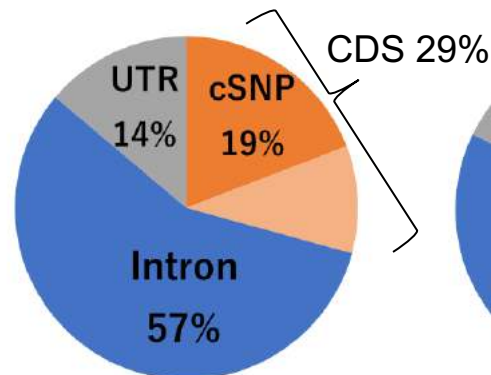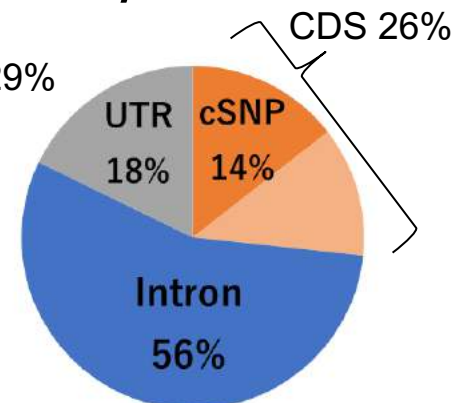
H. spruceana

72.7 M bp

	Countries	Parentage
RRIM 600	Malaysia Thailand	Tjir 1 x PB 86
GT 1	(sterility)	Primer clone
BPM 1	Indonesia	AV 163 x AV 308

H. nitida
105.0 M bp

H. spruceana
72.7 M bp

H. brasiliensis

GT 1
14.0 M bp

BPM 1
14.1 M bp

5.9 M bp

6.0 M bp

8.1 M bp

Summary and Future study
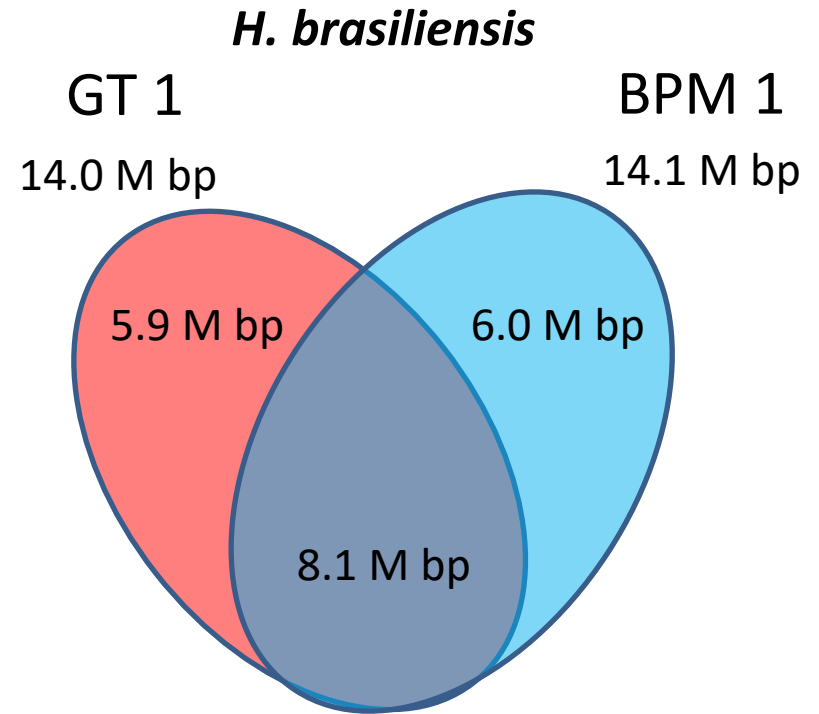
- For sustainable development and climate change
  - Examine growth environment of Hevea species.
  - Examine characteristics of Hevea species.
  - Compare genome between *H. brasiliensis* and other Hevea species.
  - Examine SNPs and transcriptome data of H. species.