Climate change and Hevea species
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
気候変動への対応

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—Prediction—Experiment—Data collection
d4PDF is an ensemble climate prediction database

- 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

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Calculated span</th>
<th>members</th>
</tr>
</thead>
<tbody>
<tr>
<td>Past experiment</td>
<td>61 yrs. (1951~2011)</td>
<td>100</td>
</tr>
<tr>
<td>Non-Global warming experiment</td>
<td>61 years</td>
<td>100</td>
</tr>
<tr>
<td>2ºC increase</td>
<td>61 years</td>
<td>54</td>
</tr>
<tr>
<td>4ºC increase</td>
<td>61 years</td>
<td>90</td>
</tr>
</tbody>
</table>
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

Future vision
Low input,
Low fertilizer
High population

Social Implementation
Collaboration with companies
And International partners

Field trial and data collection

Observation

Other scenario

Change and Challenge

Experiment (G x E)

Prediction

17 GOALS TO TRANSFORM OUR WORLD
Genome x Environment

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

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)

- DNA variants
- SNPs

**Traits**

- Phenotypic data

**Candidates**

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
For latex productivity and disease resistance

Photos kindly provided by Mohd Adi Faiz Ahmad Fauzi, MRB

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**
<table>
<thead>
<tr>
<th>Species</th>
<th>Latex</th>
<th>SALB (M. ulei)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>H. brasiliensis</em></td>
<td>Main commercial source</td>
<td>Susceptible</td>
</tr>
<tr>
<td><em>H. nitida</em></td>
<td>Anti-coagulant latex</td>
<td>Not infected naturally</td>
</tr>
<tr>
<td><em>H. spruceana</em></td>
<td>Watery and Low quality (high proportion of resin)</td>
<td>Susceptible (It is used in breeding programmes to improve the disease resistance of <em>H. brasiliensis</em>)</td>
</tr>
</tbody>
</table>
GWAS (Genome Wide Accession Study) is a powerful method to elucidate the strong correlation between SNPs with traits. DNA polymorphism from SNPs includes three SNPs (SNP1, SNP2, SNP3) with three genetic variations: G/C, A/G, and T/G. Each clone (A, B, C, J, K, L) has different combinations of these genetic variations.

- **Aim:**
  - Identify multiple causative genes

- **Traits:**
  - Phenotypic data

- **Correlation:**
  - Latex productivity
    - Low
    - High
    - A shows lower latex productivity
    - G shows higher latex productivity

- **Applications:**
  - Disease resistance
  - Drought resistance
  - etc.

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

<table>
<thead>
<tr>
<th>Latex</th>
<th>H. brasiliensis</th>
<th>H. nitida</th>
<th>H. spruceana</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Intergenic</strong></td>
<td>Main commercial source</td>
<td>Anti-coagulant latex</td>
<td>Low quality (high proportion of resin)</td>
</tr>
<tr>
<td><strong>Gene</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>UTR</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>CDS</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Intron</strong></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

H. nitida
105.0 M bp

H. spruceana
72.7 M bp

H. nitida
CDS 29%
UTR 14%
cSNP 19%
Intron 57%

H. spruceana
CDS 26%
UTR 18%
cSNP 14%
Intron 56%
Num of SNPs inside H. brasiliensis

<table>
<thead>
<tr>
<th>Countries</th>
<th>Parentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>RRIM 600</td>
<td>Malaysia Thailand Tjir 1 x PB 86</td>
</tr>
<tr>
<td>GT 1</td>
<td>(sterility) Primer clone</td>
</tr>
<tr>
<td>BPM 1</td>
<td>Indonesia AV 163 x AV 308</td>
</tr>
</tbody>
</table>

- **H. nitida**
  - GT 1: 105.0 M bp

- **H. spruceana**
  - BPM 1: 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.