



yamamoto.yoshiharu.h5@f.gifu-u.ac.jp

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- Figure 3. Comparison of the genome sizes and divergence times of *Arabis* and *Arabidopsis* species. The phylogenetic tree shows the relationships between *Arabis serrata* (2n = 32; 568 Mbp), *Arabis stelleri* (2n = 32), *Arabis hirsuta/nipponica*, *Arabis hirsuta* (2n = 32; 583 Mbp), *Arabis alpina* (2n = 16; 300 Mbp), *Arabidopsis halleri* (2n = 16; 250 Mbp), *Arabidopsis lyrata* (2n = 16; 200 Mbp), and *Arabidopsis thaliana* (2n = 10; 120 Mbp). The divergence times are indicated by the scale bar (16.80 MYA, 3.6 MYA, 1.5 MYA). The green diamond indicates the divergence time of *Arabis* species, and the green triangle indicates the divergence time of *Arabidopsis* species. The species names are followed by their genome sizes and the locations of their native habitats.

作業仮説

ゲノム重複イベント

里山種

高山種

砂浜種

高成長性の喪失

低湿・強光・紫外線耐性獲得

乾燥・高温・栄養耐性獲得

- ・ 新種遺伝子の発生なし
- ・ 発芽プロファイルの再チューニングのみ
- ・ キー転写因子のプロモーターに注目
- ・ 日本へ射撃で発生

A. hirsuta
high growth & high nutrition requiring

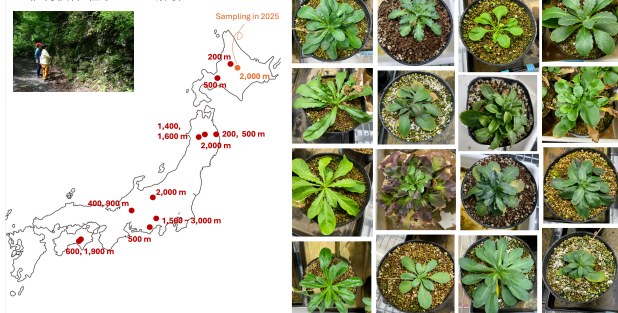
A. serrata
field, HL & UV resistant

A. stelleri
low nutrition resistant, drought & salt resistant

A. stelleri
0 m

alpine species:
Cold/HL/UV stress resistant

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分布状況から考えると、北半球に広く生息するヤマハタザオから日本朝鮮半島に局在するハマハタザオ及びイワハタザオが出現したということになる。我々は属内に全ゲノム重複イベント（WGD）を同定しており、これがハマハタザオ属の活発な種形成（属内に~180種ある）と極端な生息地への適応を可能にした、と考えている。

❖ ゲノムシーケンシング



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graph TD
    A[Single plant from Neo in Gifu] --> B[HiFi reads (Revio, PacBio):  
8.3 kb x 6.4 M reads = 54 Gb]
    B --> C[Genome assembly  
Hifiasm]
    B --> D[Organelle genome assembly  
Oatkit]
    C --> E[2,216 contigs (793 Mb)]
    E --> F[Remove organelle-derived contigs  
Nucmer]
    F --> G[1,706 contigs (787 Mb)]
    G --> H[Remove heterozygous contigs  
Redundans]
    H --> I[231 contigs (568 Mb)]
    D --> J[Organelle contigs]
    I --> K[Chromosome-level scaffolding  
RagTag scaffold]
    J --> K
    K --> L[58 contigs (568 Mb)]
    I --> L
    L --> M[N50 = 36 Mb  
BUSCO: complete/examined = 254/255]
  
```

Single plant from Neo in Gifu

HiFi reads (Revio, PacBio):
8.3 kb x 6.4 M reads = 54 Gb

Genome assembly
Hifiasm

2,216 contigs (793 Mb)

Remove organelle-derived contigs
Nucmer

1,706 contigs (787 Mb)

Remove heterozygous contigs
Redundans

231 contigs (568 Mb)

Organelle genome assembly
Oatkit

Organelle contigs

Chromosome-level scaffolding
RagTag scaffold

58 contigs (568 Mb)

N₅₀ = 36 Mb
BUSCO: complete/examined = 254/255

❖ 遺伝子構成とプロモーター構造の比較

