# Laboratory of Population Genetics

Prof. KAWABE, Akira.

## **Research projects**

We focused on the maintenance mechanisms of DNA variation in Plant species. We are interested in the following topics.

#### 1) Evolutionary process of Centromere regions

Centromere is an important area for accurate chromosome segregation but is also one of the fastest evolving regions in the genome. By using Arabidopsis relatives, we are analyzing evolutionary pattern of centromeric sequences. We found novel repeat from *Turritis glabra* with no homology to previously known centromeric repeat from any species. *T. galbra* also has very complicated repeat structure with chromosome specificities.

#### 2) Patterns of Transposable Element Evolution

Transposon families with an integration specificity to the centromere region were characterized in Brassicaceae species and their evolutionary patterns were analyzed. In *Arabidopsis thaliana*, only the Columbia strains have been analyzed so far, but we have identified different families in other strains. The analysis of the Columbia lineage did not target the centromere in *A. thaliana*. Similarly, another family was identified in which the transition was not to the centromere but to the gene region. The insertion specificity to the centromere is probably lost in *A. thaliana*. In several Brassicaceae species, we found different types of subgroups in the centromere region and in the other regions. We believe that further analysis of different species will allow us to verify how transposons of the same family maintain centromere specificity and how they have evolved.

### 3) RNA editing evolution among Brassicaceae species

We determined complete chloroplast genomes of several Brassicaceae species to analyse RNA editing in chloroplast genome. We analysed RNA editing in chloroplasts of several species of Brassicaceae, and have searched for loss-of-function mutations in PPR genes involved in RNA editing to analyze the diversity of RNA editing among Arabidopsis lines and its causes. In addition, we are planning to elucidate the evolutionary pattern of RNA editing in the entire Brassicaceae family.



Flower of Arabidopsis helleri ssp. gemmifera