### Plant Genome Assembly

**Aim:**

The study uses several genomic and bioinformatics approaches. In this project, participants will be required to reproduce the genomic analysis carried out in the study. The data will be available from NCBI. You are expected to: Download the sequence data programmatically, carry out DNA sequence pre-processing and de novo assembly and perform genome annotation of the plant of interest.

Manuscript:

Xia, E., Li, F., Tong, W., Yang, H., Wang, S., Zhao, J., Liu, C., Gao, L., Tai, Y., She, G., Sun, J., Cao, H., Gao, Q., Li, Y., Deng, W., Jiang, X., Wang, W., Chen, Q., Zhang, S., … Wan, X. (2019). The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data. Scientific Data 2019 6:1, 6(1), 1–9. <https://doi.org/10.1038/s41597-019-0127-1>

**Objectives:** Come with a detailed report answering the following:

* Are you able to determine genome location associated with crucial agronomic traits?
* Are you able to arrive at similar conclusions as those in the paper? Why or why not?
* Are the descriptions in the methodology section detailed for reproducibility? If not, what could you have done to improve reproducibility?