# **Outline: EEOB563 Final project - Evolution of cultivated wheats**

My final project is based on the activities done by [Piotr Gornicki](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Gornicki%2C+Piotr), [Huilan Zhu](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Zhu%2C+Huilan), [Junwei Wang](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Wang%2C+Junwei), [Ghana S. Challa](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Challa%2C+Ghana+S), [Zhengzhi Zhang](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Zhang%2C+Zhengzhi), [Bikram S. Gill](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Gill%2C+Bikram+S), [Wanlong Li](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Li%2C+Wanlong), ***The chloroplast view of the evolution of polyploid wheat (2014),*** <https://doi.org/10.1111/nph.12931>. The premise of this paper is the search for the female parent for two lineages of triticum genus by investigating the evolution of the chloroplast genome.

Cultivated wheat belongs to the genus Triticum L. which includes cultivated and wild species. Triticum is made up of six species; *Tritucum monococcum* (AA genome), *Triticum urartu* (AA genome), *Triticum Turgidum* (AABB genome), *Triticum timopheevii* (AAGG genome)*, Triticum aestivum* (AABBDD genome) and *Triticum zhukovskyi* (AAAAGG genome). The species are further grouped into those belonging to diploid species (monococcon), tetraploid (Dicoccoidea) and Triticum (consisting of hexaploid species). The hexaploid arose under cultivation after the domestication of diploid and tetraploid species in the last 10,000 years. *T. aestuvim* arose from the hybridization between cultivated *T. turgidum* and diploid goatgrass Aegilop tauschii with DD genome, while *T. zhukovskyi* originated from hybridization of *T. monococcum* a diploid with *T.timopheevii*. The two hexaloid make up two lineages of polyploid wheat;one, Emmer lineage that consists of *T. aestivum* and *T. turgidum, while T.timopheevii* and *T. zhukovskyi* make up the Timopheevii lineage.

*Triticum urartu*  with AA genome is believed to be the male parent contributing to the A genome in both lineages, while *A. speltoides* is the female donor contributing the G genome and cytoplasm to the Timopheevii lineage. Debates over the origin of the B genome and therefore the cytoplasm of *T. turgidum* have spanned over decades with several hypotheses of the origin proposed. In one hypothesis, *A. speltoides* is proposed as a possible donor, in which B and G genomes could have been derived from different genotypes of *A. speltoides*. This is possible due to its diverse plasmon and outcrossing nature of *A. speltoides.* Although the second hypothesis was contradicted by molecular and morphological data, it postulates the origin of the B genome to be in the *Sitopsis* section of *Aegilops*. And lastly, the donor of B genome could be extinct or has yet to be collected.

Despite the availability of genomic information, the origin of the B and G genome had been more difficult to decipher from nuclear genome data. In a bid to understand the evolutionary history of the B and G genome, plasmon (in this case chloroplast) and nuclear marker data of *Aegilops and tritucum* species was used to reveal the origin of the chloroplast in the Emmer and Timopheevii lineage.

**METHOD**

1. **Material**

I collected the data used in this analysis from Genbank using the accession provided in the paper.

|  |  |  |
| --- | --- | --- |
| Species | Ssp. | Number of accessions per species |
| *T. aestivum* | *spelta* | 1 |
| *T.turgidum* | *carthlicum* | 3 |
|  | *durum* | 2 |
|  | *dicoccoides* | 6 |
| 1. *speltoides* |  | 2 |
| 1. *sharonensis* |  | 4 |
| 1. *longissima* |  | 2 |
| 1. *kotschyi* |  | 2 |
| *T. urartu* |  | 2 |
| *T. tauschii* |  | 2 |

**2. Phylogeny Analysis**

My goal for this project is to re make the phylogenetic analysis done by Gornicki et al. The differences in the analysis here will be from the tool/programs used to perform various phylogenetic analytical steps. Once the genotypic data is established, I will perform a sequence alignment analysis in MAFFT. Gaps produced from the analysis will be removed manually. Next I will use PAUP to perform NJ using Juke-Cantor’s distances and a bootstrap analysis using 1000 reps. I will also build a majority rule maximum likelihood tree in RAxML using GTR-G model. I will also build a majority rule tree after partitioning the nucleotides based on codon. Finally, I will estimate the best nucleotide substitution model using bayesian information criterion in Mr. Bayes.

**References**

[Piotr Gornicki](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Gornicki%2C+Piotr), [Huilan Zhu](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Zhu%2C+Huilan), [Junwei Wang](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Wang%2C+Junwei), [Ghana S. Challa](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Challa%2C+Ghana+S), [Zhengzhi Zhang](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Zhang%2C+Zhengzhi), [Bikram S. Gill](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Gill%2C+Bikram+S), [Wanlong Li](https://nph.onlinelibrary.wiley.com/action/doSearch?ContribAuthorStored=Li%2C+Wanlong), The chloroplast view of the evolution of polyploid wheat (2014)***,*** *New Phytologist, 204(3), 74-714*