*Pedigree Relationships Between NAM Parents*

The NAM founders were based on two cycles of intermating within the UMN breeding program, which originated from material in at The Land Institute (TLI). Pedigree records at TLI trace maternal families back to the TLI founder individuals, as random intermating was conducted without male parent pollen control (DeHaan et al., 2018). As genotypic data was collected in UMN Cycle 2, we used historical breeding data to identify the paternal parents of the NAM founders allowing complete grandparent origin for NAM genets, and maternal pedigrees six generations back from the NAM genets to be constructed (Zhang et al., 2016)(Supplementary Figure 2).

Genotyping-by-sequencing (GBS) data from UMN Cycle 2, a subset of SRA Bioproject PRJNA608473, experiment [SRX7814130](https://www.ncbi.nlm.nih.gov/sra/SRX7814130), and the genotypic data from the NAM population were combined to identify SNPs for parent analysis. The GBS libraries were prepared using a two enzyme approach similar to the methods of Poland et al. (2012). SNP calling was completed with the TASSEL v2 GBS pipeline (Glaubitz et al., 2014) using the IWG reference genome (access provided by the *Thinopyrum intermedium* Genome Sequencing Consortium, https://phytozome-next.jgi.doe.gov/info/Tintermedium\_v2\_1) . Filtering was completed using VCFtools (Danecek et al., 2011) and custom scripts that insured all SNPs 1). Maintained a minor allele frequency greater than 0.05. 2). Allowed less than 1% missing genotypes per marker. 3). Aligned to exactly one location in the genome. 4). Required SNPs to be biallelic, triallelic or presence/absence were discarded. 5.) Required less than 30% heterozygosity per loci across all individuals. 6). Insured that homozygous SNPs were required to have a read depth of four, while heterozgyous SNPs could be called with two contrasting tags. This filtering strategy resulted in 2,303 SNP to use for parentage analysis. Paternity was assigned using Cervus 3.0.7 (Kalinowski et al., 2007) where the following parameters were used: a minimum of 300 typed loci were required, 250,000 progeny were simulated, and a test for self-fertilization was completed. All other parameters were maintained at the default value, with paternity assignment being completed at the 95% confidence level. The *visPedigree* R package was used to create pedigree diagrams (Luan, 2020).

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