Outline the first predictive breeding study using whole genome markers in kelp

**Intro**

Predictive breeding in animals and in plants, how is GS being performed?

(the real on-going breeding program study only. No simulation/empirical analysis)

Kelp potential, any Asian kelp breeding programs strategies?

Identify gap in current kelp breeding strategies. Elaborate the potential of using predictive breeding

**M&M**

Kelp breeding efforts in details (past two years)

* Phenotyping effort
* Genotyping effort
* Compose pedigree+ marker based relationship matrix
* Report both diploid and haploid methods?
* GS model, rrBLUP
* GS model, GCA+SCA (BGLR)

**Results**

1. ANOVA Experimental effects across two years (avoid dup from 2019 data by Umanzor et al 2020)
2. Compare relationship matrix results from diploid vs haploid methods?
3. *Cor (using lsmeans?)* on both years’ data (Supplemental figure and cite 2019 data cor figure Umanzor et al. 2020*)---- Multi-trait BGLR, genetic correlation between traits (Marnin,installation from github); this same correlation between same trait\_from both years*
4. Heritabilities within year and between years
5. Predicted BVs via rrBLUP changes over generations
6. GS CV schemes via rrBLUP to predict the hybrid SP itself
   1. TP data from one year SP -> Predict Population (PP): another year (partial borrowing information, as not all the same lines were repeated in both years)
   2. TP: a proportion of data from all locations -> the other proportion of data from those same locations
   3. TP data from a few locations -> PP: new location (e.g. PP: 3 loc, within or between 2 locs)
   4. TP: SPs from 2 GPs both had marker data (#) -> PP: SPs in c. and d.
   5. TP: SPs from 2 GPs one pedigree, another one marker data (#) > PP: SPs in b. and d.
   6. TP: SPs from 2 GPs neither have marker data (??) ->PP: SPs in b. and c.
7. GS CV schemes with the BGLR for above TP->PP combination
   1. GCA
   2. GCA+SCA
   3. GCA+SCA+GCA\*Year+SCA\*Year
8. 7. And 8. Model, but used for predicting the GPs BVs, Compare BVs values coming out of different models?
9. Any ways to look into GCA for female and male differences? Unequal family size and maternal effects? Predicting SPs, with data only from FGs
10. TP: Founder SPs (individual measurements) -> predicted GCA on the FGs, cor that to those Phenotypic values on the plot level SPs coming out of the FGs

**Discussion**