Development of genomic tools for breeding superior sugar kelp (Saccharina latissima) cultivars for food and fuel

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Outline

- Background
- General project objectives
- Current progress
- Future work
- Acknowledgements



Kelp on the rope, Domenic Manganell, 2019



Sugar kelp (Saccharina latissima)

- Brown seaweed, a winter crop
- Human food and animal feed
- Source of alginates, possible biofuel
- New economic opportunities
- Two-stage life cycle



Bio oil. Credit: Chang Dou, UW https://wsg.washington.edu/community-outreach/kelp-aquaculture/



ps://www.amazon.com/Maine-Coast-Kelp-Kombu-Organic/dp/B001HTKNFA





The ARPA-E MARINER program



General project objectives

- Germplasm foundation
- Gametophytes culture collection
- Sequencing and variants detection
- Sporophytes cultivation and phenotypic evaluation
- Statistical model construction
- Breeding selection and improvement of next generation



A harvested kelp plot, David Bailey, 2019

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General project objectives Current progress Future work Acknowledgements Background

Founder population construction



Map by David Bailey, 2019

- 189 wild kelp samples from 15 locations
- Two regions: GOM (Gulf of Maine) and SNE (Southern New England)
- Female and male gametophytes from each wild kelp sample were isolated
- Around 400 available gametophytes in the lab currently

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Parental sporophyte sequencing

DArT sequencing ٠ Black Ledge Fort Wetherill 4905 SNP markers **Giant's Staircase** Lubec Dock Lubec Light Cape Cod Canal 149 samples from 15 locations for PCoA Downeast Institute Mt Desert Rock Fisher's Island Nubble Light analysis Orr's Island Fort Stark . Pine Island Isles of Shoals Newcastle PC2 (5%) 10 cm **SNE** GOM 15 0 10 PC1 (15.2%) Sullivan Falls Orr's Island Thimble Island Pine Island Fort Wetherill

Mao et al, 2020

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Reference genome

- A female gametophyte (haploid) from Connecticut
- Two step sequencing
- Illumina sequencing
- PacBio sequencing
- Reference genome V1 available



Gametophytes resequencing

- 285 gametophytes (three 96 plates) that represent the diversity of the collection will be resequenced
- Two plates have been finished and SNPs were called using the reference genome
- All the available gametophytes (except the resequenced) will be sequenced using the skim-sequencing methods



Male (up) and female (down) gametophytes at UCONN Stamford, Schery Umanzor, 2020

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Phenotyping for the crosses



- Two experimental farm sites
- GOM in the New Hampshire
- SNE at the Long Island Sound
- Around 600 crosses have been evaluated for plot level and blade level traits
- Large variation for different crosses
- High heritability for several traits

Background General project objectives *Current progress* Future work Acknowledgements

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Future work



2. Use genomic tools estimating the gametophytes breeding values

Jean-Luc Jannink, 2018

 Genomic prediction model

- Improved database
- High yield strains
- GWAS
- Marker development

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Acknowledgements













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Thank you so much for your attention!