1st International Seaweed Conference USA

Seagriculture

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SEAGRICULTURE INNOVATION AWARD 2022

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Company / organization: Woods Hole Oceanographic Institution, University of Connecticut, and University of Southern California

Description of the Innovation (ca. 250 words):

Our organizations have developed a method for selecting, breeding and improving sugar kelp that are infertile. With our collection of over 1,000 accessions of gametophytes (now publicly available at the National Center for Marine Algae at Bigelow Labs), including many that have been whole genome sequenced, we have employed bioinformatic screening methods to identify pairs of parents that will produce “sporeless” or sterile progeny. We do this by selecting individuals with naturally occurring mutations (recessive alleles) for genes that confer sterility. Then we breeding them with complementary individuals so that the allele for sterility is homozygous and is expressed. For example, since meiosis is a crucial step for spore production, natural mutations found on meiosis checkpoint genes often result in sporophytes that will not produce spores and thus will be sterile. Such a cross can be achieved within one generation using gene sequencing to identify appropriate mutations on genes interfering with functional fertility.

Infertility is an important management feature for breeding programs because most national and state regulators are risk averse, and are not ready to permit selectively bred farmed strains for fear they may impact natural resources. There is a poor understanding of the probability of interbreeding between wild kelp and selectively improved strains, and the possible effect on the wild. So far, we have tested 25 putatively sterile strains, and two have been either late ripening (> 6 weeks post “harvest time”) or sterile. We have a patent pending, “Improved Strains of Algae and Uses Thereof”, U.S. Provisional Patent Application No. 63/318,475 that covers our method for making infertile kelp.

What makes your innovation unique compared with other products? (ca. 400 words)

There is no comparable product. The sugar kelp industry relies primarily on wild collected and untested seed each year hoping for commercially viable results, unlike most agricultural practices . We have developed strains that can produce harvests over 15 kg/m (about 2 to 3 times typical commercial harvests), and some strains yielded over 20 kg/m, and as much as 28 kg/m. Virtually all successful business plans are driven by how much one can harvest in a permitted growing area. Use of select kelp strains can ensure the most profitable results.

However, the cited improvements above are practically useless without regulatory approval to plant them on commercial farms. Alongside our germplasm collection, we have developed an annotated reference genome which will be published soon. The reference genome opens up a “Rosetta stone” of possibilities for understanding the inner workings of genes that regulate sugar kelp growth, composition, resilience, AND

infertility. Using this and other reference genomes, we have examined the gene sequences of sugar kelp parents (male and female gametophytes) to predict which crosses might contain complementary natural mutations to produce infertile or "sporeless" sporophytes. Once we can consistently produce infertile sporophytes, it should clear the way for environmental and regulatory compliance. "Superior" strains will be permitted to planted on farms because they can't potentially interbreeding with wild kelp. This may also open the door to cross breeding different kelp species for farming (for example Asian "kombu" with North Atlantic sugar kelp) possibly producing vastly different and superior cultivars.

What special new advantages does your innovation bring in terms of for example commercial, environmental and social factors? (ca. 400 words)

One major factor that is holding seaweed farming back from reaching its potential is the inability to consistently produce selectively bred and sporeless seed that satisfy regulatory concerns. Our selective breeding and sporeless kelp innovation (and the associated open-source tools we have developed) could transform the industry, and enable the expansion of profitable production in the Northeastern US, and serve as a model for other regions of the world.

Commercial value:
The US Department of Energy (MARINER Program) and the World Wildlife Fund along with matching funds from academic and industry partners have invested over $5 million in the last 4 years to enable our achievements. On-farm implementation of selectively bred strains could double harvested yields and would contribute 50 to 75% more revenue per unit area – if such strains were permitted.

Environmental value:

There are many examples of deliberate plant and algae introductions that have caused unintended environmental changes (e.g. *Undaria* in Europe). Long-term breeding programs can create strains that are every different from the wild, and are akin to new species. We need to be prepared to manage those strains, and stop their proliferation. Our innovation will help protect kelp forests even as it helps to expand kelp farming.

Social value:

Currently, there is a lot of uncertainty, lack of information, and confusion on the part of regulators and the public regarding the potential environmental risks with planting selectively bred kelp strains – even those that are not even one generation removed from the wild like most of our current collection in the NE US. This creates conflict between regulatory obligations and socio-economic goals. The development and use of infertile strains via our bio-informatic tools will solve this problem. An easier regulatory path to the adoption and expansion of seaweed farming leads to greater economic and social benefits for coastal communities; revitalized working waterfronts, business diversification for fisherman and shellfish/finfish farmers, new processing opportunities, and employment.

For which market and target group was your innovation mainly developed? Who is likely to be the key customer group? (ca. 200 words).

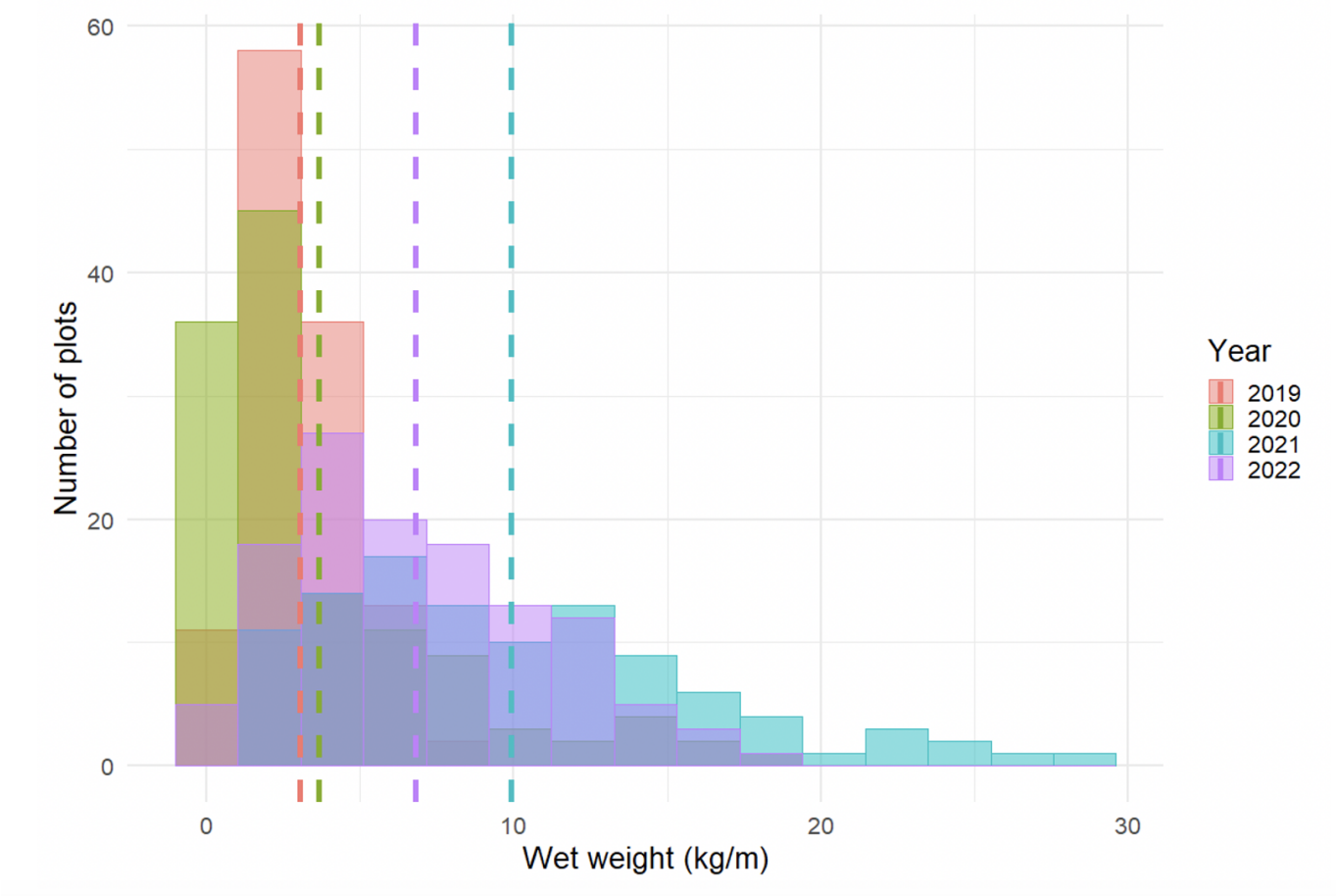
The customers are ultimately farmers, many of whom we are cooperating to extensively test strains on a research scale. But the immediate and practical customer will be commercial hatcheries that either use the publicly available germplasm (genotyped gametophytes) or develop their own. In either case genomic tools may be adopted to predict and test which crosses will be infertile.

Please give very briefly 3 reasons why you believe your innovation should win the Seagriculture 2022 Innovation Award:

1. Our innovation is a relatively-low cost, non-GMO method of creating infertile farmed kelp
2. Our innovation can be applied to selectively improved strains of sugar kelp which have significantly higher yield and other desirable traits

3. Our innovation allows the breeding and planting of infertile sugar kelp that can be widely permitted without fear of impacting wild kelp. If this was widely adopted successfully, it could radically improve kelp farming worldwide.

Figure 1. Wet weight per meter of sugar kelp harvested from plots (different families) farm-tested over 4 MARINER Program growing seasons, 2019 to 2022, and their mean wet weight per meter (kg/m) .



Reference genome

- Multiple sequencing results can be combined
- Comparative genetic analysis
- Useful for other breeding programs
- Gene discovery
- Maker development

JGI PhycoCosm THE ALGAL GENOMICS RESOURCE

JGI HOME GENOME PORTAL

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Status

[June 2021] The *Saccharina latissima* SL-CT1-FG3 v1.0 genome was sequenced with PacBio and assembled with HiFiAsm by the HudsonAlpha Genome Sequencing Center. The resulting assembly was polished using RACON, scaffolded using HiC data, and screened for contaminants. Aquatic genomes can often harbor contaminants that are difficult to identify, so Illumina depth was employed to assist in contaminant screening. The transcriptome was sequenced with Illumina by HudsonAlpha, and then assembled with Trinity by the Joint Genome Institute (JGI). Subsequently, the JGI Annotation Pipeline was used to generate structural and functional annotations.

Genome Assembly	
Genome Assembly size (Mbp)	615.55
Sequencing read coverage depth	185.23x
# of contigs	1513
# of scaffolds	1180
# of scaffolds >= 2Kbp	1180
Scaffold N50	109
Scaffold L50 (Mbp)	1.35
# of gaps	333
% of scaffold length in gaps	0.5%
Three largest Scaffolds (Mbp)	11.32, 8.81, 7.48

Reference Genome annotated and to be published in 2022

Top Ranked Plot

- 28 kg/m wet weight
- 4 kg/m dry weight
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