Cropomics
Our vision for making bioproducts profitable
What is the primary constraint for increased commercialization of bioproducts?

The cost of the feedstock compared to the value.

We need to increase margins

*We need to increase yield*
But???

• Won’t farmers make less money?
  – More yield/Ha same profit/farm

• What about food production?
  – Increase yield by decreasing protein
  – Fuel crops displacing less food crops
  – Choices for farmers

• Is it possible without increasing inputs?
  – There is no a priori genetic reason to think that this is not possible.

• Does anyone really have a better idea?
Transgenic approaches

• I am dubious
  – Yield is a function of how a plant responds to a variable environment.
  – You don’t improve a motor by sticking things in it.
    • You need to rebuild it.
There are two types of genetic variation.

- Segregation
- Recombination

Plant breeding over the last 100 years is largely based on segregation.

There is an untapped reservoir of variation in genetic linkage.
Plant breeding with self-pollination

Parent A
Good
Bad

Parent B
Bad
Good

F1 (progeny)
Good
Bad

X

F6 (progeny)
Good
Bad

Good
Bad

Bad
Good

Good
Bad

Probability of recombination may be too low to be selected. Chromosomes segregate, linkage groups are maintained.
Cropomics

Using the power of biotechnology to access natural variation.
Crop plants have more genes than they should.

25,000 genes 20,000 genes 24,000 genes

40,000 genes???
Genes have been duplicated

Five alpha-amylase inhibitor genes in 50 kb.
- Sequences vary between genes
What do we need to do to access this variation?

1. Characterize sequence differences within target enzymes
2. Identify desirable recombination events
3. Direct where we want recombination to occur
4. Test hypotheses regarding sequence variation
What have we achieved?

1. Developed high throughput proteomics platform.
   – Protein purification capacity
   – Access to MS/MS peptide sequencing (UWO/Sickkids)
   – Developed our own software for analysis

2. Applied platform to the identification of 42 sequence differences in two families of proteins within wheat.
S4 Program

- Input gene sequence
  - Generate all possible single and double point mutations
  - Translate mutation database to protein database
  - Remove redundant sequences
  - Screen plausible sequence space
Controlling recombination

We are working on this.
I'm not interested in the philosophy of this change. I'm damn interested in making the change, seeing it happen.

Norman Borlaug
Thank you

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