Plant Breeding & Genetics Group

Shaun Townsend
Co-Director PBG
Outline

- Introduction
- PBG Genetic Research
  - Program personnel
  - Research areas
- Questions
Introduction

- PBG is one part of a larger genetic research component at OSU
- Plant-based genetic research
  - Primarily in support of plant breeding efforts
- Initially formed by members of Crop & Soil Sciences and Horticulture
Hops

- Two programs:
  - Shaun Townsend, OSU, Aroma Hops
  - John Henning, USDA, Aroma and bittering hops
Hop Challenges

- Expensive production system
  - Infrastructure & labor
- Plants immature until third growing season
- Brewing chemistry extremely complex
- Dioecy
Genetic Approaches

- Traditional (statistical)
  - Heritability, co-inheritance, BLUP
- Induced mutations
- Molecular biology
  - Marker development, genetic diversity, gene discovery
  - Possibly gene editing and transformation
OSU Aroma Hops

- Task is to develop new aroma hop cultivars suitable for the craft beer industry and adapted to Oregon growing conditions.
- Traits include yield, maturity date, disease resistance, brewing profile
Traditional Approaches

- Understanding heritability of important traits
  - **Best Linear Unbiased Predictor (BLUP)**
  - Provides information to guide breeding strategy by partitioning observed or measured variation for a trait into genetic and non-genetic causes
  - Superior male genotypes identified
Traditional Approaches

- Induced mutations
  - Subtle changes
  - Limited genetic change
  - Replacement hop cultivars
USDA Hops Program

- Led by John Henning
- Started in 1933
- Most public hop cultivars developed by this program
Molecular Approaches

- Marker development for **Marker-Assisted Selection (MAS)**
  - Disease resistance, plant sex
- Sequence the genome
  - Gene discovery
- Fix pedigree errors
- Assess genetic diversity
Barley

*Hordeum vulgare*

2n = 2x = 14

5.3 Gbp

~ 30,000 genes

Self-pollinated (hermaphroditic)
The OSU Barley Project

Crossing

Doubled haploids

Genetics and Breeding

Publication, Variety/Germplasm release

Integrating genetics and breeding at a Land Grant University

<table>
<thead>
<tr>
<th>Locus/alleles</th>
<th>Phenotype</th>
<th>Mechanism</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Vrn1, Vrn2, Vrn3</em></td>
<td>Growth habit</td>
<td>Loss of function deletions</td>
</tr>
<tr>
<td><em>Ppd1, Ppd2</em></td>
<td>Flowering time</td>
<td>Loss of function deletions</td>
</tr>
</tbody>
</table>
Barley contributions to beer flavor

Deschutes + 6 and the Oregon Promise
Hazelnut Program

- Led by Shawn Mehlenbacher
- Only hazelnut breeding program in the U.S.
- Hazelnut production is centered in Oregon
Hazelnut Breeding Objectives

A. **Blanched kernel market** (for chocolate, baked goods)
   (93% of world crop is sold as kernels, 7% sold in-shell)

   1. Bud mite resistance
   2. Round nut shape
   3. High percent kernel
   4. Precocity
   5. High yield
   6. Few defects
   7. Early maturity
   8. Free-falling nuts
   5. Easy pellicle removal

B. **Resistance to eastern filbert blight (EFB)**

   1. Simply inherited resistance (‘Gasaway’ & >50 others)
   2. Quantitative resistance (e.g. ‘Tonda di Giffoni’, ‘Sacajawea’)


<table>
<thead>
<tr>
<th>Trait</th>
<th>Heritability (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Good Kernels</td>
<td>42</td>
</tr>
<tr>
<td>Doubles</td>
<td>84</td>
</tr>
<tr>
<td>Moldy Kernels</td>
<td>61</td>
</tr>
<tr>
<td>Poorly Filled Nuts</td>
<td>25</td>
</tr>
<tr>
<td>Nut Length</td>
<td>68</td>
</tr>
<tr>
<td>Nut Shape Index</td>
<td>65</td>
</tr>
<tr>
<td>Nut Compression Index</td>
<td>88</td>
</tr>
<tr>
<td>Nut Weight</td>
<td>63</td>
</tr>
<tr>
<td>Percent Kernel</td>
<td>87</td>
</tr>
<tr>
<td>Fiber</td>
<td>56</td>
</tr>
<tr>
<td>Blanching</td>
<td>64</td>
</tr>
<tr>
<td>Relative Husk Length</td>
<td>91</td>
</tr>
<tr>
<td>Nuts per Cluster</td>
<td>67</td>
</tr>
<tr>
<td>Catkin Elongation Time</td>
<td>68</td>
</tr>
<tr>
<td>Nut Maturity</td>
<td>86</td>
</tr>
</tbody>
</table>

Most traits are highly heritable.
Mehlenbacher et al., 1993; Yao & Mehlenbacher, 2000
Eastern Filbert Blight


We now have > 100 sources of resistance. We use single R-genes and quantitative resistance.
Sources of Very High EFB Resistance in *C. avellana* (greenhouse tests)

<table>
<thead>
<tr>
<th>Accession</th>
<th>Origin</th>
<th>LG*</th>
<th>S-alleles</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Gasaway</td>
<td>Unknown</td>
<td>6</td>
<td>3 26</td>
</tr>
<tr>
<td>1. Zimmerman</td>
<td>Barcelona x Gasaway</td>
<td>6</td>
<td>1 3</td>
</tr>
<tr>
<td>2. Ratoli</td>
<td>Spain</td>
<td>7</td>
<td>2 10</td>
</tr>
<tr>
<td>3. Georgian OSU 759.010</td>
<td>Rep. of Georgia</td>
<td>2</td>
<td>4 20</td>
</tr>
<tr>
<td>4. OSU 408.040</td>
<td>Univ. Minnesota</td>
<td>6</td>
<td>15 27</td>
</tr>
<tr>
<td>5. OSU 495.072</td>
<td>Southern Russia (VIR)</td>
<td>6</td>
<td>6 30</td>
</tr>
<tr>
<td>6. Culpla</td>
<td>Spain</td>
<td>6</td>
<td>9 10</td>
</tr>
<tr>
<td>7. Crvenje</td>
<td>Serbia</td>
<td>6</td>
<td>6 23</td>
</tr>
<tr>
<td>8. Uebov</td>
<td>Serbia</td>
<td>6</td>
<td>12 16</td>
</tr>
<tr>
<td>9. Moscow N02</td>
<td>Russia (Moscow)</td>
<td>?</td>
<td>6 20</td>
</tr>
<tr>
<td>10. Moscow N23</td>
<td>Russia (Moscow)</td>
<td>?</td>
<td>6 30</td>
</tr>
<tr>
<td>11. Moscow N26</td>
<td>Russia (Moscow)</td>
<td>?</td>
<td>1 29</td>
</tr>
<tr>
<td>12. Moscow N27</td>
<td>Russia (Moscow)</td>
<td>?</td>
<td>19 23</td>
</tr>
<tr>
<td>13. Moscow N37</td>
<td>Russia (Moscow)</td>
<td>?</td>
<td>1 6</td>
</tr>
<tr>
<td>14. Farris OSU 533.029</td>
<td>Lansing, Michigan</td>
<td>?</td>
<td>3 11</td>
</tr>
<tr>
<td>15. <em>C. avellana</em> COR 157</td>
<td>Finland</td>
<td>?</td>
<td>9 25</td>
</tr>
<tr>
<td>16. Amarillo Tardio</td>
<td>Chile (Chillan)</td>
<td>?</td>
<td>2 2</td>
</tr>
</tbody>
</table>

*Linkage Group assigned using microsatellite markers*
Pacific Northwest Potato Breeding and Variety Development Program

Tri-State Potato Variety Development Team

C. Brown, Prosser, WA
R. Novy, Aberdeen, ID
J. Whitworth, Aberdeen, ID
R. Navarre, Prosser, WA

M. Pavek, Pullman, WA
R. Knowles, Pullman, WA

J. Stark, Aberdeen, ID
M. Thornton, Parma, ID
N. Olsen, Kimberly, ID
L. Ewing, Moscow, ID

V. Sathuvalli, Hermiston, OR
B. Charlton, Klamath Falls, OR
S. Yilma, Corvallis, OR
C. Shock, Ontario, OR

Jointly funded by USDA-NIFA & Potato Commissions of ID, OR & WA
- Range of ploidy: 2X, 3X, 4X and 5X
- Most cultivated potatoes are tetraploid (2n=4x=48)
- The basic chromosome number is 12
- Haploid genome size is ~900 mb

Solanum sp.
USA Potato Production 2014

PNW: 64%  
North Central: 21%  
Southwest: 10%  
Eastern: 5%

Adapted from Knowles et al (2010)
PNW Potato Industry

- **Processing Industry**
- Fresh Market – Table stock Russets
- Chipping
- Specialty – Reds, yellows, etc.
- Dehy Industry – Potato starch, flour, etc.
Breeding Objectives

- Develop new russet potatoes
  - Dual purpose russet varieties (ID)
  - Individual market oriented russet varieties (OR)

- Breeding for resistance to major pests and diseases
  - PVY, Verticillium wilt, Zebra Chip, TRV, PMTV, CRKN, Scab etc.

- Breeding of specialty potatoes
  - Reds/yellows/purples
  - High anthocyanins, minerals, carotenoids, Nutrients, Flavor

- Breeding for cold sweetening resistance and high nutrient efficiency
  - Low acrylamide, low N input

**Overall Goal:**
Release & commercialize new potato varieties that will directly benefit all segments of the PNW potato industry
Serious pathogen - cause severe disease on potato

A gene, $R_{Mc1(blb)}$, controlling resistance derived from *Solanum bulbocastanum* has been identified and used in breeding resistant potato lines.
Solanum bulbocastanum
Dunal

- Wild, diploid potato
- Source of late blight resistance genes
- Source of tuber resistance to Columbia Root Knot Nematode (CRKN)
- Accession SB22 (PI 275187)
Identification of Molecular Markers

Population Segregating for CRKN Resistance

- PA99N82-4 x CRKN susceptible selection
- Progeny segregating resistant:susceptible

Illumina Hi-seq 2000

- Genome alignments
- SNP calling

SB22 genome

Illumina Sequences Obtained Per Sample

- CRKN-susceptible clones
- CRKN-resistant clones

68,180 contigs

- Resistant
- Susceptible

68,180 genome contigs
1-225 SNPs per contig

Candidate resistance markers

- Resistant pool
- Susceptible pool
Genetically Engineered Trees

Steve Strauss  
Distinguished Professor  
Oregon State University  
Steve.Strauss@OregonState.Edu
Focus in Strauss lab

- Genetic engineering approaches to tree breeding, with a focus on poplar (cottonwood) and eucalypts
  - Emphasis on containment for social and regulatory acceptance given wild relatives, long distance gene flow capability
- Genomic analysis of role of structural polymorphisms in poplar heterosis
- GWAS analysis of genes that control variation in capability for genetic engineering (major new, $4 million NSF project)
Study organisms: Poplar plantations
FT overexpression induces precocious flowering and normal reproductive development in Eucalyptus

Amy L. Klocko1, Cathleen Ma1, Sarah Robertson1, Elahe Esfandian1, Ove Nilsson2 and Steven H. Strauss1,

1Department Forest Ecosystems & Society, Oregon State University, Corvallis, OR, USA
2Department of Forest Genetics and Plant Physiology, Umeå Plant Science Centre, Swedish University of Agricultural Sciences, Umeå, Sweden

Summary

Eucalyptus trees are among the most important species for industrial forestry worldwide. However, as with most forest trees, flowering does not begin for one to several years after planting which can limit the rate of conventional and molecular breeding. To speed flowering, we transformed a Eucalyptus grandis × urophylla hybrid (S7) with a variety of constructs that enable overexpression of FLOWERING LOCUS T (FT). We found that FT expression led to very early flowering, with events showing floral buds within 1–5 months of transplanting to the glasshouse. The most rapid flowering was observed when the cauliflower mosaic virus 3SS promoter was used to drive the Arabidopsis thaliana FT gene (AtFT). Early flowering was also observed with AtFT overexpression from a 4095 ubiquitin promoter and under heat induction conditions with Populus trichocarpa FT1 (PtFT1) under control of a heat-shock promoter. Early flowering trees grew robustly, but exhibited a highly branched phenotype compared to the strong apical dominance of nonflowering transgenic and control trees. AtFT-induced flowers were morphologically normal and produced viable pollen grains and viable self- and cross-pollinated seeds. Many self-seedlings inherited AtFT and flowered early. FT overexpression-induced flowering in Eucalyptus may be a valuable means for accelerating breeding and genetic studies as the transgene can be easily segregated away in progeny, restoring normal growth and form.

Keywords: Eucalyptus, breeding, transgenic, forest biotechnology, flowering Locus T, genetic engineering.
Field trials: Coleopteran resistant Bt-cottonwoods in eastern Oregon field trial
RNA interference for sterility (suppression of endogenous flowering genes)
Policy analysis relevant to GE crops and trees – many lab contributions

BIOTECHNOLOGY

Genetically engineered trees: Paralysis from good intentions
Forest crises demand regulation and certification reform

By Steven H. Strauss¹, Adam Costanza², Armand Séguela³

Intensive genetic modification is a longstanding practice in agriculture, and, for some species, in woody plant horticulture and forestry (4). Current regulatory systems for genetically engineered (GE) trees, however, restrict them to a small number of species. This situation is due in part to the lack of a broad framework for integration with other existing regulations and policies (1-3).

Although only a few forest tree species might be subject to GE in the foreseeable future, regulatory and market obstacles prevent most of these from even being subjects of translational laboratory research. There is also little commercial activity: Only two types of pest-resistant poplars are authorized for commercial use in small areas in China and another under lengthy review in Brazil and another under lengthy review in the USA (5).

METHOD-FOCUSED AND MISGUIDED

Many high-level science reports state that the GE method is no more risky than conventional breeding, but regulations around the world essentially presume that GE is hazardous and requires strict containment. Many European countries still ban GE tree trials.
Vegetable Breeding & Genetics

- Various species
  - Snap beans
  - Snap peas
  - Broccoli
  - Tomatos
  - Cucurbits
- Traditional and organic production
Disease Resistance in Bean

- Genetic resistance in beans to *Fusarium* root rot
- Screened 148 bean varieties in Oregon
- Associated morphological traits to resistance
- Used **Single Nucleotide Polymorphism** (SNP) to identify markers for MAS
- Created a linkage map
Indigo Rose Tomato

- Introgressed chromosomal segments from a wild relative into tomato
- High levels of healthful flavanoids
Ornamental Breeding & Genetics

- Various landscape ornamentals
  - Maples
  - Cape hyacinth
  - Sweetbox
  - Flowering currant
  - Many others
Genetic work to support plant breeding effort
- Ploidy manipulation to induce sterility (ie. triploids) in nonnative species
- Mutagenesis via chemical and physical means
- Traditional genetic research (ex. heritability)
Genetic Work

- Interspecific hybridization in Lilac
- Heritability of floral traits in *Hibiscus syriacus*
- Cytogenetics of various woody shrubs
Winter Wheat Breeding Program

- Soft white winter wheat
  - Cakes, cookies, pancakes
- Hard white winter wheat
  - Noodles, bread
- Hard red winter wheat
  - Bread, rolls, cereal

Bob Zemetra
Program Goal

- Increase profitability of growing wheat for Oregon producers

How:
- Boost production - yield
- Decrease costs - disease resistance
- Boost demand - high quality
In some cases, genetic resistance is the only option

- Barley Yellow Dwarf (BYDV)
- Wheat Mosaic Virus (sbWMV)

Viruses have a great impact on yield and quality
Barley Yellow Dwarf Virus

- 30-40% yield loss
- Resistance gene bdv2 from Oklahoma germplasm
- Moving gene into Oregon germplasm
Wheat Mosaic Virus

- Soil-borne
- Only control is genetic resistance
- sbwm1 gene from midwest and New York
Disease can also reduce quality - Fusarium head blight
Fusarium head blight

- Fungal disease that infects the head and seed
- Disease reduces yield and seed quality
- Pathogen produces a toxin making the seed useless for animal and human consumption
- Source of resistance gene Fhb1 and QTLs
- Michigan and New York germplasm
- Breeding program transferring Fhb1 and QTL for FHB resistance into OSU germplasm
Other Programs

- Jennifer Kling - Quantitative genetics
- Kelly Vining - Mint breeding & genomics
- Laurent Deluc - Grape genomics
- Chad Finn - USDA, Berry breeding & genetics