

Overview

- Brief Background
- Application of genomics to . . .
 - 1) Fingerprinting for clone identification
 - 2) Candidate gene discovery and marker development
 - 3) SNP genotyping and QTL detection

Acknowledgments

- Students and Lab Members
 - Alan Chambers
 - **Sujeet Verma** 
 - Colleen Kennedy
 - Jozer Mangandi
 - Yanina Perez
 - Jack Roach
 - Tomas Hasing
 - Catalina Moyer
 - Luis Osorio
 - David Moore
 - Jim Sumler
 - Angelita Arredondo
 - Kelsey Cearley
- Selected Collaborators
 - Kevin Folta
 - Anne Plotto
 - Dave Clark
 - Thomas Colquhoun
 - Natalia Peres
 - Charlie Sims
- RosBREED collaborators
- Funding and Support

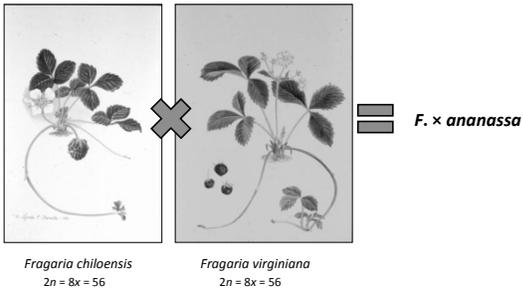


Why have breeding applications of genomics been so slow in strawberry?

- Highly heterozygous allo-octoploid
- Genomic resources and \$ limiting
- Germplasm highly divergent across regions



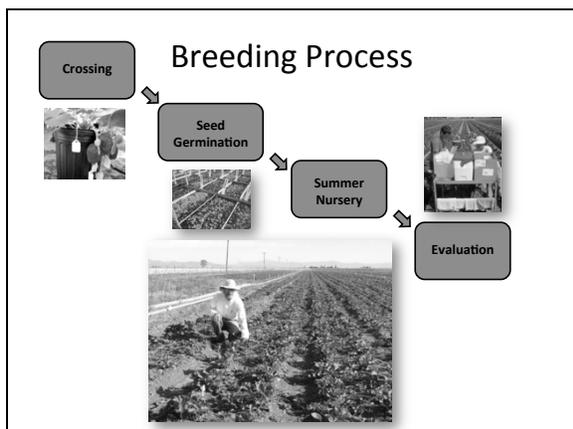
Origins of the Cultivated Strawberry

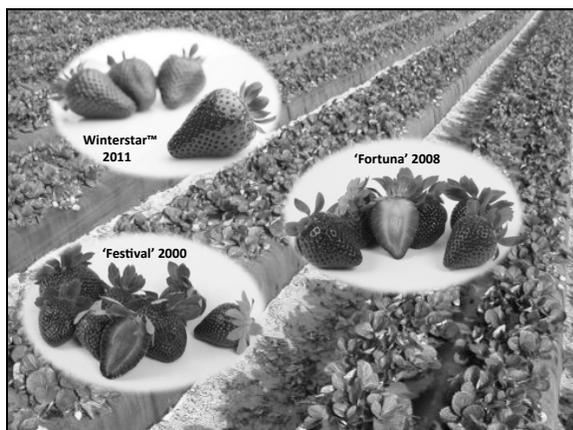


New Resources!

- Reference genome (*F. vesca* $2n = 2x = 14$)
- High throughput DNA and RNA sequencing
- Affymetrix Axiom® IStraw90 SNP Array

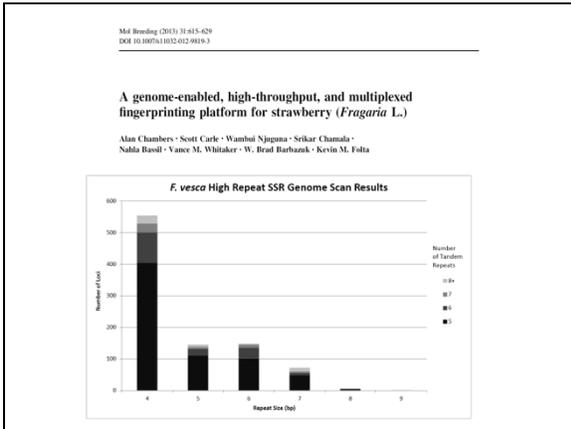


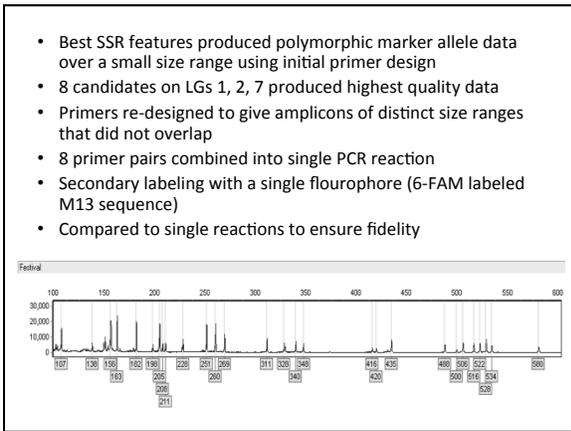


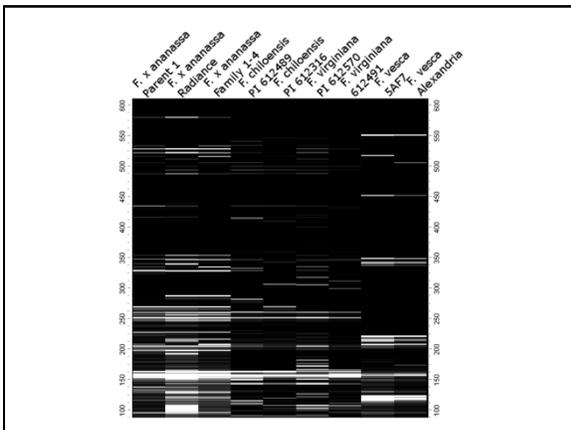


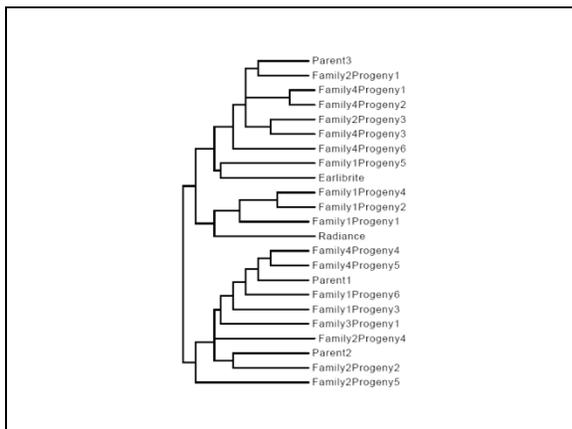
Part 1

Application of Genomics to
Fingerprinting for Clone
Identification









Applications

- For sorting out mixups in grower fields, breeding nursery, repository
- Across highly related or diverse germplasm, across species, across ploidy levels
- For IP protection
- For diversity analyses

Part 2

Application of Genomics to Candidate Gene ID and Marker Development

Chambers et al. BMC Genomics 2014, 15:217
<http://www.biomedcentral.com/1471-2164/15/217>



RESEARCH ARTICLE **Open Access**

Identification of a strawberry flavor gene candidate using an integrated genetic-genomic-analytical chemistry approach

Alan H Chambers¹, Jeremy Pillet¹, Anne Plotto², Jirhe Bai², Vance M Whitaker³ and Kevin M Folta^{1,4*}

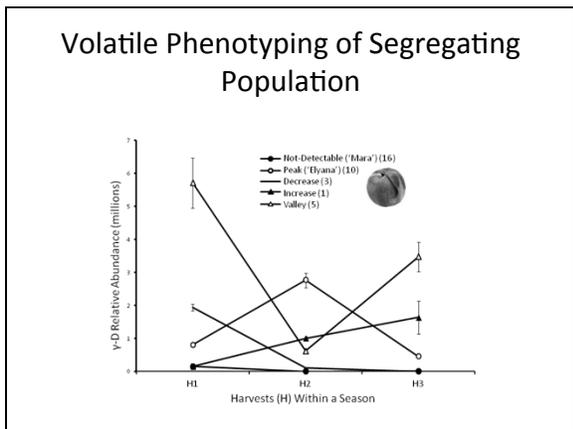
Transcriptome Sorting Approach

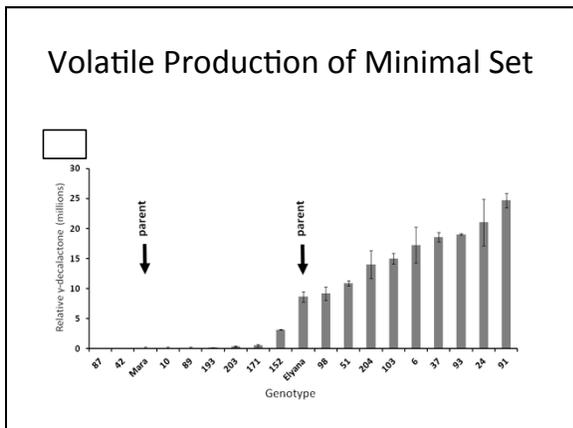
1. Use GC/MS to identify presence/absence of fruit volatiles in two cultivars

	
Volatile A Volatile B	present (+) not detected
	not detected(-) present

Transcript Validation

<p>Accumulation with ripening</p>  <p>volatile candidate</p>  <p>PASS!</p>	<p>Presence/absence with environment</p>  <p>+ - - + - -</p> <p>+ - - + - -</p> <p>PASS!</p>	<p>Presence/absence in other cultivars</p>  <p>- - - + - -</p> <p>- - - + - -</p> <p>PASS!</p>
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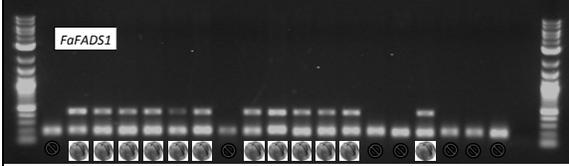
A Single Candidate

Reducing octoploid complexity – bars shown to scale

- ~34,000 Predicted genes in *F. vesca* genome
- ~17,000 Genes with transcript evidence
- ~2,200 Genes differentially expressed between parents
- 1 Gene differentially expressed between phenotypic groups
- 1 Gene validated using qRT-PCR
- 1 Gene validated using molecular marker

- FaFADS1 – putative fatty acid desaturase
- Functional allele absent in non-producers (deletion?)
- Primers designed in genic region for functional marker

DNA Diagnostic Test for GD



Transcriptome Sorting Summary

- Rapid identification of a candidate gene for GD production
- Validation using transcript abundance in fruit ripening and environmental series
- Robust gene-based marker works across breeding germplasm, cultivars and wild species
- Can re-sort RNAseq data using barcodes for other volatiles
- Limitation: works best with presence/absence phenotypes and single dominant genes

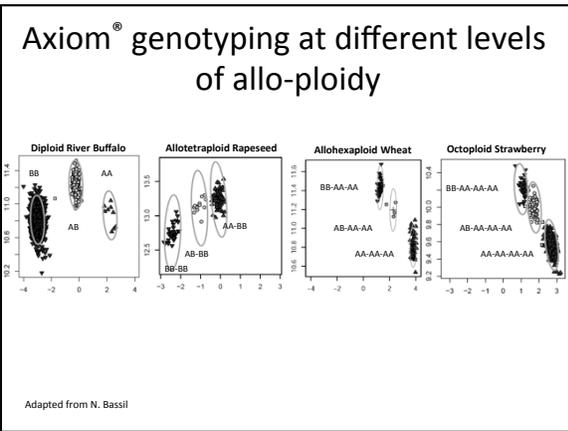
Part 3

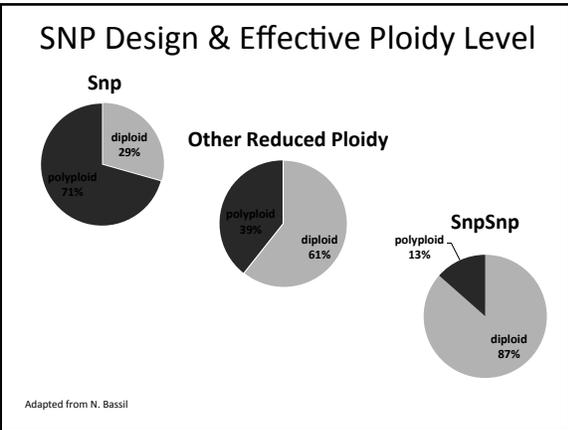
Application of Genomics to SNP Genotyping and QTL Discovery

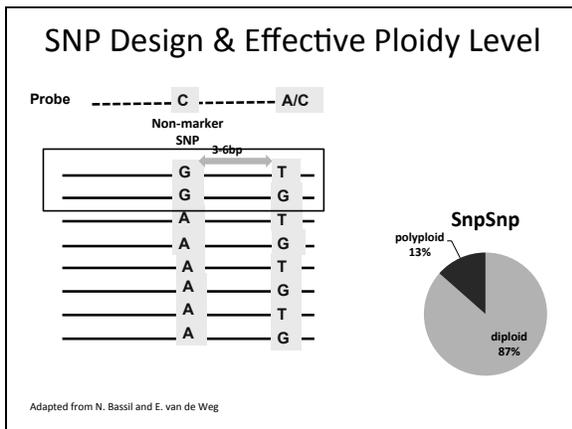
RosBREED
Enabling marker-assisted breeding in Rosaceae

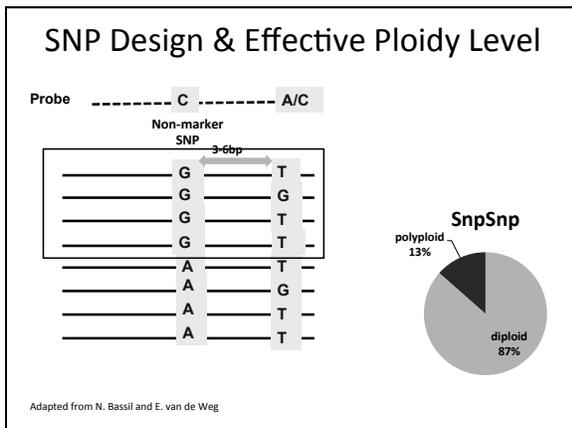
IStraw90®
A High Throughput Genotyping Chip for Strawberry

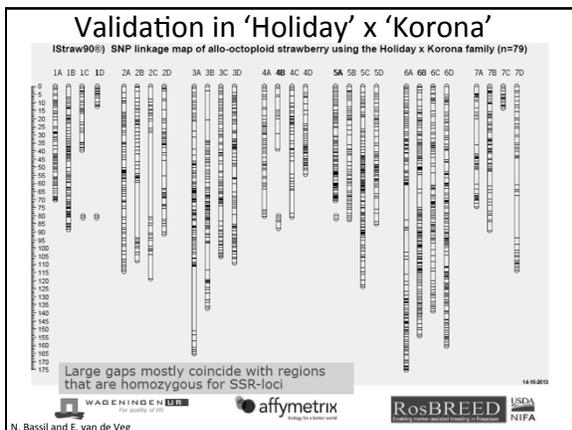
- Released October, 2013
- 90K SNP Array
- Focus on "ploidy reduction"
- SNP detection – deep sequencing of 9 octoploid genotypes (important founders)

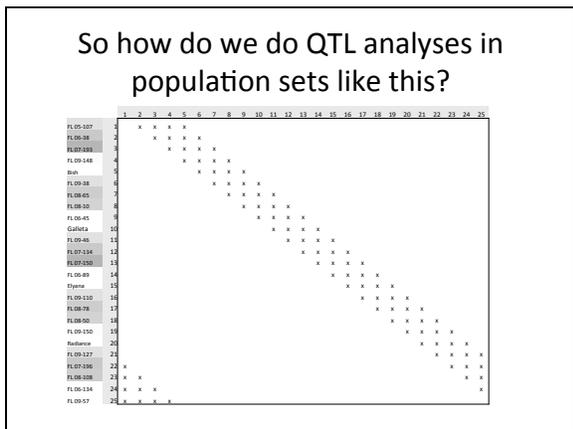


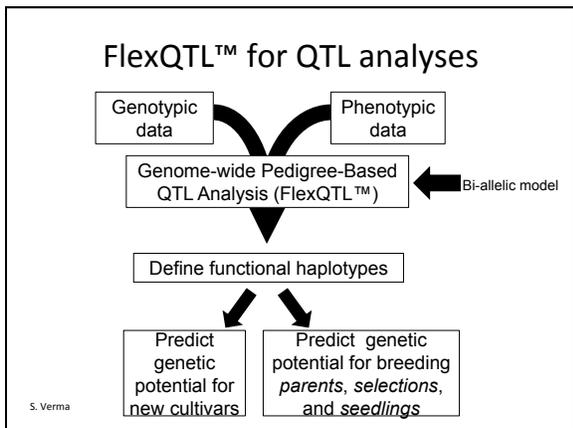


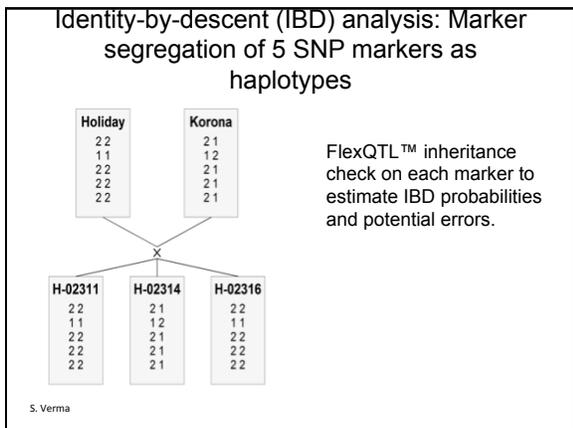


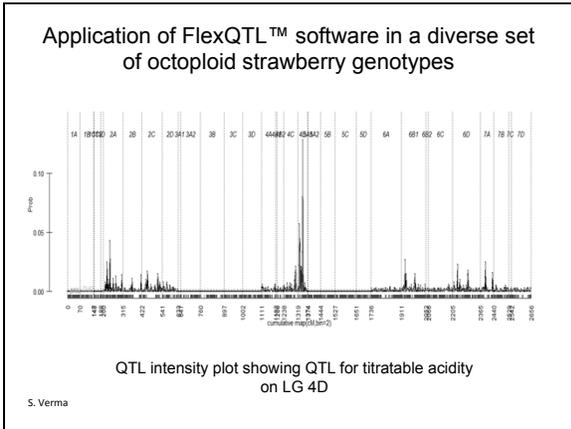


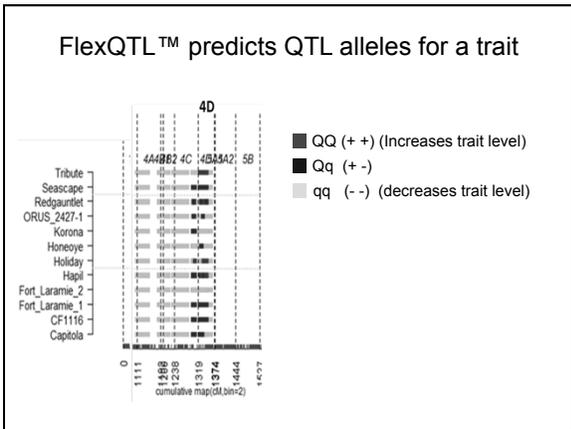












- SNP Array Summary**
- SNP design key to reducing ploidy
 - 21,000 high resolution SNPs show diploid clustering
 - 6,000 initially mapped in H x K
 - Segregation according to pedigree in broad germplasm
 - Initial QTL analyses performed using FlexQTL™

Webinar Summary

- New approaches and tools allowing applications of genomics to breeding in strawberry
- Fingerprinting, MASS, MAPS
- Next Steps
 - Uncover genomic architecture of many important traits
 - Reduce cost of whole-genome SNP scans
 - Test genomic selection methodologies