

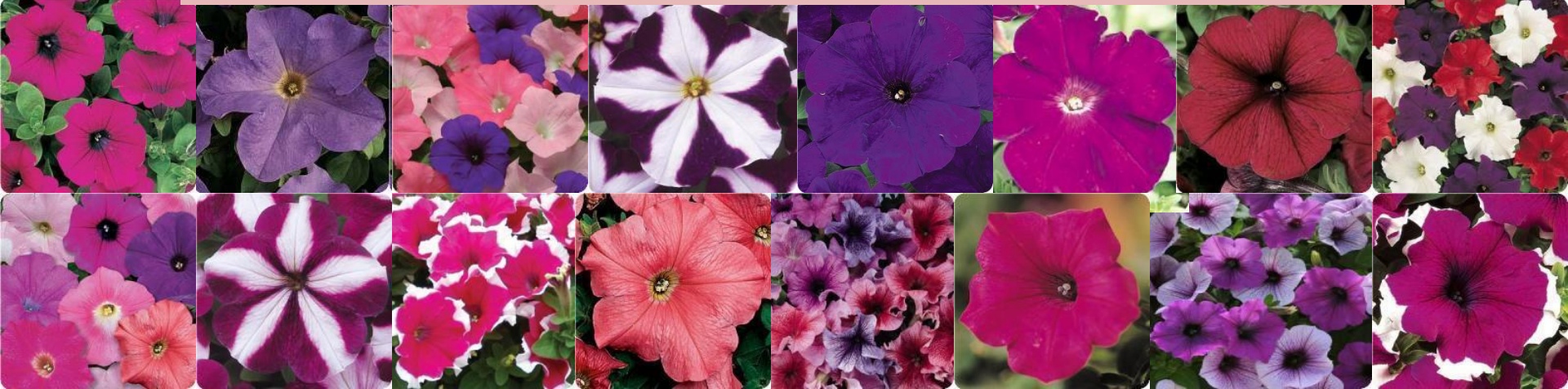


The Petunia Genome Project

**Sequencing and Comparison of the Genomes
of *Petunia inflata* & *Petunia axillaris***

Thomas Sims, Northern Illinois University

The Petunia Platform & BGI



The Petunia Platform (www.petuniaplatform.net)



The Petunia Platform

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12th World Petunia Days 2012

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Project Goals

- Determine genomic DNA sequence of two *Petunia* genomes:
 - *Petunia axillaris*
 - *Petunia inflata*
 - Chosen because these are the progenitors to *Petunia hybrida* (commercial garden petunia)
- Annotate and compare genomic sequences
 - To each other
 - With other species in the Solanaceae
 - With other sequenced species
- Release data to the public via SGN (Solanum Genomics Network)

Why Petunia?

- Well characterized
- Known genetics, phylogeny
- Large flowers, easily pollinated
- Easily transformed
- Model species for biochemical investigations
- Genomic tools already available

P. axillaris (SC)



P. integrifolia (SI)



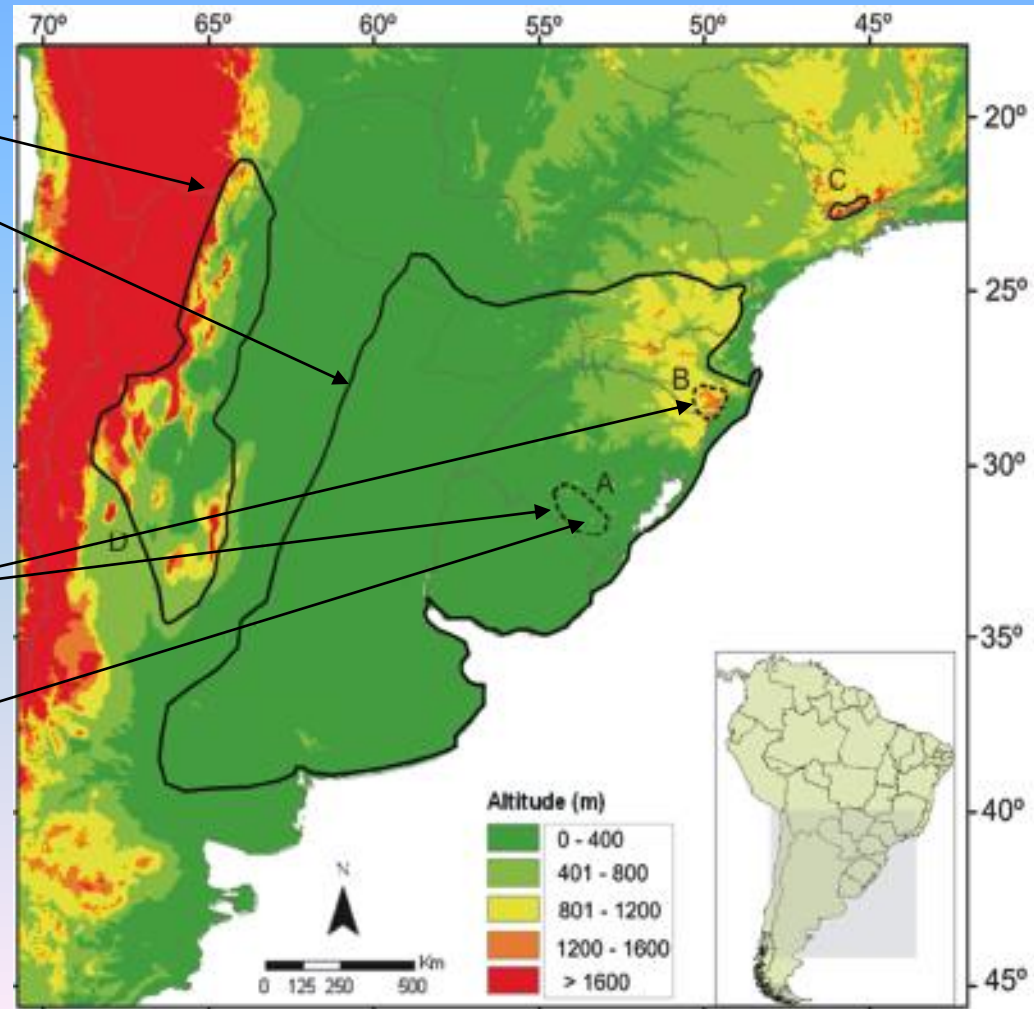
Petunia hybrida

Native to South America (Brazil) numerous sub-habitats

Species distribution

Centers of species diversity

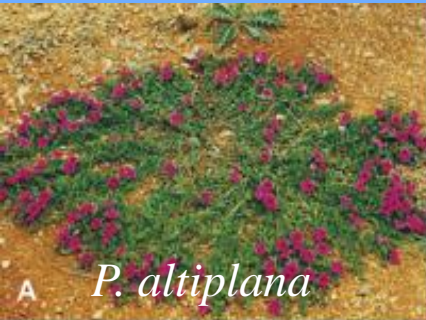
Serra do Sudeste (*P. axillaris* &
P. integrifolia)



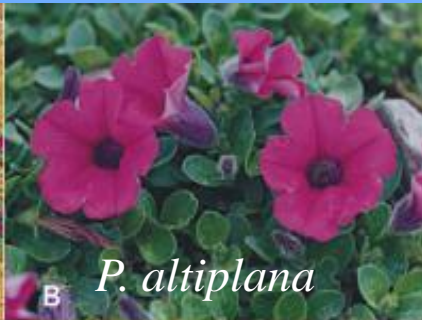
Petunia species

JR Stehmann et al., The Genus *Petunia*, 2009

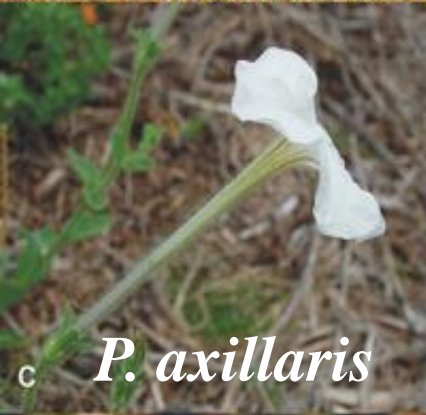
14 species; $2n = 14$



A *P. altiplana*



B *P. altiplana*



C *P. axillaris*



D *P. bajeensis*



E *P. bonjardinensis*



F *P. exserta*



A *P. integrifolia*



B *P. mantiqueirensis*



C *P. scheideana*



D *P. saxicola*



E *P. reitzii*



F *P. secreta*

Petunia as a Model Organism

- Pigmentation, synthesis & regulation
- Volatiles, production & regulation
- Pollination syndromes
- Reproduction and self-incompatibility
- Floral induction and senescence
- Transcription factors in floral organ development
- Vegetative branching
- Arbuscular mycorrhizal symbiosis

#1 Floriculture Crop in overall sales

USDA Wholesale Value 2010 (\$ millions)

Crop	Flats	Baskets	Total
Petunia	65.9	30.21	96.11
Pansies	66.7	4.95	71.65
New Guinea Impatiens	3.1	18.48	21.58
Marigolds	36.2	0.3	36.5
Impatiens	70.6	13.43	84.03
Geraniums	9	28.88	37.88
Begonias	34.2	9.56	43.76



Current Genomic Resources

- Genetic maps
 - *P. axillaris* x *P. inflata* BC₁ mapping population
- Numerous mutants
- BAC libraries
- Insertional mutant libraries (*dTph1*)
- EST and RNA-Seq databases
- Related species in Solanaceae sequenced

Timeline

- Genomic DNA for *P. axillaris*, *P. inflata* sterile, homozygous lines (done)
- BGI has carried out Illumina sequencing of the separate genomes (done)
- Assembly by BGI, BTI-Cornell (in progress)
- Annotation by BTI-Cornell, Northern Illinois University, University of Verona (starting)
- Publication & Release later in 2012
- Sequencing of other spp. (e.g. *P. exserta*)?

Assembly & Annotation

- Assembly
 - SOAPdenovo
 - ABySS, possibly ALLPATHS
- Annotation
 - MAKER

Sequencing Progress

- *Petunia inflata*
 - Genome sequenced, Assembled by BGI. Reassembly in-process by BTI-Cornell
- *Petunia axillaris*
 - Genome sequences, Assembly in-process by BTI-Cornell
- RNA-Seq
 - RNA-Seq from *P. inflata* (fertilized ovary, floral bud, inflorescence, callus, seedling), University of Verona

Assembly Statistics

(Aureliano Bombarely Gomez, BTI-Cornell)

Parameters				Scaffolds				
Species	Group	k-mer	Total (Gb)	Longest	N90 length	N90 number	N50 length	N50 number
P. inflata	BGI-HK	17	1.32	786641	127	388342	79287	4341
P. inflata	BTI	31	0.52	46180	100	2579079	147	790123
P. inflata	BTI	47	1.06	529569	121	1853247	11360	18764
P. inflata	BTI	63	1.39	741287	127	2133222	20769	13883
P. axillaris	BTI	31	0.48	5931	102	2256321	158	686259
P. axillaris	BTI	47	1.07	769100	126	1450576	19305	12624
P. axillaris	BTI	63	1.34	1055557	127	1765676	35416	9015

NIU



Sims



Johns

Radboud Univ
Nijmegen



Gerats

VU Amsterdam



Quattrocchio

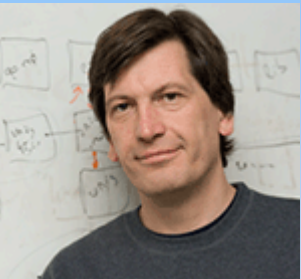


Univ. Verona



Delledonne

Boyce-
Thompson



Mueller



Gomez



Pezzotti