

# Diversity analyses and genetic mapping in seashore paspalum

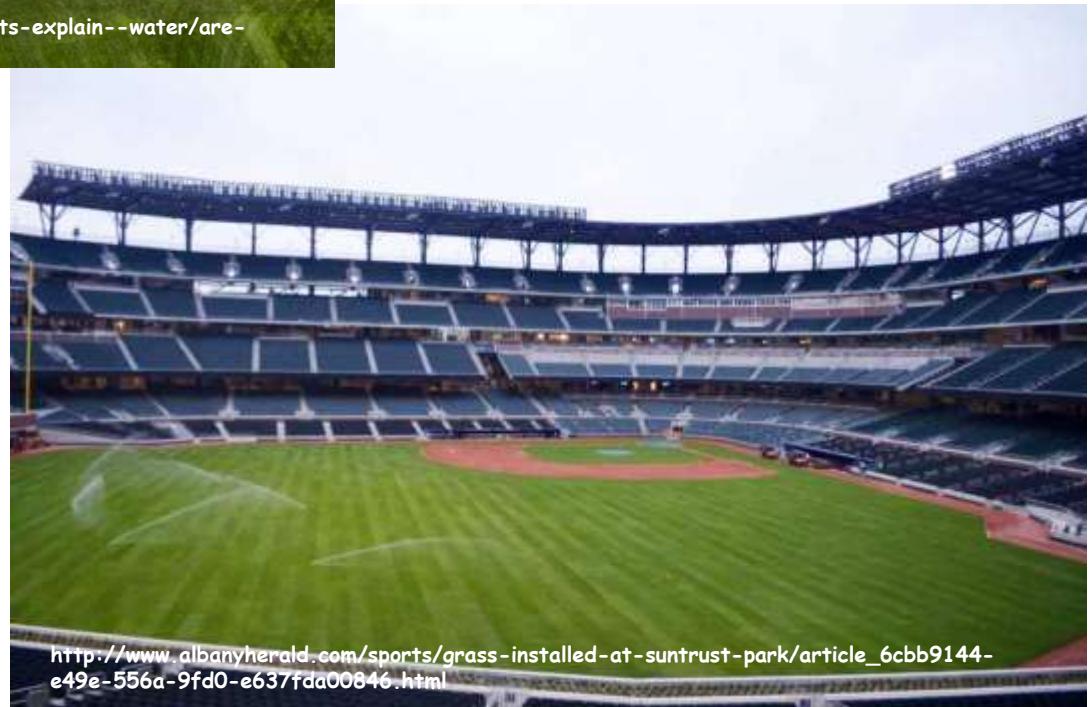
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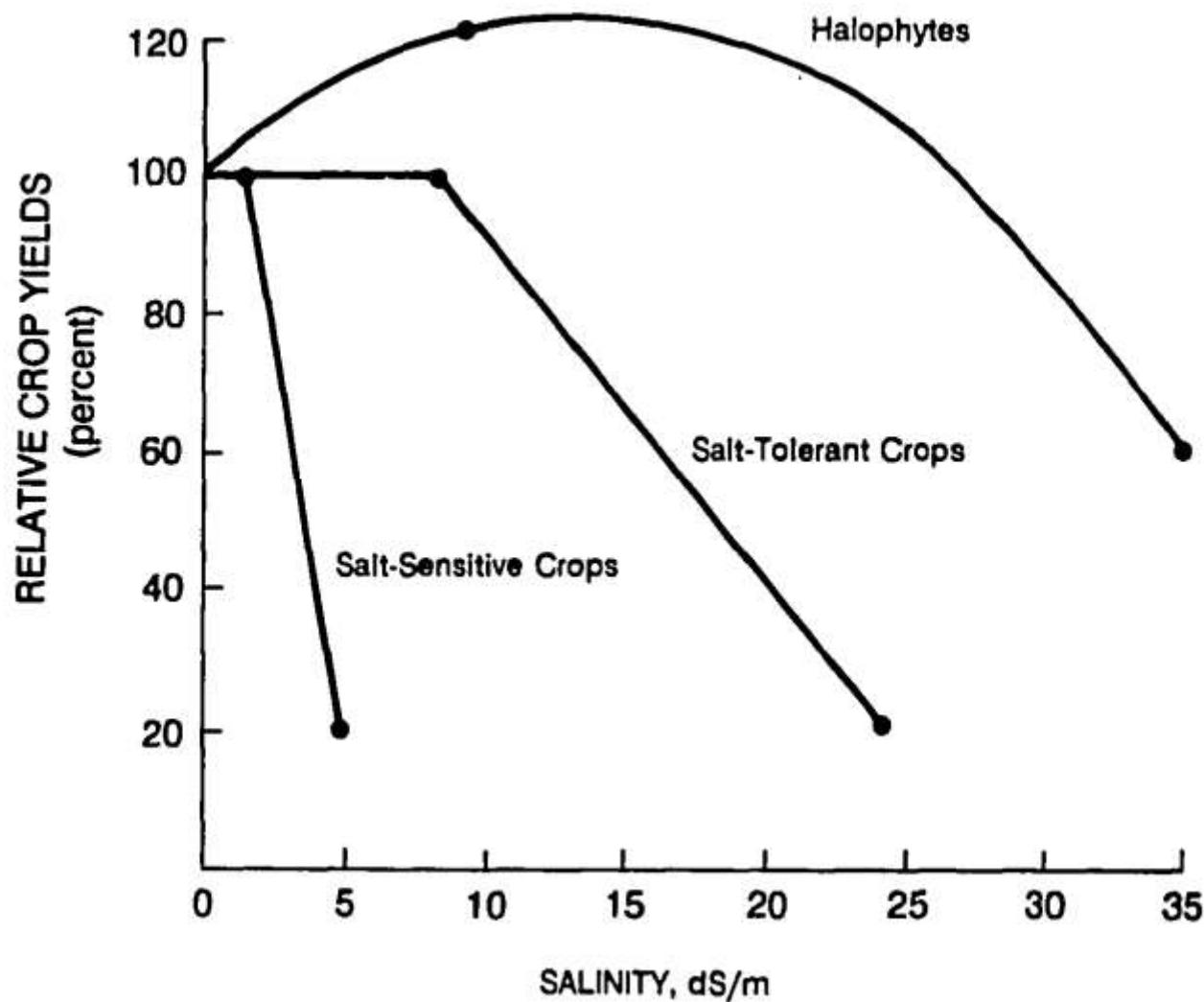
<http://www.usga.org/course-care/water-resource-center/our-experts-explain--water/are-there-grasses-that-can-be-irrigated-with-sea-water.html>

## Seashore paspalum, a sustainable turfgrass



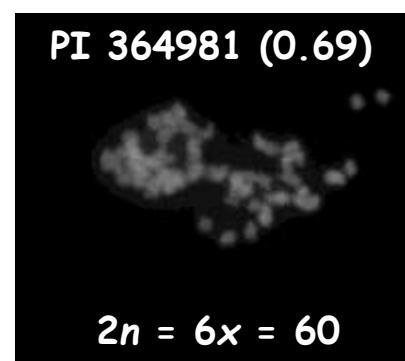
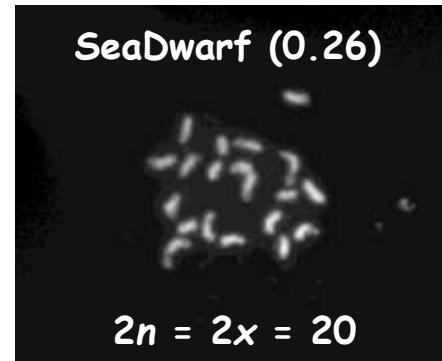
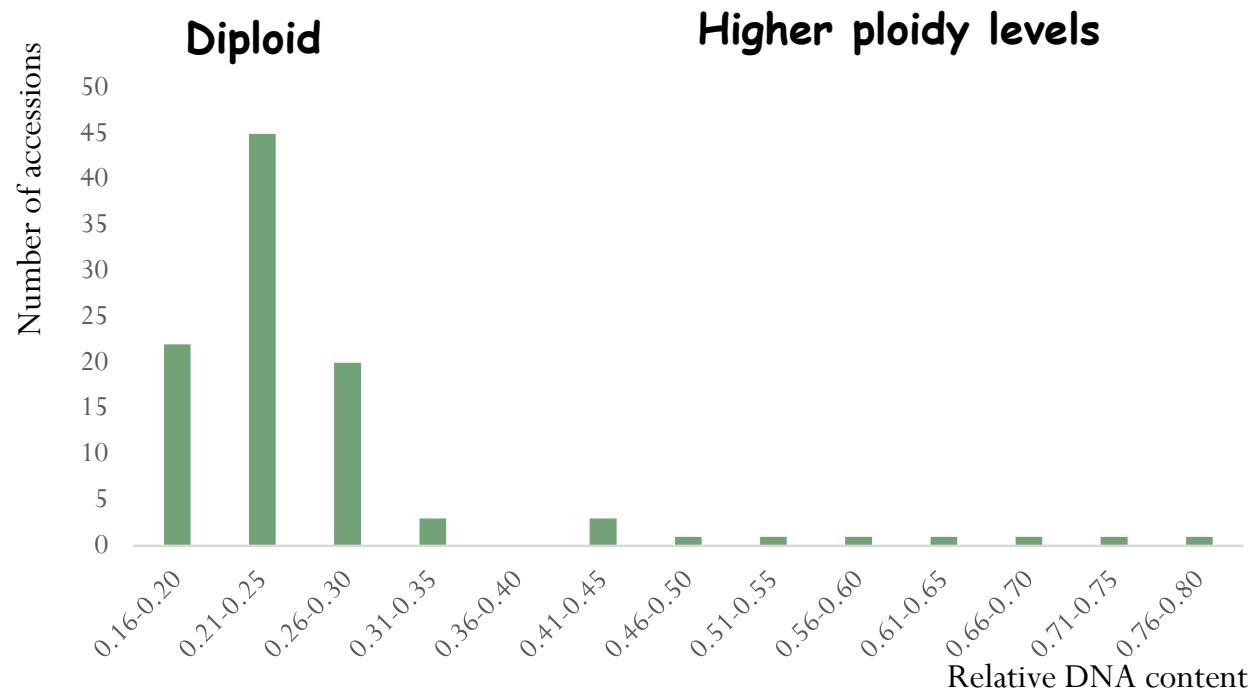
[http://www.albanyherald.com/sports/grass-installed-at-suntrust-park/article\\_6cbb9144-e49e-556a-9fd0-e637fda00846.html](http://www.albanyherald.com/sports/grass-installed-at-suntrust-park/article_6cbb9144-e49e-556a-9fd0-e637fda00846.html)

## Growth response to salinity

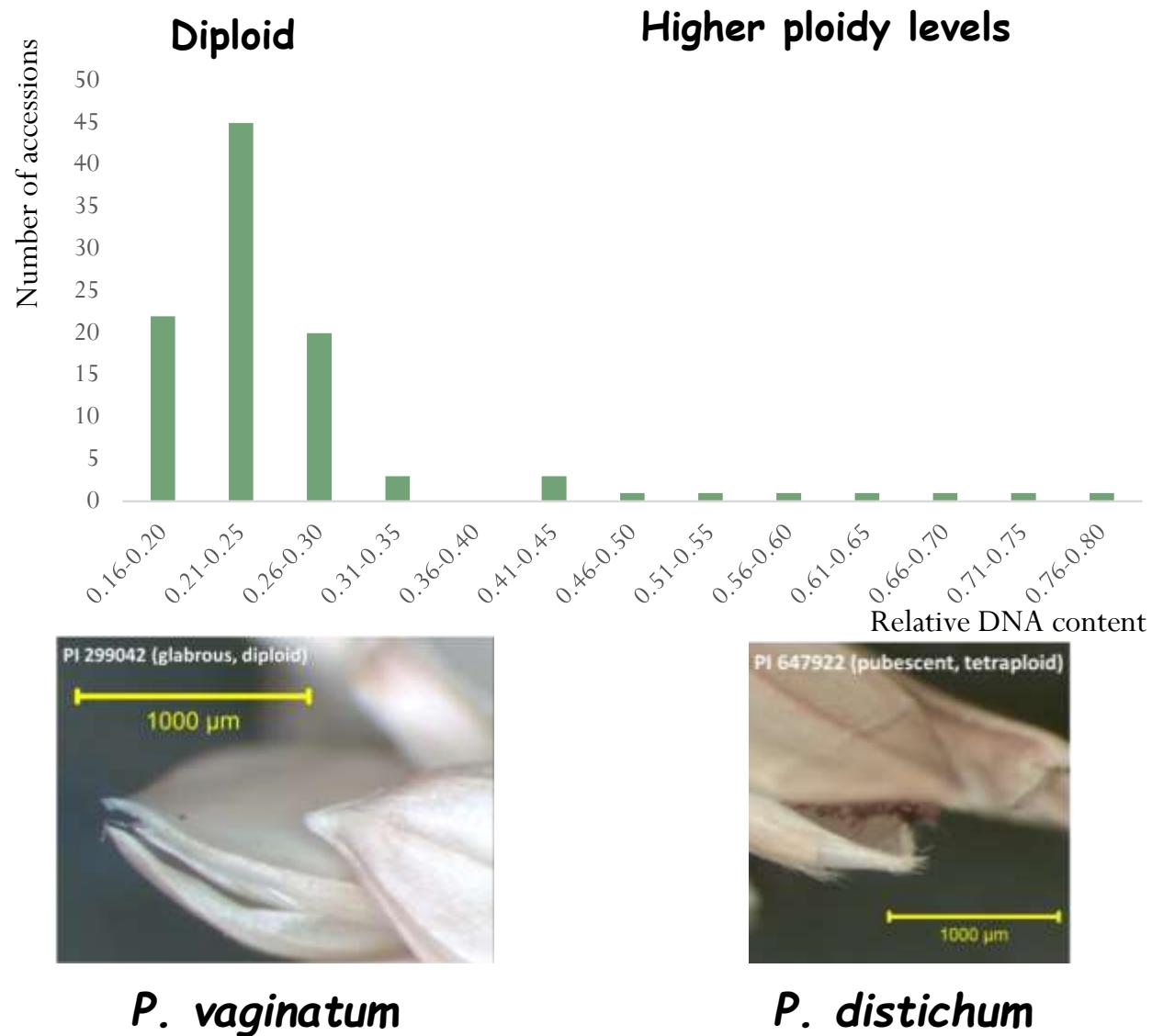




# Most *P. vaginatum* accessions are diploid



# Most *P. vaginatum* accessions are diploid



*P. vaginatum* and *P. distichum* are not completely separated by ploidy level

## Diploids:

Glabrous → *P. vaginatum*

Except: Two diploid pubescent accessions

## Polyploids:

Pubescent → *P. distichum*

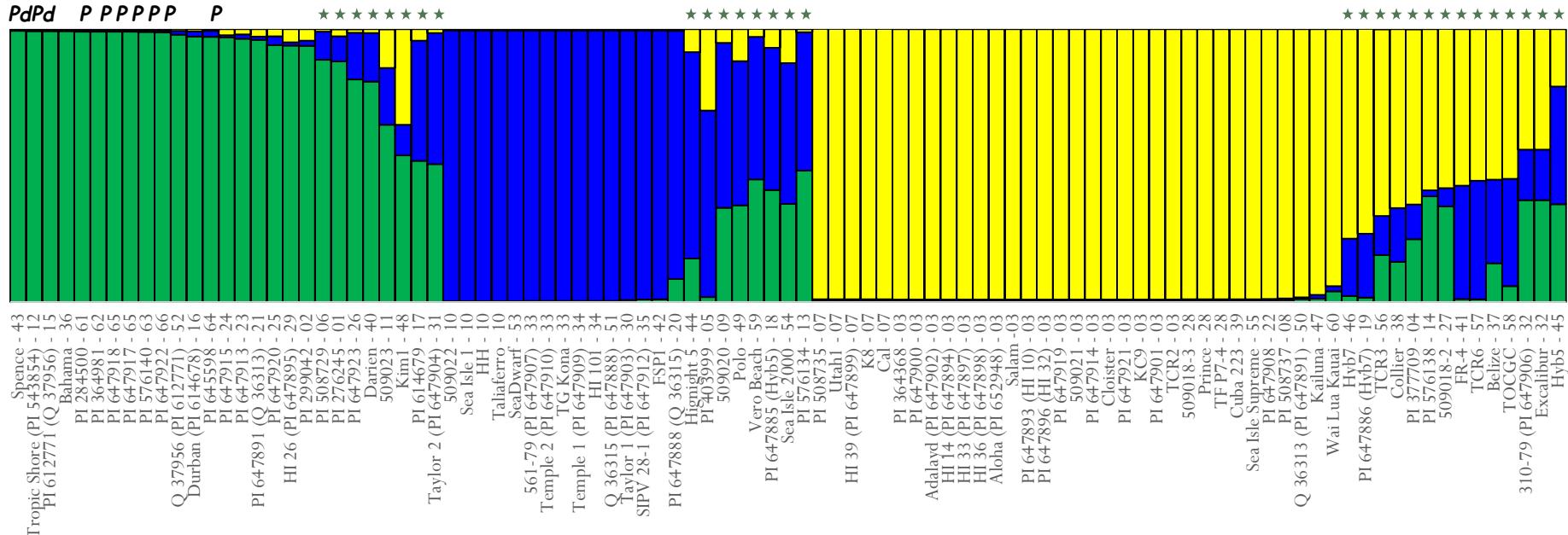
Except: three triploid glabrous accessions

Are *P. vaginatum* and *P. distichum* truly different species?

# Paspalum germplasm groups in three subpopulations

- 43 SSRs developed
  - 97 accessions
  - 66 unique multilocus genotypes

\* = Admixed  
P = Polyploid  
*Pd* = *P. distichum*

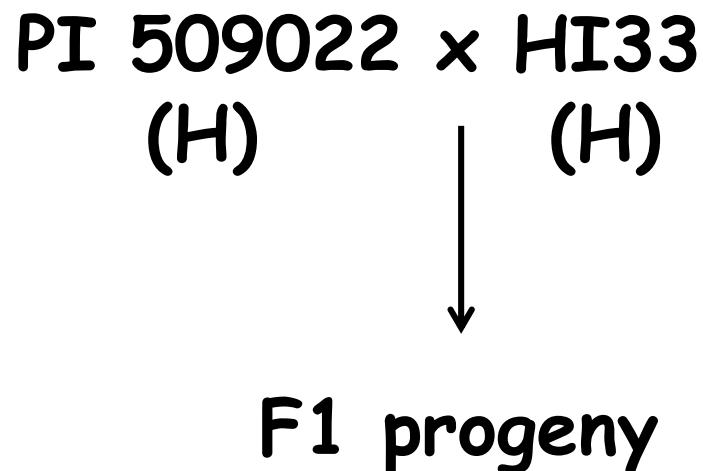


# No geographic patterning

A genetic map was constructed in a cross between two divergent parents

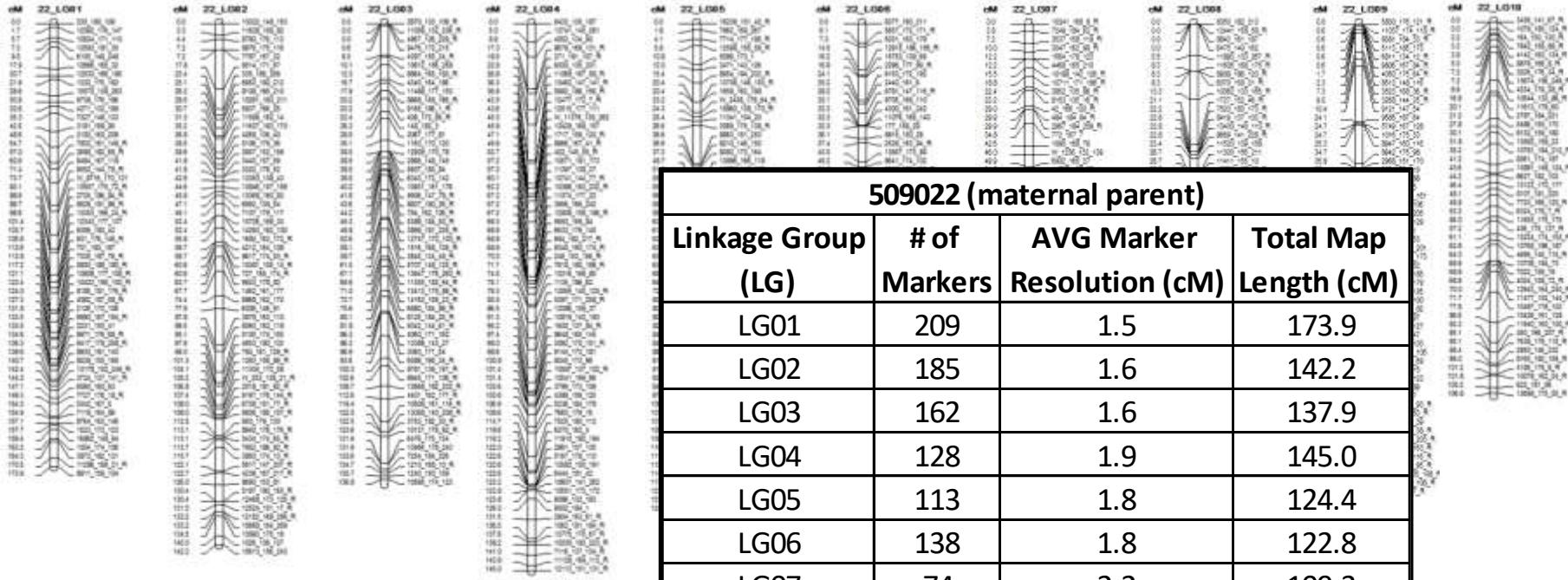
Origin: Argentina (inland)  
Subpopulation: Blue  
Salt tolerance: Intermediate

Origin: GA (coast)  
Subpopulation: Yellow  
Salt tolerance: High



Map F1 progeny using genotyping-by-sequencing

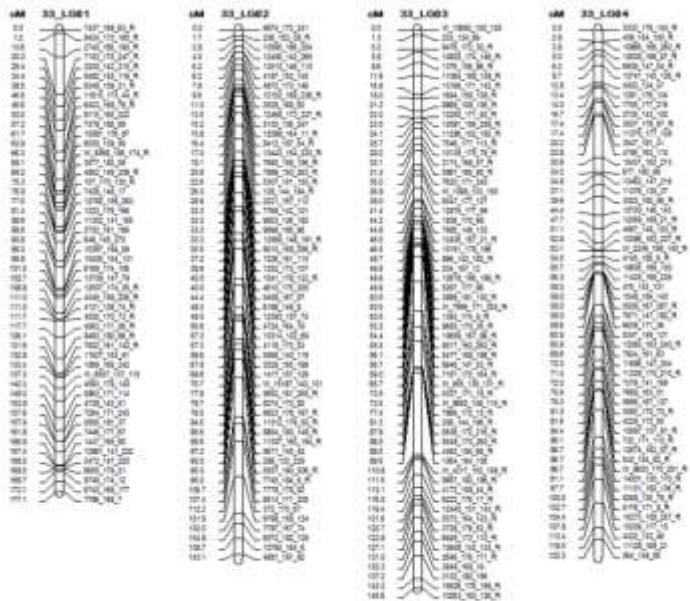
# PI 509022 genetic map with 1262 SNP markers



**509022 (maternal parent)**

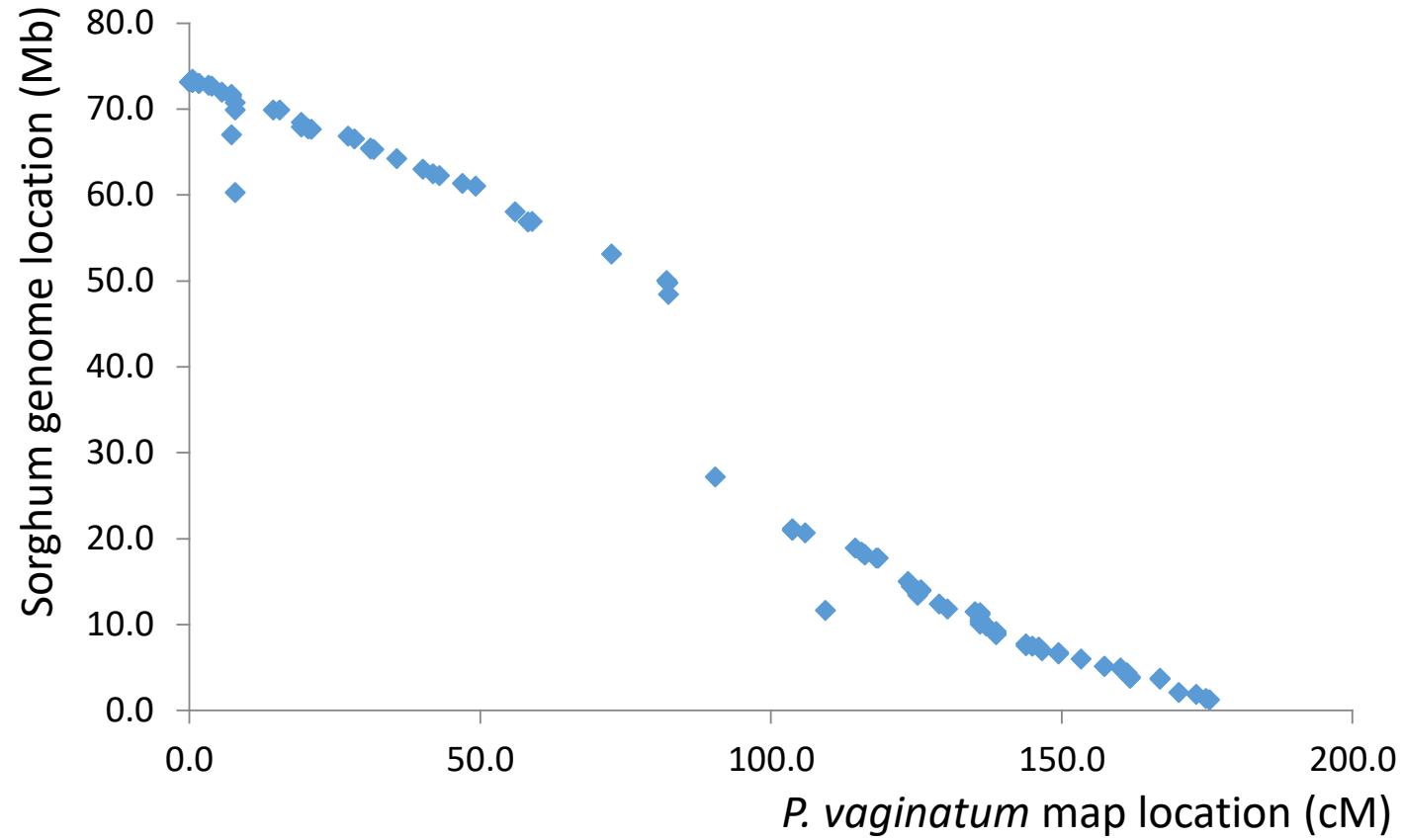
| Linkage Group<br>(LG) | # of<br>Markers | AVG Marker<br>Resolution (cM) | Total Map<br>Length (cM) |
|-----------------------|-----------------|-------------------------------|--------------------------|
| LG01                  | 209             | 1.5                           | 173.9                    |
| LG02                  | 185             | 1.6                           | 142.2                    |
| LG03                  | 162             | 1.6                           | 137.9                    |
| LG04                  | 128             | 1.9                           | 145.0                    |
| LG05                  | 113             | 1.8                           | 124.4                    |
| LG06                  | 138             | 1.8                           | 122.8                    |
| LG07                  | 74              | 2.2                           | 109.3                    |
| LG08                  | 56              | 2.4                           | 83.3                     |
| LG09                  | 109             | 1.9                           | 113.8                    |
| LG10                  | 88              | 1.9                           | 107.4                    |
| <b>TOTAL</b>          | <b>1262</b>     | <b>1.9</b>                    | <b>1260.0</b>            |

# HI33 genetic map with 1092 SNP markers



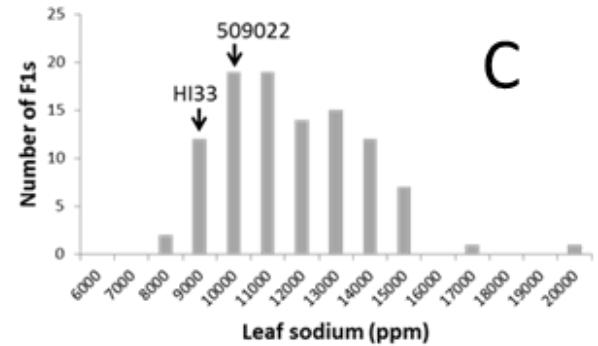
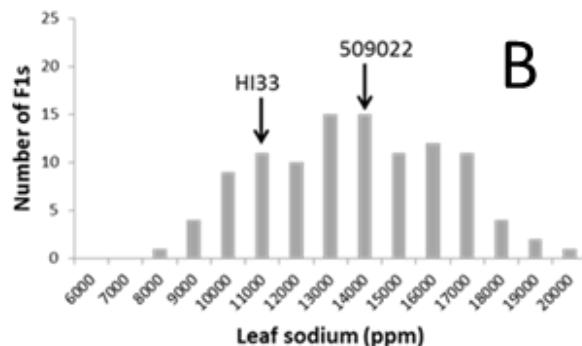
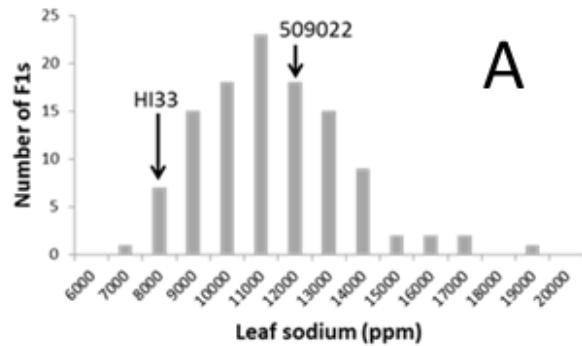
| HI33 (paternal parent) |              |                            |                       |
|------------------------|--------------|----------------------------|-----------------------|
| Linkage Group (LG)     | # of Markers | AVG Marker Resolution (cM) | Total Map Length (cM) |
| LG01                   | 197          | 1.6                        | 177.1                 |
| LG02                   | 112          | 2.0                        | 144.4                 |
| LG03                   | 119          | 1.9                        | 145.6                 |
| LG04                   | 112          | 1.8                        | 126.5                 |
| LG05                   | 104          | 2.3                        | 178.7                 |
| LG06                   | 80           | 1.9                        | 113.2                 |
| LG07                   | 75           | 2.1                        | 99.4                  |
| LG08                   | 68           | 2.0                        | 96.7                  |
| LG09                   | 100          | 2.1                        | 135.2                 |
| LG10                   | 125          | 1.7                        | 117.6                 |
| <b>TOTAL</b>           | <b>1092</b>  | <b>1.9</b>                 | <b>1334.4</b>         |

# The *P. vaginatum* genome is highly colinear with the sorghum genome

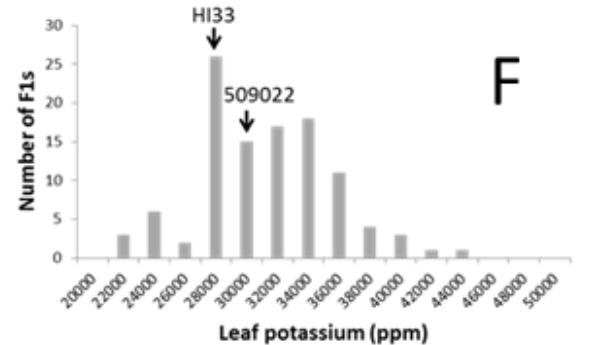
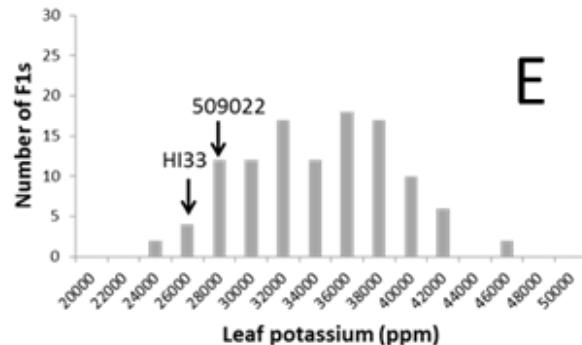
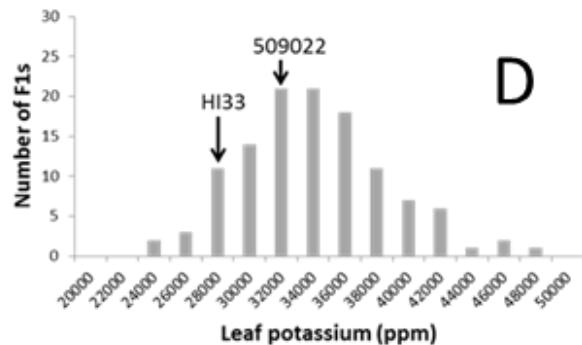


# Phenotyping the mapping population for salt tolerance

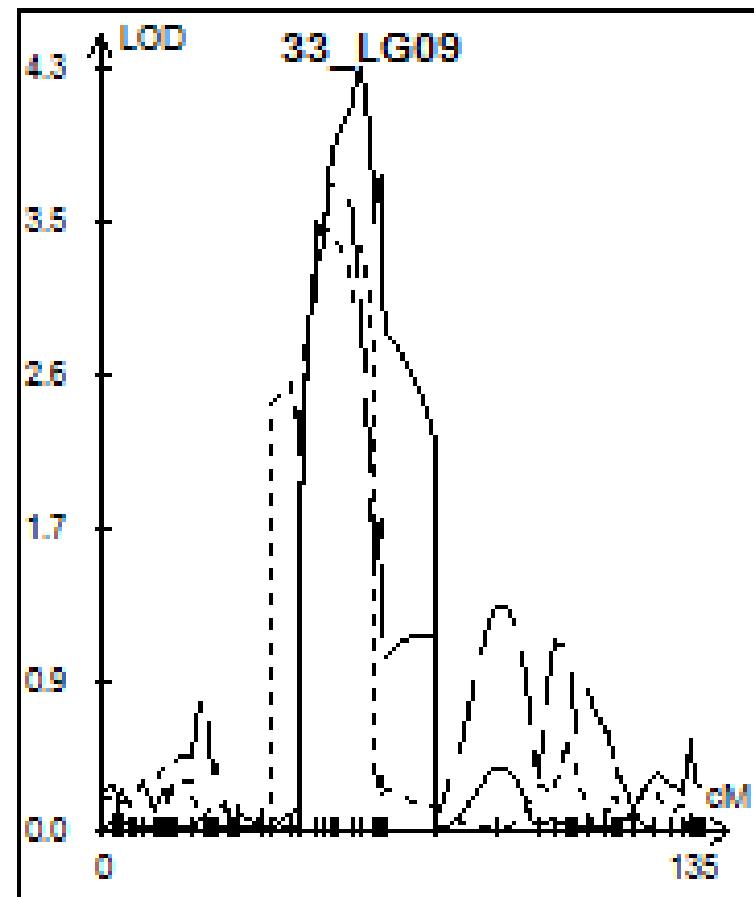
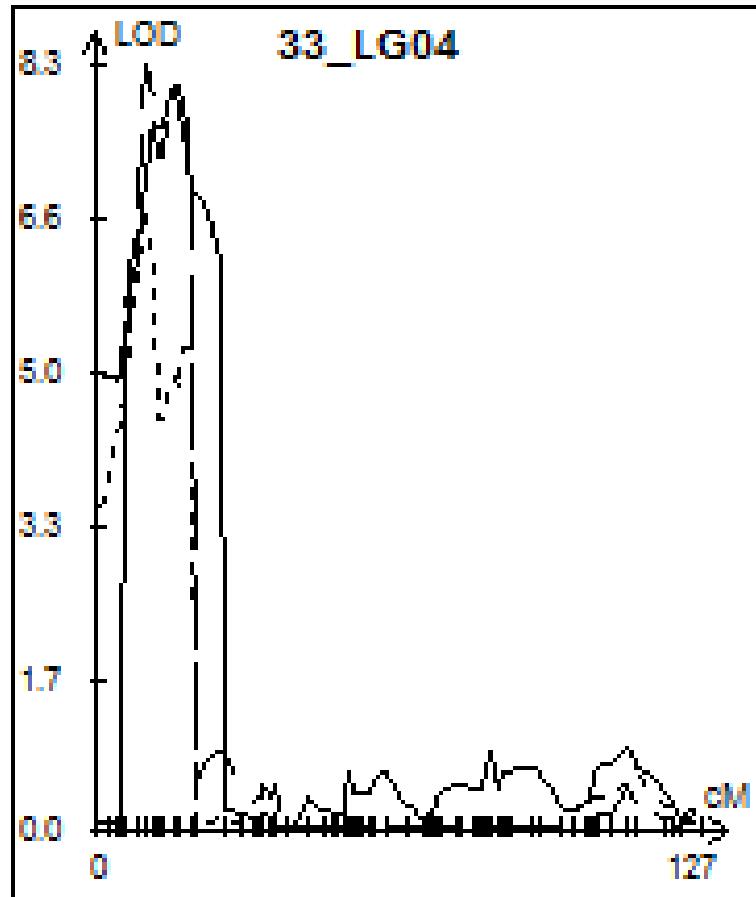
## Leaf sodium



## Leaf potassium



# QTL for K and Na are found on LG4 and LG9, respectively, in HI33



Explains ~20% of the variation

Explains ~12% of the variation

## Take-home messages

- ❖ Three genetic subpopulations; two 'turfy'; one mixed
- ❖ Genetic subpopulations do not correspond to geographic patterns
- ❖ Unclear whether *P. vaginatum* and *P. distichum* are different species
- ❖ Genome size of *P. vaginatum*: ~600 Mb
- ❖ Genetic maps of 1000+ SNP markers
- ❖ QTL for K and Na identified on LGs 4 and 9, respectively

# Acknowledgements



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# *P. vaginatum* likely has a sodium exclusion mechanism

