Kochia scoparia: Basic Research in Biology and Ecology

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Kochia Genome 1.0

The Kochia Genome 1.0 is published with the manuscript in Genome Biology and Evolution:

- NCBI: SNQN00000000

Sup. Table 2. A statistical summary of the kochia genome assembly.

Metric	Count	Percentage
Number of scaffolds	19,671	
Total size of scaffolds (bp)	711,356,803	
Longest scaffold (bp)	770,912	
Shortest scaffold (bp)	897	
Scaffold length/genome size		83.70%
Number of scaffolds > 1K nt	19,594	99.6%
Number of scaffolds > 10K nt	14,701	74.7%
Number of scaffolds > 100K nt	1,286	6.5%
Mean scaffold size (bp)	36,163	
N50 scaffold length (bp)	61,675	
%A		28.8%
%C		16.4%
%G		16.4%
%T		28.5%
%N		9.5%
Num. of contigs	61,353	
Num. of contigs in scaffolds	54,776	
Total size of contigs	643,547,114	

ACCEPTED MANUSCRIPT

The Draft Genome of *Kochia scoparia* and the Mechanism of Glyphosate Resistance via Transposon-Mediated *EPSPS* Tandem Gene Duplication

Eric L Patterson, Christopher A Saski, Daniel B Sloan, Patrick J Tranel, Philip Westra, Todd A Gaines

Genome Biology and Evolution, evz198, https://doi.org/10.1093/gbe/evz198

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- Bassia 1 *Click on organism name to get more information.*
  - Bassia angustifolia
  - Bassia arabica
  - Bassia diffusa
  - Bassia dinteri
  - Bassia eriantha
  - Bassia eriophora
  - Bassia hyssopifolia
  - Bassia indica
  - Bassia laniflora
  - Bassia lasiantha
  - Bassia littorea
  - Bassia muricata
  - Bassia odontoptera
  - Bassia pilosa
  - Bassia prostrata
  - Bassia salsoloides
  - Bassia scoparia 1
  - Bassia stellaris
  - Bassia tianschanica
  - Bassia tomentosa
  - Bassia villosissima
  - Bassia sp. Palmer 50

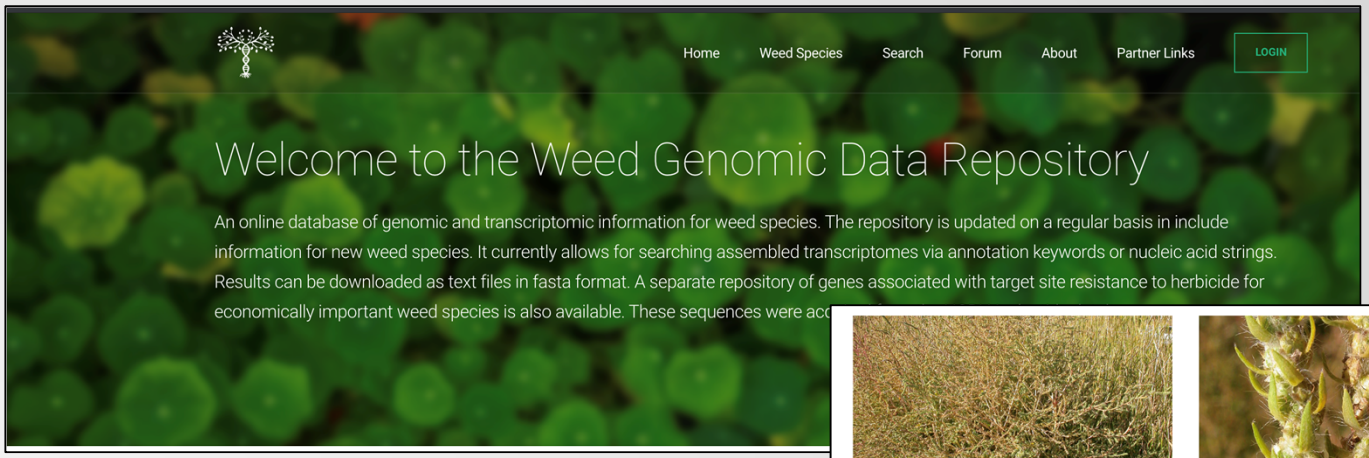
Kochia Genome 2.0

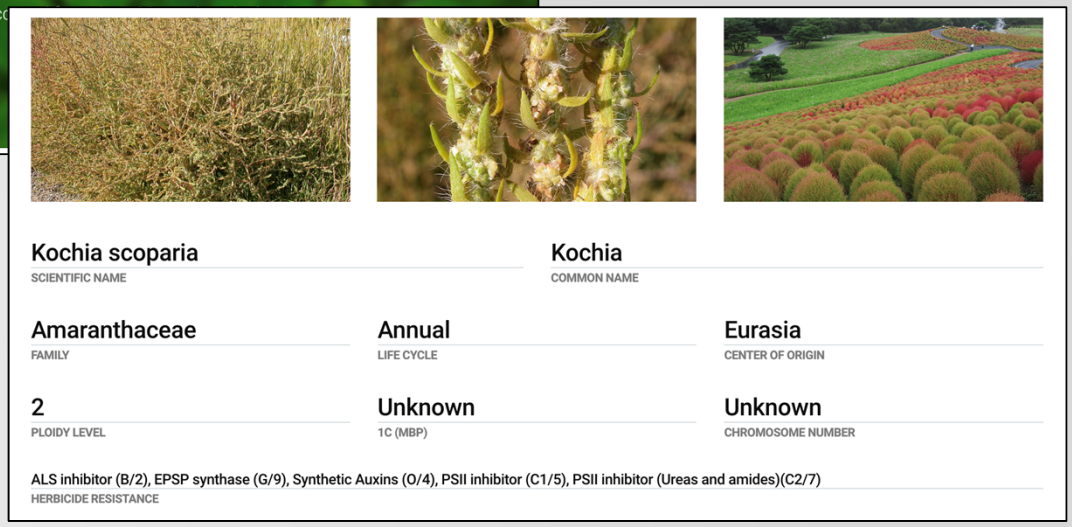
Number of scaffolds	2802	
Total size of scaffolds	1387336952	
Longest scaffold	39592204	
Shortest scaffold	5303	
Number of scaffolds > 1K nt	2802	100.0%
Number of scaffolds > 10K nt	2790	99.6%
Number of scaffolds > 100K nt	838	29.9%
Number of scaffolds > 1M nt	261	9.3%
Number of scaffolds > 10M nt	15	0.5%
Mean scaffold size	495124	
Median scaffold size	54736	
N50 scaffold length	4069025	
L50 scaffold count	88	
scaffold %A	31.28	
scaffold %C	18.69	
scaffold %G	18.69	
scaffold %T	31.25	
scaffold %N	0.09	
scaffold %non-ACGTN	0.00	
Number of scaffold non-ACGTN nt	0	

* We are now generating an optical map for further scaffolding and to increase continuity.

The Kochia Genome

Deposited soon with the IWGC and Weedgenomics.com





The Future of the Kochia Genome

Understanding the molecular biology of weedy traits….

1. Chromosome or near chromosome level scaffolding will allow techniques such as GWAS and QTL-seq to be implemented for for gene discovery
   - Herbicide Resistance
   - Other abiotic stress (namely cold, salt, and drought)
2. Genome resequencing to ask questions about genome dynamics, genetic diversity, novel variations, etc. (pan-genome?)
3. Cross species comparisons to other chenopod weeds (Lambsquarter and Russian thistle)
4. Better population genetics and modeling
   - Tracking movement of populations and quantifying gene flow
   - Identify true biotypes/locally adapted populations

Kochia Seedling Emergence and Seed Bank

Weed Science 2017 65:614–625

Kochia (*Kochia scoparia*) Emergence Profiles and Seed Persistence across the Central Great Plains

J. Anita Dille, Phillip W. Stahlman, Juan Du, Patrick W. Geier, Jarrett D. Riffel, Randall S. Currie, Robert G. Wilson, Gustavo M. Sbatella, Philip Westra, Andrew R. Kniss, Michael J. Moechnig, and Richard M. Cole*

Major Findings:

1. >95% of seed dies after 2 years.
2. Seed viability >80% after they are buried for 6 months (oct-march), <5% at 1 year
3. Burial (depth) did not change viability; however, deeper seeds would not be able to emerge
4. High seedling emergence in the (Early) spring emphasizes the importance of pre-emergent control

Seedling Emergence Timing

Weed Science 2018 66:25–35

Emergence Dynamics of Kochia (*Kochia scoparia*) Populations from the U.S. Great Plains: A Multi-Site-Year Study

Vipan Kumar, Prashant Jha, J. Anita Dille, and Phillip W. Stahlman*

Major Findings:

1. Emergence windows vary greatly depending on biotype and environment.
    1. Understanding the emergence pattern of your local kochia population can help make management recommendations or predict optimal application timing

Modeling Kochia Population in Response to Control Options

Modeling Population Dynamics of Kochia (*Bassia scoparia*) in Response to Diverse Weed Control Options

O. Adewale Osipitan[1], J. Anita Dille[2], Muthukumar V. Bagavathiannan[3] and Stevan Z. Knezevic[4]

Major Findings:

1. a diversified management program, including glyphosate, could provide excellent control of kochia, even if glyphosate resistance plants are present
    1. Diversity in control methods can even result in the loss of GR biotypes
2. The most successful scenario was a diverse control strategy that included:
    1. one or two preplant tillage operations
    2. A preplant or PRE application of herbicides with residual activities
    3. POST application of glyphosate
3. This strategy reduced seedling recruitment, survival, and seed production during the growing season,
    1. Huge negative impacts on long-term population growth and resistance risk in kochia.

Future Work in Kochia Ecology

1. More to do on kochia's life cycle:
   - How can we customize weed control methods for local biotypes
   - What new control methods can we develop for new stages in the lifecycle (how do we control the seedbank)
   - How is kochia different in rangeland versus cropland?

2. How is Kochia interacting with other ecological factors?
   - How does kochia interact with pathogens and insects?

Other ideas….

Understanding the evolution of resistance and informing management practices

Managing the evolution of herbicide resistance

Jeffrey A Evans,[a*] Patrick J Tranel,[b] Aaron G Hager,[b] Brian Schutte,[c] Chenxi Wu,[b] Laura A Chatham[b] and Adam S Davis[a]

1. The main determining factor for whether or not a particular grower has resistance is their management practices.
   - Bad practices lead to resistance evolution
   - Even if it did come from a neighboring field, good practices can usually control those *trans-plants* before they are a larger problem
2. Could we use a combination of field use data, population genetics, molecular biology, and other basic techniques to help inform growers about best practices?