Kochia scoparia: Basic Research in Biology and Ecology

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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.

<table>
<thead>
<tr>
<th>Metric</th>
<th>Count</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of scaffolds</td>
<td>19,671</td>
<td></td>
</tr>
<tr>
<td>Total size of scaffolds (bp)</td>
<td>711,356,803</td>
<td></td>
</tr>
<tr>
<td>Longest scaffold (bp)</td>
<td>770,912</td>
<td></td>
</tr>
<tr>
<td>Shortest scaffold (bp)</td>
<td>897</td>
<td></td>
</tr>
<tr>
<td>Scaffold length/genome size</td>
<td>83.70%</td>
<td></td>
</tr>
<tr>
<td>Number of scaffolds &gt; 1K nt</td>
<td>19,594</td>
<td>99.6%</td>
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<tr>
<td>Number of scaffolds &gt; 10K nt</td>
<td>14,701</td>
<td>74.7%</td>
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<tr>
<td>Number of scaffolds &gt; 100K nt</td>
<td>1,286</td>
<td>6.5%</td>
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<tr>
<td>Mean scaffold size (bp)</td>
<td>36,163</td>
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</tr>
<tr>
<td>N50 scaffold length (bp)</td>
<td>61,675</td>
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</tr>
</tbody>
</table>

%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
* 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 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
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

**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 Oshipitan¹, J. Anita Dille², Muthukumar V. Bagavathiannan³ and Stevan Z. Knezevic⁴

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?
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?