

# Constructing a Gene Expression Atlas of Chia (*Salvia Hispanica*)

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- *Salvia hispanica*, also known as Chia, is an annual plant of the mint family, Lamiaceae. Chia is a vascular plant with perennating buds initially formed at or within the soil surface. Chia grows to roughly one meter tall at maturity, with leaves growing in opposite arrangement, small purple flowers, and black, grey, or white oval shaped seeds between 1 and 2mm lengthwise.
- More known for its ornamental use in the terra cotta pot "Chia-pet", Chia has been a staple in human diets since pre-Columbian times. Currently Chia is popularly used for its health properties. Chia's high concentrations of Omega-3 fatty acids offer health benefits in childhood development as well as in lowering risks of cardiovascular disease and diabetes in adults. Chia seeds consist of between 25 and 40 percent oil, of which 80% are essential omega oils. Chia is promising as a diversified field crop in its ability to grow well in arid environments.
- Our research is focused on achieving broad understanding of the transcriptomic profile of chia, based on selected tissues at various stages of development, in order to provide knowledge and understanding of its Omega oils and broader potential as a human food source. The chia subspecies, *Salba*, was used for this study.

## Methods

### Sample Collection

Chia plants were kept in a greenhouse under a 12 hour light/dark cycle. Samples were collected in test tubes and immediately placed into a liquid nitrogen containing container, and were transferred to a -80C freezer.

### RNA Isolation

RNA was isolated from tissues by using RNA plant reagent (Invitrogen INC., USA), RNeasy kits (Qiagen INC., USA), and treated with RNase-free DNase (Life Technologies INC., USA). RNA concentration and quality were determined using the Bioanalyzer 2100 (Agilent Technologies INC., USA).

## Sample Selection



### Seedlings

- Cotyledons
- Stems
- Initial true leaves



### Vegetative growth

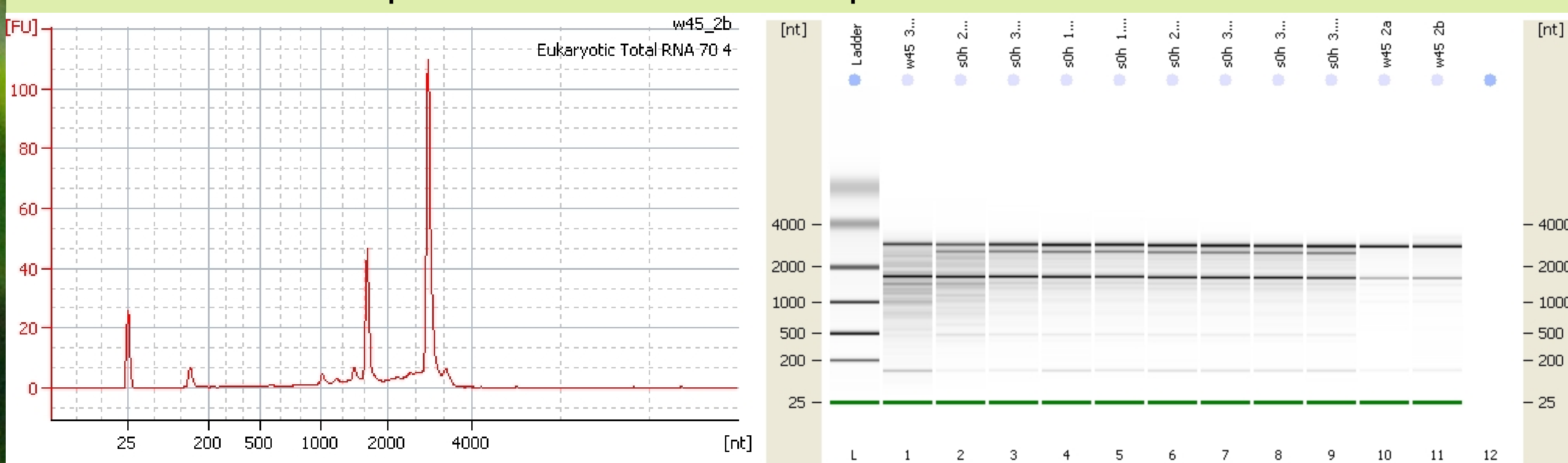
- True leaves



### Flowers

## Quality Control of RNA

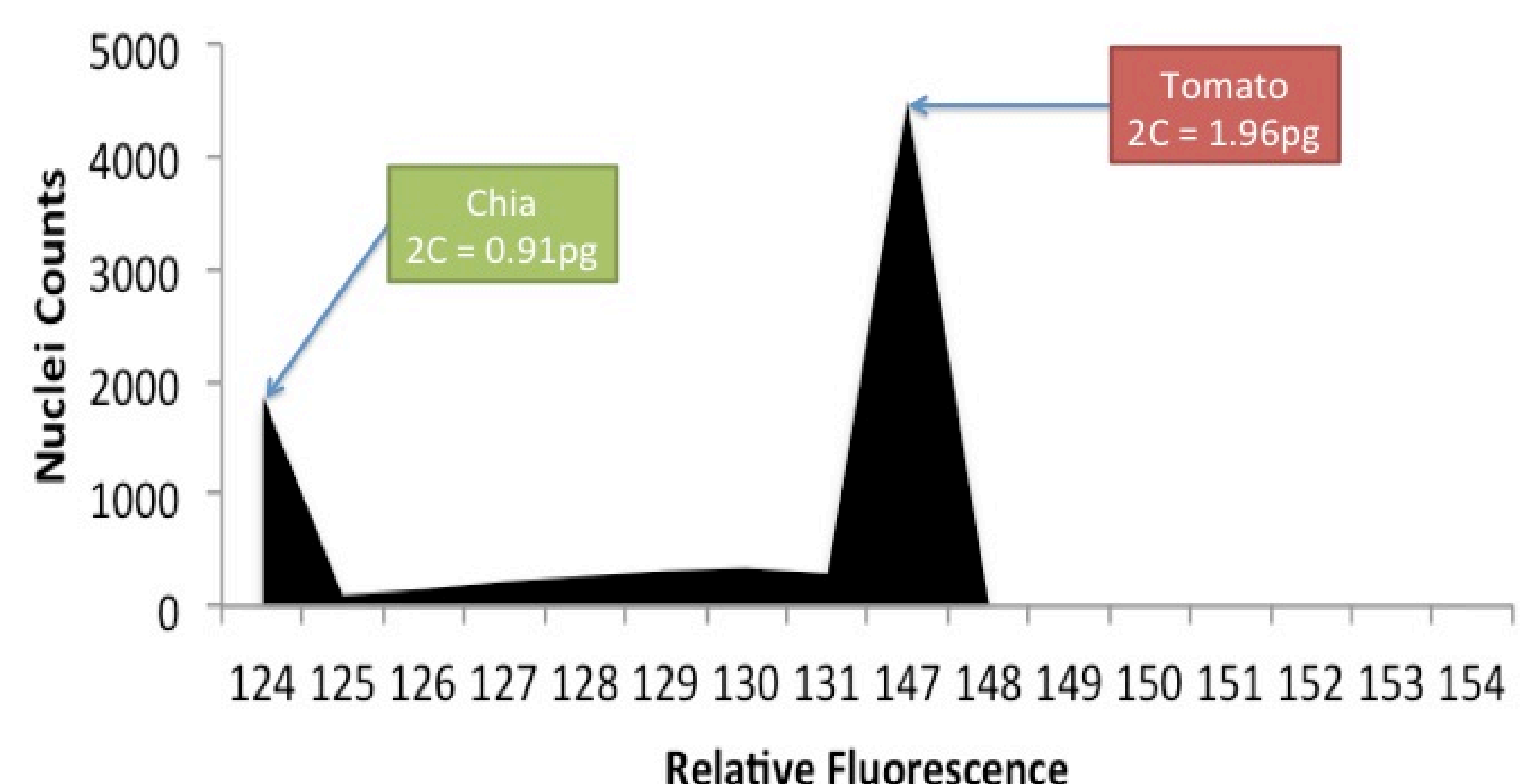
To check sample quality for sequencing, isolated RNA was run on an Agilent Technologies Bioanalyzer 2100 at the Oregon State University Center for Genome Research and Biocomputing. After RNA was extracted, samples were submitted to measure RNA quality, and a RNA Integrity Number (RIN) was assigned. RIN values above 7.0 were deemed acceptable for RNA-seq.



## Estimating the genome size of Chia

Genome size was estimated by flow cytometry. This process involves comparing the simultaneous analysis of the experimental sample (Chia) with a reference sample with a known genome size (Tomato: 2C = 1.96pg). The peak average of these sets is used in the calculations between the two samples.

## Comparison of genome size of tomato and chia



## Acknowledgements

Flow cytometry materials and assistance was provided by Jason Lattier and Dr. Ryan Contreras. Background slide image obtained from [http://www.ars.usda.gov/images/docs/13119\\_13313/Chia-Nov09%20\(06\).JPG](http://www.ars.usda.gov/images/docs/13119_13313/Chia-Nov09%20(06).JPG). Address correspondence to [jaiswalp@science.oregonstate.edu](mailto:jaiswalp@science.oregonstate.edu)