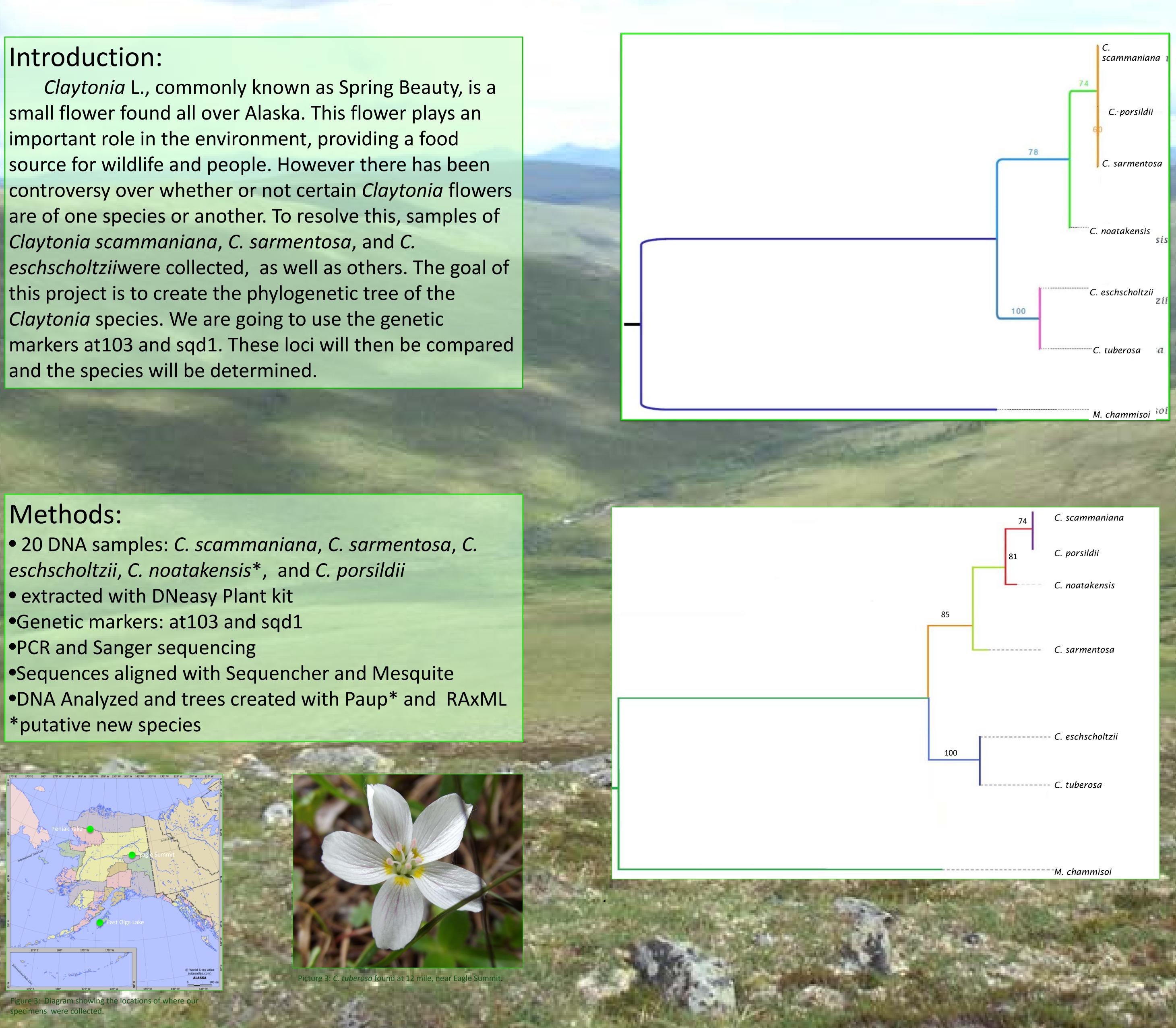


Genetic Variation and Speciation in Alaskan Claytonia



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Results:

Figure 1(top middle): Maximum likelihood tree showing bootstrap values - the sequences used in this particular tree were from sqd1 and Montia chammisoi was used as the root.

Figure 2(bottom middle): Maximum likelihood tree consisting of the same species but using at103 as the marker. Montia chammisoi was also used as the root here

Discussion:

We found that C. tuberosa and C. eschscholtzii are more closely related to each other than the others. While on the other clade C. scammaniana, C. sarmentosa, C. porsildii and C. noatakensis* share appear to share a common ancestor. These relationships were reflected in both trees with the different markers, providing further support for these relationships. While the precise relationships between the C. scammaniana clade are not as supported and could use further resolution, separation from the clade containing C. tuberosa is well supported and provides some resolution within Alaskan species. Further repetition would be able to provide more evidence of this.

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Picture 2: *C. scammaniana* found at Eagle Summi