What is claimed is

1. An isolated nucleic acid molecule comprising SEQ ID NO: 1-12, or a nucleic acid sequence having at least 90% sequence identity to SEQ ID NO: 1-12 that includes G at position 51 of SEQ ID NO:1, a G at position 51 of SEQ ID NO:2, a G at position 49 of SEQ ID NO:3, a G at position 49 of SEQ ID NO:4, a G at position 50 of SEQ ID NO:5, a G at position 50 of SEQ ID NO:6, a G at position 48 of SEQ ID NO;7, a T at position 50 of SEQ ID NO:8, A G at position 50 of SEQ ID NO:9, a G at position 51 of SEQ ID NO:10, a G at position 50 of SEQ ID NO: 11, or a C at position 49 of SEQ ID NO:12.

2. An isolated nucleic acid molecule for detecting a molecular marker representing a polymorphism in Lettuce DNA, wherein said nucleic acid molecule comprises at least 15 nucleotides that include or are immediately adjacent to said polymorphism, wherein said nucleic acid molecule is at least 90% identical to a sequence of the same number of consecutive nucleotides in either strand of DNA that include or are immediately adjacent to said polymorphism, and wherein said molecular marker is selected from the group of SEQ ID NOs: 1-12.

3. The isolated nucleic acid molecule of claim 2~~56~~, wherein the polymorphism is G at position 51 of SEQ ID NO:1, a G at position 51 of SEQ ID NO:2, a G at position 49 of SEQ ID NO:3, a G at position 49 of SEQ ID NO:4, a G at position 50 of SEQ ID NO:5, a G at position 50 of SEQ ID NO:6, a G at position 48 of SEQ ID NO;7, a T at position 50 of SEQ ID NO:8, A G at position 50 of SEQ ID NO:9, a G at position 51 of SEQ ID NO:10, a G at position 50 of SEQ ID NO: 11, or a C at position 49 of SEQ ID NO:12 as set forth in SEQ ID NOS 1-12.

4. A method of identifying a Lettuce plant for use in a plant breeding program comprising at least one allele associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) in a Lettuce plant comprising:

a) genotyping at least one Lettuce plant with at least one nucleic acid marker selected from the group of SEQ ID NOs: 1-12; and

b) selecting based upon said genotyping at least one Lettuce plant comprising an allele of

at least one of said nucleic acid markers that is associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) for breeding.

5. The method according to claim 4, wherein the at least one Lettuce plant genotyped in step (a) and/or the at least one Lettuce plant selected in step (b) is a Lettuce plant from a population generated by a cross.

6. The method of claim 5, wherein said population is generated by a cross of at least one Lettuce plant having plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) with at least one Lettuce plant having no trait.

7. The method of claim 5, wherein said population is a segregating population.

8. The method of claim 5, wherein said cross is a backcross of at least one Lettuce plant having plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2)ing with at least one Lettuce plant having no trait to introgress plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) into a Lettuce germplasm.

9. The method of claim 5 further comprising the step of crossing the Lettuce plant selected in step (b) to another Lettuce plant.

10. The method of claim 9, further comprising the step of obtaining seed from the Lettuce plant selected in step (b).

11. A Lettuce plant obtained by the method of claim 5, wherein said Lettuce plant comprises an allele of at least one nucleic acid molecule selected from SEQ ID NOs: 1-12 that is associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2), and produces the same traits.

12. A method of introgressing a plant (canopy) diameter (cm), plant height (cm),

number of leaves, and overall leaf area (cm2) locus allele into a Lettuce plant, the method comprising the steps of:

a) crossing at least one first Lettuce plant comprising the plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) locus allele, wherein the allele comprises one or more of SEQ ID NOs: 1-12, with at least one second Lettuce plant in order to form a segregating population;

b) screening said segregating population with one or more nucleic acid markers to determine if one or more Lettuce plants contain the plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) locus allele comprising one or more of SEQ ID NOs: 1-12; and

c) selecting said plants based upon said screening from said segregating population one or more Lettuce plants comprising said plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) locus allele for further breeding.

13. The method according to claim 12, wherein at least one of the nucleic acid markers is located within 100 Kb of the plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) locus.

14. The method according to claim 12, wherein at least one of the nucleic acid markers is located within 5 cM of the plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) locus.

15. The method according to claim 12, wherein at least one of the nucleic acid markers exhibits a LOD score of greater than 2.0 with the plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) locus.

16. The method according to claim 12, wherein said population is generated by a cross of at least one Lettuce plant having plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) with at least one Lettuce plant having no trait.

17. A Lettuce plant obtained by the method of claim 12.

18. The Lettuce plant according to claim 17, wherein said Lettuce plant comprises an allele of at least one nucleic acid marker selected from the group of SEQ ID NOs: 1-12 that is associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2).

19. The Lettuce plant according to claim 17, wherein said Lettuce plant is homozygous for said allele.

20. A method of creating a population of Lettuce plants each comprising at least one allele associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2), the method comprising the steps of:

a) genotyping a first population of Lettuce plants, said population or said plants containing at least one allele associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2), the at least one allele associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) comprising one or more of SEQ ID NOs: 1-12;

b) selecting from said first population of Lettuce plants based upon said genotyping one or more Lettuce plants containing said at least one allele associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2); and

c) producing from said selected one or more Lettuce plants a second population of Lettuce plants comprising at least one allele associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) comprising one or more of SEQ ID NO: 1-12.

21. The method of claim 20, wherein said producing comprises crossing the selected one or more Lettuce plants having the plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) allele with a Lettuce plant having no trait to produce a second population of Lettuce plants having plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2), thereby creating a population of

Lettuce plants comprising at least one allele associated with plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) comprising one or more of SEQ ID NOs: 1-12.

22. The method according to claim 20, wherein the first population of Lettuce plants genotyped in step (a) is a population generated by a cross.

23. The method according to claim 20, wherein said selected Lettuce plant(s) of step (b) produces superior plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2).

24. The method of claim 20, wherein said first population of Lettuce plants is generated by a cross of at least one Lettuce plant having plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2) with at least one Lettuce plant having no trait.

25. The method of claim 20, wherein said first population of Lettuce plants is a segregating population.

26. A population of Lettuce plants obtained by the method of claim 20, wherein the Lettuce plants produce superior plant (canopy) diameter (cm), plant height (cm), number of leaves, and overall leaf area (cm2).

27. An isolated nucleic acid molecule for detecting a molecular marker representing a polymorphism in Lettuce DNA, wherein said nucleic acid molecule comprises at least 15 nucleotides that include or are immediately adjacent to said polymorphism, wherein said nucleic acid molecule is at least 90% identical to a sequence of the same number of consecutive nucleotides in either strand of DNA that include or are immediately adjacent to said polymorphism, and wherein said molecular marker is selected from the group of SEQ ID NOs: 1-12.

28. The isolated nucleic acid molecule of claim 27 wherein the polymorphism is G at position 51 of SEQ ID NO:1, a G at position 51 of SEQ ID NO:2, a G at position 49 of SEQ ID NO:3, a G at position 49 of SEQ ID NO:4, a G at position 50 of SEQ ID NO:5, a G at position 50 of SEQ ID NO:6, a G at position 48 of SEQ ID NO;7, a T at position 50 of SEQ ID NO:8, A G at position 50 of SEQ ID NO:9, a G at position 51 of SEQ ID NO:10, a G at position 50 of SEQ ID NO: 11, or a C at position 49 of SEQ ID NO:12 as set forth in SEQ ID NOS 1-12.