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Introduction

Circadian Rhythms are biological cycles with a period of 24 hour that are observed in most of the organisms from cyanobacteria to fungi to humans. Circadian rhythms has two properties: period and entrained phase. Disruption of phase property of circadian rhythm has been linked to many chronic diseases, such as obesity, diabetes, sleep disorder, etc. Even though genes that are responsible for period are known, genes that are responsible for phase have remained unknown. Since phase is quantitative trait, quantitative genetics approach helps identify multiple genetic loci for responsible for complex phenotype. My project will try to identify and characterize the phase QTL gene of chromosome 6 in *Neurospora crassa*. This project will give insight about molecular understanding of phase property of circadian rhythm.

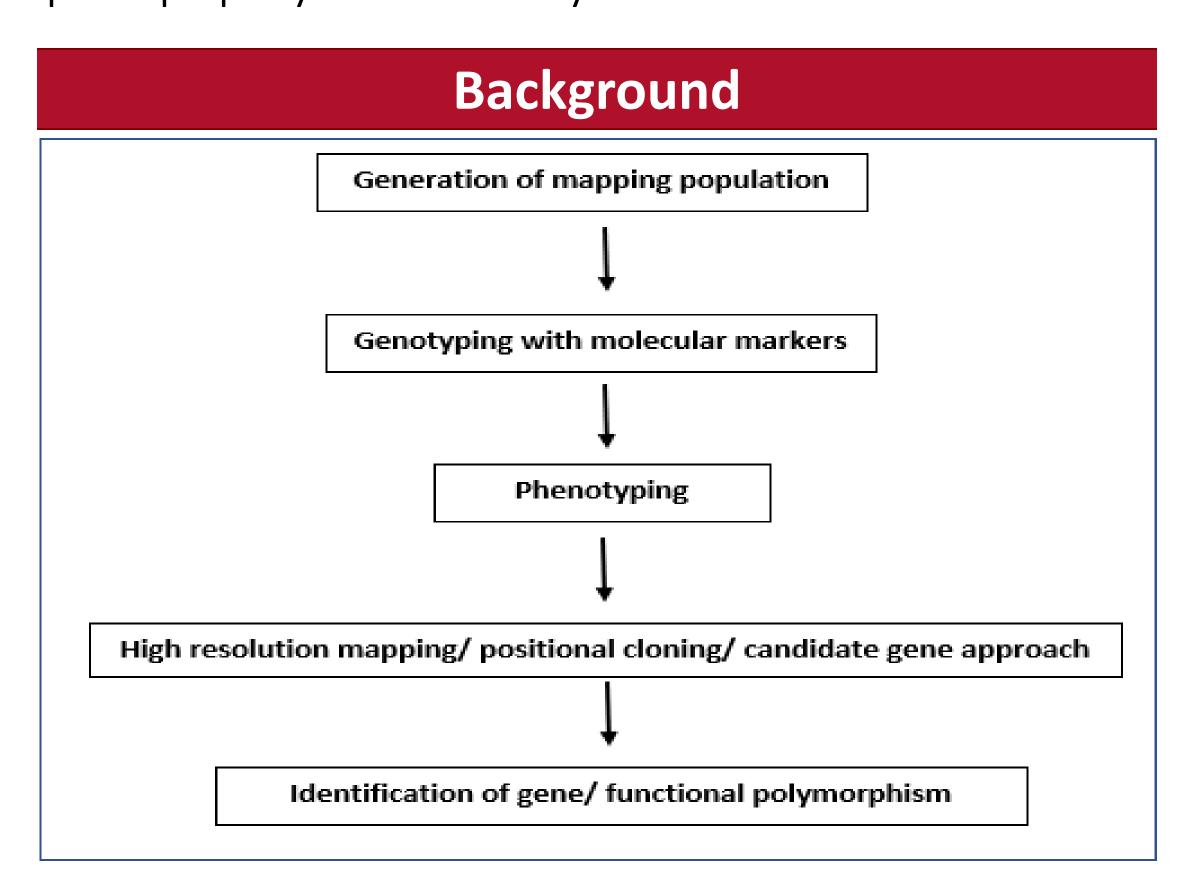
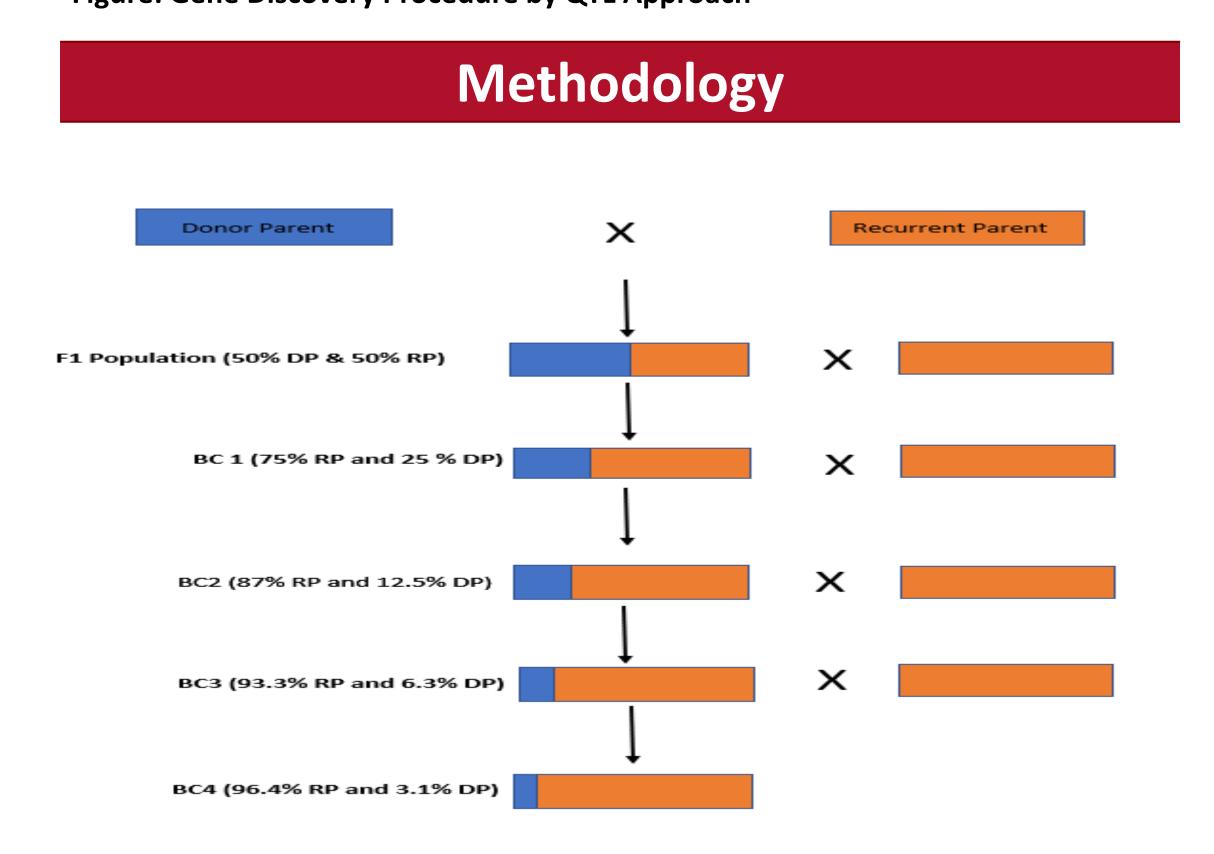
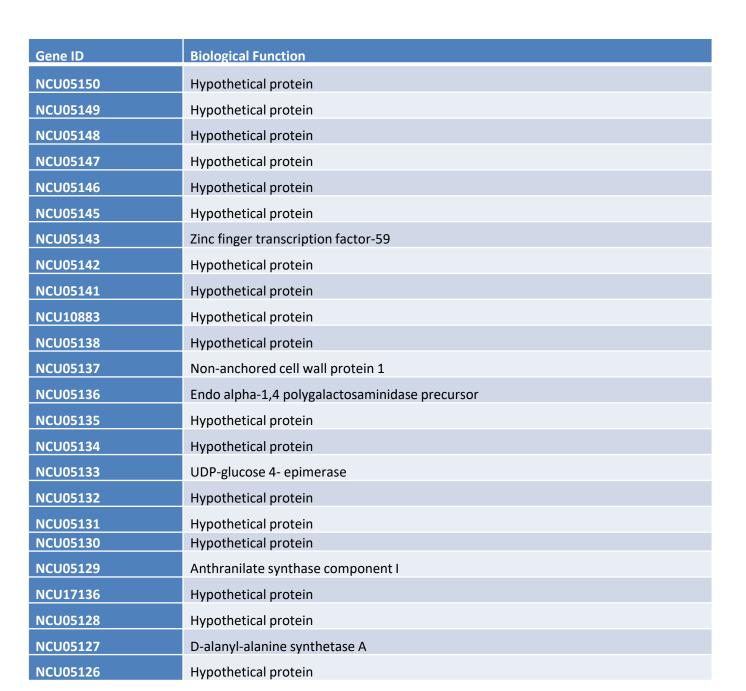


Figure: Gene Discovery Procedure by QTL Approach



N6F1 donor Physical Position vs Minor Allele Frequency Physical Position vs Minor Allele Frequency N662 donor Physical Position vs Minor Allele Frequency N663 donor Physical Position vs Minor Allele Frequency N664 donor Physical Position vs Minor Allele Frequency N663 donor Physical Position vs Minor Allele Frequency Region B Region B

Figure: Cleaning up of genetic background during backcross in chromosome 6



Physical Position

Figure: Candidate genes in Region A

Gene ID Biological Function NCU04077 Assimilatory sulfite reductase NCU04078 Alcohol dehydrogenase-11 NCU12107 Hypothetical protein NCU04079 Hypothetical protein NCU04080 Palmitoyltransferase SWF1 NCU04081 Guanine triphosphate binding-20

Physical position

Figure: Candidate genes in Region B

Discussion

- Donor segments were reduced in half in each backcross (50%- 25%-12.5%- 6.25%). That is how genetic background was cleared.
- After fourth backcross, two QTL regions were identified.
- Using Fungidb, 30 genes were found in these two regions.
- Region A had 24 genes total, in which 15 were genes located on the forward strand, and 11 genes were located on the reversed strand.
- Region B had 6 genes total, in which 4 genes were located on the forward strand, and 2 genes were located on the reversed strand.
- Out of 30 genes, the function of 20 genes have remained unknown.
- We believe genes that are responsible for phase phenotype could be from these 20 genes.

Conclusions and Directions for Future Research

- Thirty genes are found using fungidb.org from two QTL regions. From these 30 genes, genes that are possibly responsible for phase phenotype will be further identified and characterized.
- By using knockout library, race tube analysis will be performed to further identify the genes that are linked with phase phenotype.

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References

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