# Exploring autoinducer binding domain of LuxR regulators for quorum sensing in gram-positive bacteria

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## INTRODUCTION

- Quorum Sensing (QS) is cell-to-cell communication among microbes.
- It is driven by various quorum sensing signaling molecules like N-acyl homoserine lactone (AHL) synthesized by LuxI and sensed by LuxR regulators.
- LuxR regulators are vital component of signaling cascade known as quorum sensing (QS) and widely distributed among Gram-negative bacteria to sense as well as respond N-acyl homoserine lactone (AHL).

## OBJECTIVES

- Present study is focused to cognize the existence of autoinducer binding domain (ABD) of LuxR regulators in Gram-positive bacteria on the basis of phylogeny, conservation and potential functions.

## METHODOLOGY

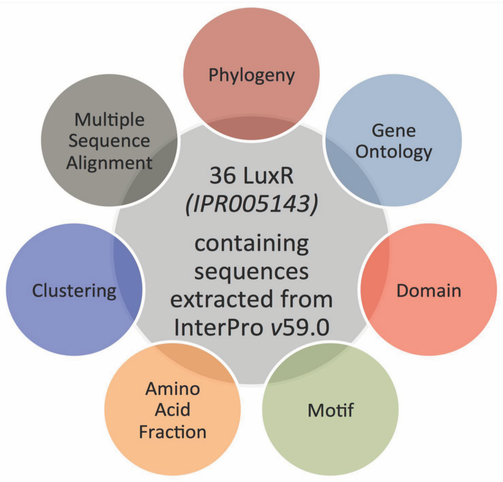
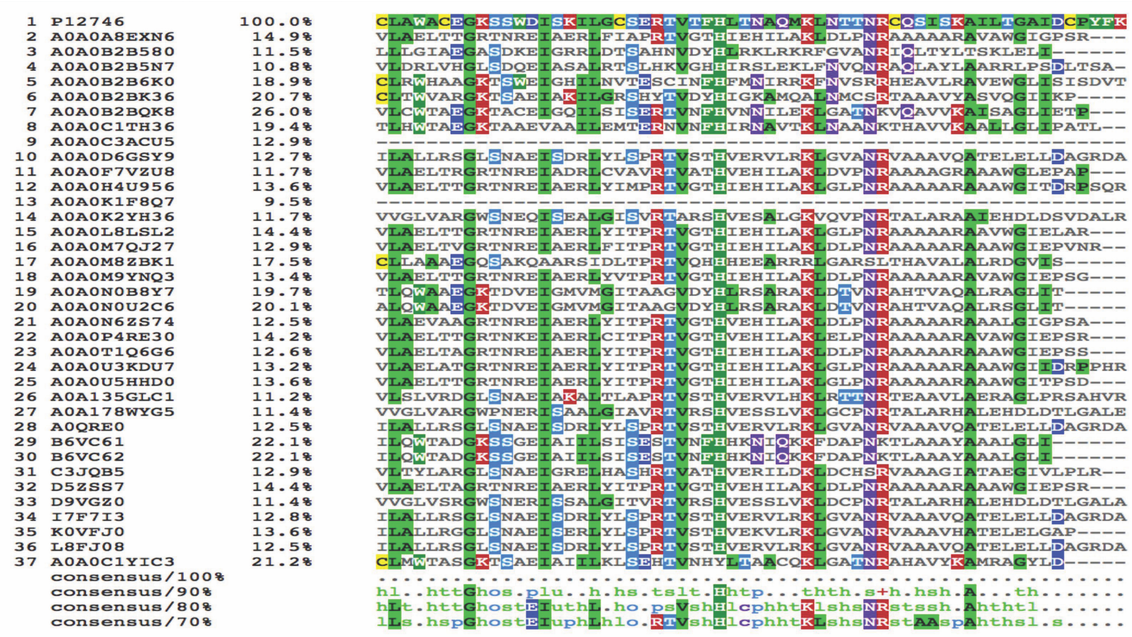
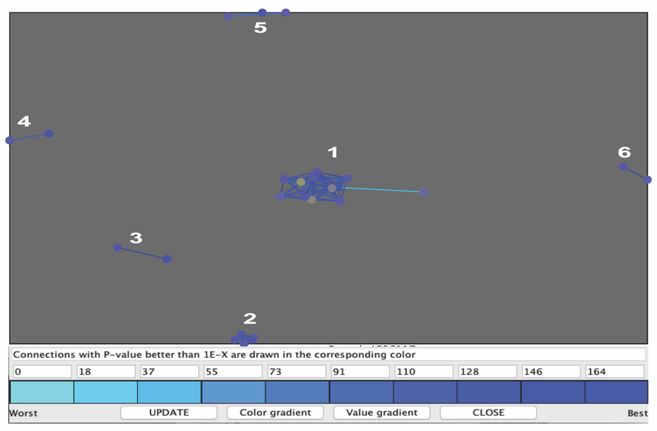



*Diagram showing various analyses methods exploited for exploring LuxR regulators in Gram-positive bacteria*

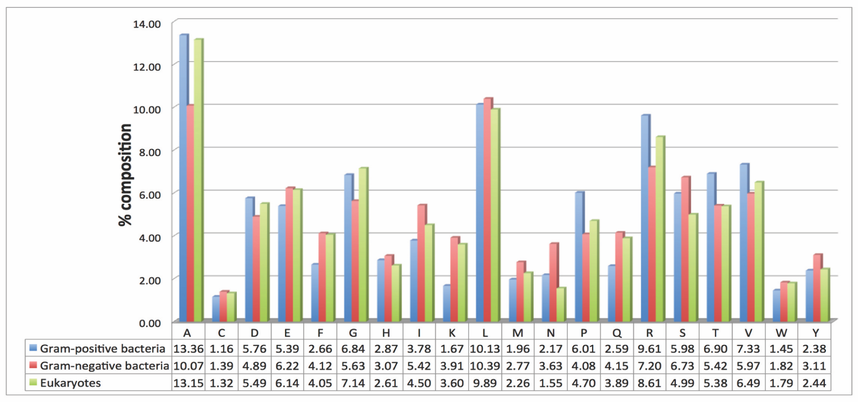
## RESULTS



***I**. Multiple sequence alignment using CLUSTAL OMEGA software of 36 Gram-positive bacteria against Vibrio fischeri LuxR*



***II**. Clustering analysis done using CLANS software of 36 LuxR containing sequences of Gram-positive bacteria.*

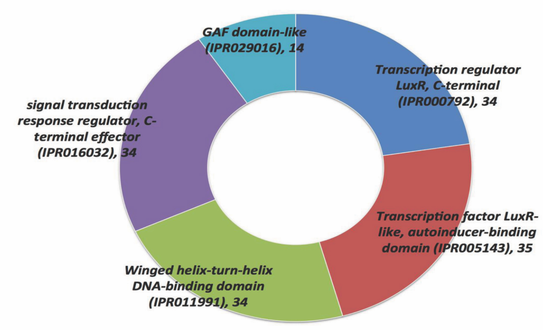


| | A | C | D | E | F | G | H | I | K | L | M | N | P | Q | R | S | T | V | W | Y |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Gram-positive bacteria | 13.36 | 1.16 | 5.76 | 5.39 | 2.66 | 6.84 | 2.87 | 3.78 | 1.67 | 10.13 | 1.96 | 2.17 | 6.01 | 2.59 | 9.61 | 5.98 | 6.90 | 7.33 | 1.45 | 2.38 |
| Gram-negative bacteria | 10.07 | 1.39 | 4.89 | 6.22 | 4.12 | 5.63 | 3.07 | 5.42 | 3.91 | 10.39 | 2.77 | 3.63 | 4.08 | 4.15 | 7.20 | 6.73 | 5.42 | 5.97 | 1.82 | 3.11 |
| Eukaryotes | 13.15 | 1.32 | 5.49 | 6.14 | 4.05 | 7.14 | 2.61 | 4.50 | 3.60 | 9.89 | 2.26 | 1.55 | 4.70 | 3.89 | 8.61 | 4.99 | 5.38 | 6.49 | 1.79 | 2.44 |

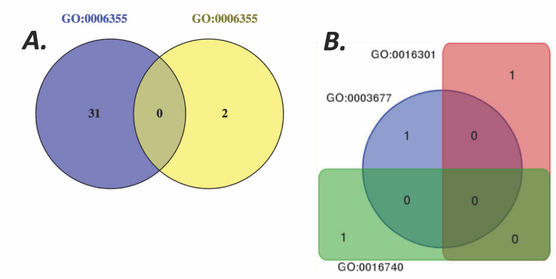
***III**. Comparison of the Amino Acid Composition of LuxR containing sequence of Gram-positive bacteria, Gram-negative bacteria and Eukaryotes*

| S. No | Motif logo | Motif Width | Sequence coverage |
|---|---|---|---|
| Motif 1 | | 50 | 34 |
| Motif 2 | | 41 | 22 |
| Motif 3 | | 50 | 12 |
| Motif 4 | | 29 | 17 |
| Motif 5 | | 21 | 17 |
| Motif 6 | | 15 | 11 |
| Motif 7 | | 21 | 05 |
| Motif 8 | | 38 | 09 |
| Motif 9 | | 29 | 05 |
| Motif 10 | | 21 | 05 |

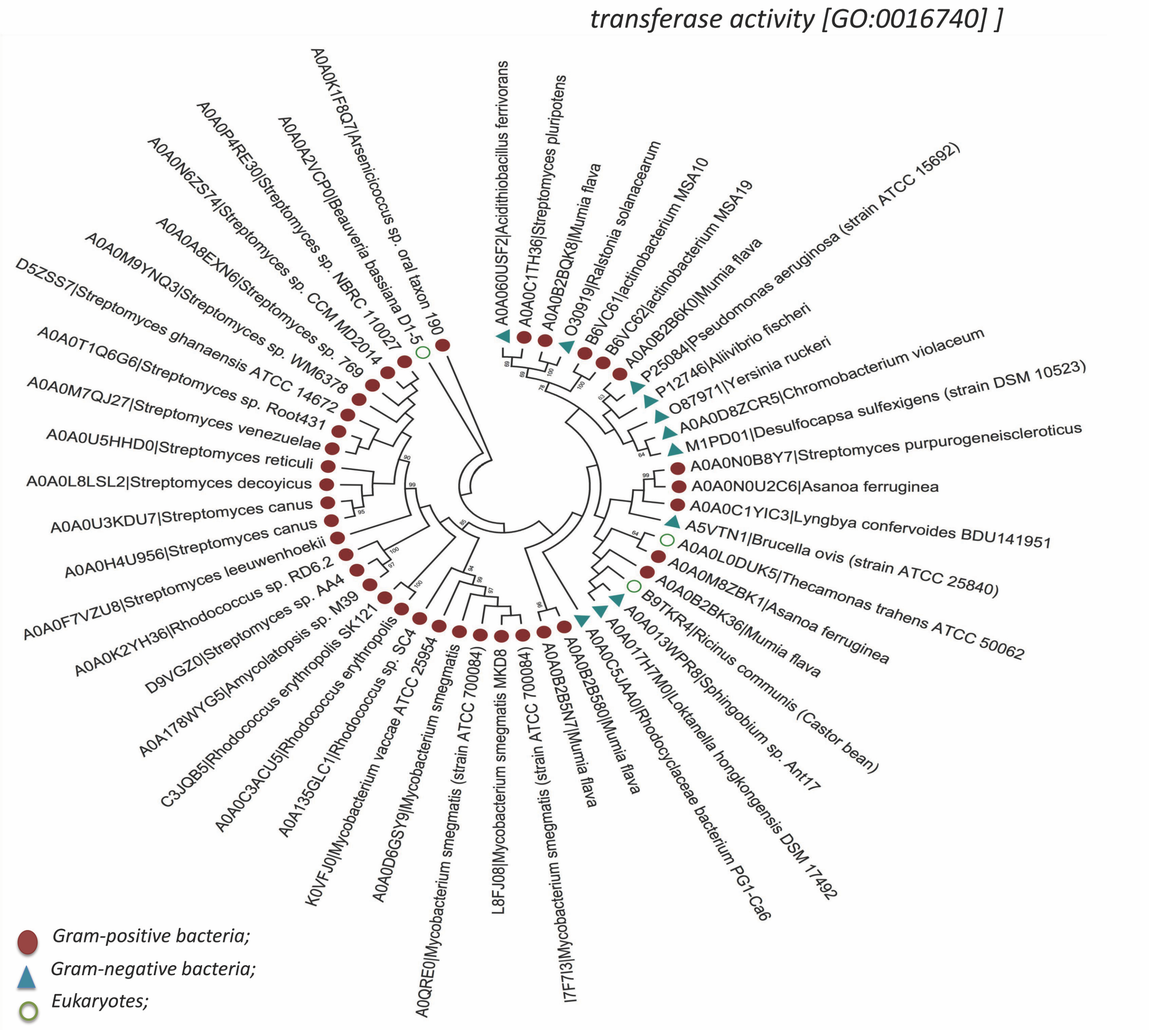
***IV.** Motif extraction of 36 LuxR-containing sequences of Gram-positive bacteria using MEME/MAST software*




***V.** Domain scanning in LuxR containing sequences of Gram-positive bacteria*




***VI.** Gene ontology based annotation of LuxR-containing sequences of Gram-positive bacteria: **A)** Biological processes [regulation of transcription, DNA-templated [GO:0006355]; transcription, DNA-templated [GO:0006351]] **B)** Molecular function [DNA binding [GO:0003677]; kinase activity [GO:0016301]; transferase activity [GO:0016740] ]*




***VII**. Phylogenetic reconstruction (Maximum likelihood)of the LuxR-incorporating sequences of 36 Gram-positive bacteria, 11 Gram-negative bacteria and 03 eukaryotes using MEGA 7.0 (LG+G+F model, 1000 Bootstrap values)*

## CONCLUSION

- Our study showed the coevolution of LuxR containing sequences of plant-associated soil-borne Gram-positive with that of Gram-negative bacteria may help in intraspecies and interspecies signaling.

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