

The Homeodomain-Leucine Zipper genes family regulate the response of *Oryza sativa* to *Nilaparvata lugens*, *Laodelphax striatellus*, and Jinggangmycin

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Table S1: Primer sequences for RT-qPCR.

<i>Genes</i>	Primer's sequence (5'to3')
<i>OsHDZ3</i>	F: GATCCAATCCATAAGGCCAAAC R: CTCCGAAGACGAGTCCATTCATAC
<i>OsHDZ4</i>	F: GGTGTTGCTGTTCCGGTGAGGTGCT R: TCCGCCGCTGCCTCGTCGTCGTA
<i>OsHDZ10</i>	F: GCAGCAACCGCAGCGAGAATAGC R: AGAACGGGATCATGCCGCCACC
<i>OsHDZ15</i>	F: GCAGACGGAGGTGGACTGCGAGTT R: GCGCTGGAGTTGTTATTGGTGTGGA
<i>OsHDZ20</i>	F: TGAATGGCATGGGAGGGAGAAGC R: GCGGCACATTGTCCATCGCGTAT
<i>OsHDZ28</i>	F: TCGTCGGTGAAGGAGGAGGAGGACC R: TTGAGAAGCTGCCCCGTGGAAGAACA
<i>OsHDZ37</i>	F: GCACTACGGCACATCAGACAAA R: CACCCATGACAGACCAACCATC
<i>OsHDZ40</i>	F: CGACGCAATACTGTGCTGTTCT R: AGCGAGATGTCCTGGAGGTTGA
<i>ACTIN</i>	F: TCCATCTTGGCATCTCTCAG R: GTACCCGCATCAGGCATCTG

Table S2: Types and number of cis-acting regulatory elements analysis involved in the growth and development, stress and hormonal response.

	Site Name	Function
Hormones	AuxRR-core	<i>Cis</i> -acting regulatory element involved in auxin responsiveness
	CGTCA-motif	<i>Cis</i> -acting regulatory element involved in the MeJA responsiveness
	CGTCA-motif	<i>Cis</i> -acting regulatory element involved in the MeJA responsiveness
	P-box	gibberellin-responsive element
	TCA-element	<i>Cis</i> -acting element involved in salicylic acid responsiveness
	TCA-element	<i>Cis</i> -acting element involved in salicylic acid responsiveness
	ABRE	<i>Cis</i> -acting element involved in the abscisic acid responsiveness
	GARE-motif	gibberellin-responsive element
	ABRE	<i>Cis</i> -acting element involved in the abscisic acid responsiveness

Stress and growth	<u>G-Box</u>	<i>Cis</i> -acting regulatory element involved in light responsiveness
	<u>G-Box</u>	<i>Cis</i> -acting regulatory element involved in light responsiveness
	ATCT-motif	part of a conserved DNA module involved in light responsiveness
	ACE	<i>cis</i> -acting element involved in light responsiveness
	GC-motif	enhancer-like element involved in anoxic specific inducibility
	ARE	<i>Cis</i> -acting regulatory element essential for the anaerobic induction
	MBS	MYB binding site involved in drought-inducibility/resistance
	TATA-Box	core promoter element around -30 of transcription start
	<u>CAAT-box</u>	common <i>cis</i> -acting element in promoter and enhancer regions
	<u>LTR</u>	<i>cis</i> -acting element involved in low-temperature responsiveness
	<u>MBS1</u>	MYB binding site involved in flavonoid biosynthetic genes regulation
	TC-rich repeats	<i>cis</i> -acting element involved in defense and stress responsiveness
	CAT-box	<i>cis</i> -acting regulatory element related to meristem expression

Table S3: Domain distribution and structure of *OsHDZIP* genes in *Oryza sativa*.

No	Motif Logo	Motif Sequence
1		LGLEPRQVKVWFQNRRARWKTQ
2		RLTKEQVRALERSFKECPKLDPKQ
3		CRRLPSGCLIQEMPNGYSKVTWVEHVELD
4		LKRENEALREENRRL
5		NGTJQLMYAELQVPSPLVPTREVWFLRYCKQLADG
6		CTDASGSLVYAPVDIPAMNVVMNGGDPSYVALLPSGFAL
7		GGSLLTVAFQILVNSVPTAKLSLESVATVNSLIACTIEKIK
8		PERVDFLREDESSRSEWDILSNGGVVQEMAHIKGRDHGNCVSL
9		KEALSNA SCPCGGPAALGEMSFEEHHLRIENARLKDEJDRISAJAAKYL
10		ITTPEGRRSMLKLAERMVASFCAGVSASSAHZWTTLSGSG

Table S4 Predicted functional partners of *OsHDZIP* proteins

RoC9	Homeobox-leucine zipper protein ROCP; Probable transcription factor; belongs to the HDZIP homeobox family. Class IV subfamily. (816aa)
	Predicted functional partners:
Q3V826	Os02g0682500 protein
A0A0N7KLN2	Os02g0183800 protein
OSHAP3E	cDNA clone: 002-134-B07, full insert sequence

Q0JAK5	cDNA clone: J03305D05, full insert sequence
Q7F3D6	cDNA clone: 002-141-A12, full insert sequence
LFL1	B3 domain-containing protein LFL1; Transcription repressor involved in flowering time regulations.
Q8GVN6	Os07g0531600 protein
AP2-5	APETALA2-like protein 5; Transcription factor. Involved in spikelet transition and development.
A0A0P0VDU4	Os02g0114400 protein
A0A0P0WRG0	Os05g0586300 protein