

Thirty-four farmers from three villages withheld irrigation following agro-advisory in nearly 26.5 ha area, thus saving 18,550 m<sup>3</sup> irrigation water. This also saved nearly 53 man-days that otherwise would have been spent in irrigating the crop. Total irrigation water saved by dry sowing and withholding irrigation was 23,800 m<sup>3</sup> (Table 2). Energetics in terms of irrigation water, electricity and labour saved was calculated. It was observed that dry sowing and withholding irrigation in 34 ha area saved total 50,246.56 MJ energy (Table 3).

Thus, the agro-advisory services provided through E-Chara Kendra not only benefit the farmers in effective crop planning and management, but also in conserving NR. India's total geographical area is 329 m ha. Out of this, 195 m ha is gross cropped area while net irrigated area is only 65.3 m ha. Rest of the land is rainfed. We can save 1,365,000,000 m<sup>3</sup> irrigation water by withholding irrigation or dry sowing by following weather-based agro-advisory in just 1% of the gross cropped area (1.95 m ha). That means we can generate additional irrigation potential in 1.95 m ha area for one irrigation. This will also save 3.9 million man-days and 2881.788 million MJ energy. Therefore,

weather based agro-advisory services should be promoted in a big way through IT services and awareness programmes for NR conservation and welfare of farmers.

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## Mitochondrial genome sequence of *Oryza sativa* indica cultivar RP Bio-226

Mitochondria play a key role in plant development, energy production, metabolism and cell homeostasis<sup>1–3</sup>. Plant and animal mitochondria differ with respect to their genomes. Plant mitochondrial genome is generally larger compared to those of animals (208 kb–11.3 Mb) and is present in relatively fewer copies<sup>4–6</sup>. Sequencing and understanding the mitochondrial genomes of individual cultivars of crop plants like rice is essential to know their role in crop yield<sup>7,8</sup>. Further, understanding the mitochondrial genome is important in the context of cytoplasmic male sterility<sup>9,10</sup>. In our effort to understand the genomic basis of yield of the bacterial leaf blight-resistant indica rice cultivar RP Bio-226, we have gener-

ated the genomic resources for this cultivar. We have recently sequenced the total genome of RP Bio-226 and assembled the nuclear genome<sup>11</sup>. Further, we have sequenced the urea responsive transcriptome of this cultivar<sup>12</sup>. Mitochondrial genome can be sequenced by separating the mitochondria from other cell contents and selectively isolating the mitochondrial DNA, or it can be sequenced along with the nuclear genome from the whole genomic DNA<sup>13–16</sup>. Following the second approach, we assembled the mitochondrial genome of RP Bio-226 using the whole genomic reads, annotated it and the results are reported here.

The paired end genomic reads of *O. sativa* indica cultivar RP Bio-226 were

used for mitochondrial genome assembly<sup>11</sup>. The reads were aligned to the reference genome (93-11 indica rice mitochondrial genome) using Bowtie2 (ver. 2.2.4)<sup>17</sup>. Out of 69,377,450 whole genomic reads used, 2.2% of them assembled onto the mitochondrial reference

**Table 1.** RP Bio-226 mitochondrial genome characteristics

Genome size	488.615 kb
SNP	37
Indels	11
Protein coding genes	27
rRNA	4
tRNA	29

**Table 2.** Genes identified in RP Bio-226 mitochondrial genome

Gene	Start	Stop	Strand	Length
<i>trnP(tgg)</i>	9,776	9,850	+	75
<i>nad1-1</i>	11,046	11,411	+	366
<i>cox3-1</i>	17,233	18,018	-	786
<i>nad5-1</i>	22,037	23,248	+	1212
<i>trnM(cat)</i>	26,688	26,760	+	73
<i>trnH(gtg)</i>	32,742	32,815	-	74
<i>trnP(tgg)</i>	35,761	35,834	+	74
<i>trnW(cca)</i>	35,977	36,050	+	74
<i>trnQ(ttg)</i>	45,677	45,748	-	72
<i>atp8</i>	53,966	54,052	+	87
<i>trnM(cat)</i>	54,826	54,898	-	73
<i>nad6</i>	60,130	60,648	-	519
<i>nad1-3</i>	61,936	62,091	-	156
<i>trnM(cat)</i>	64,625	64,698	-	74
<i>trnD(gtc)</i>	65,424	65,497	+	74
<i>trnN(gtt)</i>	66,188	66,259	-	72
<i>trnK(ttt)</i>	70,357	70,429	-	73
<i>trnP(tgg)</i>	104,836	104,910	+	75
<i>nad1-0_a</i>	106,106	106,471	+	366
<i>cox3-0</i>	112,293	113,078	-	786
<i>nad5-2_a</i>	116,016	116,240	+	225
<i>nad5-0</i>	117,097	118,308	+	1212
<i>trnM(cat)</i>	121,748	121,820	+	73
<i>trnH(gtg)</i>	127,802	127,875	-	74
<i>trnP(tgg)</i>	130,821	130,894	+	74
<i>trnW(cca)</i>	131,037	131,110	+	74
<i>trnQ(ttg)</i>	140,737	140,808	-	72
<i>nad3</i>	176,612	176,926	+	315
<i>trnL1(cag)</i>	185,013	185,077	-	65
<i>trnM(cat)</i>	189,610	189,683	-	74
<i>nad4</i>	201,166	201,744	+	579
<i>cox2</i>	215,025	215,399	+	375
<i>atp6</i>	226,237	226,743	-	507
<i>nad5-2_c</i>	233,544	233,867	-	324
<i>nad1-0_b</i>	240,789	241,025	-	237
<i>trnS2(tga)</i>	262,560	262,646	+	87
<i>atp9</i>	264,083	264,298	+	216
<i>rrnS</i>	284,095	285,065	-	971
<i>nad4l</i>	299,796	300,086	+	291
<i>cob-0</i>	304,872	305,957	-	1086
<i>nad1-2</i>	315,989	316,165	-	177
<i>cox1</i>	339,524	341,080	+	1557
<i>nad5-2_b</i>	349,309	349,452	-	144
<i>trnF(gaa)</i>	360,445	360,517	+	73
<i>trnY(gta)</i>	364,070	364,152	+	83
<i>nad2-0</i>	367,329	367,847	+	519
<i>trnE(ttc)</i>	377,031	377,102	+	72
<i>rrnL</i>	382,925	384,488	+	1564
<i>trnG(gcc)</i>	390,383	390,441	-	59
<i>trnC(gca)</i>	391,769	391,839	-	71
<i>cob-1</i>	396,837	397,373	+	537
<i>nad2-2</i>	404,738	404,944	-	207
<i>trnS1(tct)</i>	408,205	408,276	-	72
<i>rrnS</i>	415,051	416,021	-	971
<i>nad5-3</i>	430,422	430,544	-	123
<i>trnF(gaa)</i>	441,558	441,630	+	73
<i>trnY(gta)</i>	445,183	445,265	+	83
<i>nad2-1</i>	448,442	448,960	+	519
<i>trnE(ttc)</i>	458,144	458,215	+	72
<i>rrnL</i>	464,038	465,601	+	1564

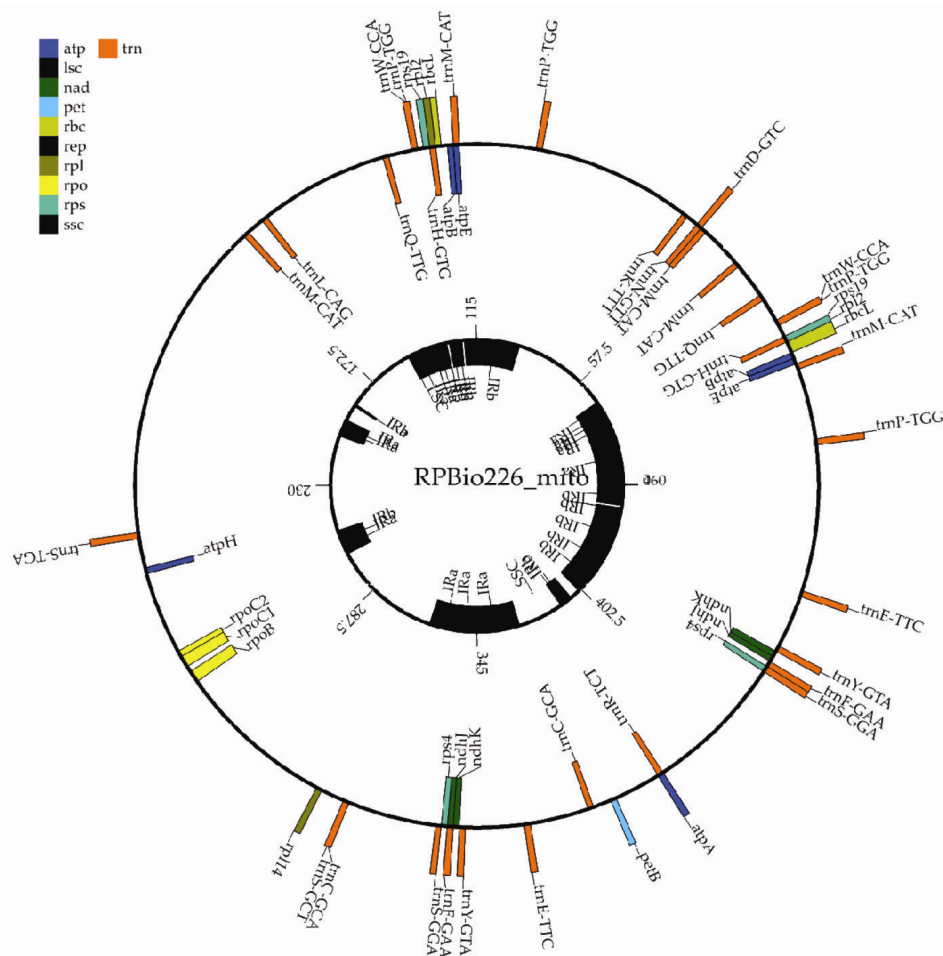
genome. The mitochondrial genomic consensus sequence of RP Bio-226 was generated using the Bam file derived from the Sam file generated in the above assembly with the mpileup function of Samtools. The mitochondrial genome was 488.615 kb in size. Variations in RP Bio-226 mitochondrial genome were studied in comparison with the 93-11 reference mitochondrial genome using Samtools<sup>18</sup>. The RP Bio-226 mitochondrial genome showed 37 SNPs and 11 indels (Table 1).

Annotation of the mitochondrial genome for identification of protein coding genes, rRNA and tRNA coding genes was done using Dogma<sup>19</sup>, CpGAVAS<sup>20</sup> and MitoSsoftware<sup>21</sup>. RP Bio-226 mitochondrial genome contained 27 protein coding genes, 29 tRNA coding genes and four rRNA genes (Table 2). The genome also contained repetitive elements both short and long tandem repeats. Table 3 lists the repeats identified with RepeatMasker<sup>22</sup> (<http://www.repeatmasker.org>). The genome map (Figure 1) was drawn with both CpGAVAS and CGview tools<sup>20,23</sup>.

RP Bio-226 mitochondrial genome sequence was reconstructed from the whole genome reads. The mitochondrial genome shows variations in comparison with the reference genome (93-11 indica rice mitochondrial genome). The reference genome contained an additional tRNA coding gene compared to RP Bio-226. Two and five copies of trnE and trnM respectively, were present in RP Bio-226 mitochondrial genome, while only one and four copies were present in 93-11 mitochondrial genome. Gene coding for trnX is absent in RP Bio-226,

**Table 3.** Differences between the RP Bio-226 and 93-11 indica mitochondrial genomes

	RP Bio-226	93-11 indica
Protein coding genes	27	27
tRNA coding genes	29	30
rRNA coding genes	4	4
Retro elements	17	20
LINES	-	2
L1/CIN4	-	2
LTR elements	17	18
Gypsy/DIRS1	11	12
Small RNA	6	6
Simple repeats	31	35
Low complexity	16	17
Unclassified	-	1



**Figure 1.** Mitochondrial genome map of *Oryza sativa indica* rice cultivar RP Bio-226.

while it is present in 93-11. RP Bio-226 mitochondrial genome contains 31 simple repeats, 16 low complexity repeats (A, G and GA-rich) and 17 LTRs (long terminal repeats) which are less in number compared to the reference mitochondrial genome.

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