

# Impacts of elevated CO<sub>2</sub> on exogenous *Bacillus thuringiensis* toxins and transgene expression in transgenic rice under different levels of nitrogen

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## Supplementary legends:

**Supplementary Fig. 1** Methylation maps of P1 fragment in the fused *Cry IAb/Ac* transgene region in leaves of transgenic *Bt* rice grown under ambient CO<sub>2</sub> with different N-fertilizer rates. (n=minimum of 10 clones for each treatment. Positions of cytosines (CGN, CHG and CHH) on the analyzed regions are represented in Fig. 7. Filled symbols indicate cytosine methylation. Red, blue and green circles represent CGN, CHG and CHH sites respectively, whereas H = A, T or C.

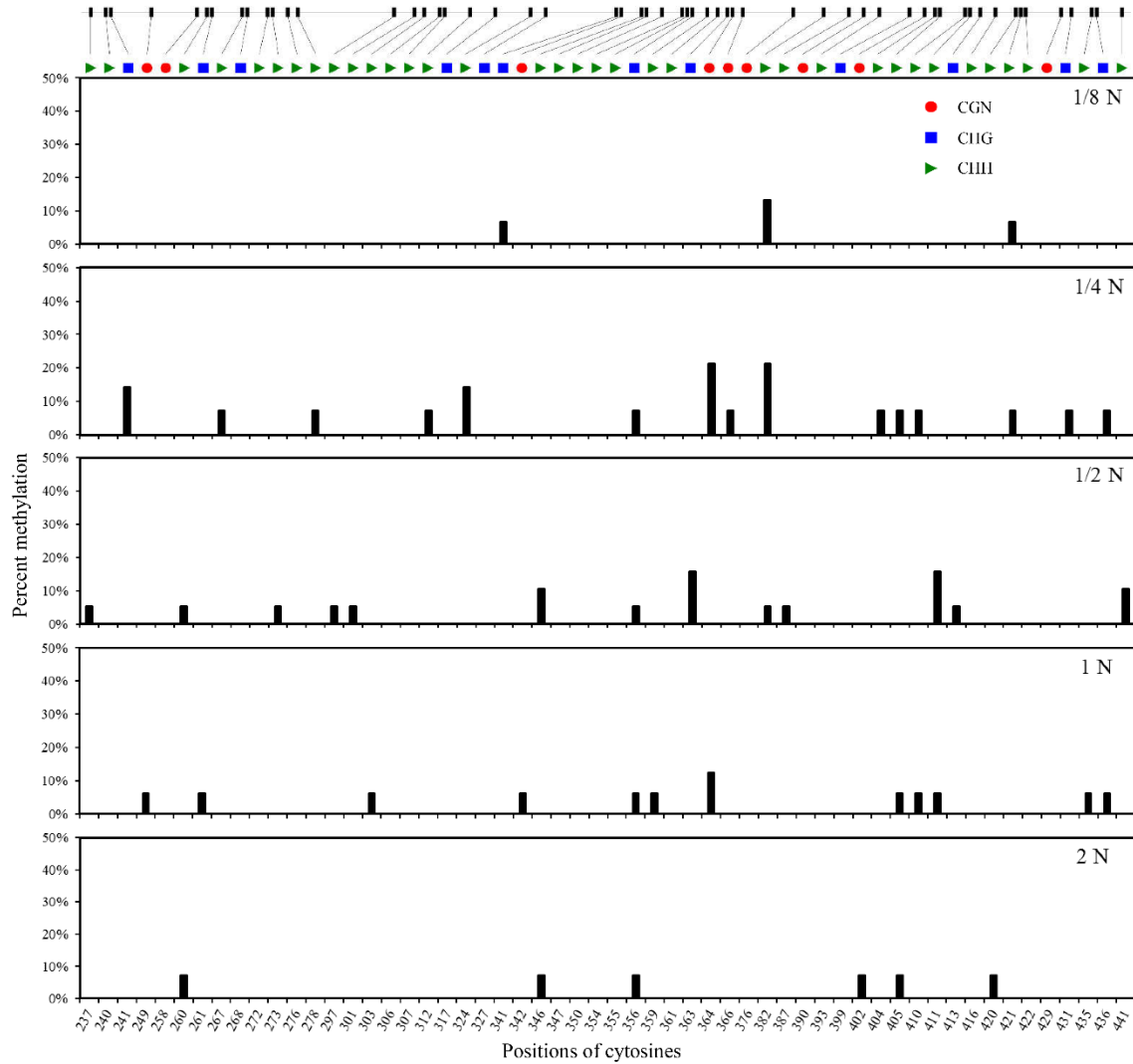
**Supplementary Fig. 2** Methylation maps of P1 fragment in the fused *Cry IAb/Ac* transgene region in leaves of transgenic *Bt* rice grown under elevated CO<sub>2</sub> with different N-fertilizer rates. (n=minimum of 10 clones for each treatment. Positions of cytosines (CGN, CHG and CHH) on the analyzed regions are represented in Fig. 7. Filled symbols indicate cytosine methylation. Red, blue and green circles represent CGN, CHG and CHH sites respectively, whereas H = A, T or C.

**Supplementary Fig. 3** Methylation maps of P2 fragment in the fused *Cry IAb/Ac* transgene region in leaves of transgenic *Bt* rice grown under ambient CO<sub>2</sub> with different N-fertilizer rates. (n=minimum of 10 clones for each treatment. Positions of cytosines (CGN, CHG and CHH) on the analyzed regions are represented in Fig. 7. Filled symbols indicate cytosine methylation. Red, blue and green circles represent CGN, CHG and CHH sites respectively, whereas H = A, T or C.

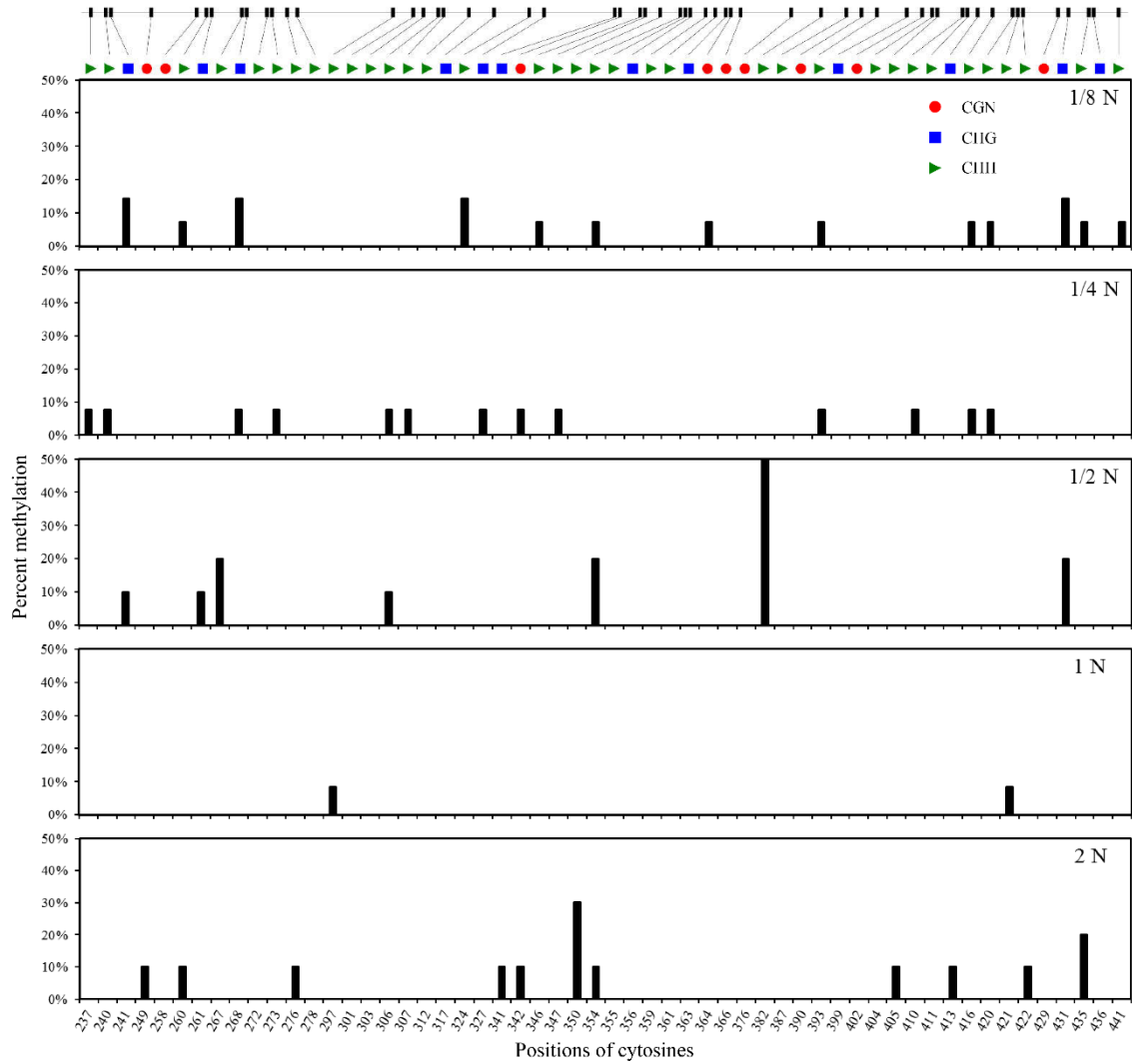
**Supplementary Fig. 4** Methylation maps of P2 fragment in the fused *Cry IAb/Ac* transgene region in leaves of transgenic *Bt* rice grown under elevated CO<sub>2</sub> with different N-fertilizer supply (n=minimum of 10 clones for each treatment. Positions of cytosines (CGN, CHG and CHH) on the analyzed regions are represented above. Filled symbols indicate cytosine methylation. Red, blue and green circles represent CGN, CHG and CHH sites respectively, whereas H = A, T or C.

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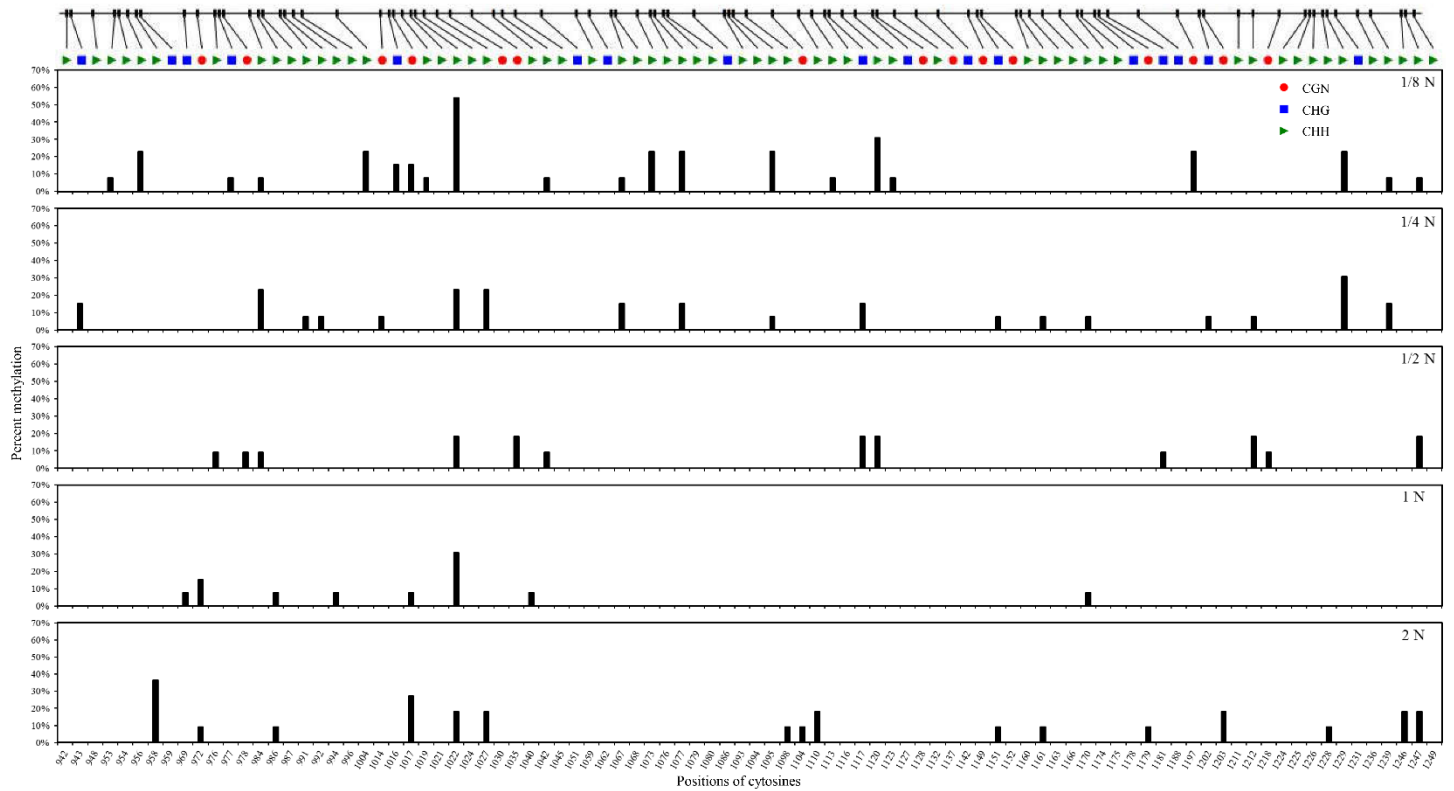
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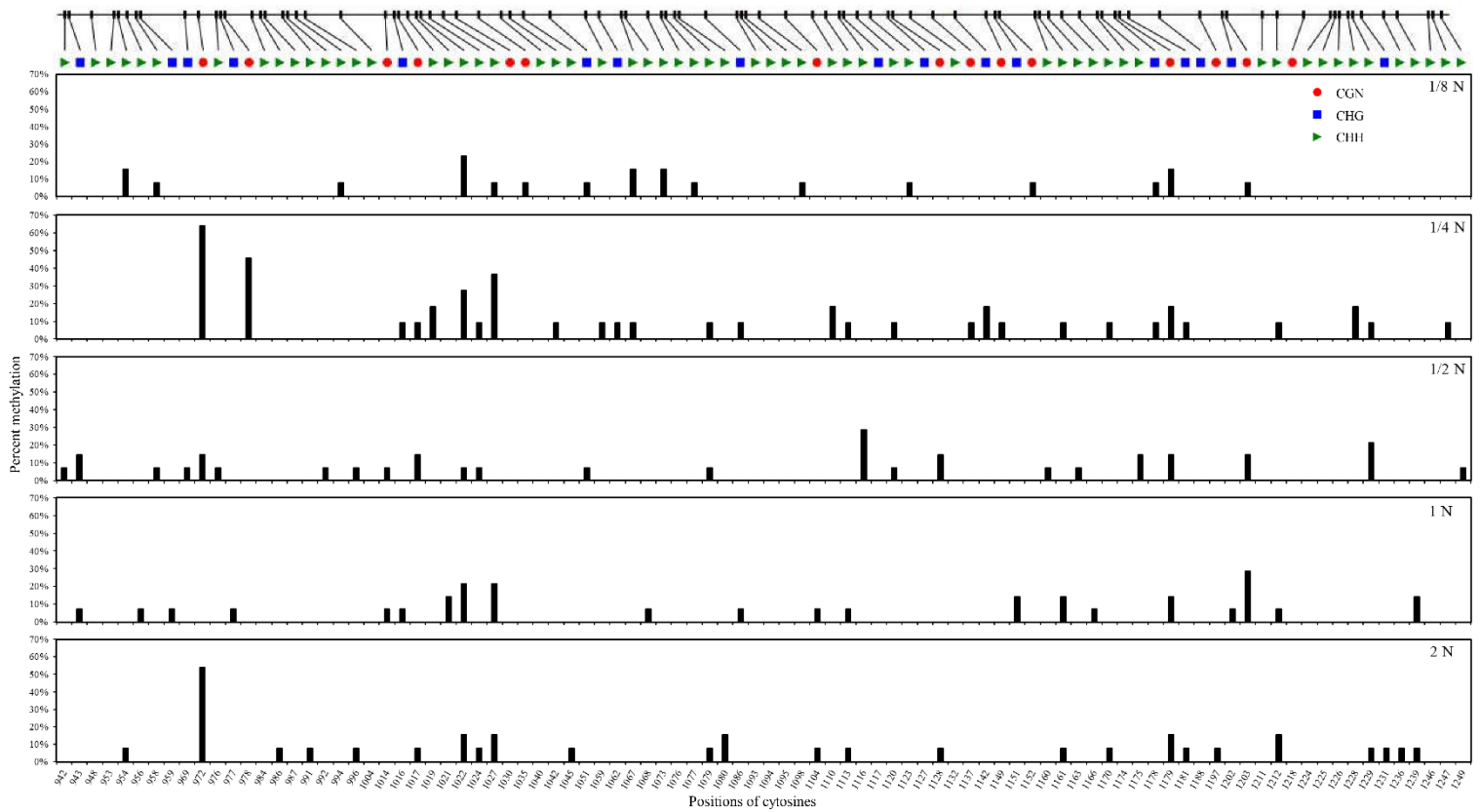
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**Supplementary Fig. 2** Methylation maps of P1 fragment in the fused *Cry IAb/Ac* transgene region in leaves of transgenic *Bt* rice grown under elevated CO<sub>2</sub> with different N-fertilizer rates (n=minimum of 10 clones for each treatment). Positions of cytosines (CGN, CHG and CHH) on the analyzed regions are represented in Fig 7. Filled symbols indicate cytosine methylation. Red, blue and green circles represent CGN, CHG and CHH sites respectively, whereas H = A, T or C).



**Supplementary Fig. 3** Methylation maps of P2 fragment in the fused *Cry IAb/Ac* transgene region in leaves of transgenic *Bt* rice plant grown under ambient CO<sub>2</sub> with different N-fertilizer supply (On the average of at least 10 clones for each treatment. Positions of cytosines (CGN, CHG and CHH) on the analyzed regions are represented above. Filled symbols indicate cytosine methylation. Red, blue and green circles represent CGN, CHG and CHH sites respectively, whereas H = A, T or C.)



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