Supplementary Files

Evaluation of plant growth promotion properties and induction of antioxidative defense mechanism by tea rhizobacteria of Darjeeling, India

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Table S1: Rhizobacterial consortium composition using a randomized design

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Figure S1. Evaluation of plant-growth promoting traits upon individual treatments of selected tea rhizobacterial isolates on the Early Golden Bantam variety of maize seedlings. Seven days old seedlings were treated with individual rhizobacterial isolates, and the growth parameters such as (a) wet weight, (b) dry weight, (c) root length, and (d) shoot length were measured 15 days post-treatment. A two-sided t-test determined the significance level, and data are mean ± SD. (a: P-value- 0.05–0.01, b: P-value 0.01–0.001, and c: P-value less than 0.001)

Figure S2. Evaluation of Chlorophyll concentration upon individual treatments of selected tea rhizobacterial isolates on the Early Golden Bantam variety of maize seedlings. Seven days old seedlings were treated with individual rhizobacterial isolates, and the total chlorophyll concentration was measured 15 days post-treatment. A two-sided t-test determined the significance level, and data are mean ± SD. (a: P-value- 0.05–0.01, b: P-value 0.01–0.001, and c: P-value less than 0.001)

Figure S3. Effect of rhizobacterial treatment on (a) ascorbate peroxidase (APX), (b) catalase (CAT), (c) chitinase, and (d) phenylalanine ammonia-lyase (PAL) activity in root fraction of IR64 variety of rice seedlings. Five days old rice seedlings were treated with individual rhizobacterial isolates, and the antioxidative defense enzymes were measured in the root lysate preparation 14 days post-treatment. A two-sided t-test determined the significance level, and data are mean ± SD. (a: P-value- 0.05–0.01, b: P-value 0.01–0.001, and c: P-value less than 0.001)

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Table S1. Rhizobacterial consortium composition using a randomized design

Consortium	Rhizobacterial isolates
Group I	*Arthrobacter* sp. AB200, *Staphylococcus pasteuri* AB212, *Bacillus* sp. AB233, *Bacillus altitudinis* AB242, *Pseudomonas stutzeri* AB266
Group II	*Exiguobacterium mexicanum* AB201, *Bacillus nakamurai* AB214, *Bacillus cereus* AB236, *Bacillus wiedmannii* AB246, *Ochrobactrum haematophilum* AB286
Group III	*Leifsonia lichenia* AB203, *Bacillus atrophaeus* AB228, *Bacillus flexus* AB255, *Staphylococcus cohnii* AB312, *Ochrobactrum anthropi* AB285
Group IV	*Bacillus niacini* AB209, *Bacillus velezensis* AB230, *Bacillus velezensis* AB237, *Bacillus megaterium* AB320, *Micrococcus luteus* AB321
Group V	*Bacillus subtilis* AB267, *Staphylococcus gallinarum* AB328, *Bacillus thuringiensis* AB341, *Staphylococcus haemolyticus* AB336, *Bacillus pumilus* AB276
Group VI	*Bacillus paralicheniformis* AB330, *Staphylococcus edaphicus* AB331, *Ochrobactrum* sp. AB345, *Lysinibacillus fusiformis* AB332, *Bacillus nitratireducens* AB304

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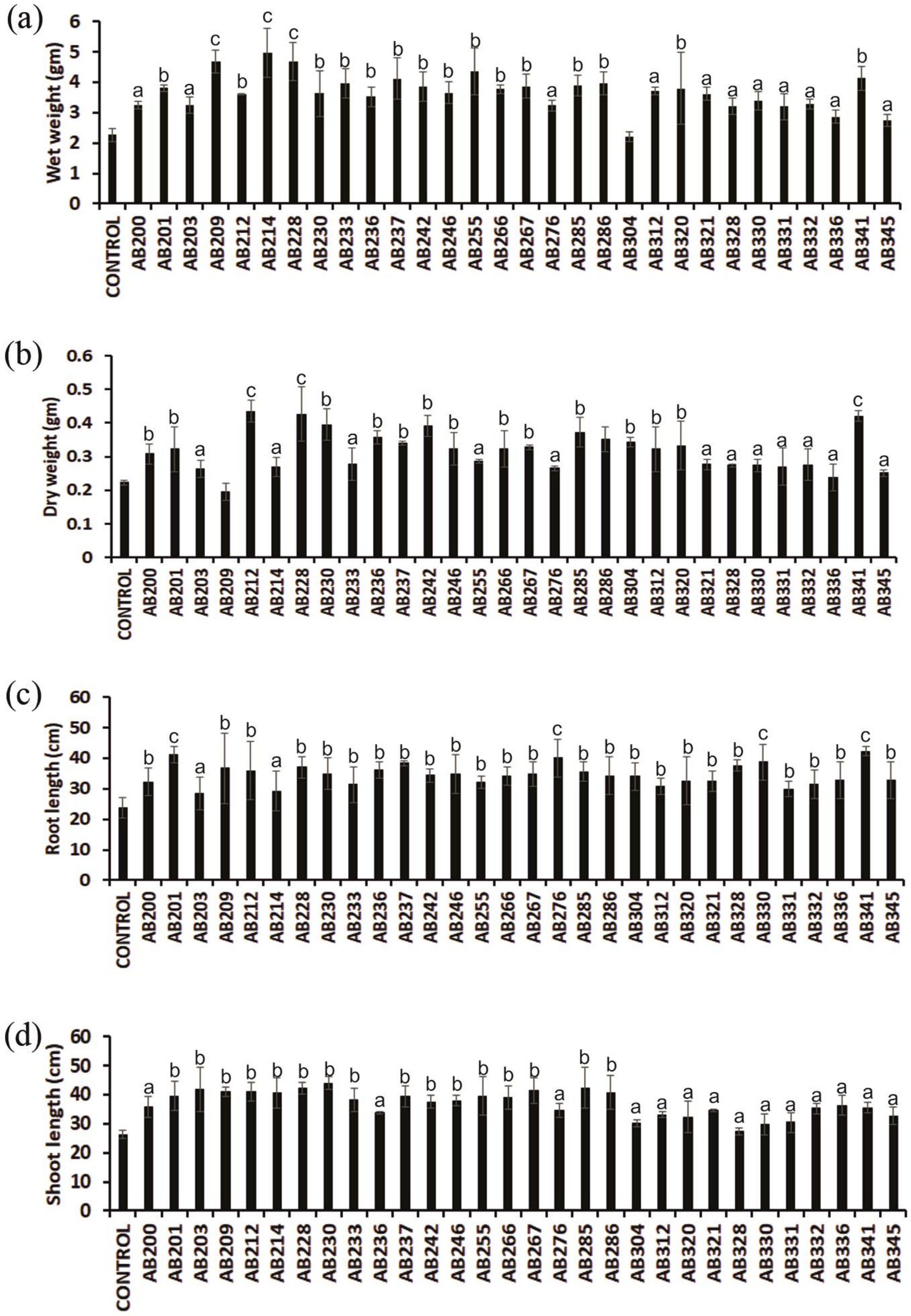

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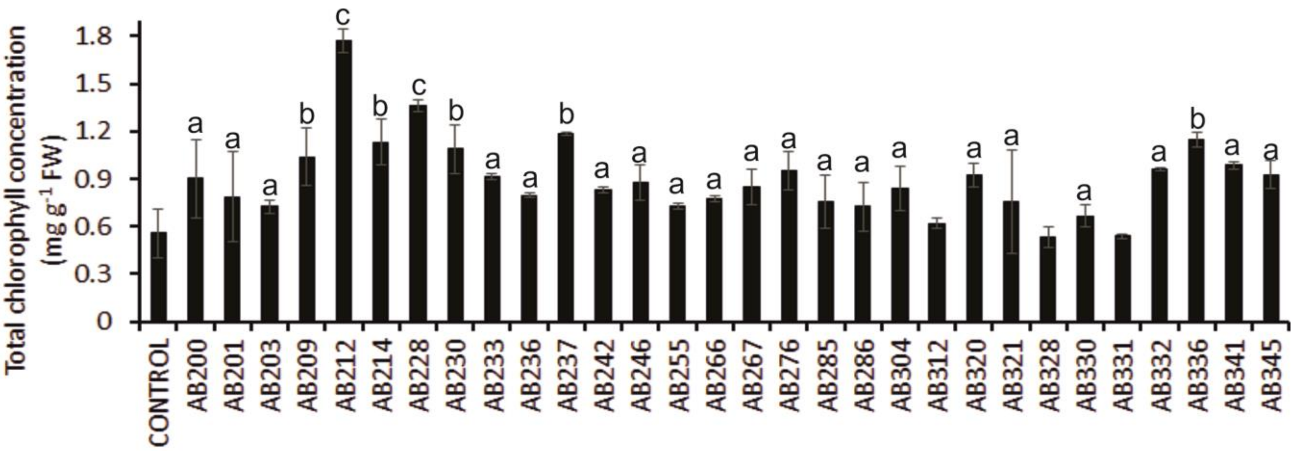
Figure S2. Evaluation of Chlorophyll concentration upon individual treatments of selected tea rhizobacterial isolates on the Early Golden Bantam variety of maize seedlings. Seven days old seedlings were treated with individual rhizobacterial isolates, and the total chlorophyll concentration was measured 15 days post-treatment. A two-sided t-test determined the significance level, and data are mean ± SD. (a: P-value- 0.05–0.01, b: P-value 0.01–0.001, and c: P-value less than 0.001)



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