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Supplementary Materials: Identification of Two Diamondback Moth Parasitoids, *Diadegma fenestrale* and *Diadegma semiclausum*, Using LAMP for Application in Biological Control

Hwayeun Nam, Min Kwon, Srinivasan Ramasamy and Juil Kim

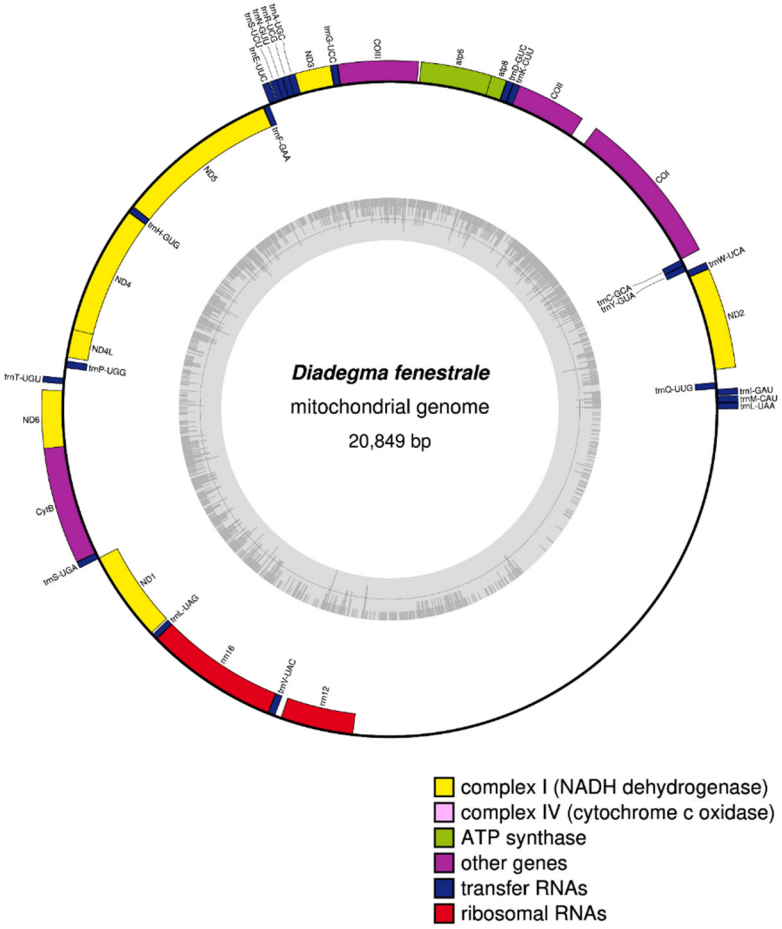

Figure S1. Organization of the mitochondrial genome of Korean population of *Diadegma fenestrale* (MN599978). ND: NADH dehydrogenase components (complex I) is shown in yellow. COX: cytochrome oxidase subunits (complex VI) is shown in pink. ATP synthase is shown in green. CYPB: cytochrome oxidase b is shown in purple. Ribosomal RNA genes are shown in red, and tRNA genes are shown in blue. Noncoding regions are not colored.

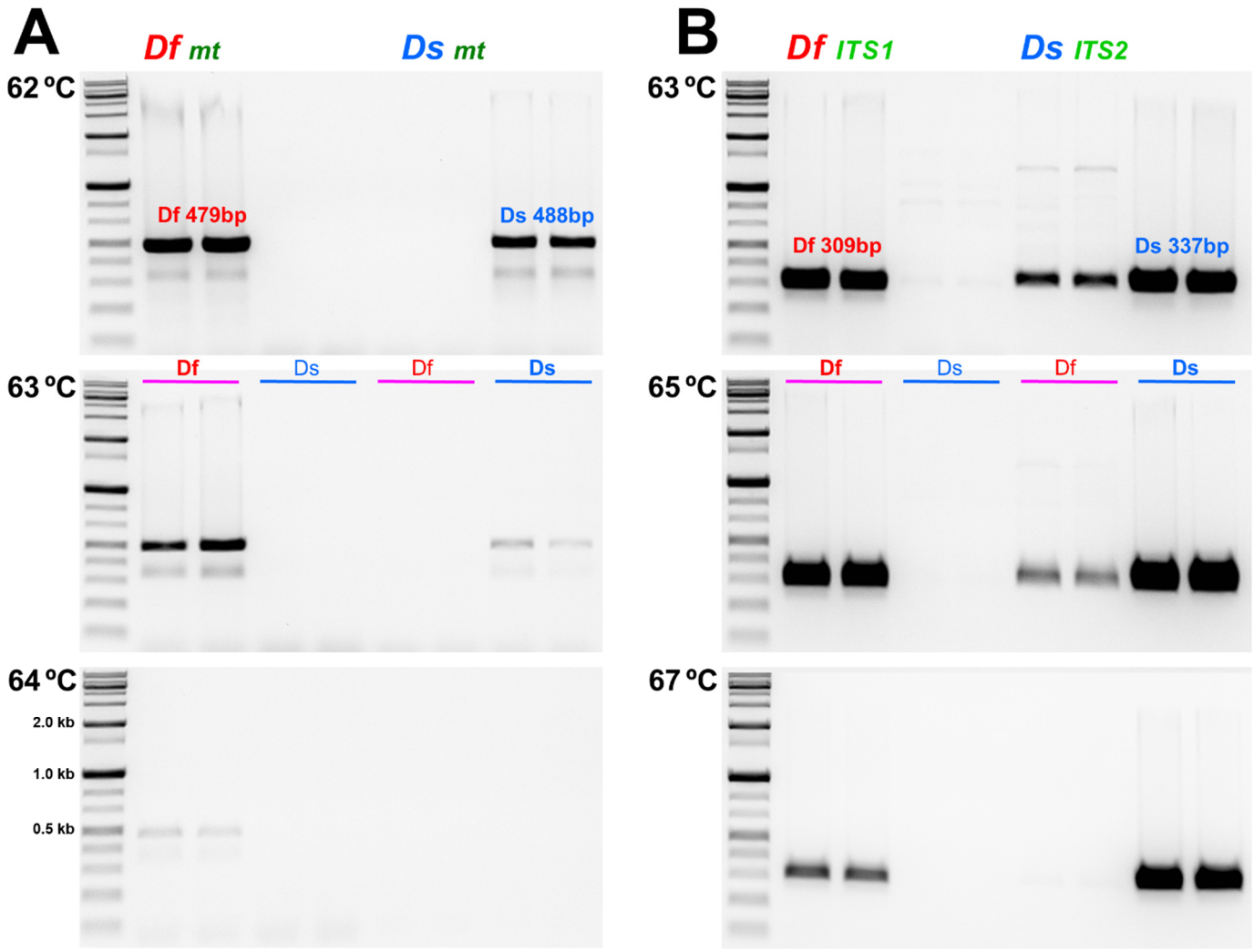

Figure S2. Conventional polymerase chain reaction (PCR) to distinguish Df and Ds by using specific primers in mt genome, ITS1, and ITS2. PCR with LAMP external primer set (**A**) based on mt genome used at three temperature conditions (62, 63, and 64 °C) and (**B**) based on ITS1 and ITS2 used at three temperature conditions (63, 65, and 67 °C). Df, *Diadegma fenestrale*; Ds, *Diadegma semiclausum*; DBM, diamondback moth; LAMP, loop-mediated isothermal amplification. PCR was performed under the following thermal conditions: initial denaturation at 95 °C for 1 min, followed by 35 cycles of 95 °C for 15 s, various annealing temperatures for 15 s, and 68 °C for 15 s, and final extension for 1 min at 68 °C.