

Abstract

Bamboo is used for making structures, bamboo crafts, furniture, and bamboo shoot and foods, tourism of ecology and culture are additional bamboo-farming culture as well as a source of food in Korea. In addition, 'Traditional land use structure in rural Damyang bamboo-field area' is formed in 'forest - bamboo field-village-cultivation area-stream' formation, and rich agro-biodiversity and cultural landscape of bamboo farming and crafting are fruitful results of the structure. One of the emerging diseases of bamboo in the country is the bamboo witches' broom (BWB). However, studies and information about BWB in the country remain lacking and largely unexplored. In this study, we bamboo leaf and stem samples which showed BWB symptoms were collected from in five major bamboo plantation area, and the samples were subject to high-throughput sequencing, for identify pathogen that causes BWB. One fungi which is *Aciculosporium take* was identified in bamboo libraries. *A. take* (Ascomycota; Clavicipitaceae) causes continuous shoot growth but maintains normal leaf-arrangement and branching patterns in the host plant, which eventually resulting in witches' broom disease of bamboo. Colonized shoots by *A. take* continue to grow in an acropetal sequence with very thin stems and little leaves, although normal bamboo shoots cease to grow when three to five leaves develop. For rapid and specific detection of *A. take*, we developed Taqman probe-based qPCR methods. Then, we investigate the occurrence patterns of BWB in Damyang. A total of 150 bamboo leaf samples, 150 bamboo stems samples, and 150 roots samples were collected randomly and tested for infection using qPCR. More than 50% of the tested samples were infected with *A. take*. The infection rate in collected leaf samples was 26.7%, stem samples was 27.3%, and root samples was 0.7%.

Results

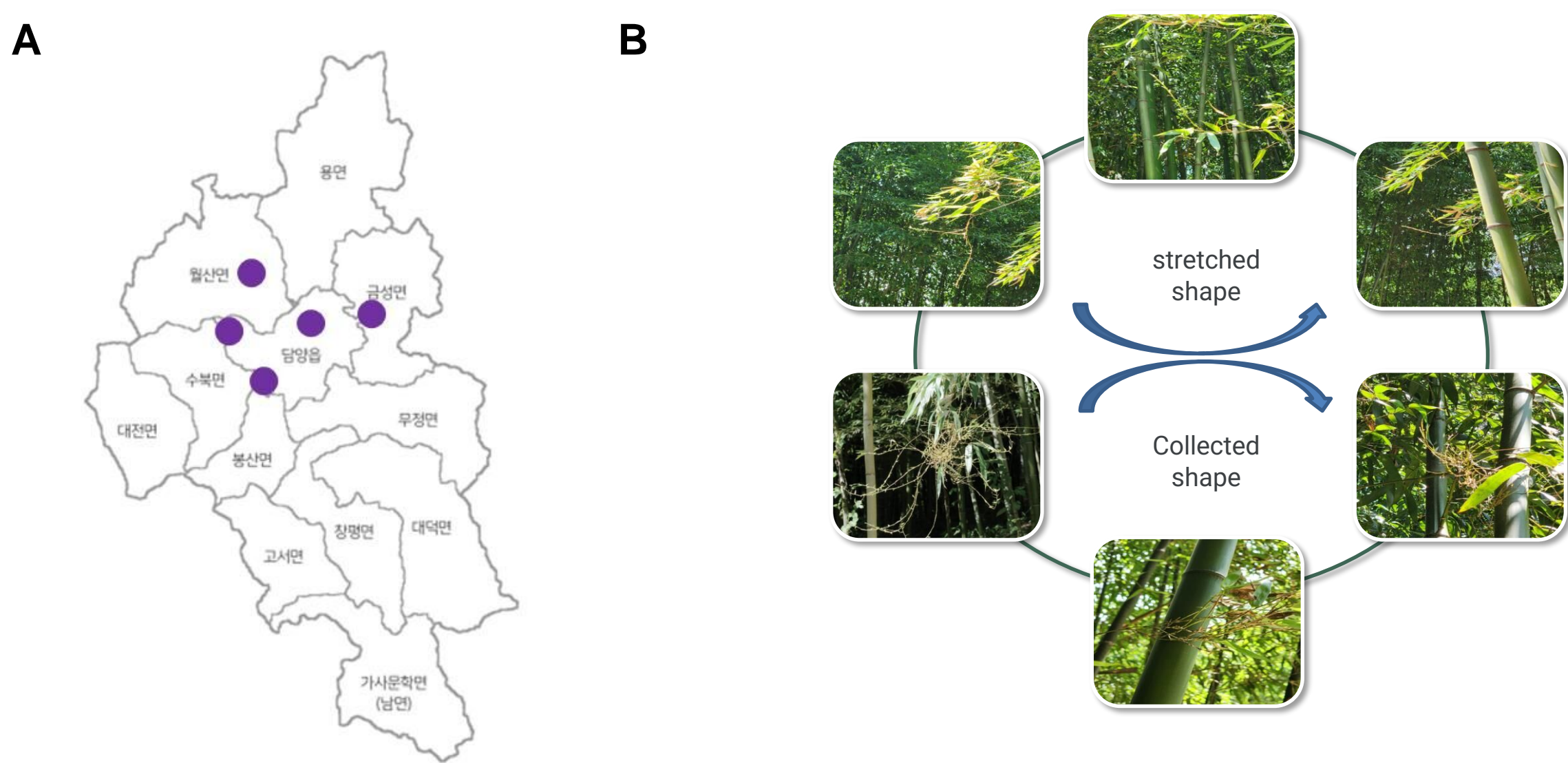


Fig. 1. The phenotypes of bamboo and map of Damyang areas surveyed in 2024. (A) Map of Damyang showing areas surveyed in 2024. (B) Symptoms of bamboo witches' broom (BWB) infection on bamboo in Korea.

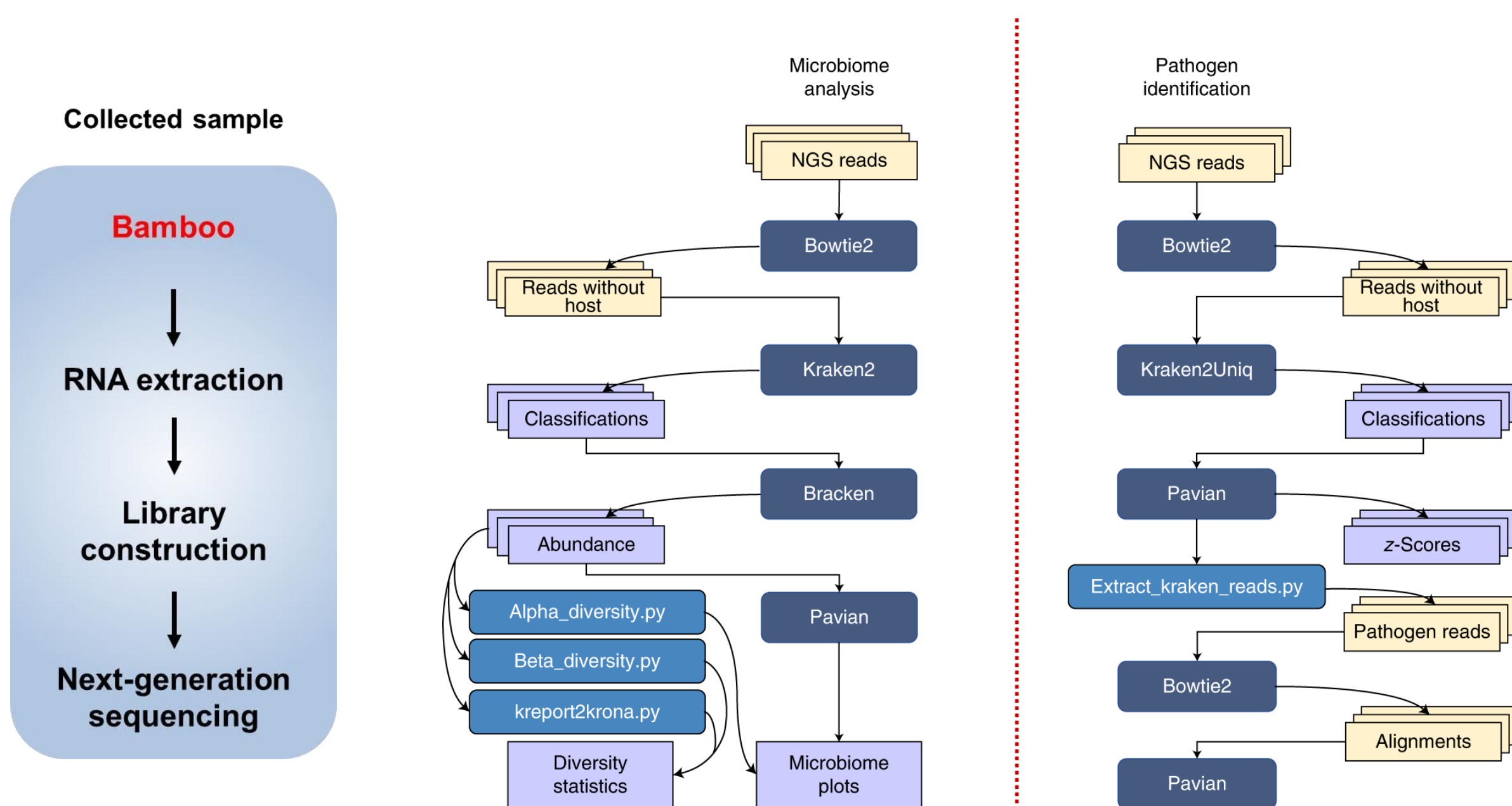


Fig. 2. The experimental scheme. Overview of two workflows (1) pathogen identification and (2) microbiome analysis.

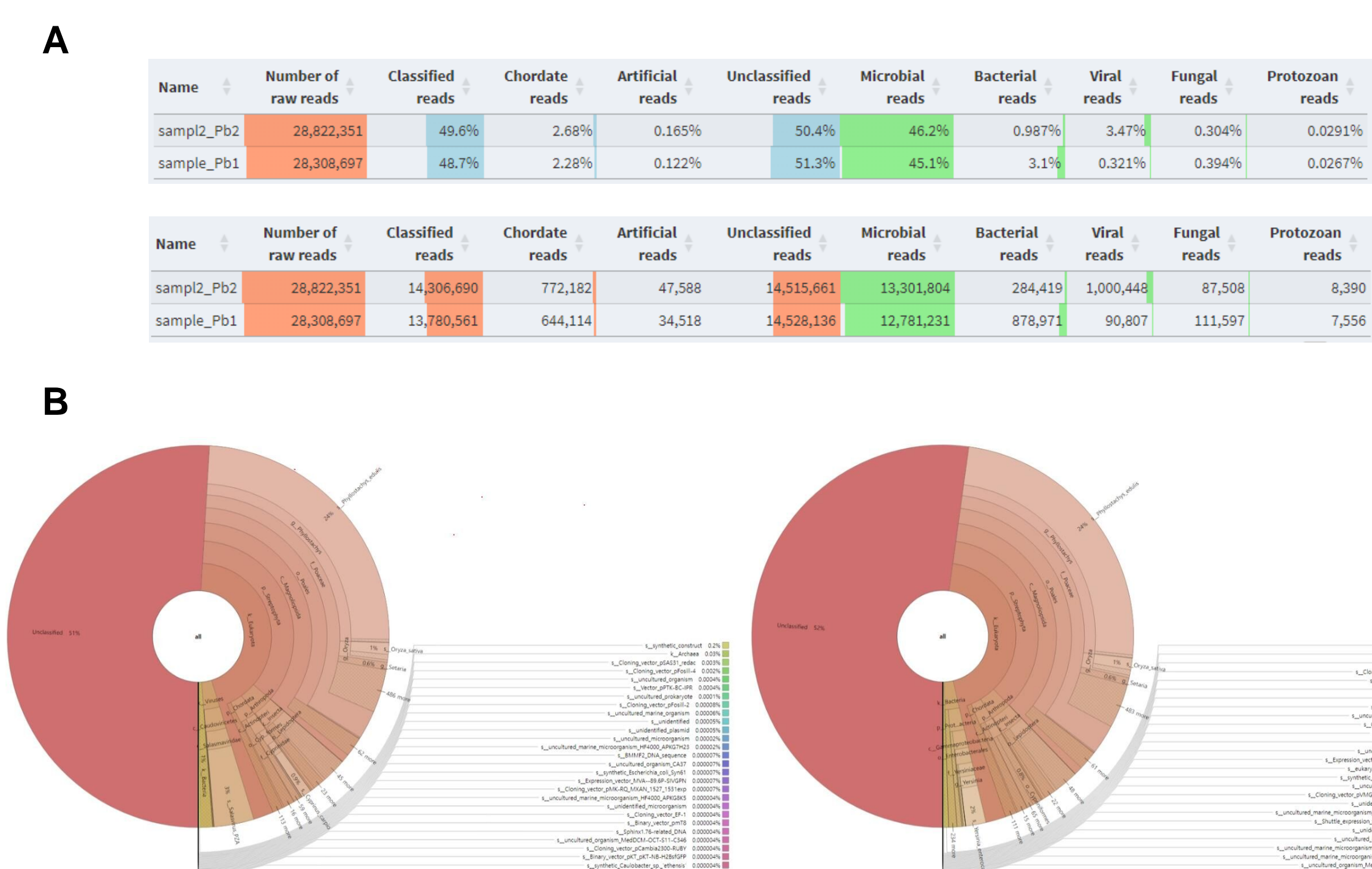


Fig. 3 Classification results of bamboo samples. (A) Sample set summary (B) The Krona RSF display. The bacterioplankton metagenome from a vertical profiling of the North Pacific Subtropical Gyre was imported from METAREP and displayed using Krona.

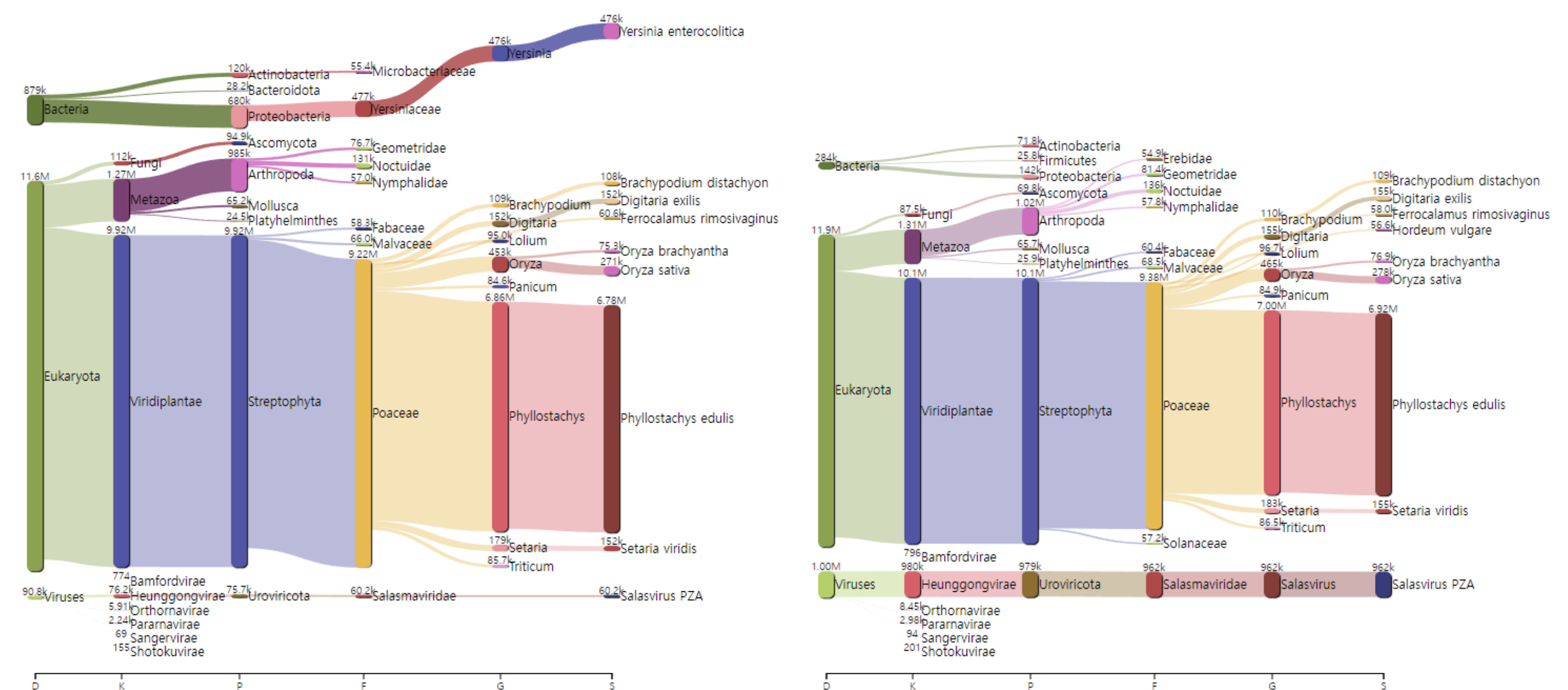


Fig. 4. Sankey visualization of the absolute read counts as estimated by Kraken/Bracken from the bamboo samples. D, Domain; P, Phylum; F, family; G, genus; D, domain.

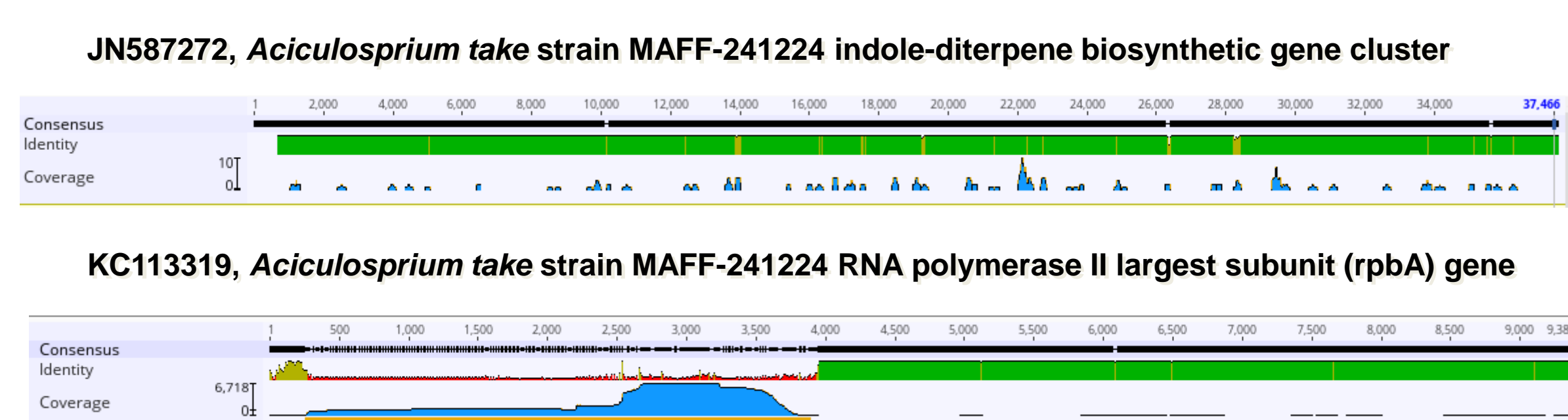


Fig. 5. Read mapping to reference sequences using geneious program. Reference sequence: *Aciculosporium take*

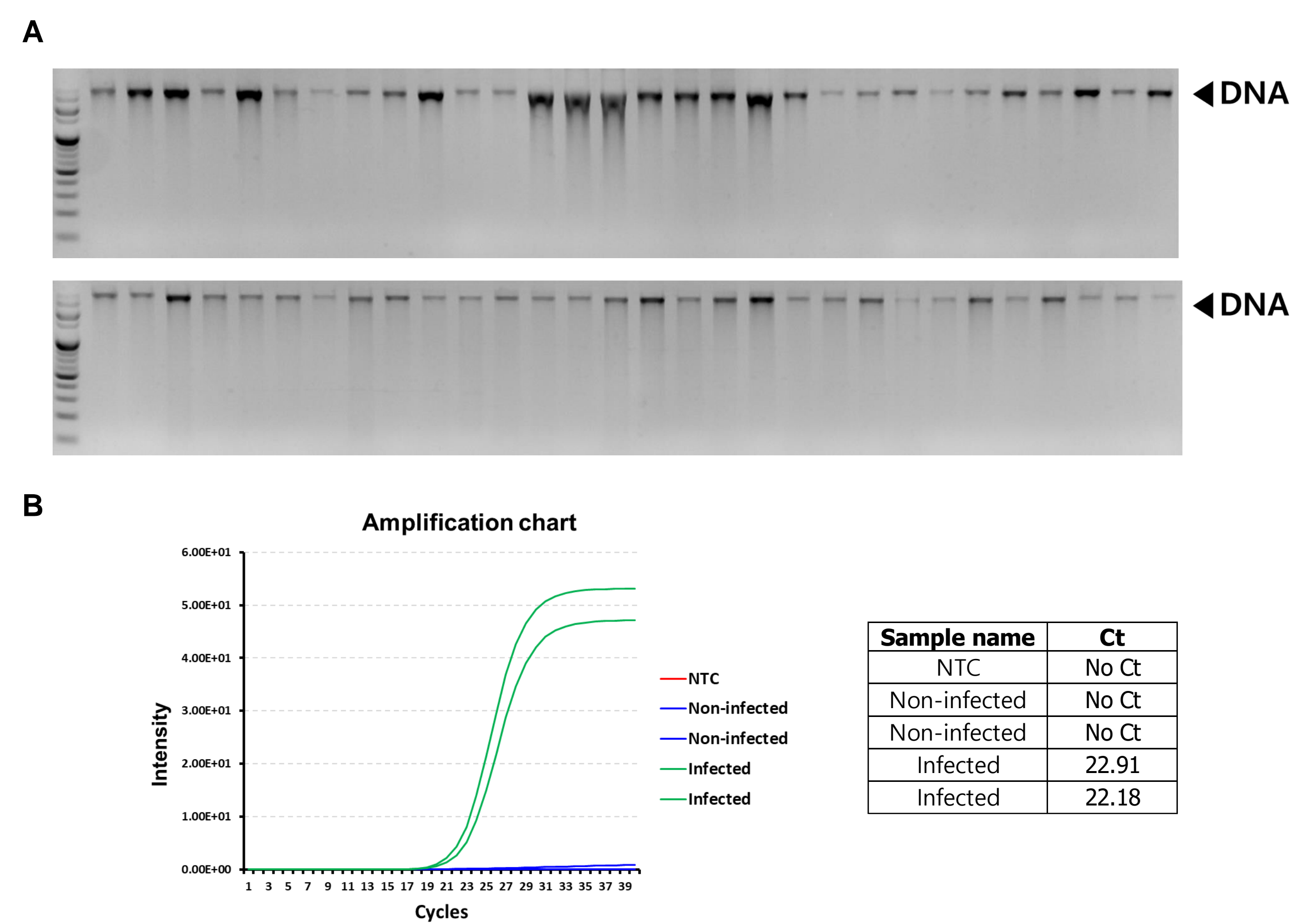


Fig. 6. DNA extraction results and real-time PCR results. (A) The analysis of 1% agarose gel electrophoresis of extracted DNA from bamboo samples (B) Real-time PCR amplification plot of the assay targeting *A. take*

	Region1	Region2	Region3	Region4	Region5	Total (ea)
Leaf	6	0	20	11	3	40
Stem	13	0	9	19	0	41
Root	0	1	0	0	0	1
Total	19	1	29	30	3	82

	Region1	Region2	Region3	Region4	Region5	Total (%)
Leaf	8.6	0.0	100.0	55.0	15.0	26.7
Stem	18.6	0.0	45.0	95.0	0.0	27.3
Root	0.0	5.0	0.0	0.0	0.0	0.7
Total	9.0	1.7	48.3	50.0	5.0	18.2

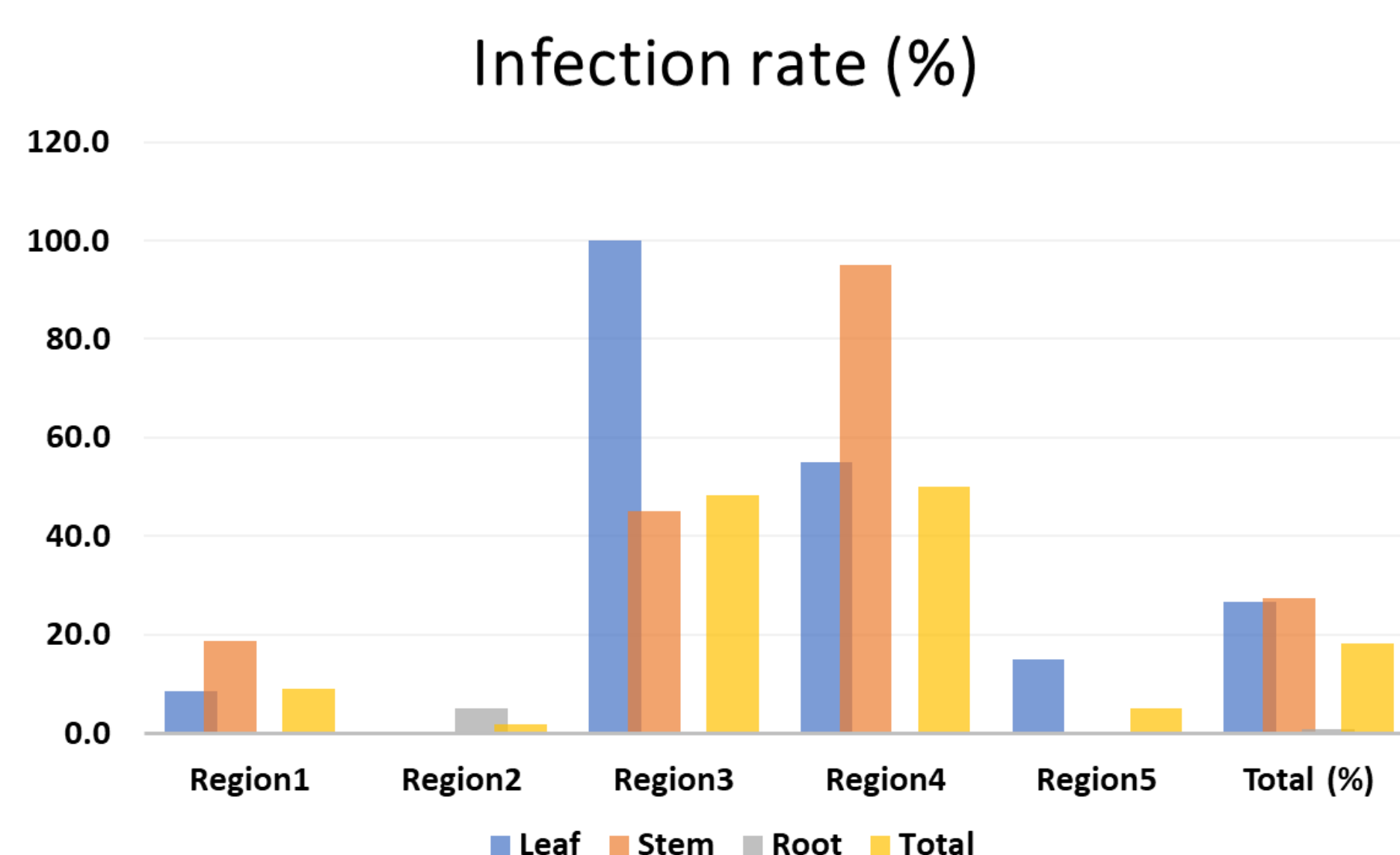


Fig. 7. Survey on bamboo witches' broom (BWB) infection for bamboo in Damyang.