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Prophage Diversity and Conservation in Burkholderia Pseudomallei: Implications for Virulence and Environmental Adaptation

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Burkholderia pseudomallei is an environment bacterium that often caused potentially fatal disease melioidosis. Genetic diversity of environment isolates was largely unknown despite of almost all infections emerging from environmental exposure. Prophage DNA acquired via horizontal gene transfer significantly contributes to genetic diversity, virulence and environment adaptability. In this study, nine whole genome sequences of Sri Lankan clinical isolates and 50 clinical isolates from other geographic origins (Australia, India, Thailand, China, Malaysia, Taiwan) were analyzed for prophages using PHASTEST online tool. Hypothetical proteins in intact prophages used NCBI protein BLAST. The whole genome sequences were downloaded in FASTA format from NCBI. Diversity of intact prophages were high in the genomes of B. pseudomallei reported from Australia, Thailand as compared to that of from Sri Lanka. The most commonly detected intact prophages include PHAGE_Burkho_phi52237_NC_007145, PHAGE_Burkho_phiE202_NC_009234, PHAGE_Burkho_KL3_NC_015266, PHAGE_Burkho_phiE12_2_NC_009236. PHAGE_Bacill_AR9_NC_031039, PHAGE_Burkho_KS10_NC_011216C,PHAGE_Burkho_KS10_NC_011216, PHAGE_Burkho_phi1026b_NC_005284, PHAGE_Entero_Arya_NC_031048, and PHAGE_Escher_vB_EcoM_ECO1230_10_NC_027995. Comparative genome analysis of prophage DNA showed co-evolutionary relationship of intact prophages in B. pseudomallei from various geographic regions. PHAGE_Burkho _phiE202_NC_009234 was the most common intact prophage found in Sri Lankan isolates. Further, results in this study indicated that highly conserved prophage proteins were present among different strains. Presence of marR, BrnT family toxin immunity 32, PAAR motif genes suggest they might play key roles in B. pseudomallei's prophage acquisition, virulence, and adaptation. Phylogenetic analysis demonstrated a co-evolutionary relationship among strains with different geographic origins. This high conservation indicates that prophages play a crucial role in the genetic diversity, virulence, and environmental adaptability of B. pseudomallei.

Keywords: *Burkholderia pseudomallei, melioidosis, prophage diversity, co-evolutionary relationship, comparative genome analysis, Sri Lanka*