106 年度生醫系專題研究競賽報名表

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題目(中文)：藉以電腦輔助設計胜肽疫苗-豬圓環病毒之豬隻 T 輔助細胞抗原決定位分析

題目(英文)：Analysis of Porcine T helper cell epitopes about porcine circovirus

摘要：

Background and motivation

Post-weaning multisystemic wasting syndrome (PMWS) represents a major disease of Porcine circovirus associated disease (PCVAD) cause by Porcine circovirus (PCV type ii), which can cause diarrhea and weight loss of a growing pig. To resist the infection of porcine circovirus, we use bioinformatic methods to discover potential peptide vaccines of this non-enveloped, icosahedron and smallest single-stranded DNA virus.

Method

In our peptide vaccine design pipeline, it contains several steps, including peptide sequences analysis, filtering, homology modeling, energy minimization, and pocket calculation. The optimized procedures (homology modeling, energy minimization, and pocket calculation) can enhance the binding affinity of peptides.

Result

First step, we collected peptide sequence (T cell epitope and B cell epitope) from immune epitope database (IEDB) and predicted T cell epitope in whole PCV genome sequence by ProPred (MHC Class ii binding peptide prediction server). And we had 27 T cell epitopes and 25 B cell epitopes. Second step, deleted the sequence that had defective point and classified all peptide sequences by the profiles that on the sequences. Third step, using human leukocyte antigen (HLA) three-dimension data and Porcine histocompatibility antigens (SLA) two-dimension data to execute homology modeling and minimized the peptide structure's energy (Scwrl and Chimera). Forth step, calculating the pockets at the position 1, 4, 6, 7, and 9 of the epitopes then applied this information to the original sequences.

Conclusion and future works

In concluded, we create a better binding affinity antigen (peptide sequence). For now, we had finished position 1, 4, 6, 7, and 9 of the epitopes for MHC class ii optimization, in future works, we will optimize the other side of immune binding sites.