豬瘟病毒與邊境病毒共同抗原決定位之研究

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摘要

瘟疫病毒屬(pestivirus)包含幾個感染經濟動物之重要病毒，如豬瘟病毒(classical swine fever virus; CSFV)、牛病毒性下痢(bovine viral diarrhea virus; BVDV)與邊境病毒(border disease virus; BDV)。這幾種病毒皆會感染豬隻且具相似之抗原性，造成豬隻血清抗體之交叉反應，因而干擾豬瘟血清學上之診斷。有鑑於此，找出豬瘟病毒之特異性與不同瘟疫病毒之間共同之抗原決定位，將有助於瞭解造成血清抗體交叉反應之機制。本研究使用不同病毒來源之六個單株抗體與不同瘟疫病毒株分析其反應，更進一步使用表現分段及變異之豬瘟病毒及邊境病毒 E2 醣蛋白分析與單株抗體之作用，找出各單株抗體所辨認之抗原決定位。本研究共找出四個單株抗體辨認所需之重要胺基酸，此四個胺基酸位於 E2 醣蛋白 domain B/C，共組成兩個抗原決定位，其中 G725 與 V738/I738 位於具豬瘟病毒特異性之抗原決定位，而 P709/L709 與 E713 位於另一個豬瘟病毒與邊境病毒共同之抗原決定位。3D 結構分析顯示此兩個抗原決定位皆位在 E2 醣蛋白表面。本研究結果可更深入瞭解 E2 醣蛋白之抗原性結構，並有助於豬瘟與其它瘟疫病毒之區別診斷。

Identification of a common conformational epitope on the glycoprotein E2 of classical swine fever virus and border disease virus

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Abstract

Classical swine fever virus (CSFV) shares high structural and antigenic homology with bovine viral diarrhea virus (BVDV) and border disease virus (BDV). Because all three viruses can infect swine and elicit cross-reactive antibodies, it is necessary to differentiate among them with regard to serological diagnosis of classical swine fever. To understand the mechanism of crossreactivity, it is important to define common or specific epitopes of these viruses. For this purpose, epitope mapping of six monoclonal antibodies (mAbs) was performed using recombinant expressed antigenic domains of CSFV and BDV E2 proteins. One CSFV-specific conformational epitope and one CSFV and BDV common epitope within domain B/C of E2 were identified. Site-directed mutagenesis confirmed that residues G725 and V738/I738 of the CSFV-specific epitope and P709/L709 and E713 of the second epitope are important for mAbs binding. 3D structural modeling suggested that both epitopes are exposed on the surface of E2. These findings will further enhance the understanding of the structural and antigenic topography of glycoprotein E2 and will improve the differential diagnosis of porcine pestivirus infections.