

行政院農業委員會家畜衛生試驗所

106 年第四季禽流感病毒分析訊息

本季分析病毒株為 2017 年 12 月 22 日由南投縣家畜疾病防治所採送主動監測檢體所檢出之 2 場鴨源 H5N6 亞型低病原性禽流感病毒株(編號 17A0759 與 17A0760)，此 2 場為同一畜主，2 株病毒 8 段基因呈現 99.6~99.9 %相似度。兩場案例的 HA 基因序列與 GenBank 資料庫比對後，與 2005~2013 年臺灣鴨隻的 14 株 H5N2 亞型病毒株最相近，核苷酸相似度為 93~97%；而與其餘地區之歐亞野鳥病毒群 HA 基因之核苷酸相似度均在 83%以下（圖一），HA 基因源自臺灣特有之低病原性禽流感病毒群，而非境外移入之禽流感病毒。8 段基因於 GenBank 資料庫比對結果如表一。特別的是在 NA stalk 區域有 13 個連續胺基酸的缺損（deletion），有文獻指出 NA stalk 的缺損可能增進病毒對陸禽之適應性，因而提高跨物種傳播之風險。

(本季病毒核酸序列若有學者有研究參考需求，請逕向畜衛所洽取。)

Sequences producing significant alignments:

Select: All None Selected:0

Alignments		Download	GenBank	Graphics	Distance tree of results		
	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Influenza A virus (A/duck/Taiwan/11213/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2843	2843	95%	0.0	97%	KJ162796.1
☐	Influenza A virus (A/duck/Taiwan/11254/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2832	2832	95%	0.0	97%	KJ162804.1
☐	Influenza A virus (A/duck/Taiwan/758/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2828	2828	95%	0.0	97%	KJ162724.1
☐	Influenza A virus (A/duck/Taiwan/4379/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2826	2826	95%	0.0	97%	KJ162780.1
☐	Influenza A virus (A/duck/Taiwan/755/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2826	2826	95%	0.0	97%	KJ162716.1
☐	Influenza A virus (A/duck/Taiwan/4380/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2822	2822	95%	0.0	97%	KJ162788.1
☐	Influenza A virus (A/duck/Taiwan/4378/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2820	2820	95%	0.0	97%	KJ162772.1
☐	Influenza A virus (A/duck/Taiwan/4355/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2820	2820	95%	0.0	97%	KJ162740.1
☐	Influenza A virus (A/duck/Taiwan/4374/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2817	2817	95%	0.0	97%	KJ162784.1
☐	Influenza A virus (A/duck/Taiwan/4360/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2817	2817	95%	0.0	97%	KJ162748.1
☐	Influenza A virus (A/duck/Taiwan/4372/2013(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2815	2815	95%	0.0	97%	KJ162756.1
☐	Influenza A virus (A/duck/Taiwan/DV30-2/2005(H5N2)) hemagglutinin (HA) gene, complete cds	2564	2564	98%	0.0	93%	CY110933.1
☐	Influenza A virus (A/Taiwan/DV413/2006(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2532	2532	98%	0.0	93%	KP792300.1
☐	Influenza A virus (A/Taiwan/DV518/2006(H5N2)) segment 4 hemagglutinin (HA) gene, complete cds	2523	2523	98%	0.0	93%	KP792308.1
☐	Influenza A virus (A/goose/Hong Kong/23/1978(H5N3)) segment 4, complete sequence	1605	1605	100%	0.0	83%	CY006028.1
☐	Influenza A virus (A/greater white-fronted goose/Netherlands/5/2010(H5N3)) segment 4 hemagglutinin (HA) gene, complete cds	1600	1600	100%	0.0	83%	KX978851.1
☐	Influenza A virus (A/duck/Potsdam/1402-6/1986(H5N2)) segment 4, complete sequence	1600	1600	100%	0.0	83%	CY014642.1
☐	Influenza A virus (A/mallard duck/Netherlands/19/2009(H5N3)) segment 4 hemagglutinin (HA) gene, complete cds	1594	1594	100%	0.0	83%	KX978032.1
☐	Influenza A virus (A/mallard duck/Netherlands/20/2009(H5N3)) segment 4 hemagglutinin (HA) gene, complete cds	1589	1589	100%	0.0	83%	KX978388.1

圖一、HA 序列與 GenBank 資料庫比對結果。

表一、南投 H5N6 低病原性禽流感病毒株 8 段基因序列比對結果

基因	17A0759	17A0760
PB2	A/duck/Hokkaido/10/2015(H3N6) (97.9%)	A/duck/Hokkaido/10/2015(H3N6) (97.8%)
PB1	A/duck/Mongolia/709/2015(H10N7) (98.2%)	A/duck/Mongolia/709/2015(H10N7) (98.2%)
PA	A/wild bird/Jiangxi/P419/2016(H6N8) (98.3%)	A/wild bird/Jiangxi/P419/2016(H6N8) (98.1%)
HA	A/duck/Taiwan/11213/2013(H5N2) (97.0%)	A/duck/Taiwan/11213/2013(H5N2) (97.0%)
NP	A/duck/Ganzhou/GZ5/2015(H4N6) (97.8%)	A/duck/Ganzhou/GZ5/2015(H4N6) (97.8%)
NA	A/duck/Mongolia/127/2015(H4N6) (97.3%)	A/duck/Mongolia/127/2015(H4N6) (97.1%)
M	A/duck/Hokkaido/W280/2014(H5N3) (98.2%)	A/duck/Hokkaido/W280/2014(H5N3) (97.8%)
NS	A/chicken/Wuhan/WHJF/2014(H5N2) (98.4%)	A/chicken/Wuhan/WHJF/2014(H5N2) (98.1%)