

Table S4. Mean migration rates of H6 subtype viruses between avian ecosystems across sampling locations. Statistically supported interactions are shown in bold.

Origin		Destination													
		Domestic							Wild						
		Japan/ S Korea	E China	C China	W China	SE Asia	Europe	North America	Japan/ S Korea	E China	C China	SE Asia	Middle East	Europe	North America
Domestic	Japan/ S Korea	-	0.33	0.32	0.19	0.19	0.15	0.15	0.68	0.29	0.23	0.24	0.26	0.29	0.20
	E China	0.68	-	1.26	0.33	1.10	0.26	0.17	0.56[†] (0.01, 1.42)	0.74	0.45	0.26	0.32	0.47	0.44
	C China	0.59	2.42[§] (1.07, 4.01)	-	0.61[§] (0.08, 1.28)	0.65[†] (0.09, 1.29)	0.17	0.09	0.56	0.61[†] (0.02, 1.43)	2.55[§] (1.23, 3.94)	0.21	0.14	0.31	0.59
	W China	0.42	0.36	0.49	-	0.41	0.29	0.39	0.32	0.47	0.35	0.61	0.42	0.37	0.42
	SE Asia	0.37	0.35	0.27	0.32	-	0.41	0.22	0.34	0.41	0.36	1.68[§] (0.40, 3.26)	0.28	0.25	0.32
	Europe	0.34	0.29	0.36	0.28	0.38	-	0.37	0.39	0.35	0.30	0.39	0.45	1.35	0.57
	North America	0.27	0.26	0.38	0.31	0.37	0.27	-	0.48	0.39	0.39	0.36	0.32	0.55	0.60[§] (0.01, 1.49)
Wild	Japan/ S Korea	1.36[†] (0.12, 2.81)	0.66	1.46[§] (0.03, 3.82)	0.41	0.33	0.40	0.28	-	0.60	0.40	0.43	0.39	0.68	1.58[§] (0.21, 3.27)
	E China	1.68[†] (0.31, 3.12)	0.78	3.05[§] (0.17, 5.76)	0.93[†] (0.14, 1.95)	0.32	0.46	0.25	1.16[‡] (0.17, 2.46)	-	0.43	0.39	0.40	0.80[†] (0.09, 1.61)	1.19[†] (0.17, 2.35)
	C China	0.42	0.52	0.46	0.47	0.37	0.24	0.35	0.52	0.79	-	0.36	0.35	0.53	0.77
	SE Asia	0.31	0.29	0.36	0.37	0.38	0.35	0.45	0.32	0.32	0.30	-	0.43	0.29	0.39
	Middle East	0.39	0.36	0.40	0.42	0.56	0.30	0.43	0.46	0.41	0.27	0.67[§] (0.04, 1.62)	-	0.42	0.56
	Europe	0.17	0.18	0.22	0.20	0.15	2.33[§] (0.53, 4.17)	0.19	0.27	0.27	0.23	0.32	0.61[§] (0.06, 1.26)	-	0.35
	North America	0.10	0.12	0.15	0.17	0.10	0.12	0.41[§] (0.07, 0.86)	0.12	0.28	0.21	0.10	0.09	0.23[§] (0.01, 0.53)	-

BSSV statistically supported migration rates with 95% Bayesian credible intervals (BCI), where the Bayes factor was >12. [†] 12 > BF ≥ 30; [‡] 30 > BF ≥ 100; [§] BF > 100