

## **Quantification of Avian Influenza A Virus (H5N1) via Enzymatic Reactions and Glucometer Test Strips**

### **Supplementary Information**

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**Table S1.** Performance comparison of the present H5N1 detection method with representative recent platforms (as reported in the cited sources).

Method / Platform	Target	Detection Format	Matrix	LOD (reported)	Reference
This work (binding buffer, artificial saliva, tap water)	H5N1 virus (via HA)	Amperometric (glucose strip)	Binding buffer / Artificial saliva / Tap water	$7.78 \times 10^5 - 1.46 \times 10^6$ RNA copies mL <sup>-1</sup>	This work
Paper-based electrochemical immunosensor	H5N1 HA antigen	DPV electrochemical	PBS	55.7 pg mL <sup>-1</sup> (0.95 pM)	Lee et al., 2022 <sup>1</sup>
Capacitive biosensor	H5N1 viral RNA	Capacitive response	Aerosol samples	56 RNA copies mL <sup>-1</sup>	Kumar et al., 2025 <sup>2</sup>
RT-RAA + CRISPR-Cas13a + LFD	H5 subtype AIV (HA gene)	Lateral flow	Clinical poultry samples	0.1 copy $\mu$ L <sup>-1</sup>	Li et al., 2023 <sup>3</sup>
RT-RAA + CRISPR-Cas13a	Pan-AIV (M gene)	Fluorescence / LFA	—	1 copy $\mu$ L <sup>-1</sup> (fluorescence); 10 copies $\mu$ L <sup>-1</sup> (LFA)	Yang et al., 2025 <sup>4</sup>
SPR biosensor	H5N1 virus	SPR ( $\Delta$ RU)	Poultry samples	2.24 Hemagglutination unit	Prayugo et al., 2025 <sup>5</sup>
Commercial rapid antigen & POC molecular tests	H5N1 strains	LFA / Molecular amplification	Nasal swab	1.55–7.75 TCID <sub>50</sub> /swab (molecular); 78–1550 TCID <sub>50</sub> /swab (LFA)	Bassit et al., 2025 <sup>6</sup>

Units are reproduced as reported in the original publications. Due to differences in reporting formats (RNA copies, TCID<sub>50</sub>, PFU, antigen mass, HAU), direct numerical comparison should be interpreted cautiously.

**Table S2.** Comparison of conventional ALP–PNPP colorimetric detection (UV–Vis, A405) and electrochemical strip-based amperometric detection for H5N1 quantification. The PNPP reaction mixture (200  $\mu\text{L}$ , 37  $^{\circ}\text{C}$ , 15 min) was divided into two equal aliquots for absorbance measurement and electrochemical analysis. Absorbance values represent the mean  $\pm$  standard deviation of three replicate measurements ( $n = 3$ ). Electrochemical currents were obtained using three independent glucose test strips, and values represent mean  $\pm$  standard deviation. Relative precision was evaluated using the coefficient of variation (CV%).

Electrochemical signal was quantified as the mean current (nA) averaged over 3–20 s of each chronoamperometric trace and summarized across three independent strips.

H5N1 (RNA copies $\text{mL}^{-1}$ )	A405 Mean $\pm$ SD	A405 CV (%)	Electrochemical Mean $\pm$ SD (nA)	Electrochemical CV (%)
Blank	0.023 $\pm$ 0.003	11.5	74 $\pm$ 3	4.2
$5.90 \times 10^6$	0.032 $\pm$ 0.003	9.4	84 $\pm$ 4	4.3
$2.21 \times 10^7$	0.085 $\pm$ 0.004	4.1	111 $\pm$ 7	6.1

**Table S3.** Spike–recovery, accuracy, and precision analysis of H5N1 detection across tested matrices.

Expected concentrations were prepared independently in each matrix. Measured values were back calculated from calibration curves. Intra-assay CV% represents variability across strips (n=3). Inter-assay CV% represents variability across independent runs performed on two different days.

Matrix	Expected (RNA copies mL <sup>-1</sup> )	Measured (RNA copies mL <sup>-1</sup> )	Recovery (%)	Intra-assay CV (%)	Inter-assay CV (%)
Binding buffer	2.94 × 10 <sup>6</sup>	2.43 × 10 <sup>6</sup>	82.59	—	11.13
Tap water	2.94 × 10 <sup>6</sup>	9.83 × 10 <sup>5</sup>	33.44	25.73	—
Artificial saliva	2.94 × 10 <sup>6</sup>	1.86 × 10 <sup>6</sup>	63.41	10.60	—
Binding buffer	5.90 × 10 <sup>6</sup>	5.21 × 10 <sup>6</sup>	88.23	—	6.49
Tap water	5.90 × 10 <sup>6</sup>	4.89 × 10 <sup>6</sup>	82.80	19.13	—
Artificial saliva	5.90 × 10 <sup>6</sup>	5.55 × 10 <sup>6</sup>	94.15	15.09	—
Binding buffer	1.47 × 10 <sup>7</sup>	1.64 × 10 <sup>7</sup>	111.80	—	5.03
Tap water	1.47 × 10 <sup>7</sup>	1.76 × 10 <sup>7</sup>	119.66	10.67	—
Artificial saliva	1.47 × 10 <sup>7</sup>	1.65 × 10 <sup>7</sup>	112.38	7.44	—
Binding buffer	2.21 × 10 <sup>7</sup>	2.15 × 10 <sup>7</sup>	97.44	—	1.91
Tap water	2.21 × 10 <sup>7</sup>	2.22 × 10 <sup>7</sup>	100.79	12.16	—
Artificial saliva	2.21 × 10 <sup>7</sup>	2.16 × 10 <sup>7</sup>	98.09	5.46	—
Binding buffer	5.88 × 10 <sup>7</sup>	5.76 × 10 <sup>7</sup>	98.01	—	1.73
Tap water	5.88 × 10 <sup>7</sup>	5.38 × 10 <sup>7</sup>	91.54	13.60	—
Artificial saliva	5.88 × 10 <sup>7</sup>	5.69 × 10 <sup>7</sup>	96.82	1.96	—

Table S4. Composition of the ZeptoMetrix respiratory pathogen pools used for selectivity testing.

Pool	Number	Pathogen name
Pool 1	1	Influenza A H1N1 (A/NY/02/09)
	2	Parainfluenza Type 4A
	3	Parainfluenza Type 4B
	4	Rhinovirus (1A)
	5	Adenovirus Type 3
Pool 2	1	Influenza A H1 (A/New Caledonia/20/99)
	2	Respiratory Syncytial Virus A
	3	Parainfluenza Type 1
	4	Coronavirus NL63
	5	<i>Mycoplasma pneumoniae</i> (M129)
Pool 3	1	Influenza A H3 (A/Brisbane/10/07)
	2	Respiratory Syncytial Virus B (CH93(18)-18)
	3	Coronavirus OC43
	4	Coronavirus HKU-1 (Recombinant)
Pool 4	1	Influenza B (B/Florida/02/06)
	2	Parainfluenza Type 3
	3	Human Metapneumovirus (Peru6-2003)
	4	<i>Legionella pneumophila</i> (Philadelphia)
Pool 5	1	Parainfluenza Type 2
	2	Coronavirus 229E
	3	Human Bocavirus
	4	<i>Chlamydomydia pneumoniae</i> (CWL-029)

Reference:

1. D. Lee, J. Bhardwaj and J. Jang, *Sci. Rep.*, 2022, 12, 2311.
2. J. Kumar, M. Xu, Y. A. Li, S. W. You, B. M. Doherty, W. D. Gardiner, J. R. Cirrito, C. M. Yuede, A. Benegal, M. D. Vahey, A. Joshi, K. Seehra, A. C. M. Boon, Y. Y. Huang, J. V. Puthussery and R. K. Chakrabarty, *ACS Sens.*, 2025, 10, 3381–3389.
3. Y. Li, J. Shang, J. Luo, F. Zhang, G. Meng, Y. Feng, W. Jiang, X. Yu, C. Deng, G. Liu and H. Liu, *Front. Microbiol.*, 2023, 14, 1283210.
4. Y. Yang, Z. Yang, X. Zhang, B. Niu, Q. Huang, Y. Li, H. Yin, X. Zhang, M. Liao and W. Jia, *Poult. Sci.*, 2025, 104, 104745.
5. A. D. Prayugo, W. Widayat, T. Subroto, W. Arnafia, M. Yusuf, G. Gumilar, Y. F. Achmad, B. Sundari, A. K. Nissa and D. Sibit, *Talanta Open*, 2025, 12, 100577.
6. L. Bassit, G. L. Damhorst, H. B. Bowers, C. Sabino, J. Sullivan, E. B. Kennedy, J. Khouri, P. Miller, E. Lai, R. F. Schinazi, W. A. Lam, N. R. Pollock and A. Rao, *J. Clin. Microbiol.*, 2025, 63, e0054825.