World Organisation for Animal Health

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WOAH Collaborative Centre Reports Activities 2024

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CENTRE INFORMATION

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TOR 1 AND 2: SERVICES PROVIDED

1. Activities as a centre of research, expertise, standardisation and dissemination of techniques within the remit of the mandate given by WOAH

Category	Title of activity	Scope
		1. In 2024, we collected 59,914 swab

		samples from avian species, 530 swabs from dogs and cats, 2,946 swabs from pigs for zoonotic and animal diseases surveillance in China; we collected 7,040 avian sera, 3,168 swine sera, and 8,200 bovine sera for antibody surveillance. 2. Recently, an outbreak of highly pathogenic avian influenza A (H5N1), has been prevalent among North American bird populations since the winter of 2021, was reported in dairy cows in the United States. Notably, The US Food and Drug Administration reported that around 20% of tested retail milk samples contained H5N1 viruses, with a higher percentage of positive results from regions with infected cattle herds. Data are scant regarding how effectively pasteurization inactivates the H5N1 virus in milk. We evaluated the thermal stability of the H5 clade 2.3.4.4b viruses, along with one human H3N2 virus and other influenza subtype viruses, including H1, H3, H7, H9, and H10 subtype viruses. We also assessed the effectiveness of pasteurization in inactivating these viruses. We found that the avian H3 virus exhibits the highest thermal stability, whereas the H5N1 viruses that belong to clade 2.3.4.4b display moderate thermal stability. Importantly, our data provide direct evidence that the standard pasteurization methods used by dairy companies are effective in inactivating all tested subtypes of influenza viruses in raw milk. Our findings indicate that thermally pasteurized milk products do not pose a safety risk to consumers. 3. The sugC gene of Streptococcus suis (S. suis) is a coding gene for the ATP-binding transporter-associated protein with strong pathogenicity. In order to reveal the effect of the sugC gene on the virulence of S. suis serotype 2, a wild-type strain of TJS75, isolated from fattening pigs' brain tissue samples, was used as a parent strain, and a knockout sugC gene (DeltasugC) and complementary strain (CDeltasugC) were successfully constructed, and the

		biological characteristics of TJS75, DeltasugC and CDeltasugC were compared and analyzed through growth curves, biochemical characteristics, hemolysis characteristics, cell infection tests and pathogenicity tests on BALB/c mice. The results of the growth characteristic experiments in vitro showed that the plateau stage growth period of DeltasugC was delayed compared to the TJS75 strain, but there was no difference in the total number of bacteria. The biochemical characteristics and hemolysis ability of DeltasugC in sheep blood had no difference compared with TJS75, but its adhesion and invasion abilities in PK-15 cells were decreased. Knockout of the sugC gene had no impact on the expression levels of adhesion-related genes in TJS75 in real-time PCR analysis. In addition, the LD(50) of DeltasugC in BALB/c mice was seven times higher than that of TJS75. These results illustrate that the deletion of sugC reduced the virulence of TJS75 to BALB/c mice. In summary, this study provides evidence that the sugC gene is a virulence-related gene in the S. suis serotype 2 strain and plays a crucial role in the adhesion and invasion of S. suis. This study lays a foundation for the further exploration of the potential virulence factors and pathogenesis of S. suis. 4. Classically, all hepatitis E virus (HEV) variants causing human infection belong to the genus Paslahepevirus (HEV-A). However, the increasing cases of rat HEV infection in humans since 2018 challenged this dogma, posing increasing health threats. Herein, we investigated the underlying mechanisms dictating the zoonotic potentials of different HEV species and their possible cross-protection relationships. We found that rat HEV virus-like particles (HEV(VLPs)) bound to human liver and intestinal cells/tissues with high efficiency. Moreover, rat HEV(VLPs) and infectious rat HEV particles penetrated the cell membrane and entered human target cells postbinding. In contrast, ferret

Epidemiology, surveillance, risk assessment, (true)	1. Pathogens and antibody surveillance 2. Pasteurization inactivation test of avian influenza virus in cow milk. 3. Characterization Studies on the sugC Gene of Streptococcus suis Serotype 2 in Adhesion, Invasion, and Virulence in Mice. 4. Cell binding tropism of rat hepatitis E virus is a pivotal determinant of its zoonotic transmission to humans. 5. NLRP1 restricts porcine deltacoronavirus infection via IL-11 inhibiting the phosphorylation of the ERK signaling pathway. 6. Epidemiology and biological characteristics of influenza A (H4N6) viruses from wild birds. 7. Emergence of a novel pathogenic porcine G1P[7] rotavirus in China.	HEV(VLPs) showed marginal cell binding and entry ability, bat HEV(VLPs) and avian HEV(VLPs) exhibited no binding and entry potency. Structure-based three-dimensional mapping identified that the surface spike domain of rat HEV is crucial for cell binding. Antigenic cartography indicated that rat HEV exhibited partial cross-reaction with HEV-A. Intriguingly, sera of HEV-A infected patients or human HEV vaccine Hecolin(R) immunized individuals provided partial cross-protection against the binding of rat HEV(VLPs) to human target cells. In summary, the interactions between the viral capsid and cellular receptor(s) regulate the distinct zoonotic potentials of different HEV species. The systematic characterization of antigenic cartography and serological cross-reactivity of different HEV species provide valuable insights for the development of species-specific diagnosis and protective vaccines against zoonotic HEV infection. 5. Porcine deltacoronavirus (PDCoV) is a newly emerging enterotropic swine coronavirus that causes large-scale outbreaks of severe diarrhea disease in piglets which poses a significant risk of cross-species transmission. Nucleotide-binding oligomerization domain-like receptor (NLR) family pyrin domain-containing 1 (NLRP1) has a key role in linking host innate immunity to microbes and the regulation of inflammatory pathways. We revealed a role for NLRP1 in the control of PDCoV infection. Overexpression of NLRP1 remarkably suppressed PDCoV infection, whereas knockout of NLRP1 led to a significant increase in PDCoV replication. A mechanistic study revealed that NLRP1 suppressed PDCoV replication in cells by upregulating IL-11 expression, which in turn inhibited the phosphorylation of the ERK signaling pathway. Furthermore, the ERK phosphorylation inhibitor U0126 effectively hindered PDCoV replication in pigs. Together, our results demonstrated

		that NLRP1 exerted an anti-PDCoV effect by IL-11-mediated inhibition of the phosphorylation of the ERK signaling pathway, providing a novel antiviral signal axis of NLRP1-IL-11-ERK. 6. During the active surveillance, we isolated nine H4N6 subtype influenza A viruses from wild birds in China. To reveal the epidemiology and biology characteristics of H4 subtype influenza A virus from wild birds, we investigated H4 subtype viruses available in the public source, and found that the H4 viruses have been detected in at least 37 countries to date, and more than 73.6% of the viruses were from wild Anseriformes. Bayesian phylogeographic analysis showed that Mongolia worked as the important transmission centre for Eurasian lineage H4 viruses spreading. Phylogenetic analysis of HA genes indicated that global H4 influenza A viruses were divided into Eurasian and North American lineage, our nine H4N6 isolates fell into the Eurasian lineage. Recombination analysis suggested that nine H4N6 isolates underwent complex gene recombination with various subtypes of influenza A viruses and formed two genotypes. Notably, nine H4N6 isolates acquired mammalian virulence-increasing residues. Two representative H4N6 viruses possessed dual receptor binding specificity, they could efficiently replicate in MDCK and 293 T cells in vitro infection, also could cross the species barrier to infect mice directly without prior adaption in vivo experiments. These findings emphasize the public health issues represented by H4 viruses, and highlight the need to strengthen the active surveillance of H4 viruses from wild birds. 7.Among group A rotaviruses (RVAs), the G1 genotype is the main genotype causing diarrhea in children, but it has rarely been reported in pigs. During our epidemiological investigation, we detected G1P[7] rotavirus infection in piglets across several provinces in China and then isolated a porcine G1P[7]

		rotavirus strain (CN1P7). Sequencing revealed that the virus constellation was G1-P[7]-I5-R1-C1-M1-A8-N1-T1-E1-H1. Phylogenetic analyses revealed that CN1P7 most likely emerged due to genetic reassortment among porcine, human, giant panda and dog rotavirus strains. In vivo experiments were conducted on two-day-old piglets, which revealed that the CN1P7 strain was pathogenic to piglets. The virus was shed through the digestive tract and respiratory tract. In addition to the intestine, the CN1P7 strain displayed extraintestinal tropisms in piglets. Histopathological analysis revealed that the lung and small intestine were the targets of CN1P7. This study is the first to explore the molecular and pathogenic characterization of a pig-origin G1P[7] rotavirus.
		1. We screened 974 natural compounds and identified Tubeimosides I, II, and III as pan-coronavirus and filovirus entry inhibitors that target NPC1. Using in-silico, biochemical, and genomic approaches, we provide evidence that NPC1 also binds SARS-CoV-2 spike (S) protein on the receptor-binding domain (RBD), which is blocked by Tubeimosides. Importantly, NPC1 strongly promotes productive SARS-CoV-2 entry, which we propose is due to its influence on fusion in late endosomes. The Tubeimosides' antiviral activity and NPC1 function are further confirmed by infection with SARS-CoV-2 variants of concern (VOC), SARS-CoV, and MERS-CoV. 2. Streptococcus suis is an important bacterial pathogen that affects the global pig industry and poses threats to public health. We aimed to uncover the role of pyroptosis in cellular necrosis in thymic cells of S. suis-infected mice. Confocal microscopy revealed that S. suis activated the M1 phenotype and primed pyroptosis in the macrophages of atrophied thymus. Live cell imaging further confirmed that S. suis could induce porcine alveolar macrophage

		(PAM) pyroptosis in vitro, displaying cell swelling and forming large bubbles on the plasma membrane. Meanwhile, the levels of p-p38, p-extracellular signal-regulated kinase (ERK) and protein kinase B (AKT) were increased, which indicated the mitogen-activated protein kinase (MAPK) and AKT pathways were also involved in the inflammation of S. suis-infected PAMs. Furthermore, significant mRNA expression of pro-inflammatory mediators, including interleukin (IL)-1beta, IL-6, IL-18, tumor necrosis factor (TNF)-alpha and chemokine CXCL8. The data indicated that the inflammation induced by S. suis was in parallel with pro-inflammatory activities of M1 macrophages, pyroptosis and MAPK and AKT pathways. Pyroptosis contributes to necrotic cells and thymocyte reduction in the atrophied thymus of mice. 3. Influenza virus infection is initiated by the attachment of the viral haemagglutinin (HA) protein to sialic acid receptors on the host cell surface. Most virus particles enter cells through clathrin-mediated endocytosis (CME). However, it is unclear how viral binding signals are transmitted through the plasma membrane triggering CME. Here we found that metabotropic glutamate receptor subtype 2 (mGluR2) and potassium calcium-activated channel subfamily M alpha 1 (KCa1.1) are involved in the initiation and completion of CME of influenza virus using an siRNA screen approach. Influenza virus HA directly interacted with mGluR2 and used it as an endocytic receptor to initiate CME. mGluR2 interacted and activated KCa1.1, leading to polymerization of F-actin, maturation of clathrin-coated pits and completion of the CME of influenza virus. Importantly, mGluR2-knockout mice were significantly more resistant to different influenza subtypes than the wild type. Therefore, blocking HA and mGluR2 interaction could be a promising host-directed antiviral strategy. 4. Mycoplasmas are minimal but notorious bacteria that

Zoonoses (true)	1. Tubeimosides are pan-coronavirus and filovirus inhibitors. 2. Streptococcus suis Induces Macrophage M1 Polarization and Pyroptosis. 3. Influenza virus uses mGluR2 as an endocytic receptor to enter cells. 4. Mycoplasma glycine cleavage system key subunit GcvH is an apoptosis inhibitor targeting host endoplasmic reticulum. 5. Non-proteolytic ubiquitination of HBx controls HBV replication. 6. IFITM3 restricts porcine deltacoronavirus infection by targeting its Spike protein. 7. Structural insights into Semiliki forest virus receptor binding modes indicate novel mechanism of virus endocytosis. 8. Altered landscape of total RNA, tRNA and sncRNA modifications in the liver and spleen of mice infected by Toxoplasma gondii. 9. Palmitoylation-dependent association with Annexin II directs hepatitis E virus ORF3 sorting	infect humans and animals. Using Mycoplasma bovis as a model, we demonstrate that mycoplasma glycine cleavage system (GCS) H protein (GcvH) targets the endoplasmic reticulum (ER) to hijack host apoptosis facilitating bacterial infection. Mechanically, GcvH interacts with the ER-resident kinase Brsk2 and stabilizes it by blocking its autophagic degradation. Brsk2 subsequently disturbs unfolded protein response (UPR) signaling, thereby inhibiting the key apoptotic molecule CHOP expression and ER-mediated intrinsic apoptotic pathway. CHOP mediates a cross-talk between ER- and mitochondria-mediated intrinsic apoptosis. The GcvH N-terminal amino acid 31-35 region is necessary for GcvH interaction with Brsk2, as well as for GcvH to exert anti-apoptotic and potentially pro-infective functions. Notably, targeting Brsk2 to dampen apoptosis may be a conserved strategy for GCS-containing mycoplasmas. Our study reveals a novel role for the conserved metabolic route protein GcvH in Mycoplasma species. 5. We found that non-proteolytic ubiquitination of HBx controls HBV replication. The expression level of TRIM21 in patients is negatively correlated with the replication and integration of HBV. TRIM21 was found to trigger non-proteolytic ubiquitination of X protein of HBV. This study proposes that the PRYSPRY and RING domains in TRIM21 dimer can form a docking conformation for HBx binding. TRIM21-mediated HBx ubiquitination disrupts the DDB1 recruitment to HBx and stabilize Smc6. 6. The discovery of antiviral molecules is crucial for controlling porcine deltacoronavirus (PDCoV). Previous studies have provided evidence that the IFN-inducible transmembrane protein 3 (IFITM3), which is coded by an interferon-stimulated gene, prevents the infections of a number of enveloped viruses. Nevertheless, the involvement of IFITM3 in PDCoV infection remains unexplored.

	into vesicles and quasi-enveloped virions.	We observed that the overexpression of IFITM3 successfully restrictes the infection of PDCoV in cell cultures. Conversely, the suppression of IFITM3 facilitates the infection of PDCoV in IPI-2I and IPEC-J2 cells. Further studies revealed that IFITM3 limits the attachment phase of viral infection by interacting with the S1 subunit of the PDCoV Spike (S) protein. In addition, IFITM3 is verified as a member of the CD225 family, the GxxxG conserved motif of this family is important for it to limit PDCoV infection. In summary, this study reveals the mechanism of IFITM3 as an antiviral molecule to inhibit PDCoV infection, and also provides theoretical supports for screening effective anti-PDCoV drugs. 7. The Very Low-Density Lipoprotein Receptor (VLDLR) is an entry receptor for the prototypic alphavirus Semliki Forest Virus (SFV). However, the precise mechanisms underlying the entry of SFV into cells mediated by VLDLR remain unclear. We found that of the eight class A (LA) repeats of the VLDLR, only LA2, LA3, and LA5 specifically bind to the native SFV virion while synergistically promoting SFV cell attachment and entry. Furthermore, the multiple cryo-electron microscopy structures of VLDLR-SFV complexes and mutagenesis studies have demonstrated that under physiological conditions, VLDLR primarily binds to E1-DIII of site-1, site-2, and site-1' at the twofold symmetry axes of SFV virion through LA2, LA3, and LA5, respectively. These findings unveil a novel mechanism for viral entry mediated by receptors, suggesting that conformational transitions in VLDLR induced by multivalent binding of LAs facilitate cellular internalization of SFV, with significant implications for the design of antiviral therapeutics. 8. We investigated the effect of Toxoplasma gondii infection on host RNA modification profiles and explored how these modifications may influence the host-parasite interaction. We analyzed the modification levels of

		approximately 80 nt tRNA and 17-50 nt sncRNAs in mouse liver, spleen, and serum using liquid chromatography and tandem mass spectrometry analysis. The results revealed alterations in RNA modification profiles, particularly during acute infection. The liver exhibited more differentially abundant RNA modifications than the spleen. RNA modification levels in serum were mostly downregulated during acute infection compared to control mice. Correlations were detected between different RNA modifications in the liver and spleen during infection and between several RNA modifications and many cytokines. Alterations in RNA modifications affected tRNA stability and protein translation. These findings provide new insight into the role of RNA modifications in mediating the murine host response to T. gondii infection. 9. Historically considered to be nonenveloped, hepatitis E virus (HEV), an important zoonotic pathogen, has recently been discovered to egress from infected cells as quasi-enveloped virions. These quasi-enveloped virions circulating in the blood are resistant to neutralizing antibodies, thereby facilitating the stealthy spread of infection. Despite abundant evidence of the essential role of the HEV-encoded ORF3 protein in quasi-enveloped virus formation, the underlying mechanism remains unclear. Here, we demonstrate that the HEV ORF3 protein possesses an inherent capacity for self-secretion and that palmitoylation at two cysteine residues within the ORF3 N-terminal region is essential for its secretion and quasi-enveloped virus formation. We further found that only palmitoylated ORF3 proteins hijacked Annexin II for transport to the cytoskeleton and are then directed into multivesicular bodies through the nSMase-endosomal sorting complexes required for transport-III pathway for secretion. Finally, we show that infection of gerbils with HEV mutants harboring mutations at palmitoylation

		sites within ORF3 showed no fecal viral shedding but competent replication in the liver. Our study fills a gap in the understanding of the assembly and release of quasi-enveloped virions mediated by ORF3 and offers the potential for designing therapeutic strategies to control HEV infection.
		1. We developed a triplex real-time quantitative polymerase chain reaction (qPCR) assay based on a TaqMan probe for the detection of H. parasuis, S. suis serotype 2, and P. multocida. Primers and probes were designed to target the conserved regions of the H. parasuis OmpP2 gene, the S. suis serotype 2 gdh gene, and the P. multocida Kmt1 gene. By optimizing the reaction system and conditions, a triplex qPCR method for simultaneous detection of H. parasuis, S. suis serotype 2, and P. multocida was successfully established. The amplification efficiencies of the standard curves for all three pathogens were found to be highly similar, with values of 102.105% for H. parasuis, 105.297% for S. suis serotype 2, and 104.829% for P. multocida, and all R(2) values achieving 0.999. The specificity analysis results showed that the triplex qPCR method had a strong specificity. The sensitivity test results indicated that the limit of detection can reach 50 copies/muL for all three pathogens. Both intra- and inter-assay coefficients of variation for repeatability were below 1%. This triplex qPCR method was shown to have good specificity, sensitivity, and reproducibility. 2. Toxoplasmosis is an important zoonotic disease caused by Toxoplasma gondii that can infect almost all warm-blooded animals worldwide, including humans. The high prevalence of T. gondii infection and its ability to cause serious harm to humans and animals, especially immunodeficient individuals, make it a key public health issue. Accurate diagnostic tools with high sensitivity are needed for controlling T. gondii infection. In the current study, we compared the

Diagnosis, biotechnology and laboratory (true)	1. Development of a Triplex qPCR Assay Based on the TaqMan Probe for the Detection of Haemophilus parasuis, Streptococcus suis Serotype 2 and Pasteurella multocida. 2. GRA3 is a priming antigen in serological tests for detecting T. gondii infection. 3. Development and application of Colloid gold test strip for Brucella antigen detection. 4. A CRISPR-Cas12a-based platform facilitates the detection and serotyping of Streptococcus suis serotype 2.	performance of recombinant SAG2, GRA6, and GRA7 in ELISA for the serological diagnosis of T. gondii infection in cats. We further investigated the antigenicity of recombinant dense granule protein 3 (rGRA3), rGRA5, rGRA8, and rSRS29A expressed in a plant-based, cell-free expression system for detecting antibodies in T. gondii-infected cats. In summary, our data suggest that GRA7 is more sensitive than the other two antigens for the serodiagnosis of T. gondii infection in cats, and GRA3 expressed in the cell-free system is also a priming antigen in serological tests for detecting T. gondii infection in cats. 3. Streptococcus suis (SS) cause major economic losses in pig farming industry and is a serious threat to public health safety. It has multiple serotypes, with poor cross-protection between serotypes, and effective typing methods are lacking. We developed a quadruplex TaqMan fluorescence quantitative PCR assay that can differentiate between Streptococcus suis types 2, 7 and 9 by using the gdh gene, a generic gene for Streptococcus suis, and cps2J, cps7H and cps9J, genes encoding podocarp-associated genes for types 2, 7 and 9, respectively, as targets. The method is specific to accurately type Streptococcus suis pigmentosus without detecting non-target pathogens (Escherichia coli, Pasteurella multocida, Staphylococcus aureus, Streptococcus agalactiae, Streptococcus pneumoniae and et al). The sensitivity was high, with a minimum lower detection line of 10 copies for P-SS and P-SS9, and 100 copies for P-SS2 and P-SS7. The standard curves generated showed good linearity with R(2) of 0.999, 0.999, 0.997 and 0.998 respectively. The repeatability was good, with coefficients of variation between batch to batch and batch to batch tests ranging from 0.21% to 1.10%. Testing of 156 samples yielded 68 positive and 88 negative samples, of which the positive rate of SS was 5.77% (9/156), SS2 was

		20.51% (32/156), SS7 was 8.33% (13/156) and SS9 was 9.6% (15/156), which was in line with the existing fluorescent quantitative PCR assay of 93.75%~100%, which was higher than the detection rate of conventional PCR. 4. Streptococcus suis serotype 2 is a zoonotic pathogen that causes septicemia, arthritis, and meningitis in pigs and humans. In this study, we developed a high-fidelity detection and serotyping platform for S. suis serotype 2 based on recombinase polymerase amplification (RPA) and a clustered regularly interspaced short palindromic repeat (CRISPR)-Cas12a system called Cards-SSJ/K. Cards-SSJ had a detection limit of 10 CFU, takes <60 min, and no cross-reaction was found with other S. suis serotypes, closely related Streptococcus spp., or common pig pathogens, and Cards-SSK could differentiate serotype 2 from serotype 1/2. Results from Cards-SSJ and qPCR were equivalent in detecting S. suis serotype 2 in tissue samples. Analysis indicated that despite a relatively high reagent cost compared to PCR and qPCR, Cards-SSJ was less time-consuming and had low requirements for equipment and personnel. Thus, it is an excellent method for point-of-care detection for S. suis serotype 2.
		1. The H9N2 subtype of the avian influenza virus (AIV) poses a significant threat to the poultry industry and human health. We constructed two recombinant MDV type 1 strains. The HA gene of H9N2 AIV was inserted in UL41 and US2 of the MDV type 1 vector backbone to obtain recombinant viruses rMDV-UL41/HA and rMDV-US2/HA, respectively. An indirect immunofluorescence assay showed sustained expression of HA protein in both recombinant viruses. The insertion of the HA gene in UL41 and US2 did not affect MDV replication in cell cultures. After immunization of specific pathogen-free chickens, although both the rMDV-

Vaccines (true)	1. recombinant MDV type 1 virus carrying the hemagglutinin (HA) gene of AIV provide dual protection against both AIV and MDV. 2. Safety and immunogenicity of a SARS-CoV-2 mRNA vaccine (SYS6006) in minks, cats, blue foxes, and raccoon dogs. 3. Cell-penetrating peptides TAT and 8R functionalize P22 virus-like particles to enhance tissue distribution and retention in vivo. 4.	UL41/HA and rMDV-US2/HA groups exhibited similar levels of hemagglutination inhibition antibody titers, only the rMDV-UL41/HA group provided complete protection against the H9N2 AIV challenge, and also offered complete protection against challenge with MDV. These results demonstrated that rMDV-UL41/HA could be used as a promising bivalent vaccine strain against both H9N2 avian influenza and Marek's disease in chickens. 2. Minks, cats, and some other species of carnivores are susceptible of SARS-CoV-2 and have a high risk of transmitting SARS-CoV-2 to humans. We developed an mRNA vaccine SYS6006 and further evaluated the safety and immunogenicity of SYS6006 as an animal COVID-19 vaccine candidate for SARS-CoV-2 susceptible animals or wild animals. SYS6006 was safe and immunogenic in mice and completely protected mice against mouse-adapted SARS-CoV-2 infection in the upper and lower respiratory tracts. SYS6006 was able to induce neutralizing antibodies against the SARS-CoV-2 wild-type, Delta, and Omicron BA.2 strain on day 7 after prime immunization, and two doses of immunization could enhance the neutralizing antibody responses and produce long-lasting potent antibodies for more than 8 months in minks and cats, blue foxes, and raccoon dogs, while all immunized animals had no abnormal clinical signs during immunization. These results provided here warrant further development of this safe and efficacious mRNA vaccine platform against animal COVID-19. 3. Virus-like particles (VLPs) are used as nanocontainers for targeted drug, protein, and vaccine delivery. The phage P22 VLP is an ideal macromolecule delivery vehicle, as it has a large exterior surface area, which facilitates multivalent genetic and chemical modifications for cell recognition and penetration. Arginine-rich cell-penetrating peptides (CPPs) can increase cargo transport

		efficiency in vivo. However, studies on the tissue distribution and retention of P22 VLPs mediated by TAT and 8R are lacking. We aimed to analyze the TAT and 8R effects on the P22 VLPs transport efficiency and tissue distribution both in vitro and in vivo. We used a prokaryotic system to prepare P22 VLP self-assembled particles and expressed TAT-or 8R-conjugated mCherry on the VLP capsid protein as model cargoes and revealed that the level of P22 VLP-mCherry penetrating the cell membrane was low. However, both TAT and 8R significantly promoted the cellular uptake efficiency of P22 VLPs in vitro, as well as enhanced the tissue accumulation and retention of P22 VLPs in vivo. At 24 h postinjection, TAT enhanced the tissue distribution and retention in the lung, whereas 8R could be better accumulation in brain. Thus, TAT was superior in terms of cellular uptake and tissue accumulation in the P22 VLPs delivery system. Understanding CPP biocompatibility and tissue retention will expand their potential applications in macromolecular cargo delivery.

TOR 3: HARMONISATION OF STANDARDS

2. Proposal or development of any procedure that will facilitate harmonisation of international regulations applicable to the main fucus area for which you were designated

Proposal title	Scope/Content	Applicable Area
Specification for genetic quality control in experimental pigs	Specification for experimental animals	Laboratory Expertise
Specification for genetic quality control of SPF ducks	Specification for experimental animals	Laboratory Expertise
Specification for SPF duck breeding	Specification for experimental animals	Laboratory Expertise

Technical Specification for RT-PCR detection of experimental swine parainfluenza virus type 5	Specification for experimental animals	Laboratory Expertise

3. In exercising your activities, have you identified any regulatory research needs* relevant for WOAH?

No

4. Did your Collaborating Centre maintain a network with other WOAH Collaborating Centres (CC), Reference Laboratories (RL), or organisations designated for the same specialty, to coordinate scientific and technical studies?

Yes

Name of WOAH CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose
Surveillance and Control of animal protozoan Diseases	Japan	Asia y el Pacífico	To cooperate in the research for surveillance and control of animal protozoan diseases
Biotechnology-based Diagnosis of Infectious Diseases	Sweden	Europa	To have cooperation on the research of zoonoses and other animal diseases

TOR 4 AND 5: NETWORKING AND COLLABORATION

5. Did your Collaborating Centre maintain a network with other WOAH Collaborating Centres, Reference laboratories, or organisations in other disciplines, to coordinate scientific and technical studies?

Yes

Name of WOAH CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose
the WOAH cc- of Biotechnology-based Diagnosis of Infectious Diseases in Veterinary Medicine National Veterinary Institute, Sweden	Sweden	Europe	To have cooperation on the research of swine fever

RL of Marek's Disease	UK	Europe	To have cooperation on the research of Marek's Disease

TOR 6: EXPERT CONSULTANTS

6. Did your Collaborating Centre place expert consultants at the disposal of WOAH?

Yes

Name of expert	Kind of consultancy	Subject
ZHONG Gongxun	Conselor	UNSGM "Future Pandemic Testing" Exercise – Results, performance and geographical participation. To participate in the ninth UNSGM designalted laboratories workshop, in Spiez, Switzerland, 11 September 2024.
ZHONG Gongxun	Member of the WOAH Collaborating Centre Network	Quarterly Meeting: Network of WOAH Collaborating Centres on Wildlife Health
ZHONG Gongxun	Member of ZOSP	Quarterly Meeting: Network of WOAH Collaborating Centres on Wildlife Health
LIU Jinxiong	Conselor	Recombinant duck enteritis virus bearing the hemagglutinin genes of H5 and H7 influenza viruses is an ideal multivalent live vaccine in ducks. To participate in the 23rd Federation of Asian Veterinary Associations Congress in Daejeon, South Korea, 15 November 2024.
CHEN Hualan	Conselor	Pandemic potential of different avian influenza viruses. To participate in the 23rd Federation of Asian Veterinary Associations Congress in Daejeon, South Korea, 15 November 2024.
CHEN Hualan	Conselor	Control of highly pathogenic avian influenza through vaccination. To participate in the 23rd Federation of Asian Veterinary Associations Congress in Daejeon, South Korea, 15 November 2024.
WENG Changjiang	Conselor	Illumination of pig reproductive and respiratory syndrome virus immune escape mechanism by virus and host protein interaction. To participate in the International Porcine Reproductive and Respiratory Syndrome Symposium—The International PRRS Symposium, IPRRSS, in

		Yantai, China, 7 August 2024.
QIU Huaji	Conselor	Drops in the ocean-selected work on ASFV in Qiu lab. To participate in the 2nd Animal Disease and Health Forum, in Nanjing, China, 16 November 2024.
QIU Huaji	Conselor	New technologies applied to vaccine development: what can we expect? To participate in the 27th International Pig Veterinary Society Congress and the 15th European Symposium of Porcine Health Management, in Leipzig, Germany, 4-7 June 2024.
CHEN Hualan	Conselor	Highly pathogenic avian influenza epidemic and Progress in its prevention and control. To participate in The 16th Workshop of Biotechnology Branch of Chinese Association of Animal Science and Veterinary Medicine and Veterinary Immunology Branch of the Chinese Society for Immunology, in Harbin, China, 7 August 2024.
PAN Qiao	Conselor	Molecular mechanism of mycoplasma GcvH protein targeting the host ER induced apoptosis inhibition. To participate in The 16th Workshop of Biotechnology Branch of Chinese Association of Animal Science and Veterinary Medicine and Veterinary Immunology Branch of the Chinese Society for Immunology, in Harbin, China, 7 August 2024.
HU Seng	Conselor	The Epidemic of Brucellosis in China and Development of DIVA vaccine（M5-90Δ26）. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
WANG Xiumei	Conselor	Control of Contagious Bovine Pleuropneumonia (CBPP) in China. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
CHEN Weiye	Conselor	Development of Vaccines for Peste Des Petits Ruminants. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
		Characterization of African Swine Fever Viruses in China. To participate in the China-East Africa Animal Disease Control and One Health

DING Leilei	Conselor	Approach Exchange Meeting, in Sanya, China, 21 November 2024.
BU Zhigao	Conselor	Novel Vaccines and Diagnostic Technology for Brucellosis & Rabies. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
HAN Zongxi	Conselor	Brief Introduction of Epidemiology and Control of Newcastle Disease and Infectious Bronchitis in China. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
YANG Huanliang	Conselor	Surveillance and characterization of Eurasian Avian-like H1N1 swine influenza viruses in China. To participate in the OFFLU Swine Influenza Virus (SIV) Technical Meeting, in Paris, 3-4 April 2024.
ZENG Xianying	Conselor	Control of highly pathogenic avian influenza through vaccination. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
JIANG Yongping	Conselor	Development of avian influenza (H5+H7) trivalent DNA vaccine. To participate in the 23rd Federation of Asian Veterinary Associations Congress in Daejeon, South Korea, 15 November 2024.
CHEN Weiye	Conselor	Development of Vaccines for Peste Des Petits Ruminants. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
CHEN Weiye	Conselor	Establishment of goat infection model of the Peste des petits ruminants virus isolated in China for vaccine efficacy evaluation. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
LIU Jinxiong	Conselor	Brief Introduction of Epidemiology and Control of Newcastle Disease and Infectious Bronchitis in China. To participate in the Workshop on Prevention and Control Technologies for new-Emerging and re-Emerging Significant Infectious Animal Diseases in Cairo, Egypt, 5 November 2024.

LI Chengjun	Conselor	Successful control of HPAI in China by vaccination and vaccine development for other countries. To participate in the China-East Africa Animal Disease Control and One Health Approach Exchange Meeting, in Sanya, China, 21 November 2024.
CHEN Pucheng	Conselor	Development of polyvalent herpesvirus of turkey (HVT) vector vaccine against H5 and H7 subtype highly pathogenic avian influenza virus. To participate in the 23rd Federation of Asian Veterinary Associations Congress in Daejeon, South Korea, 15 November 2024.
DENG Guohua	Conselor	A broad-spectrum vaccine candidate against H5viruses bearing different sub-clade 2.3.4.4 HA genes. To participate in the OPTIONS XII for the Control of INFLUENZA, in Brisbane, Australia, 29 September 2024.
KONG Huihui	Conselor	The SUMO-interacting motif in NS2 promotes adaptation of avian influenza virus to mammals. To participate in the OPTIONS XII for the Control of INFLUENZA, in Brisbane, Australia, 29 September 2024.
SHI Jianzhong	Conselor	Evolution of H7N9 highly pathogenic avian influenza virus in the context of vaccination. To participate in the OPTIONS XII for the Control of INFLUENZA, in Brisbane, Australia, 29 September 2024.
LI Chengjun	Conselor	ABTB1 facilitates the replication of influenza A virus by counteracting TRIM4-mediated degradation of viral NP protein. To participate in the OPTIONS XII for the Control of INFLUENZA, in Brisbane, Australia, 29 September 2024.
JIA Honglin	Conselor	A novel scramblase is required for the IMC biogenesis in Toxoplasma gondii. To participate in the 4th global Virtual Symposium on Toxoplasmosis, on-line in 20 March 2024.
CHEN Hualan	Conselor	Genomic Epidemiology of Highly Pathogenic H5 Viruses in China. To participate the Regional Technical Consultation on Reassortant Avian Influenza in Southeast Asia, in Bangkok, Thailand, 25 July 2024.
CHEN Hualan	Conselor	Identification of the key receptor for influenza virus entry into cells. To participate the UK-China Avian Flu Control Workshop and Flu-Trail Map Workshop on 11 and 12 November 2024 at The Pirbright Institute, UK.
		Development of Epitope-based Diva Vaccines

MENG Fandan	Conselor	for Senecavirus A. To participate in the 2nd International Conference on Vaccine Research and Development, in Munich, Germany, 22 April 2024.

TOR 7: SCIENTIFIC AND TECHNICAL TRAINING

7. Did your Collaborating Centre provide advice/services to requests from Members in your main focus area?

Yes

We maintain a Joint Laboratory of Animal Diseases Prevention and Control with Cairo University. We provided advice and diagnostic technique for prevention of zoonoses and other avian diseases, and vaccines against highly pathogenic avian influenza to Egypt.

We maintain the China- Kazakhstan Joint Laboratory on Agricultural Sciences and provided advice and diagnostic technique for prevention of zoonoses and other avian diseases, especially in surveillance capacity for avian influenza, Newcastle disease and brucellosis.

We maintain the China-Burundi Arthropod-Transmitted Animal Disease Prevention and Control and One Health Joint Laboratory, providing scientific and technical training in research on zoonotic diseases and overall preventive veterinary techniques.

8. Did your Collaborating Centre provide scientific and technical training, within the remit of the mandate given by WOAH, to personnel from WOAH Members?

Yes

a) Technical visit : 0

b) Seminars : 70

c) Hands-on training courses: 0

d) Internships (>1 month) : 6

Type of technical training provided (a, b, c or d)	Content	Country of origin of the expert(s) provided with training	No. participants from the corresponding country
B	China-Central Asia Animal Disease Prevention and Control Technology Workshop	Kazakhstan, Turkmenistan, Tajikistan, Kyrgyzstan	20
B	China-East Africa Animal Disease Control and One Health Approach Exchange Meeting	Burundi, Ethiopia, Congo (Kim), Tanzania, Kenya	20
B	Workshop on prevention and control technologies for new-emerging and re-emerging significant infectious animal disease	Egypt	30

D	Provide scientific and technical training in research and overall preventive veterinary techniques	Pakistan	6

TOR 8: SCIENTIFIC MEETINGS

9. Did your Collaborating Centre organise or participate in the organisation of scientific meetings related to your main focus area on behalf of WOAH?

Yes

National/International	Title of event	Co-organiser	Date	Location	No. Participants
Internationally	Quarterly Meeting: Network of WOAH Collaborating Centres on Wildlife Health	WOAH	2024-03-19	On line	20
Internationally	Quarterly Meeting: Network of WOAH Collaborating Centres on Wildlife Health	WOAH	2024-06-19	On line	20
Internationally	Quarterly Meeting: Network of WOAH Collaborating Centres on Wildlife Health	WOAH	2024-09-19	On line	20
Internationally	Meeting with the ZODIAC Ad-Hoc Scientific Panel (ZOSP)	IAEA, WOAH	2024-11-24	On line	21
Internationally	the ninth UNSGM designalted laboratories workshop	UNODA, Spiez Lab, WOAH	2024-09-11	Spiez, Switzerland	50
Internationally	1st International Forum on Chanllenges of and Responses to Zoonoses	Shanxi Agricultural University；Zoonoses Periodical Office	2024-10-19	Taiyuan, China	500
Internationally	The 16th Workshop of Biotechnology Branch of Chinese Association of Animal Science and Veterinary Medicine and Veterinary Immunology Branch of	Harbin Veterinary Research Institute, Chinese Academy of AgriculturalSciences	2024-08-07	Harbin, China	500

	the Chinese Society for Immunology				
Internationally	Workshop on Prevention and Control Technologies for new-Emerging and re-Emerging Significant Infectious Animal Diseases	Harbin Veterinary Research Institute, Chinese Academy of AgriculturalSciences; Cairo University; Animal Health Research Institute, Agricultura Research Center of Egypt	2024-11-05	Cairo, Egypt	100
Internationally	China-Central Asia Animal Disease Preventionand Control Technology Workshop	Harbin Veterinary Research Institute, Chinese Academy of AgriculturalSciences; China-Kazakhstan Joint Laboratory on Agricultural Sciences	2024-11-24	Sanya, China	100
Internationally	Regional Workshop on Avian Disease Prevention and Control in Asia and the Pacific	WOAH; The Ministry of Agriculture, Food and Rural Affairs (MAFRA), Republic of Korea	2024-08-26	Seoul, Republic of Korea	100
Internationally	The 23rd Federation of Asian Veterinary Associations Congress (FAVA 2024)	Federation of Asian Veterinary Associations; Korean Veterinary Medical Association	2024-10-15	Daejeon, South Korea	200
Internationally	OPTIONS XII for the control of influenza	WOAH; FAO; WHO	2024-09-30	Brisbane, Australia	100
Internationally	the 27th International Pig Veterinary Society Congress; the 15th European Symposium of Porcine Health Management	the International Pig Veterinary Society, the European College of Porcine Health Management; the Veterinary Practitioner Council; the Local Organizing Committee	2024-06-04	Leipzig, Germany	2700
Internationally	2nd Animal Disease and One Health Forum	FAO; Huazhong Agriculture University; Jiangsu Academy of Agricultural Sciences Nanjing Agricultural University; South China Agricultural University	2024-11-15	Nanjing, China	500
	China-East Africa Animal Disease Control	Harbin Veterinary Research Institute, Chinese			

Internationally	and One Health Approach Exchange Meeting	Academy of AgriculturalSciences	2024-05-31	Harbin, China	50
Internationally	UK-China Avian Flu Control Workshop and Flu-Trail Map Workshop	The Pirbright Institute, UK	2024-11-11	Surrey, UK	200
Internationally	Global Conference on Animal Health Innovation, Reference Centres and Vaccines	FAO	2024-09-23	Rome, Italy	50
Internationally	World Influenza Conference 2024: From Influenza to respiratory infectious diseases	Chinese Preventive Medical Association; Asia-Pacific Influenza Control Alliance; Chinese Center for Disease Control and Prevention, Chinese Academy of Medical Sciences	2024-07-06	Boao, China	500
Internationally	the 5th International Symposium on Neglected Influenza Viruses	International Society for Inlufenza and other Respiratory Virus Diseases	2024-04-08	Lexington, Kentucky, USA	150
Internationally	2024 NAPRRS/NC229: International Conference of Swine Viral Diseases	University of Illinois	2024-12-08	Chicago, USA	500
Internationally	OFFLU Swine Influenza Virus (SIV) Technical Meeting	WOAH, FAO, WHO	2024-04-03	Paris, France	21

TOR 9: DATA AND INFORMATION DISSEMINATION

10. Publication and dissemination of any information within the remit of the mandate given by WOAH that may be useful to Members of WOAH

a) Articles published in peer-reviewed journals:

29

1. Chen Y, Yu Q, Fan W, Zeng X, Zhang Z, Tian G, Liu C, Bao H, Wu L, Zhang Y, Liu Y, Wang S, Cui H, Duan Y, Chen H, Gao Y. 2024. Recombinant Marek's disease virus type 1 provides full protection against H9N2 influenza A virus in chickens. Vet Microbiol 298:110242.

2. Cui P, Zhuang Y, Zhang Y, Chen L, Chen P, Li J, Feng L, Chen Q, Meng F, Yang H, Jiang Y, Deng G, Shi J, Chen H, Kong H. 2024. Does pasteurization inactivate bird flu virus in milk? Emerg Microbes Infect 13:2364732.

3. Dong Z, Li C, Tian X, Guo X, Li X, Ren W, Chi J, Zhang L, Li F, Zhu Y, Zhang W, Yan M. 2024. Characterization Studies on the sugC Gene

of Streptococcus suis Serotype 2 in Adhesion, Invasion, and Virulence in Mice. Vet Sci 11.
4. Guo H, Xu J, Situ J, Li C, Wang X, Hou Y, Yang G, Wang L, Ying D, Li Z, Wang Z, Su J, Ding Y, Zeng D, Zhang J, Ding X, Wu S, Miao W, Tang R, Lu Y, Kong H, Zhou P, Zheng Z, Zheng K, Pan X, Sridhar S, Wang W. 2024. Cell binding tropism of rat hepatitis E virus is a pivotal determinant of its zoonotic transmission to humans. Proceedings of the National Academy of Sciences of the United States of America 121:e2416255121.
5. He H, Li Y, Chen Y, Chen J, Li Z, Li L, Shi D, Zhang X, Shi H, Xue M, Feng L. 2024. NLRP1 restricts porcine deltacoronavirus infection via IL-11 inhibiting the phosphorylation of the ERK signaling pathway. J Virol 98:e0198223.
6. Huo H, Wang J, Li C, Xiao S, Wang H, Ge J, Zhong G, Wen Z, Wang C, Lang Q, Chen L, Wang Z, Wang J, Wang X, He X, Guan Y, Shuai L, Bu Z. 2024. Safety and immunogenicity of a SARS-CoV-2 mRNA vaccine (SYS6006) in minks, cats, blue foxes, and raccoon dogs. Front Cell Infect Microbiol 14:1468775.
7. Khan I, Li S, Tao L, Wang C, Ye B, Li H, Liu X, Ahmad I, Su W, Zhong G, Wen Z, Wang J, Hua RH, Ma A, Liang J, Wan XP, Bu ZG, Zheng YH. 2024. Tubeimosides are pan-coronavirus and filovirus inhibitors that can block their fusion protein binding to Niemann-Pick C1. Nature communications 15:162.
8. Lan T, Liu Q, Ge J, Wang Y. 2024. A novel approach for efficient co-expression of two foreign genes based on the reverse genetic system of Newcastle disease virus. Front Microbiol 15:1442551.
9. Li K, Zhang Y, Luo T, Li C, Yu H, Wang W, Zhang H, Chen H, Xia C, Gao C. 2024. Development of a Triplex qPCR Assay Based on the TaqMan Probe for the Detection of Haemophilus parasuis, Streptococcus suis Serotype 2 and Pasteurella multocida. Microorganisms 12.
10. Li S, Chen T, Gao K, Yang YB, Qi B, Wang C, An T, Cai X, Wang S. 2024. Streptococcus suis Induces Macrophage M1 Polarization and Pyroptosis. Microorganisms 12.
11. Liu T, Cao Y, Weng J, Gao S, Jin Z, Zhang Y, Yang Y, Zhang H, Xia C, Yin X, Luo Y, He Q, Jiang H, Wang L, Zhang Z. 2024. Hepatitis E virus infects human testicular tissue and Sertoli cells. Emerg Microbes Infect 13:2332657.
12. Ni Z, Wang J, Yu X, Wang Y, Wang J, He X, Li C, Deng G, Shi J, Kong H, Jiang Y, Chen P, Zeng X, Tian G, Chen H, Bu Z. 2024. Influenza virus uses mGluR2 as an endocytic receptor to enter cells. Nat Microbiol 9:1764-1777.
13. Pan Q, Zhang Y, Liu T, Xu Q, Wu Q, Xin J. 2024. Mycoplasma glycine cleavage system key subunit GcvH is an apoptosis inhibitor targeting host endoplasmic reticulum. PLoS Pathog 20:e1012266.
14. Sabukunze S, Gu H, Zhao L, Jia H, Guo H. 2024. Comparison of the performance of SAG2, GRA6, and GRA7 for serological diagnosis of Toxoplasma gondii infection in cats. Front Vet Sci 11:1423581.
15. Sheng X, Yang Y, Zhu M, Zhou L, Zhu F, Zhu Y, Dong S, Kong H, Wang H, Jiang J, Wan M, Feng M, Deng Q, Xu Y, You Q, Hu R. 2024. Non-proteolytic ubiquitination of HBx controls HBV replication. Virol Sin 39:338-342.
16. Shi Q, Zhao R, Chen L, Liu T, Di T, Zhang C, Zhang Z, Wang F, Han Z, Sun J, Liu S. 2024. Newcastle disease virus activates diverse signaling pathways via Src to facilitate virus entry into host macrophages. J Virol 98:e0191523.
17. Song X, Li Y, Wu H, Qiu H, Sun Y. 2024. T-Cell Epitope-Based Vaccines: A Promising Strategy for Prevention of Infectious Diseases. Vaccines (Basel) 12.
18. Song X, Tian J, Li M, Bai X, Zhao Z, Shi J, Zeng X, Tian G, Guan Y, Chai H, Li Y, Chen H. 2024. Epidemiology and biological characteristics of influenza A (H4N6) viruses from wild birds. Emerg Microbes Infect 13:2418909.
19. Su S, Shen X, Shi X, Li X, Chen J, Yang W, Sun M, Tang YD, Wang H, Wang S, Cai X, Lu Y, An T, Yang Y, Meng F. 2024. Cell-penetrating peptides TAT and 8R functionalize P22 virus-like particles to enhance tissue distribution and retention in vivo. Front Vet Sci 11:1460973.
20. Su W, Ahmad I, Wu Y, Tang L, Khan I, Ye B, Liang J, Li S, Zheng YH. 2024. Furin Egress from the TGN is Regulated by Membrane-Associated RING-CH Finger (MARCHF) Proteins and Ubiquitin-Specific Protease 32 (USP32) via Nondegradable K33-Polyubiquitination. Adv Sci (Weinh) 11:e2403732.
21. Sun Z, Wang Y, Jin X, Li S, Qiu HJ. 2024. Crosstalk between Dysfunctional Mitochondria and Proinflammatory Responses during Viral Infections. Int J Mol Sci 25.
22. Wang H, Chen J, Sun Y, An T, Wang Y, Chen H, Yu C, Xia C, Zhang H. 2024. Development and application of a quadruplex TaqMan fluorescence quantitative PCR typing method for Streptococcus suis generalis, type 2, type 7 and type 9. Front Cell Infect Microbiol 14:1475878.
23. Wang L, Sun J, Zhao J, Bai J, Zhang Y, Zhu Y, Zhang W, Wang C, Langford PR, Liu S, Li G. 2024. A CRISPR-Cas12a-based platform facilitates the detection and serotyping of Streptococcus suis serotype 2. Talanta 267:125202.
24. Wu J, Tang R, Zhang X, Gao M, Guo L, Zhang L, Shi D, Zhang X, Shi H, Song H, Feng L, Chen J. 2024. IFITM3 restricts porcine deltacoronavirus infection by targeting its Spike protein. Vet Microbiol 288:109953.

25. Wu L, Jing Z, Pan Y, Guo L, Li Z, Feng L, Tian J. 2024. Emergence of a novel pathogenic porcine G1P[7] rotavirus in China. Virology 598:110185.
26. Yang D, Wang N, Du B, Sun Z, Wang S, He X, Wang J, Zheng T, Chen Y, Wang X, Wang J. 2024. Structural insights into Semiliki forest virus receptor binding modes indicate novel mechanism of virus endocytosis. PLoS Pathog 20:e1012770.
27. Yuan H, Wei W, Zhang Y, Li C, Zhao S, Chao Z, Xia C, Quan J, Gao C. 2024. Unveiling the Influence of Copy Number Variations on Genetic Diversity and Adaptive Evolution in China's Native Pig Breeds via Whole-Genome Resequencing. Int J Mol Sci 25.
28. Zhang XX, Sun YZ, Wang W, Gao Y, Wei XY, Sun HC, Wang CR, Ni HB, Yang X, Elsheikha HM, Guo HP. 2024. Altered landscape of total RNA, tRNA and sncRNA modifications in the liver and spleen of mice infected by Toxoplasma gondii. PLoS Negl Trop Dis 18:e0012281.
29. Liu X, Liu T, Shao Z, Xiong X, Qi S, Guan J, Wang M, Tang YD, Feng Z, Wang L, Yin X. 2025. Palmitoylation-dependent association with Annexin II directs hepatitis E virus ORF3 sorting into vesicles and quasi-enveloped virions. Proceedings of the National Academy of Sciences of the United States of America 122:e2418751122.

b) International conferences:

c) National conferences:

d) Other (Provide website address or link to appropriate information):

11. What have you done in the past year to advance your area of focus, e.g. updated technology?
To fulfilling the terms of reference to the benefit of WOAH Members, we provide our expertise more internationally in the past year.
As the WOAH Collaborating Centre for Zoonoses of Asia-Pacific, we also extend our contribution as a member of Network of WOAH Collaborating Centres on Wildlife Health.
We continue to providing advice on the prevention of future pandemics caused by zoonotic diseases as member of the ZODIAC Ad-Hoc Scientific Panel (ZOSP).
We organized a Secretary-General's Mechanism for Investigation of Alleged Use of Chemical and Biological Weapons (UNSGM) "Future Pandemic Testing" Exercise, as one of the UNSGM designated analytical laboratories and on behalf of a WOAH Collaborating Centre.

12. Additional comments regarding your report:
None.