

ALLEGATO B

UNIVERSITÀ DEGLI STUDI DI MILANO

selezione pubblica per n. 1 posto di Ricercatore a tempo determinato ai sensi dell'art.24, comma 3, lettera b) della Legge 240/2010 per il settore concorsuale 07/H3 - Malattie Infettive e Parassitarie degli Animali, settore scientifico-disciplinare VET/06 - Parassitologia e Malattie Parassitarie degli animali presso il Dipartimento di MEDICINA VETERINARIA, (avviso bando pubblicato sulla G.U. n. 53 del 05/07/2019) Codice concorso 4141

Alice Fusaro **CURRICULUM VITAE**

INFORMAZIONI PERSONALI (NON INSERIRE INDIRIZZO PRIVATO E TELEFONO FISSO O CELLULARE)

COGNOME	FUSARO
NOME	ALICE
DATA DI NASCITA	01-01-1982

WORK EXPERIENCE

January 2014 - present

Professional Technical Collaborator - Organizational position

Organizational position (permanent position) in the sequencing, genetics and bioinformatics research group (8 technicians/fellows) at the OIE, European and National Reference Laboratory for avian influenza & Newcastle disease, FAO Reference Centre for animal influenza and Newcastle disease, Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe), viale dell'Università, 10, Legnaro (PD), Italy. <http://www.izsvenezie.it>.

My current research focuses on the evolutionary genetics of RNA viruses responsible of animal infections, with special emphasis on the major mechanisms of virus evolution, the molecular epidemiology of important emerging pathogens and the roles played by mutations, natural selection, recombination, and gene flow in shaping patterns of genetic diversity on RNA viruses. Thanks to the application of high-throughput whole-genome next-generation sequencing (NGS) technologies and bioinformatics analyses, my recent studies have helped to provide a better understanding of the inter- and intra-host genetic diversity of influenza viruses and to shed light on the critical mechanisms central to viral evolution, parthenogenesis, transmission, host adaptation and emergence of viruses with pandemic potential. Moreover, I performed metagenomic studies for virus discovery. Currently, I am also involved in a research project that aims to investigate the roles of viral and host factors in the transition of low pathogenic avian influenza virus to highly pathogenic form in poultry, using the RNA-Seq technology.

My studies concentrate on different RNA viruses, most notably Avian Influenza virus, Newcastle disease virus, Rabies virus and Infectious Bronchitis virus.

I have a broad experience with phylogenetic, phylogeographic and evolutionary analyses using several bioinformatics tools. I am also currently working with Next Generation Sequencing data.

I had been involved in several European and National (Italian Ministry of Health) projects on avian influenza and other major viral diseases and I have been responsible of operational units in three national projects.

I collaborate with several research institutes, including the University of Glasgow (Glasgow, UK), KU Leuven (Leuven, Belgium), Fogarty International Center at the National Institute of Health (Washington DC, USA)

I conducted several trainings and courses on Sanger sequencing, phylogenetic analyses and Next generation sequencing in Italy and in other countries.

December 2008 - present	Professional Technical Collaborator – Permanent position Permanent position at the OIE, European and National Reference Laboratory for avian influenza & Newcastle disease, FAO Reference Centre for animal influenza and Newcastle disease, Istituto Zooprofilattico Sperimentale delle Venezie, viale dell'Università, 10, Legnaro (PD), Italy
October 2006 – December 2008	Fellowship Fellowship at OIE and National Reference Laboratory for avian influenza & Newcastle disease, FAO Reference Centre for animal influenza and Newcastle disease, OIE Collaborating Centre for Diseases at the Human-Animal Interface, Istituto Zooprofilattico Sperimentale delle Venezie, viale dell'Università, 10, Legnaro (PD), Italy. http://www.izsvenezie.it <ul style="list-style-type: none"> ■ Main activities: Sanger sequencing and phylogenetic analyses of the whole genome of various subtypes of avian influenza viruses and other RNA viruses.
February-July 2006	Trainee Department of Public Health, Compared Pathology and Veterinary Hygiene, University of Padua, Padua, Italy <ul style="list-style-type: none"> ■ Main activities: Isolation and characterization of single nucleotide polymorphisms in the genome of gilt-head bream (<i>Sparus aurata</i>) with the aim of assuring the traceability of this food product.
March-July 2004	Trainee Department of Biology, University of Padua, Padua, Italy <ul style="list-style-type: none"> ■ Main activities: Creation of a genetic map of common gilt-head bream (<i>Sparus aurata</i>, L.) using microsatellites as genetic markers. This research was carried out under the European project BRIDGE-MAP
EDUCATION	
24 March 2014	Phd in Veterinary Science Department of Public Health, Compared Pathology and Veterinary Hygiene, University of Padua Tutor: Dr. Enrico Massimiliano Negrisolo. Title of thesis: Evolutionary dynamics of RNA viruses with zoonotic potential
July 2006	Master degree in Biotechnology for food products Department of Public Health, Compared Pathology and Veterinary Hygiene, University of Padua Marks: 110/110 with honours
July 2004	Bachelor degree in Sanitary Biotechnology Department of Public Health, Compared Pathology and Veterinary Hygiene, University of Padua Marks: 110/110 with honours
September 2001	Scientific high school certificate Scientific High School “G. Berto”, Mogliano Veneto (VE) Marks: 77/100

TRAINING COURSES



7-12 September 2014	19th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology. Rome, Italy Course content: analysis of Next Generation Sequencing data
5 June-29 August 2014	Bioinformatics course. BMR Genomics, Padua, Italy. Course content: Linux, bash command, databases
27-31 August 2012	17th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology. University of Belgrade, Faculty of Medicine, Belgrade, Serbia. Course content: Bayesian inference in phylogenetics, coalescent and phylogeographic analyses ('phylodynamics').
5-8 August 2008	Training on phylogenetic and evolutionary analyses of avian influenza viruses. University of Turin, Turin, Italy
24 April–10 May 2008	Computer laboratory course. Cambridge University, Cambridge, UK.
3 May-19 March 2007	Training course on nucleic acid sequencing. JCVI-J Craig Venter Institute- Rockville, Maryland, USA.

**RESEARCH
ACTIVITIES AT
FOREIGN
RESEARCH
INSTITUTES**

I spent several periods at foreign research institutes. These experiences allowed me to increase my knowledge and acquire experience on informatics tools and techniques for the analyses of virus genomes, but also to establish new collaborations with international research groups, as the National Institute of Health (Bethesda, USA), the University of Glasgow (Glasgow, UK) and the University of Leuven (Leuven, Belgium), which are still in place. Several publications in peer review journals resulted from these collaborations.

19-21 April 2017;	<i>Location:</i> University of Leuven (Leuven, Belgium)
12-16 March 2018	<i>Research activities:</i> investigation of the phylodynamics of highly pathogenic avian influenza viruses. The studies have been carried out under the European projects PREDEMICS (European Union's Horizon 2020 research and innovation programme grant agreement no. 278433) and DELTA-FLU (European Union's Horizon 2020 research and innovation programme, grant agreement No 727922). <i>Supervisor:</i> Prof. Philippe Lemey <i>Publication:</i> <ul style="list-style-type: none"> - Fusaro A, Monne I, Mulatti P, Zecchin B, Bonfanti L, Ormelli S, Milani A, Cecchettin K, Lemey P, Moreno A, Massi P, Dorotea T, Marangon S, Terregino C (2017). Genetic Diversity of Highly Pathogenic Avian Influenza A(H5N8/H5N5) Viruses in Italy, 2016-17. <i>EMERGING INFECTIOUS DISEASES</i>, vol. 23, p. 1543-1547, ISSN: 1080-6040 - Fusaro, A., Zecchin, B., Vrancken, B., Abolnik, C., Ademun, A.R., Akpeli, Y.P., Alassane, A., Arafa A., Awuni, J.A., Couacy-Hymann, E., Coulibaly, M., Gaidet N., Go-Maro, E., Joannis, T., Jumbo, S.D., Minoungou, G., Meseko, C., Moutari, S.M., Ndumu, D.B., Twabela, A., Wade, A., Wiersma, L., Zamperin, G., Milani, A., Lemey, P., Monne, I. Disentangling the role of the African continent in the global spread of H5 highly pathogenic avian influenza viruses. <i>Nature Communications</i>. Under review
15 April - 3 June 2013	<i>Location:</i> University of Glasgow (Glasgow, UK) <i>Research activities:</i> bioinformatics analyses of deep sequencing data of avian influenza viruses to investigate the evolutionary mechanisms governing the emergence of highly pathogenic avian influenza viruses. This collaboration has been conducted under the European project Epi-Seq (research project supported under the 2nd joint call for transnational research projects by EMIDA ERA-NET [FP7 project nr 219235]) and has been supported by a fellowship from the OECD Co-operative Research Programme: Biological Resource Management for Sustainable Agricultural Systems in 2013. <i>Supervisor:</i> Prof Pablo Murcia <i>Contact persons:</i> Prof Pablo Murcia, Joseph Hughes and Richard Orton <i>Publication:</i> Fusaro A., Tassoni L., Hughes J., Milani A., Salviato A., Schivo A., Murcia P.R., Bonfanti L., Cattoli G., Monne I. (2015) Evolutionary trajectories of two distinct avian influenza epidemics: Parallelisms and divergences. <i>Infect.Genet.Evol.</i> 34:457-466.

22 October - 7 November 2012	<p><i>Location:</i> National Institute of Health, Fogarty International Center, Bethesda USA <i>Research activities:</i> molecular epidemiological investigation of an H7 avian influenza Italian epidemic. This collaboration has been carried out under of the European project PREDEMICS (European Union's Horizon 2020 research and innovation programme grant agreement no. 278433). <i>Supervisor:</i> Dr. Mark Miller <i>Contact person:</i> Dr. Martha I. Nelson <i>Publication:</i> Monne I., Fusaro A., Nelson M.I., Bonfanti L., Mulatti P., Hughes J., Murcia P.R., Schivo A., Valastro V., Moreno A., Holmes E.C., Cattoli G. (2014) Emergence of a highly pathogenic avian influenza virus from a low-pathogenic progenitor. <i>J.Viro.</i> 88(8):4375-4388.</p>
16 March - 17 April 2009	<p><i>Location:</i> National Institute of Health, Fogarty International Center, Bethesda USA <i>Research activities:</i> phylogenetic and evolutionary analysis of HPAI H5N1 viruses isolated in Nigeria between 2006 and 2008, including spatial migration, growth of genetic diversity, and evolutionary rates. <i>Supervisor:</i> Dr. Mark Miller <i>Contact person:</i> Dr. Martha I. Nelson <i>Publication:</i> Fusaro A., Nelson M.I., Joannis T., Bertolotti L., Monne I., Salviato A., Olaleye O., Shittu I., Sulaiman L., Lombin L.H., Capua I., Holmes E.C., Cattoli G. (2010) Evolutionary dynamics of multiple sublineages of H5N1 influenza viruses in Nigeria from 2006 to 2008. <i>J.Viro.</i> 84(7):3239-3247.</p>

PROJECTS

I have been responsible of operative units in three national projects, one of them ongoing. I am currently involved in the European FP7 project DELTA-FLU as well as in four national projects. I collaborated in several European and national projects, as detailed below. I also conducted activities in the framework of the International Development's Emerging Pandemic Threat (EPT+) programme funded by the United States Agency. Several papers resulted from the research activities conducted under these projects.

20 December 2018 - present	Participation in the national project RC IZS VE 15/18: Influenza suina: determinanti antigenici dei virus circolanti in Triveneto per il corretto controllo delle infezioni animali Coordinator institute: IZSVe. Project coordinator: Dr. Alda Natale. Project running time: 2 years
1 December 2017 - present	Leader of operative unit 1 of the national project RC IZS VE 03/17: Traiettoria evolutiva del virus USUTU in aree endemiche del nord-est d'Italia e valutazione del rischio di trasmissione all'uomo tramite trasfusione di sangue. Coordinator institute: IZSVe. Project coordinator: Dr. Isabella Monne. Project running time: 3 years
1 September 2017- present	Participation in the national project RC IZS VE 07/16: Influenza D: toward a better understanding of the infection dynamics of an emerging animal virus in north-eastern Italy Coordinator institute: IZSVe Project coordinator: Dr Isabella Monne. Project running time: 3 years.
1 June 2017-present	Participation in the European project (FP7) DELTA-FLU: Dynamics of avian influenza in a changing world. Coordinator institute: Friedrich-Loeffler-Institut (FLI), Germania. Project coordinator: Prof. Thomas Mettenleiter. Project running time: 5 years.
1 September 2016- present	Participation in the national project RC IZS VE 14/2015: Epatite E nella grossa selvaggina nel nord-est italiano: epidemiologia in alcune specie di ungulati e analisi del rischio all'interfaccia tra fauna animale da reddito e popolazione umana. Coordinator institute: IZSVe – SCT2 BELLUNO. Project coordinator: Dr. Carlo V. Citterio. Project running time: 2 years.

1 September 2015- present	Participation in the national project RC IZS VE 05/14: Development and application of high-throughput sequencing strategies for identifying known and unknown viruses in biological samples from domestic rabbit and avian species with unexplained illness Coordinator institute: IZSVe. Project coordinator: Dr Isabella Monne. Project running time: 3 years.
1 August 2013–1 August 2017	Leader of operative unit 2 (from 1 February 2016 to 1 August 2017) of the national project RC IZS VE 12/12: Identificazione di micro-RNA associati alla paratubercolosi bovina. Coordinator institute: SCT1 – IZSVe Verona. Project coordinator: Dr. Nicola Pozzato. Project running time: 4 years
1 Aug 2013-31 Jul 2015	Participation in the national project RC IZS VE 21/12: Study of the genetic characteristic of APMV-1 viruses identified in Italian Columbiformes population between 1999 and 2012 and evaluation of the efficacy of homologous and heterologous oil-emulsion vaccines against contemporary virulent APMV-1 circulating in Italian Columbiformes. Project coordinator: Dr. Calogero Terregino. Project running time: 2 years.
1 Dec 2012–30 Nov 2016	Leader of operative unit 3 (from 1 February 2016 to 1 August 2017) of the national project: RF-2010-2314989: Innovative molecular platform for tick-borne diseases: suspension array and pyrosequencing for the rapid, accurate and cost-effective multi-pathogen detection in ticks and biological samples. Coordinator institute: IZSVe. Project coordinator: Dr. Gioia Capelli. Project running time: 4 years
1 may 2012-31 March 2016	Participation in the European project Epi-SEQ: Molecular epidemiology of epizootic diseases using next generation sequencing technology. 2nd Joint Call for Transnational Research Projects by EMIDA ERA-NET [FP7 project no. 219235]. Coordinator institute: CODA-CERVA, Belgio Project coordinator: Dr. Steven Van Borm Project coordinator IZSVe: Dr. Isabella Monne. Project running time: 4 years Author or co-author of the following publications: Monne et al. JVI, 2014; Fusaro et al., Infection, Genetics and Evolution, 2015; Van Borm, et al., Methods Mol Biol., 2015; Monne et al., EID, 2015.
1 Nov 2011-30 Apr 2017	Participation in the Research project supported by the European Community's Seventh Framework Programme [FP7/2007-2013] PREDEMICS: Preparedness, Prediction and Prevention of Emerging Zoonotic Viruses with Pandemic Potential using Multidisciplinary Approaches (grant agreement 278433) Coordinator institute: Institut Pasteur (IP), Francia. Project coordinator: Prof. Sylvie van der Werf. Project running time: 66 months
1 Jul 2010-31 Dec 2014	Participation in the European project (FP7) FLUPIG: Pathogenesis and Transmission of influenza in pigs (Project n.: 258084). Coordinator institute: Università di Gent, Belgio Coordinatore del progetto: Prof. Van Reeth Project running time: 54 mesi Author or co-author of the following publications: Bonfante et al., Vet Mic, 2016.
20 June 2010-20 June 2012	Partecipation in the national project RC IZS VE 14/09: Dinamiche epidemiologiche ed evolutive dell'influenza aviaria. Coordinator institute: IZSVe. Project coordinator: Dr. Isabella Monne Project running time: 2 years. Author or co-author of the following publications: Fusaro et al., JVI, 2011; Monne et al., Influenza Other Respi Viruses, 2012; Cattoli et al., Vaccine, 2011.



28-30 November 2018	Oral presentation to the peer-reviewed national conference: 2nd National Congress of the Italian Society for Virology, Rome, Italy. Presentation title: Transmission dynamics of highly pathogenic avian influenza virus A (H5N8) in Italy, 2016-2017.
9-12 November 2018	Oral presentation to the peer-reviewed international conference: International Meeting on Emerging Diseases and Surveillance (IMED 2018), Vienna, Austria. Presentation title: Origins of African Highly Pathogenic Avian Influenza H5Nx viruses and intracontinental spread.
18-20 June 2018	Oral presentation to the peer-reviewed international conference: Virus Genomics and Evolution 2018, Cambridge, UK. Presentation title: The African continent: an endpoint in the global spread of the highly pathogenic avian influenza H5Nx virus
7-10 November 2016	Invited speaker at MISMS Influenza Workshop, National Institutes of Health, Bethesda, MD, USA Presentation title: Host immunity shapes the intra-host evolution of an H3N6 avian influenza virus in ferrets.
10-13 May 2016	Oral presentation to the peer-reviewed international conference: MEEGID XIII - 13th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Anversa, Belgium Presentation title: Within-host genetic diversity of an H3N6 avian influenza virus in ferrets
13-14 October 2016	Invited speaker to the national conference: VI Workshop Nazionale di Virologia Veterinaria, Torino, Italia. Presentation title: L'effetto della pressione selettiva nell'evoluzione inter- e intra-ospite di virus influenziali aviari.
28-30 September 2016	Oral presentation to the peer-reviewed national conference: XVII Congresso Nazionale S.I.Di.LV. - Società Italiana di Diagnostica di Laboratorio Veterinario Pacengo di Lazise (VR), Italia. Presentation title: Applicazione di un approccio deep sequencing per lo studio dell'effetto della pressione immunitaria nell'evoluzione di virus influenziali aviari in ospiti mammiferi.
30 June-3 July 2014	Invited speaker at MISMS - Influenza research workshop, Bethesda, MD, USA. Presentation title: Avian influenza evolution behind the consensus genome
23-25 September 2014	Oral presentation to the peer-reviewed international conference: 8th Annual Meeting – EPIZONE, Copenhagen, Denmark
25 February- 1 March 2013	Presentation title: A deep insight into an H7N7 highly pathogenic avian influenza epidemic Invited speaker at MISMS Europe Meeting and Training Workshop, Padova, Italy Presentation title: Molecular epidemiology of avian influenza virus
30 October – 2 November 2012	Oral presentation to the peer-reviewed international conference: 11th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, New Orleans, USA Presentation title: The Emergence of a Highly Pathogenic Avian Influenza Virus - an Evolutionary Approach
4-7 September 2012	Oral presentation to the peer-reviewed international conference: ESVV – European Society for Veterinary Virology, Madrid, Spain Presentation title: The evolutionary dynamics behind the emergence of a highly pathogenic avian influenza virus from a low pathogenic progenitor
1-4 April 2012	Oral presentation to the peer-reviewed international conference: 8th International Symposium on Avian Influenza, London, UK Presentation title: Combining epidemiology with genetic data to study the dynamics of avian influenza outbreaks: the H7N1 in Italy.
4-7 February 2011	Oral presentation to the peer-reviewed international conference: IMED - International Meeting on Emerging Diseases and Surveillance, Vienna, Austria Presentation title: Impact of vaccination on the genetic evolution of H5N1 viruses in Egypt
7-8 June 2011	Oral presentation at the 2nd annual interdisciplinary workshop on influenza evolution, immunology, and epidemiology, Bethesda, MD, USA Presentation title: Evidence for differing evolutionary dynamics of A/H5N1 viruses among countries applying or not applying avian influenza vaccination in poultry
3-5 November 2010	Oral presentation to the peer-reviewed international conference: 10th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, Amsterdam, the Netherlands. Presentation title: Diversity and evolution of H9N2 viruses in the Middle East

- 23-26 June 2009 Oral presentation at IDEA Workshop, Bethesda, MD, USA.
Presentation title: Molecular epidemiology of H5N1 viruses isolated in Nigeria between 2006 and 2008.

TEACHING ACTIVITIES

One of the institutional duties of Istituto Zooprofilattico Sperimentale delle Venezie is to train providers from the animal health and food safety sectors. Specifically, as Reference Laboratory for avian influenza and Newcastle disease, my department, in cooperation with FAO, is involved in educational and international cooperation projects to train local healthcare professionals in appropriate emergency management. For this reason, I am frequently involved in teaching activities on sequencing and genetic analyses of avian influenza virus for visitors coming from developing countries, but also from European countries. Besides these routine activities, I hold the following training courses both in Italy and at foreign and international research institutes. Despite I have never taught at the University, my communication skills are good and I have a great passion for teaching.

- 19-21 September 2018 Training course: "Diagnosis of Transboundary Animal Diseases: Sequencing and Bioinformatic Analysis of Animal Pathogen Genomes", Seibersdorf, Austria.
Summoned as an expert/lecturer on "Phylogenetic and molecular analysis of avian influenza viruses", "Phylogenetic and molecular analysis of avian influenza viruses using GISAID and FluSurver" "Submission of avian influenza virus sequences in GenBank or GISAID"; "Recombination analysis"; "Phylogenetic analysis of avian avulavirus 1"; and hands-on training session on: phylogenetic and amino acid sequence analyses of avian influenza viruses, recombination analysis; genetic analyses of avian avulavirus 1 sequences
Organizer: International Atomic Energy Agency, Vienna, Austria.
Term of office: 3 days
- 15-22 September 2017 Training course: "Training on Advanced Detection and Differentiation of AI Viruses in Light of the Current Outbreaks in the Europe Region", Seibersdorf, Austria.
Summoned as an expert/lecturer on "Introduction to Next Generation Sequencing technologies", "Intra- and inter-host evolutionary dynamics of avian influenza viruses", "Introduction to NGS file formats" and hands-on training session
Organizer: International Atomic Energy Agency, Vienna, Austria.
Term of office: 5 days
- 5-8 April 2016 Training course: "EPIZONE Workshop on Next Generation Sequencing applications and Bioinformatics", Bruxelles, Belgium.
Summoned as an expert/lecturer on "Tracing avian influenza virus evolution using a deep sequencing approach" and hands-on training session.
Organizer: CODA-CERVA, Bruxelles, Belgium.
Term of office: 4 days.
- 23 November 2015 Training course (ECM) "Principi e tecniche di next generation: applicazioni nella pratica veterinaria", Portici, Italy. Summoned as an expert/lecturer on "L'utilizzo di un approccio "deep sequencing" per lo studio di virus influenzali aviari".
Organizer: Istituto Zooprofilattico Sperimentale del Mezzogiorno, Portici (NA), Italy
Term of office: 1 day.
- 27-30 January 2015 Training course "Molecular tracing of viral diseases in aquaculture", Montpellier, France.
Summoned as an expert/lecturer on "Introduction to BEAST", "Phylogeographic analysis of viral epidemic" and hands-on training session
Organizer: University of Montpellier, Montpellier, France
Term of office: 4 days.
- 29 October 2014 Training course (ECM) "Il sequenziamento di nuova generazione in IZSVe: potenzialità e applicazioni". Legnaro, Padua.
Organizer: IZSVe, Legnaro, Padua, Italy
Term of office: 1 day.
- 28-29 August 2013 Training course "European Regional Training Course on Rapid and Confirmatory Diagnosis of Avian Influenza H7N9", Seibersdorf, Austria.
Organizer: International Atomic Energy Agency, Vienna, Austria.
Term of office: 2 days
- 29 November 2012 Training course (ECM) "Biologia molecolare nella ricerca virale: nuovi approcci per lo studio degli agenti patogeni – EDIZIONE 3". Legnaro, Padua, Italy
Organizer: IZSVe, Legnaro, Padua, Italy
Term of office: 1 day

5-9 November 2012	Training course "Training on sequencing and molecular epidemiology of animal pathogens: focus on PPR, CBPP, AI, ND, FMD and capripox", Seibersdorf, Austria. Summoned as an expert/lecturer on "Submission of sequences to public databases using the sequin software", "Submission of sequences to public databases: other tools", "Live demonstration with open source software: Mega", "Molecular epidemiology of Avian Influenza and NDV", "Phylogenetic analyses: AI and NDV – applications" and hands-on training session. Organizer: International Atomic Energy Agency, Vienna, Austria. Term of office: 5 days
8 November 2011	Training course (ECM) "Biologia molecolare nella ricerca virale: nuovi approcci per lo studio degli agenti patogeni – EDIZIONE 2". Legnaro, Padua, Italy Organizer: IZSVe, Legnaro, Padua, Italy Term of office: 1 day
22 February 2011	Training course (ECM) "Biologia molecolare nella ricerca virale: nuovi approcci per lo studio degli agenti patogeni – EDIZIONE 1". Legnaro, Padua, Italy Organizer: IZSVe, Legnaro, Padua, Italy Term of office: 1 day
2-5 November 2009	Training course "EU-FLUTRAIN International Workshop", Vom, Nigeria Organizer: EU-FLUTRAIN Term of office: 4 days
21-25 September 2009	Training course "Seminario de Actualización científico-tecnica en Diagnóstico Molecular Avanzado", Campinas, Brasil. Organizer: LANAGRO, Campinas, Brasil. Term of office: 5 days

COLLABORATIONS

I collaborate with several research institutes, including:

- 2008-2009: University of Torino, Torino, Italy (Prof. Luigi Bertolotti).
- 2009-present: Fogarty International Center of the U.S. National Institutes of Health, Bethesda, MD, USA (Martha Nelson).
- 2009-present: Marie Bashir Institute for Infectious Diseases and Biosecurity, Charles Perkins Centre, School of Life and Environmental Sciences and Sydney Medical School, University of Sydney, Sydney, Australia (Prof. Edward C. Holmes).
- 2012-present: Department of Microbiology and Immunology, Rega Institute, KU Leuven, Leuven, Belgio (Prof. Philippe Lemey).
- 2013-present: MRC-University of Glasgow Center for Virus Research, Glasgow, United Kingdom (Prof. Pablo Murcia e Dr. Joseph Hughes).
- 2014-2016: Biological Control and Spatial Ecology, Université Libre de Bruxelles, Brussels, Belgium (Dr. Marius Gilbert)

REVIEWER ACTIVITY

Ad-hoc reviewer for the following International and National Scientific Journals (<https://publons.com/researcher/1516430/alice-fusaro>):

- Archives of Virology (Springer);
- Infection, Genetics and Evolution (Elsevier);
- PLoS ONE (Public Library of Science);
- Virus Research (Elsevier);
- Virology (Elsevier);
- Virus Genes (Springer);
- Molecular Phylogenetics and Evolution (Elsevier);
- PeerJ (PeerJ);
- Emerging Infectious Disease (CDC);
- SpringerPlus (SpringerOpen);
- Veterinaria Italiana (Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise);

- Avian Pathology (Taylor & Francis);
- Transboundary and Emerging Diseases (Wiley);
- Emerging Microbes & Infections (Nature Publishing Group)
- Journal of Medical Virology (Wiley);
- Viruses (MDPI)
- Influenza Research and Treatment (Hindawi)
- Virus Evolution (Oxford University Press)
- Zoonoses and Public Health (Wiley)

FELLOWSHIP AWARD

OECD's Co-operative programme fellowship award 2013. This program funds a seven week (15/04/2013-03/06/2013) research project at the University of Glasgow Centre (Prof. Pablo Murcia lab) for Virus Research to investigate the evolutionary mechanisms governing the emergence of highly pathogenic avian influenza viruses starting from Next Generation Sequencing data.

PERSONAL SKILLS

Mother tongue Italian

Other language	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken interaction	Spoken production	
English	good	excellent	good	good	good

Driving licence B

PUBLICATIONS

Publications in international journals

Scopus: H index = 18

Web of Science: H index = 17

ORCID: 0000-0002-8213-5472

1. Fusaro, A., Zecchin, B., Vrancken, B., Abolnik, C., Ademun, A.R., Akpeli, Y.P., Alassane, A., Awuni, J.A., Couacy-Hymann, E., Coulibaly, M., Go-Maro, E., Joannis, T., Jumbo, S.D., Minoungou, G., Meseke, C., Moutari, S.M., Ndumu, D.B., Twabela, A., Wade, A., Wiersma, L., Zamperin, G., Milani, A., Lemey, P., Monne, I. Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. *Int.J.Infect.Dis.* 2019 79, 9-10. <https://doi.org/10.1016/j.ijid.2018.11.041>
2. Ndumu, D.B., Zecchin, B., Fusaro, A., Arinaitwe, E., Erechu, R., Kidega, E., Kayiwa, J., Muwanga, E., Kirumira, M., Kirembe, G., Lutwama, J., Monne, I. Genetic Characterization of HPAI H5N8 Viruses Identified in Wild and Domestic Birds in Uganda, 2017. *International Journal of Infectious Diseases*, 2019. <https://doi.org/10.1016/j.ijid.2018.11.242>
3. Boumart Z, Bamouh Z, Jazouli M, Zecchin B, Fusaro A, Salviato A, Monne I, Tadlaoui KO, Harrak ME. Pathogenicity and Full Genome Sequencing of the Avian Influenza H9N2 Moroccan Isolate 2016. *Avian Dis.* 2018 Nov 16;63(1):24-30. doi: 10.1637/11941-080418-Reg.1. PubMed PMID: 31251516.
4. Dimitrov KM, Abolnik C, Afonso CL, Albina E, Bahl J, Berg M, Briand FX, Brown IH, Choi KS, Chvala I, Diel DG, Durr PA, Ferreira HL, Fusaro A, Gil P, Goujgoulova GV, Grund C, Hicks JT, Joannis TM, Torchetti MK, Kolosov S, Lambrecht B, Lewis NS, Liu H, Liu H, McCullough S, Miller PJ, Monne I, Muller CP, Munir M, Reischak D, Sabra M, Samal SK, Servan de Almeida R, Shittu I, Snoeck CJ, Suarez DL, Van Borm S,

- Wang Z, Wong FYK. Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. *Infect Genet Evol*. 2019 Jun;11:74:103917. doi: 10.1016/j.meegid.2019.103917. [Epub ahead of print] PubMed PMID: 31200111.
- 5. Awuni JA, Bianco A, Dogbey OJ, Fusaro A, Yingar DT, Salviato A, Ababio PT, Milani A, Bonfante F, Monne I. Avian influenza H9N2 subtype in Ghana: virus characterization and evidence of co-infection. *Avian Pathol*. 2019 Jun; 26:1-7. doi: 10.1080/03079457.2019.1624687. PubMed PMID: 31142135.
 - 6. Zecchin B, Schivo A, Milani A, Fusaro A, Zamperin G, Bellinati L, Ceglie L, Natale A, Bonfanti L, Cunial G, Obber F, Di Bartolo I, Citterio C, Monne I. Identification of a zoonotic genotype 3 hepatitis E subtype in wildlife in north-eastern Italy. *Infect Genet Evol*. 2019 Jul;71:16-20. doi: 10.1016/j.meegid.2019.03.005. PubMed PMID: 30876888.
 - 7. Mulatti P, Fusaro A, Scolamacchia F, Zecchin B, Azzolini A, Zamperin G, Terregino C, Cunial G, Monne I, Marangon S. Integration of genetic and epidemiological data to infer H5N8 HPAI virus transmission dynamics during the 2016-2017 epidemic in Italy. *Sci Rep*. 2018 Dec 21;8(1):18037. doi: 10.1038/s41598-018-36892-1. PubMed PMID: 30575785
 - 8. Milani A, Zamperin G, Fusaro A, Salviato A, Bano L, Zandonà L, Brunetta R, Monne I. Complete Genome Sequence of Psittacine Adenovirus 1, Identified from *Poicephalus senegalus* in Italy. *Microbiol Resour Announc*. 2018 Sep 20;7(11). pii: e01037-18. doi: 10.1128/MRA.01037-18. eCollection 2018 Sep. PubMed PMID: 30533635
 - 9. Alarcon P, Brouwer A, Venkatesh D, Duncan D, Dovas CI, Georgiades G, Monne I, Fusaro A, Dan A, Šmietanka K, Ragias V, Breed AC, Chassalevris T, Goujgoulova G, Hjulsager CK, Ryan E, Sánchez A, Niqueux E, Tammaranta N, Zohari S, Stroud DA, Savić V, Lewis NS, Brown IH. Comparison of 2016-17 and Previous Epizootics of Highly Pathogenic Avian Influenza H5 Guangdong Lineage in Europe. *Emerg Infect Dis*. 2018 Dec;24(12):2270-2283. doi: 10.3201/eid2412.171860.
 - 10. Ndumu D, Zecchin B, Fusaro A, Arinaitwe E, Erechu R, Kidega E, Kayiwa J, Muwanga E, Kirumira M, Kirembe G, Lutwama J, Monne I. Highly pathogenic avian influenza H5N8 Clade 2.3.4.4B virus in Uganda, 2017. *Infect Genet Evol*. 2018 Dec;66:269-271. doi: 10.1016/j.meegid.2018.10.010.
 - 11. Wade A, Taïga T, Fouada MA, MaiMoussa A, Jean Marc FK, Njouom R, Vernet MA, Djonwe G, Mballa E, Kazi JP, Salla A, Nenkam R, Poueme Namegni R, Bamanga H, Casimir NKM, LeBreton M, Nwobegahay JM, Fusaro A, Zecchin B, Milani A, Gaston M, Chepnda VR, Dickmu Jumbo S, Souley A, Aboubakar Y, Fotso Kamnga Z, Nkuo C, Atkam H, Dauphin G, Wiersma L, Bebay C, Nzietchueng S, Vincent T, Biaou C, Mbacham W, Monne I, Cattoli G. Highly pathogenic avian influenza A/H5N1 Clade 2.3.2.1c virus in poultry in Cameroon, 2016-2017. *Avian Pathol*. 2018 Dec;47(6):559-575. doi: 10.1080/03079457.2018.1492087.
 - 12. Wade A, Jumbo SD, Zecchin B, Fusaro A, Taiga, Bianco A, Rodrigue PN, Salomon A, Kameni JMF, Zamperin G, Nenkam R, Fouppouapouognigni Y, Abdoulkadiri S, Aboubakar Y, Wiersma L, Cattoli G, Monne I. Highly pathogenic avian Influenza virus, H5N8, Cameroon, clade 2.3.4.4. EID. 2018. *Emerg Infect Dis*. 2018 Jul;24(7):1367-1370. doi:10.3201/eid2407.172120.
 - 13. Laleye A, Joannis T, Shittu I, Meseko C, Zamperin G, Milani A, Zecchin B, Fusaro A, Monne I, Abolnik C. A two-year monitoring period of the genetic properties of clade 2.3.2.1c H5N1 viruses in Nigeria reveals the emergence and co-circulation of distinct genotypes. *Infect Genet Evol*. 2018 Jan;57:98-105. doi: 10.1016/j.meegid.2017.10.027. Epub 2017 Nov 15.
 - 14. Zecchin B, Minoungou G, Fusaro A, Moctar S, Ouedraogo-Kaboré A, Schivo A, Salviato A, Marciano S, Monne I. Influenza A(H9N2) Virus, Burkina Faso. *Emerg Infect Dis*. 2017 Dec;23(12):2118-2119. doi: 10.3201/eid2312.171294. Epub 2017 Dec 17.
 - 15. Lisowska A, Sajewicz-Krukowska J, Fusaro A, Pikula A, Domanska-Blicharz K. First characterization of a Middle-East GI-23 lineage (Var2-like) of infectious bronchitis virus in Europe. *Virus Res*. 2017 Oct 15;242:43-48. doi: 10.1016/j.virusres.2017.09.010. Epub 2017 Sep 18.
 - 16. El Romeh A, Zecchin B, Fusaro A, Ibrahim E, El Bazzal B, El Hage J, Milani A, Zamperin G, Monne I. Highly Pathogenic Avian Influenza H5N1 Clade 2.3.2.1c Virus in Lebanon, 2016. *Avian Dis*. 2017 Jun;61(2):271-273. doi: 10.1637/11544-113016-Case.1.
 - 17. Fusaro A, Monne I, Mulatti P, Zecchin B, Bonfanti L, Ormelli S, Milani A, Cecchettin K, Lemey P, Moreno A, Massi P, Dorotea T, Marangon S, Terregino C. Genetic Diversity

- of Highly Pathogenic Avian Influenza A(H5N8/H5N5) Viruses in Italy, 2016-17. *Emerg Infect Dis.* 2017 Sep;15;23(9). doi: 10.3201/eid2309.170539.
- 18. Milani A, Fusaro A, Bonfante F, Zamperin G, Salviato A, Mancin M, Mastorilli E, Hughes J, Hussein HA, Hassan M, Mundt E, Terregino C, Cattoli G, Monne I. Vaccine immune pressure influences viral population complexity of avian influenza virus during infection. *Vet Microbiol.* 2017 May;203:88-94. doi: 10.1016/j.vetmic.2017.02.016.
 - 19. Nickbakhsh S, Hall MD, Dorigatti I, Lycett SJ, Mulatti P, Monne I, Fusaro A, Woolhouse ME, Rambaut A, Kao RR. Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. *Epidemics.* 2016 Dec;17:27-34. doi: 10.1016/j.epidem.2016.10.005. Epub 2016 Oct 19.
 - 20. Beato MS, Tassoni L, Milani A, Salviato A, Di Martino G, Mion M, Bonfanti L, Monne I, Watson SJ, Fusaro A. Circulation of multiple genotypes of H1N2 viruses in a swine farm in Italy over a two-month period. *Vet Microbiol.* 2016 Nov 15;195:25-29. doi: 10.1016/j.vetmic.2016.08.015. Epub 2016 Sep 7.
 - 21. Abbadi M, Fusaro A, Ceolin C, Casarotto C, Quartesan R, Dalla Pozza M, Cattoli G, Toffan A, Holmes EC, Panzarini V. Molecular Evolution and Phylogeography of Co-circulating IHNV and VHSV in Italy. *Front Microbiol.* 2016 Aug 23;7:1306. doi: 10.3389/fmicb.2016.01306. eCollection 2016.
 - 22. Artois J, Newman SH, Dhingra MS, Chaibani C, Linard C, Cattoli G, Monne I, Fusaro A, Xenarios I, Engler R, Liechti R, Kuznetsov D, Pham TL, Nguyen T, Pham VD, Castellan D, Von Dobschuetz S, Claes F, Dauphin G, Inui K, Gilbert M. Clade-level Spatial Modelling of HPAI H5N1 Dynamics in the Mekong Region Reveals New Patterns and Associations with Agro-Ecological Factors. *Sci Rep.* 2016 Jul 25;6:30316. doi: 10.1038/srep30316.
 - 23. Tassoni L, Fusaro A, Milani A, Lemey P, Awuni JA, Sedor VB, Dogbey O, Commey AN, Meseiko C, Joannis T, Minoungou GL, Ouattara L, Haido AM, Cisse-Aman D, Couacy-Hymann E, Dauphin G, Cattoli G, Monne I. Genetically Different Highly Pathogenic Avian Influenza A(H5N1) Viruses in West Africa, 2015. *Emerg Infect Dis.* 2016 Dec;22(12):2132-2136. doi: 10.3201/eid2212.160578.
 - 24. Damena D, Fusaro A, Sombo M, Belaineh R, Heidari A, Kebede A, Kidane M, Chaka H. Characterization of Newcastle disease virus isolates obtained from outbreak cases in commercial chickens and wild pigeons in Ethiopia. *Springerplus.* 2016 Apr 18;5:476. doi: 10.1186/s40064-016-2114-8. eCollection 2016.
 - 25. Fusaro A, Tassoni L, Milani A, Hughes J, Salviato A, Murcia PR, Massi P, Zamperin G, Bonfanti L, Marangon S, Cattoli G, Monne I. Unexpected Interfarm Transmission Dynamics during a Highly Pathogenic Avian Influenza Epidemic. *J Virol.* 2016 Jun 24;90(14):6401-11. doi: 10.1128/JVI.00538-16. Print 2016 Jul 15
 - 26. Bonfante F, Fusaro A, Tassoni L, Patrono LV, Milani A, Maniero S, Salviato A, Terregino C. Spillback transmission of European H1N1 avian-like swine influenza viruses to turkeys: A strain-dependent possibility? *Vet Microbiol.* 2016 Apr 15;186:102-10. doi: 10.1016/j.vetmic.2016.02.025
 - 27. Valastro V, Holmes EC, Britton P, Fusaro A, Jackwood MW, Cattoli G, Monne I. S1 gene-based phylogeny of infectious bronchitis virus: An attempt to harmonize virus classification. *Infect Genet Evol.* 2016 Apr;39:349-64. doi: 10.1016/j.meegid.2016.02.015.
 - 28. Lee DH, Fusaro A, Song CS, Suarez DL, Swayne DE. Poultry vaccination directed evolution of H9N2 low pathogenicity avian influenza viruses in Korea. *Virology.* 2016 Jan 15;488:225-31. doi: 10.1016/j.virol.2015.11.023.
 - 29. Monne I, Meseiko C, Joannis T, Shittu I, Ahmed M, Tassoni L, Fusaro A, Cattoli G. Highly Pathogenic Avian Influenza A(H5N1) Virus in Poultry, Nigeria, 2015. *Emerg Infect Dis.* 2015 Jul;21(7):1275-7. doi: 10.3201/eid2107.150421.
 - 30. Fusaro A, Tassoni L, Hughes J, Milani A, Salviato A, Schivo A, Murcia PR, Bonfanti L, Cattoli G, Monne I. Evolutionary trajectories of two distinct avian influenza epidemics: Parallelisms and divergences. *Infect Genet Evol.* 2015 Aug;34:457-66. doi: 10.1016/j.meegid.2015.05.020.
 - 31. Van Borm S, Belák S, Freimanis G, Fusaro A, Granberg F, Höper D, King DP, Monne I, Orton R, Rosseel T. Next-generation sequencing in veterinary medicine: how can the massive amount of information arising from high-throughput technologies improve diagnosis, control, and management of infectious diseases? *Methods Mol Biol.* 2015;1247:415-36. doi: 10.1007/978-1-4939-2004-4_30. Review.
 - 32. Hill AA, Dewé T, Kosmider R, Von Dobschuetz S, Munoz O, Hanna A, Fusaro A, De

- Nardi M, Howard W, Stevens K, Kelly L, Havelaar A, Stärk K. Modelling the species jump: towards assessing the risk of human infection from novel avian influenzas. *R Soc Open Sci.* 2015 Sep;9(9):150173. doi: 10.1098/rsos.150173. PubMed PMID: 26473042
33. Bonfante F, Fusaro A, Zanardello C, Patrono LV, De Nardi R, Maniero S, Terregino C. Lethal nephrotropism of an H10N1 avian influenza virus stands out as an atypical pathotype. *Vet Microbiol.* 2014 Oct;173(3-4):189-200. doi: 10.1016/j.vetmic.2014.07.023. Epub 2014 Aug 19.
34. Monne I, Fusaro A, Nelson MI, Bonfanti L, Mulatti P, Hughes J, Murcia PR, Schivo A, Valastro V, Moreno A, Holmes EC, Cattoli G. Emergence of a highly pathogenic avian influenza virus from a low-pathogenic progenitor. *J Virol.* 2014 Apr;88(8):4375-88. doi: 10.1128/JVI.03181-13.
35. Davidson I, Fusaro A, Heidari A, Monne I, Cattoli G. Molecular evolution of H9N2 avian influenza viruses in Israel. *Virus Genes.* 2014 Jun;48(3):457-63. doi: 10.1007/s11262-014-1037-0.
36. Babiker AM, Ravagnan S, Fusaro A, Hassan MM, Bakheit SM, Mukhtar MM, Cattoli G, Capelli G. Concomitant Infection with Leishmania donovani and *L. major* in Single Ulcers of Cutaneous Leishmaniasis Patients from Sudan. *J Trop Med.* 2014;2014:170859. doi: 10.1155/2014/170859. Epub 2014 Mar 12. PubMed PMID: 24744788
37. Fusaro A, Monne I, Salomon A, Angot A, Trolese M, Ferrè N, Mutinelli F, Holmes EC, Capua I, Lemey P, Cattoli G, De Benedictis P. The introduction of fox rabies into Italy (2008-2011) was due to two viral genetic groups with distinct phylogeographic patterns. *Infect Genet Evol.* 2013 Jul;17:202-9. doi: 10.1016/j.meegid.2013.03.051.
38. Beato MS, Mancin M, Yang J, Buratin A, Ruffa M, Maniero S, Fusaro A, Terregino C, Wan XF, Capua I. Antigenic characterization of recent H5N1 highly pathogenic avian influenza viruses circulating in Egyptian poultry. *Virology.* 2013 Jan 20;435(2):350-6. doi: 10.1016/j.virol.2012.09.016.
39. Monne I, Hussein HA, Fusaro A, Valastro V, Hamoud MM, Khalefa RA, Dardir SN, Radwan MI, Capua I, Cattoli G. H9N2 influenza A virus circulates in H5N1 endemically infected poultry population in Egypt. *Influenza Other Respir Viruses.* 2013 May;7(3):240-3. doi: 10.1111/j.1750-2659.2012.00399.x
40. Panzarini V, Fusaro A, Monne I, Cappelozza E, Patarnello P, Bovo G, Capua I, Holmes EC, Cattoli G. Molecular epidemiology and evolutionary dynamics of betanodavirus in southern Europe. *Infect Genet Evol.* 2012 Jan;12(1):63-70. doi: 10.1016/j.meegid.2011.10.007
41. Cattoli G, Fusaro A, Monne I, Coven F, Joannis T, El-Hamid HS, Hussein AA, Cornelius C, Amarin NM, Mancin M, Holmes EC, Capua I. Evidence for differing evolutionary dynamics of A/H5N1 viruses among countries applying or not applying avian influenza vaccination in poultry. *Vaccine.* 2011 Nov 21;29(50):9368-75. doi: 10.1016/j.vaccine.2011.09.127. Epub 2011 Oct 12
42. Dundon WG, Heidari A, Fusaro A, Monne I, Beato MS, Cattoli G, Koch G, Starick E, Brown IH, Aldous EW, Briand FX, Le Gall-Reculé G, Jestin V, Jørgensen PH, Berg M, Zohari S, Metreveli G, Munir M, Ståhl K, Albina E, Hammoumi S, Gil P, de Almeida RS, Smietanka K, Domańska-Blicharz K, Minta Z, Van Borm S, van den Berg T, Martin AM, Barbieri I, Capua I; EPIZONE Network of Excellence Molecular Epidemiology of AI; APMV working group. Genetic data from avian influenza and avian paramyxoviruses generated by the European network of excellence (EPIZONE) between 2006 and 2011—review and recommendations for surveillance. *Vet Microbiol.* 2012 Jan 27;154(3-4):209-21. doi: 10.1016/j.vetmic.2011.08.018. Review.
43. Fusaro A, Monne I, Salvato A, Valastro V, Schivo A, Amarin NM, Gonzalez C, Ismail MM, Al-Ankari AR, Al-Blowi MH, Khan OA, Maken Ali AS, Hedayati A, Garcia Garcia J, Ziay GM, Shoushtari A, Al Qahtani KN, Capua I, Holmes EC, Cattoli G. Phylogeography and evolutionary history of reassortant H9N2 viruses with potential human health implications. *J Virol.* 2011 Aug;85(16):8413-21. doi: 10.1128/JVI.00219-11.
44. Monne I, Fusaro A, Valastro V, Citterio C, Dalla Pozza M, Obber F, Trevisiol K, Cova M, De Benedictis P, Bregoli M, Capua I, Cattoli G. A distinct CDV genotype causing a major epidemic in Alpine wildlife. *Vet Microbiol.* 2011 May 12;150(1-2):63-9. doi: 10.1016/j.vetmic.2011.01.009.
45. Bovo G, Gustinelli A, Quaglio F, Gobbo F, Panzarini V, Fusaro A, Mutinelli F, Caffara M, Fioravanti ML. Viral encephalopathy and retinopathy outbreak in freshwater fish

- farmed in Italy. *Dis Aquat Organ.* 2011 Aug;96(1):45-54. doi: 10.3354/dao02367. PubMed PMID: 21991664.
46. Smietanka K, Fusaro A, Domanska-Blicharz K, Salviato A, Monne I, Dundon WG, Cattoli G, Minta Z. Full-length genome sequencing of the Polish HPAI H5N1 viruses suggests separate introductions in 2006 and 2007. *Avian Dis.* 2010 Mar;54(1 Suppl):335-9.
 47. Fusaro A, Nelson MI, Joannis T, Bertolotti L, Monne I, Salviato A, Olaleye O, Shittu I, Sulaiman L, Lombin LH, Capua I, Holmes EC, Cattoli G. Evolutionary dynamics of multiple sublineages of H5N1 influenza viruses in Nigeria from 2006 to 2008. *J Virol.* 2010 Apr;84(7):3239-47. doi: 10.1128/JVI.02385-09.
 48. Cattoli G, Fusaro A, Monne I, Molia S, Le Menach A, Mareguya B, Nchare A, Bangana I, Maina AG, Koffi JN, Thiam H, Bezeid OE, Salviato A, Nisi R, Terregino C, Capua I. Emergence of a new genetic lineage of Newcastle disease virus in West and Central Africa—implications for diagnosis and control. *Vet Microbiol.* 2010 May 19;142(3-4):168-76. doi: 10.1016/j.vetmic.2009.09.063.
 49. Cattoli G, Fusaro A, Monne I, Capua I. H5N1 Virus Evolution in Europe-An Updated Overview. *Viruses.* 2009 Dec;1(3):1351-63. doi: 10.3390/v1031351.
 50. Fusaro A, Monne I, Cattoli G, De Nardi R, Salviato A, Moreno Martin A, Capua I, Terregino C. Gene segment reassortment between Eurasian and American clades of avian influenza virus in Italy. *Arch Virol.* 2010;155(1):77-81. doi: 10.1007/s00705-009-0550-2. Epub 2009 Nov 19.
 51. De Benedictis P, Sow A, Fusaro A, Veggiato C, Talbi C, Kaboré A, Dundon WG, Bourhy H, Capua I. Phylogenetic analysis of rabies viruses from Burkina Faso, 2007. *Zoonoses Public Health.* 2010 Dec;57(7-8):e42-6. doi: 10.1111/j.1863-2378.2009.01291.x. PubMed PMID: 19968849
 52. Cattoli G, Monne I, Fusaro A, Joannis TM, Lombin LH, Aly MM, Arafa AS, Sturm-Ramirez KM, Couacy-Hymann E, Awuni JA, Batawui KB, Awoyme KA, Aplogan GL, Sow A, Ngangnou AC, El Nasri Hamza IM, Gamatié D, Dauphin G, Domenech JM, Capua I. Highly pathogenic avian influenza virus subtype H5N1 in Africa: a comprehensive phylogenetic analysis and molecular characterization of isolates. *PLoS One.* 2009;4(3):e4842. doi: 10.1371/journal.pone.0004842. Epub 2009 Mar 17.
 53. Fusaro A, Joannis T, Monne I, Salviato A, Yakubu B, Meseko C, Oladokun T, Fassina S, Capua I, Cattoli G. Introduction into Nigeria of a distinct genotype of avian influenza virus (H5N1). *Emerg Infect Dis.* 2009 Mar;15(3):445-7. doi: 10.3201/eid1503.081161.
 54. Khan OA, Shuaib MA, Rhman SS, Ismail MM, Hammad YA, Baky MH, Fusaro A, Salviato A, Cattoli G. Isolation and identification of highly pathogenic avian influenza H5N1 virus from Houbara bustards (*Chlamydota undulata macqueenii*) and contact falcons. *Avian Pathol.* 2009 Feb;38(1):35-9. doi: 10.1080/03079450802609815.
 55. Monne I, Fusaro A, Al-Blowi MH, Ismail MM, Khan OA, Dauphin G, Tripodi A, Salviato A, Marangon S, Capua I, Cattoli G. Co-circulation of two sublineages of HPAI H5N1 virus in the Kingdom of Saudi Arabia with unique molecular signatures suggesting separate introductions into the commercial poultry and falconry sectors. *J Gen Virol.* 2008 Nov;89(Pt 11):2691-7. doi: 10.1099/vir.0.2008/004259-0.
 56. Gaidet N, Cattoli G, Hammoumi S, Newman SH, Hagemeijer W, Takekawa JY, Cappelle J, Dodman T, Joannis T, Gil P, Monne I, Fusaro A, Capua I, Manu S, Micheloni P, Ottosson U, Mshelbwala JH, Lubroth J, Domenech J, Monicat F. Evidence of infection by H5N2 highly pathogenic avian influenza viruses in healthy wild waterfowl. *PLoS Pathog.* 2008 Aug 15;4(8):e1000127. doi: 10.1371/journal.ppat.1000127.
 57. Monne I, Joannis TM, Fusaro A, De Benedictis P, Lombin LH, Ularamu H, Egbuji A, Solomon P, Obi TU, Cattoli G, Capua I. Reassortant avian influenza virus (H5N1) in poultry, Nigeria, 2007. *Emerg Infect Dis.* 2008 Apr;14(4):637-40. doi: 10.3201/eid1404.071178. Erratum in: *Emerg Infect Dis.* 2008 May;14(5):865.

**Abstract submitted to
national and
international
conferences**

1. Zecchin, B., Schivo, A., Milani, A., Fusaro, A., Zamperin, G., Bellinati, L., Ceglie, L., Natale, A., Bonfanti, L., Cunial, G., Obber, F., Di Bartolo, I., Citterio, C., Monne, I. Zootic HEV genotype 3 in wildlife in north-eastern Italy. European Congress of Virology - ECV2019 (pp. 77-78). 28 April-1 May 2019, Rotterdam, the Netherlands.
2. Fusaro, A., Zecchin, B., Zamperin, G., Schivo, A., Salomoni, A., Salviato, A., Ormelli, S., Marciano, S., Bonfanti, L., Azzolini, A., Cunial, G., Mulatti, P., Terregino, C., Monne,

- I. (2018). Strengthening outbreak investigations using a next generation approach. 10th International Symposium on Avian Influenza (p. 196). 15 - 18 April 2018, Brighton, UK
3. Fusaro, A., Zamperin, G., Milani, A., Schivo, A., Salviato, A., Monne, I. (2018). Genesis of a highly pathogenic virus: what can we learn from deep sequencing data? 10th International Symposium on Avian Influenza (p. 195). 15 - 18 April 2018, Brighton, UK
 4. Fusaro, A., Milani, A., Bonfante, F., Zamperin, G., Salviato, A., Mancin, M., Mastorilli, E., Hughes, J., Hussein A. Hussein, Hassan, M., Mundt, E., Terregino, C., Cattoli, G., Monne, I. (2018). Impact of vaccine immune pressure on avian influenza population complexity in poultry. 10th International Symposium on Avian Influenza (p. 139). 15 - 18 April 2018, Brighton, UK
 5. Mazzetto, E., Bonfante, F., Zamperin, G., Fusaro, A., Baumann, J., Milani, A., Monne, I., Matrosovich, M., Terregino, C., Cattoli, G. (2018). Selection of the G228S mutation in the hemagglutinin of a H3N6 mallard virus is favoured in ferrets with prior immunity against a H3N2 seasonal virus. 10th International Symposium on Avian Influenza (p. 84). 15 - 18 April 2018, Brighton, UK
 6. Fusaro, A., Zamperin, G., Milani, A., Schivo, A., Cavicchio, L., Mantovani, C., Monne, I., Vio, D., Schiavon, E., Giorgiutti, M., Castellan, A., Mion, M., Beato, M.S. Novel European Swine Influenza genotypes identified in Italy between 2013 and 2017. 4th International Symposium on Neglected Influenza Viruses. 18 - 20 April 2018, Brighton, UK
 7. Azzolini, A., Mulatti, P., Fornasiero, D., Cunial, G., Bonato, P., Fusaro, A., Zecchin, B., Scolamacchia, F., 2018. Characteristics of H5N8 HPAI epidemic waves in Italy in 2017. 12th Annual Meeting of EPIZONE (Abstracts, 20), 27-30 August 2018, Vienna, Austria.
 8. Beato, M.S., Fusaro, A., Zamperin, G., Milani, A., Cavicchio, L., Schivo, A., Mantovani, C., Monne, I., Vio, D., Schiavon, E., Giorgiutti, M., Castellan, A., Mion, M. Novel European Swine Influenza genotypes identified in Italy between 2013 and 2017. 4th International Symposium on Neglected Influenza Viruses (p. 34). 18-20 April 2018, Brighton, UK
 9. Bianco, A., Cavicchio, L., Fusaro, A., Rizzo, G., Milani, A., Salviato, A., Zamperin, G., Beato, M.S., Schiavon, E., Bano, L., Monne, I. Whole genome characterization of Influenza D viruses detected in cattle herds in Northern Italy between 2015 and 2017. 23rd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology - VEME 2018 (p. 30), 26-31 August 2018, Berlin, Germany.
 10. Bonfante, F., Zamperin, G., Fusaro, A., Milani, A., Mazzetto, E., Monne, I., Terregino, C., Baumann, J., Matrosovich, M., Cattoli, G. Selection of the G228S mutation in the hemagglutinin of a H3N6 mallard virus is favored in ferrets with prior immunity against a H3N2 seasonal virus. 10th International Symposium on Avian Influenza (p. 84). 15 - 18 April 2018, Brighton, UK
 11. Fusaro, A., Zamperin, G., Milani, A., Cavicchio, L., Rizzo, G., Schivo, A., Pagliari, M., Mantovani, C., Monne, I., Beato, M.S. Swine Influenza: novel European genotypes identified in North East Italy. 2nd National Congress of the Italian Society Virology. 28-30 November 2018, Rome, Italy.
 12. Fusaro, A., Zecchin, B., Mulatti, P., Zamperin, G., Schivo, A., Ormelli, S., Marciano, S., Bonfanti, L., Azzolini, A., Cunial, G., Massi, P., Moreno, A., Mandola, M.L., Marangon, S., Terregino, C., Monne, I.. Transmission dynamics of highly pathogenic avian influenza virus A (H5N8) in Italy, 2016-2017. 2nd National Congress of the Italian Society Virology. 28-30 November 2018, Rome, Italy.
 13. Fusaro, A., Zecchin, B., Vrancken, B., Abolnik, C., Ademun, A.R., Akpeli, Y.P., Alassane, A., Awuni, J.A., Couacy-Hymann, E., Coulibaly, M., Go-Maro, E., Joannis, T., Jumbo, S.D., Minoungou, G., Meseke, C., Moutari, S.M., Ndumu, D.B., Twabela, A., Wade, A., Wiersma, L., Zamperin, G., Milani, A., Lemey, P., Monne, I., 2019. Global origins of African highly pathogenic avian influenza H5Nx viruses and intracontinental spread. Int.J.Infect.Dis. 79, 9-10. Presented at the International Meeting on Emerging Diseases and Surveillance (IMED), 9-12 November 2018, Vienna Austria.
 14. Fusaro, A., Zecchin, B., Vrancken, B., Abolnik, C., Ademun, R., Akpeli, Y.P., Alassane, A., Joseph Awuni, A., Couacy-Hymann, E., Coulibaly, M., Go-Maro, E., Joannis, T., Jumbo, D.S., Minoungou, G., Meseke, C., Moutari, S.M., Ndumu, B.D., Twabela, A., Wade, A., Wiersma, L., Zamperin, G., Milani, A., Lemey, P., Monne, I. Investigating Africa's contribution to the global spread of H5Nx highly pathogenic avian influenza viruses. 2nd National Congress of the Italian Society Virology. 28-30 November 2018, Rome, Italy.
 15. Fusaro, A., Zecchin, B., Vrancken, B., Abolnik, C., Ademun, R., Alassane, A., Awuni,

- J.A., Couacy-Hymann, E., Coulibaly, M.B., Go-Maro, E., Joannis, T., Jumbo, S.D., Minoungou, G., Meseke, C., Moutari, S.M., Ndumu, D.B., Twabela, A., Wade, A., Wiersma, L., Yao,A.P.,Zamperin,G., Milani, A., Lemey, P., Monne, I., 2018. The African continent: an endpoint in the global spread of the highly pathogenic avian influenza H5Nx virus. *Virus Genomics and Evolution* 2018 (Abstract S27). 18-20 June 2018, Cambridge, UK.
16. Ndumu, D.B., Zecchin, B., Fusaro, A., Arinaitwe, E., Erechu, R., Kidega, E., Kayiwa, J., Muwanga, E., Kirumira, M., Kirembe, G., Lutwama, J., Monne, I. Genetic Characterization of HPAI H5N8 Viruses Identified in Wild and Domestic Birds in Uganda, 2017. IMED 2018 International Meeting on Emerging Diseases and Surveillance (Abstract Poster Presentation, 205), 9-12 November 2018, Vienna Austria.
 17. Rizzo, G., Cavicchio, L., Amato, L., Cunial, G., Forzan, M., Mazzei, M., Ustolin, M., Milani, A., Fusaro, A., Monne, I., Vio, D., Bonfanti, L., Beato, M.S. Norovirus GII in faeces of healthy pigs in North-East Italy. 12th Annual Meeting of EPIZONE (Abstracts, 29). 27-30 August 2018, Vienna, Austria.
 18. Venkatesh, D., Simon, G., Herve, S., Foni, E., Van Reeth, K., Beato, M.S., Fusaro, A., Larsen, L., Smietanka, K., Brookes, S., Brown, I.H., Essen, S., Seekings, J., Collins, S., Soldevilla, G.R., Vincent, A.L., Lewis, N.S. Reassortment and genetic diversity of swine influenza A viruses. 4th International Symposium on Neglected Influenza Viruses (p. 52). 18-20 April 2018, Brighton, UK
 19. Zamperin, G., Stefani, E., Fusaro, A., Bottazzari, M., Milani, A., Tondo, A., Schivo, A., Paganini, L., Monne, I., Pozzato, N. Identification of bovine microRNA as potential biomarkers of early *Mycobacterium avium* subsp. *paratuberculosis* infection. 14th International Colloquium on Paratuberculosis (p. 77). 4-8 June 2018, Riviera Maya, Mexico.
 20. Zamperin, G., Stefani, E., Fusaro, A., Bottazzari, M., Milani, A., Tondo, A., Schivo, A., Paganini, L., Monne, I., Pozzato, N. MicroRNAs associated to *Mycobacterium avium* SUBSP. *paratuberculosis* infection in cattle. 72° Convegno SISVet 2018 (p.249). 20-22 June 2018, Torino, Italy.
 21. Zecchin, B., Fusaro, A., Zamperin, G., Milani, A., Schivo, A., Salomoni, A., Salviato, A., Ormelli, S., Marciano, S., Terregino, C., Monne, I., 2018. Spatial spread of Highly Pathogenic Avian Influenza A(H5N8) in Italy, 2017-2018. 23rd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology - VEME 2018 (p. 31). 26-31 August 2018, Berlin, Germany.
 22. Zecchin, B., Schivo, A., Bellinati, L., Milani, A., Fusaro, A., Ceglie, L., Natale, A., Bonfanti, L., Cunial, G., Obber, F., Bregoli, M., Citterio, C., Monne, I. Genetic Characterization of genotype 3 Hepatitis E Viruses identified from wild boars in north-eastern Italy. 2nd National Congress of the Italian Society Virology (p. 44). 28-30 November 2018, Rome, Italy.
 23. Cavicchio,L., Fusaro, A., Rizzo,G., Milani,A., Salviato,A., Zamperin, G., Beato, M.S., Schiavon, E., Bano, L., Foni, E., Monne, I. Whole genome characterization of Influenza D viruses detected in cattle herds in Northern Italy between 2015 and 2017. 4th International Symposium on Neglected Influenza Viruses. 18 - 20 April 2018, Brighton, UK
 24. Fusaro, A., Zamperin, G., Milani, A., Cavicchio, L., Schivo, A., Mantovani, C., Monne,I., Vio,D., Schiavon,E., Mion,M., Beato, M.S. Swine influenza in northern Italy: co-circulation of different genotypes and reassortment events. XLIV MEETING ANNUALE SIPAS. 15-16 March 2018, Montichiari (BS), Italy
 25. Cuenca A, Mikkelsen S, Skall H, Panzarini V, Schütze H, Fusaro A, Korsholm H Olesen N: Molecular tracing of viral haemorrhagic septicaemia outbreaks in Denmark. In Proceedings of the 18th International Conference on Diseases of Fish and Shellfish. 4-8 September 2017; Belfast, UK. Pp: 2017:138.
 26. Fusaro, A., Zamperin, G., Milani, A., Salviato, A., Schivo, A., Bonfante, F., Terregino, C., Monne, I. (2017). Assessment of pigeon paramyxovirus type 1 virulence: exploring the molecular basis of discordant results between the in vitro and in vivo tests. 18th INTERNATIONAL SYMPOSIUM OF THE WORLD ASSOCIATION OF VETERINARY LABORATORY DIAGNOSTICIANS (WAVLD), (p. 315). 7-10 June 2017, Sorrento, Italy.
 27. Milani, A., Zamperin, G., Fusaro, A., Schivo, A., Salviato, A., Monne, I. (2017). Development of high-throughput sequencing strategies for metagenomic detection of viruses in biological samples from avian species. 18th INTERNATIONAL

- SYMPOSIUM OF THE WORLD ASSOCIATION OF VETERINARY LABORATORY DIAGNOSTICIANS (WAVLD), (p. 328). 7-10 June 2017, Sorrento, Italy.
- 28. Aiello, R., Canali, D., Calzavara, F., De Benedictis, G.M., Fusaro, A., Mutinelli, F., De Benedictis, P. & Boldrin, M. (2016). Rabies intracerebral mouse inoculation: a refined approach to reduce animal discomfort. XVII Congresso Nazionale S.I.Di.LV. - Società Italiana di Diagnostica di Laboratorio Veterinaria, (p. 103). 28-30 September 2016, Pacengo di Lazise (VR), Italy
 - 29. Aiello, R., Wasniewski, M., Mancin, M., Fusaro, A., Veggiato, C., Cliquet, F. & De Benedictis, P. (2016). Serological methods to assess post vaccination immune response in wildlife: a bayesian analysis. XVII Congresso Nazionale S.I.Di.LV. - Società Italiana di Diagnostica di Laboratorio Veterinaria, (p. 149). 28-30 September 2016, Pacengo di Lazise (VR), Italy
 - 30. Cavicchio, L., Zamperin, G., Fusaro, A., Milani, A., Mottaran, D., Schiavon, E., Zuanon, P. & Beato, M.S. (2016). Utilizzo di un approccio metagenomico per la caratterizzazione di influenza D virus in Bovini della regione Veneto. XVII Congresso Nazionale S.I.Di.LV. - Società Italiana di Diagnostica di Laboratorio Veterinaria, (p. 107). 28-30 September 2016, Pacengo di Lazise (VR), Italy
 - 31. Fusaro, A., Bonfante, F., Mastrolilli, A., Tassoni, L., Salviato, A., Romero Tejeda, A., Monne, I. & Cattoli, G. (2016). Within-host genetic diversity of an H3N6 avian influenza virus in ferrets. MEEGID XIII - 13th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, 10-13 May 2016, Antwerp, Belgium
 - 32. Fusaro, A., Tassoni, L., Milani, A., Salviato, A., Di Marino, G., Mion, M., Bonfanti, L., Watson, S.J., Monne, I. & Beato, M. (2016). Co-circulation of multiple reassortant influenza viruses in a swine farm. IMED 2016 - International Meeting on Emerging Diseases and Surveillance, 4-7 November 2016, Vienna, Austria
 - 33. Fusaro A., Zanperin G., Milani A., Salviato A., Romero A., Cattoli G., Monne I., Bonfante F (2016). Impact of host immunity in the mammalian adaptation of an H3N6 avian influenza virus. . IMED 2016 - International Meeting on Emerging Diseases and Surveillance, 4-7 November 2016, Vienna, Austria
 - 34. Fusaro, A., Zamperin, G., Milani, A., Salviato, A., Romero Tejeda, A., Cattoli, G., Monne, I. & Bonfante, F. (2016). Host immunity shapes the intra-host evolution of an H3N6 avian influenza virus in ferrets. MISMS Influenza Workshop. MISMS Influenza Workshop, Fogarty International Center, National Institutes of Health, 7-10 November 2016, Bethesda, Md, USA
 - 35. Fusaro, A., Zamperin, G., Milani, A., Salviato, A., Romero Tejeda, A., Mancin, M., Mastrolilli, E., Hussein, A., Cattoli, G., Bonfante, F. & Monne, I. (2016). L'effetto della pressione selettiva nell'evoluzione inter- e intra-ospite di virus influenziali aviari. VI Workshop Nazionale di Virologia Veterinaria, 13-14 Ottobre 2016, Torino, Italia
 - 36. Fusaro, A., Zamperin, G., Milani, A., Salviato, A., Romero, A., Cattoli, G., Monne, I. & Bonfante, F. (2016). Applicazione di un approccio deep sequencing per lo studio dell'effetto della pressione immunitaria nell'evoluzione di virus influenziali aviari in ospiti mammiferi. XVII Congresso Nazionale S.I.Di.LV. - Società Italiana di Diagnostica di Laboratorio Veterinaria, (p. 107). 28-30 September 2016, Pacengo di Lazise (VR), Italy
 - 37. Milani, A., Fusaro, A., Bonfante, F., Tassoni, L., Salviato, A., Mancin, M., Mastrolilli, E., Hussein, A., Cattoli, G. & Monne, I. (2016). Intra-host variability of an H5N1 highly pathogenic avian influenza virus in infected vaccinated poultry. MEEGID XIII - 13th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases Conference, 10-13 May 2016, Antwerp,Belgio
 - 38. Milani, A., Fusaro, A., Zamperin, G., Bonfante, F., Tassoni, L., Salviato, A., Mancin, M., Mastrolilli, E., Hussein, A., Cattoli, G. & Monne, I. (2016). Viral population diversity in vaccinated poultry host infected with H5N1 highly pathogenic avian influenza virus. IMED 2016 - International Meeting on Emerging Diseases and Surveillance, 4-7 November 2016, Vienna, Austria
 - 39. Zecchin, B., Minola, A., Aiello, R., Fusaro, A., Corti, D. & De Benedictis, P. (2016). An ELISA test to replace the rabies potency test for veterinary vaccines. XVII Congresso Nazionale S.I.Di.LV. - Società Italiana di Diagnostica di Laboratorio Veterinaria, (p. 107). 28-30 September 2016, Pacengo di Lazise (VR), Italy
 - 40. Beato, M.S., Fusaro, A., Gigli, A., Belfanti, I., Tasson, i.L., Milani, A., Bonfanti, L. & Monne, I. Emergence of multiple genetic reassortant swine influenza viruses in two months period in a swine farm in Italy. 3rd International Symposium on Neglected Influenza Viruses, (p. 57). 15-17 April, 2015, Athens, Georgia, USA

41. Bonfante, F., Fusaro, A., Tassoni, L., Leardini, S. & Terregino, C. Spill-back transmission of European H1N1 avian-like swine influenza viruses between pigs and turkeys: a strain-dependent possibility? 3rd International Symposium on Neglected Influenza Viruses, (p. 32). 15th – 17th April 2015, Athens, Georgia, USA
42. Fusaro, A., Tassoni, L., Hughes, J., Milani, A., Salviato, A., Murcia, P., Massi, P., Bonfanti, L., Cattoli, G. & Monne, i. Tracing back the emergence and transmission dynamics of an HPAI epidemic through ultra-deep sequencing analysis. 9th International Symposium on Avian Influenza - (UGA - USDA/APHIS/WS), 12-15 April 2015, Athens, Georgia, USA
43. Fusaro, A., Tassoni, L., Hughes, J., Milani, A., Salviato, A., Murcia, P., Massi, P., Bonfanti, L., Cattoli, G. & Monne, i. Ultra-deep Sequencing Analysis Revealed the Infection Transmission Pattern During an Avian Influenza Outbreak. Workshop on Next Generation Sequencing of Viruses, 20-21 May 2015, Paris, France
44. Cattoli, G. & Fusaro, A. (2014). Emergence of highly pathogenic avian influenza viruses from the avian reservoir. 12th National Congress of the Italian Society of Virology (SIV), 22-24 September 2014, Orvieto (Italy)
45. Fusaro, A., Hughes, J., Milani, A., Salviato, A., Murcia, P., Cattoli, G. & Monne, I. (2014). Inter-host evolution of an H7N7 highly pathogenic avian influenza virus. 19th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology, 7-12 September 2014, Roma (Italy)
46. Fusaro, A., Hughes, J., Milani, A., Salviato, A., Valastro, V., Murcia, P., Cattoli, G. & Monne, I. (2014). Avian influenza evolution behind the consensus genome. MISMS - Influenza research workshop, 30 June-3 July 2014, Washington DC (USA)
47. Fusaro, A., Milani, A., Hughes, J., Salviato, A., Murcia, P. & Cattoli, G. (2014). A deep insight into an H7N7 highly pathogenic avian influenza epidemic. 8th Annual Meeting - EPIZONE, 23-25 September 2014, Copenhagen (Denmark)
48. Monne, I., Valastro, V., Fusaro, A. & Cattoli, G. (2014). A phylogeny-based classification system for infectious bronchitis virus. 8th International Symposium on Avian Corona- and Metapneumoviruses and Complicating Pathogens, 17-20 June 2014, Rauschholzhausen (Germany)
49. Panzarini, V., Abbadi, M., Fusaro, A., Toffan, A., Quartesan, R., Ceolin, C., Bille, L., Dalla Pozza, M. & Cattoli, G. (2014). Molecular epidemiology and evolution of VHSV and IHNV in Northern Italy in the past 20 years. 9th International Symposium on Viruses of Lower Vertebrates, 1-4 October 2014, Malaga (Spain)
50. Fusaro A, Monne I, A Schivo, A Milani, Salviato A, A. Venturato, Capua I, M. Nelson, E.C. Holmes, P. Lemey, G Cattoli. Molecular epidemiology of avian influenza virus. MISMS Europe Meeting and Training Workshop. 25 Febbraio- 1 March. Padova. Oral presentation
51. Fusaro A, Monne I, J Hughes, A Schivo, A Salomoni, R Orton, L Bonfanti, PR Murcia, G Cattoli. Convergent evolution of H7 viruses from two distinct epidemics. Epidemics 4 - Fourth International Conference on Infectious Disease Dynamics. Amsterdam, The Netherlands, 19-22 November 2013. Poster
52. Fusaro A, Monne I, J Hughes, A Schivo, A Salomoni, R Orton, L Bonfanti, PR Murcia, G Cattoli. Evolution of H7 viruses in poultry: convergent and divergent mutations. Options for the Control of Influenza VIII. Cape Town, South Africa, 5-10 September 2013. Poster
53. Rochaa PRD, Salomoni A, Monne I, MT Capucchio, EC Souza, VL Zafino, Fusaro A, G Cattoli, P De Benedictis. Molecular analysis of rabies virus circulating in animals in the State of Mato Grosso, Brazil. Second International Congress on Pathogens at the Human Animal Interface (ICOPHAI), Porto de Galinhas, Brasile. 14-17 Agosto 2013. Poster
54. A Salomoni, P R. D. Rocha, Monne I, E C. Souza, VL Zafino, Fusaro A, M De Nardi, MT Capucchio, G Cattoli, P De Benedictis. Phylogeographic analysis of rabies virus circulating in bovines in the State of Mato Grosso, Brazil. Rabies in the Americas (RITA). Toronto, Ontario, Canada. 27-31 Ottobre 2013. Poster
55. B Zecchin, Fusaro A, M De Nardi, C Citterio, M Lorenzetto, L Bonfanti, B Crestanello, A Salomoni, A Milani, P Lemey, M Babucci, P De Benedictis, G Cattoli. Phylogeography of the rabies viruses circulating in the recent Italian epidemic And evaluation of the affected fox population dynamics through microsatellite analysis. Rabies in the Americas (RITA). Toronto, Ontario, Canada. 27-31 Ottobre 2013. Poster
56. Fusaro A, Monne I, Nelson MI, Schivo A, Valastro V, Milani A, Moreno A, Bonfanti L, Capua I, Cattoli G. The Emergence of a Highly Pathogenic Avian Influenza Virus - an

- Evolutionary Approach. In: 11th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases. New Orleans, USA, 30 ottobre-2 novembre 2012. Oral presentation
57. Monne I, Fusaro A, Valastro V, Coven F, Dakman A, Akcadag B, Bertolotti L, De Battisti C, Capua I, Cattoli G. Spatial dynamics of highly pathogenic avian influenza H5N1 identified in Turkey, 2005-2008. 8th International Symposium on Avian Influenza, London, 1-4 April 2012. Oral presentation
 58. Fusaro A, Monne I, Nelson MI, Schivo A, Valastro V, Milani A, Moreno A, Bonfanti L, Capua I, Cattoli G. Combining epidemiology with genetic data to study the dynamics of avian influenza outbreaks: the H7N1 in Italy. 8th International Symposium on Avian Influenza, Londra, 1-4 April 2012. Oral presentation
 59. Monne I, Valastro V, Fusaro A, F. Obber, C. Citterio, K. Trevisiol, M. Bregoli, Cattoli G. Monitoring canine distemper virus dynamics in alpine wild carnivore population in north-eastern Italy, 2010-2012" ESVV, Madrid, 4-7 September 2012. Poster
 60. Fusaro A, Monne I, Nelson MI, Schivo A, Valastro V, Milani A, Moreno A, Bonfanti L, Capua I, Cattoli G. The evolutionary dynamics behind the emergence of a highly pathogenic avian influenza virus from a low pathogenic progenitor. ESVV, Madrid, 4-7 September 2012. Oral presentation
 61. Fusaro A, Monne I, Nelson MI, Schivo A, Valastro V, Bonfanti L, Capua I, Cattoli G. Switch from low to high pathogenicity avian influenza virus (H7N1) is not only associated with a fast rate of evolution of the haemagglutin molecule. ESVV, Madrid, 4-7 September 2012. Poster
 62. De Benedictis P, Monne I, Fusaro A, C. De Battisti, A. Angot, A. Salomoni, S. Marciano, S. Tiozzo Caenazzo, Capua I, Cattoli G. The use of molecular tools to generate diagnostic and phylogenetic data in real-time during a rabies epidemic. ESVV, Madrid, 4-7 September 2012. Oral presentation
 63. Fusaro A, Monne I, Salviato A, Holmes EC, I Capua, G Cattoli. Evidence for a difference in the evolutionary dynamics of H5N1 viruses among countries where vaccination was or was not adopted. The 4th ESWI Influenza Conference. 11-14 September 2011. Malta. Poster
 64. Monne I, Fusaro A, V Valastro, N M Amarin, M M Ismail, O A Khan, A S M Ali5, AHedayati, J G Garcia7, I Capua, E C. Holmes, GCattoli. Evolution of H9N2 viruses: implications for human health. The 4th ESWI Influenza Conference. 11-14 September 2011. Malta. Poster
 65. Fusaro A, Monne I, Salviato A, F.Coven, A. Dakman, Capua I, Cattoli G. Impact of vaccination on the genetic evolution of H5N1 viruses in Egypt. International Meeting on Emerging Diseases and Surveillance (IMED 2011). 4-7 Febbraio 2011, Vienna, Austria. Oral presentation
 66. Monne I, Fusaro A, Valastro V, Schivo A, Burattin A, Terregino C, Capua I, Cattoli G. Genetic diversity of H1, H2 and H3 subtypes of Influenza A circulating in wild birds in Italy, 2005-2010. International Meeting on Emerging Diseases and Surveillance (IMED 2011). 4-7 Febbraio 2011, Vienna, Austria. Poster
 67. Fusaro A, Monne I, Schivo A, Cattoli G. Evolutionary history of Italian H7N1 viruses (1999-2001). 7 June 2011. 2nd annual interdisciplinary workshop on influenza evolution, immunology, and epidemiology. Bethesda, USA. Oral presentation
 68. Fusaro A, Monne I, Salviato AA, Coven F, Dakman A, Capua I, Cattoli G. Evidence for differing evolutionary dynamics of A/H5N1 viruses among countries applying or not applying avian influenza vaccination in poultry. 7 June 2011. 2nd annual interdisciplinary workshop on influenza evolution, immunology, and epidemiology. Bethesda, USA. Oral presentation
 69. Cattoli G, Fusaro A, Monne I, Milani A, B. Zecchin, Capua I. Understanding The Antigenic Drift And The Evolution Of H5N1 Viruses In Egypt (2006-2010). 4th International Influenza Conference - Influenza-2011: Zoonotic Influenza and Human Health. 7-9 September 2011 Oxford, United Kingdom. Oral presentation
 70. Panzarini V, Fusaro A, Monne I, E. Cappellozza, G. Bovo, Cattoli G. Analisi filogenetica ed evoluzionistica di ceppi di Betanodavirus isolati nel sud Europa. Dinamiche evolutive del sottotipo H9N2 in Medio Oriente. 4° Workshop Nazionale di Virologia Veterinaria. 9-10 June 2011. Oral presentation
 71. Citterio CV, Monne I, F. Obber, Fusaro A, Valastro V, M. Bregoli, D.Dellamaria, K. Trevisiol, M. Dalla Pozza, M. Toson, M. Lorenzetto, M. De Nardi, PaDe Benedictis, Capua I, Cattoli G. Descrizione dell'epidemia in corso nei carnivori selvatici dell'arco alpino italiano causata da una nuova variante del virus del cimurro. 4° Workshop

- Nazionale di Virologia Veterinaria. 9-10 June 2011.
72. Valastro V, Fusaro A, Monne I, Salviato A, Schivo A, N. M. Amarin, Gonzalez C, Ismail MM, Al-Ankari AR, Al-Blowi MH, Khan OA, Maken Ali AS, Hedayati A, Garcia Garcia J, Ziay GM, Shoushtari A, Al Qahtani KN, Capua I, Holmes EC, Cattoli G. Dinamiche evolutive del sottotipo H9N2 in Medio Oriente. 4° Workshop Nazionale di Virologia Veterinaria. 9-10 June 2011. Oral presentation
 73. Panzarini V, Fusaro A, Monne I, E. Cappellozza, G. Bovo, Cattoli G. Phylogenetic Characterization And Evolutionary Analysis Of Betanodaviruses In Southern Europe. 15th International Conference of the European Association of Fish Pathologists. Split, Croatia 12-16 September 2011. Poster
 74. Fusaro A, Monne I, Salviato A, Schivo A, N. M. Amarin, C. Gonzalez, M. M. Ismail; M. H. Al-Blowi; O. A. Khan, A. S. Maken Ali, A. Hedayati, J. Garcia Garcia, G. M. Ziay, Capua I, Cattoli G. Diversity and evolution of H9N2 viruses in the Middle East. 10th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases. November 3-5, 2010, Amsterdam, the Netherlands. Oral presentation
 75. Monne I, Coven F, Valastro V, Fusaro A, Dakman A, B. Akcadag, et al. Genetic diversity of H5N1 viruses in Turkey, 2005-2008. 10th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases. November 3-5, 2010, Amsterdam, the Netherlands. Poster
 76. Cattoli G, Fusaro A, Monne I, Abdel-Satar M. Arafa, Mohammed K. Hassan, Mona Mehrez Aly, Capua I. Higher evolutionary rate and distinct population dynamics of H5N1 HPAI viruses circulating in Egypt. Options For The Control Of Influenza Vi. 3-7 September 2010
 77. Monne I, Fusaro A, Salviato A A, Schivo A, Nadim Mukhles Amarin, Carlos Gonzalez, Mahmoud Moussa Ismail; Mohamed Hamad Al-Blowi; Owais Ahmed Khan, Ali Safar Maken Ali, Afshin Hedayati, Juan Garcia Garcia, Ghulam M. Ziay, Capua I, Cattoli G. Evolutionary dynamics of H9N2 viruses with potential human health implications in the Middle East. Options For The Control Of Influenza Vi. 3-7 September 2010.
 78. Fusaro A, Monne I, Salviato A A, Schivo A, Nadim Mukhles Amarin, Carlos Gonzales, Owais Ahmed Khan, Mohamed Hamad Al-Blowi, Mahmoud M. Ismail, Capua I, Cattoli G Molecular epidemiology of the HA gene of H9N2 viruses in the Middle East, 2004-2009. 4th Annual Meeting EPIZONE "Bridges to the Future Saint-Malo, France 7-10 June 2010
 79. Panzarini V, Fusaro A, Monne I, Rampazzo E, Cappellozza E, Toffan A, Bovo G and Cattoli G. Phylogenetic characterization of betanodavirus isolates from the mediterranean basin. 8th International Symposium on virus of lower vertebrates. Santiago de Compostela, Spain. April 26-29, 2010. Oral presentation.
 80. Monne I, Fusaro A, M M. Ismail , M H. Al-Blowi , O A. Khan, Salviato A, A Schivo, I Capua, G Cattoli. Genetic Characterisation of H9N2 Viruses Isolated From The Kingdom Of Saudi Arabia. 8th International Congress of Veterinary Virology, Budapest, 23-26 Agosto 2009.
 81. Fusaro A, Joannis T, Bertolotti L, Monne I, Salviato A, Cattoli G, Olaleye F, Capua I, Cattoli G. Genetic evolution of H5N1 Avian Influenza A Virus in Nigeria (2006-2008). 7th International Symposium on avian Influenza: Avian Influenza in Poultry and Wild Birds. University of Georgia Center for Continuing Education, Athens, Georgia, USA, 5-8 April 2009
 82. Fusaro A, Martha Nelson, Monne I, Luigi Bertolotti, Salviato A A, Tony Joannis, Lami H. Lombin, Capua I, Cattoli G. Molecular epidemiology of H5N1 viruses isolated in Nigeria between 2006 and 2008. IDEA Workshop, Fogarty Institute, NIH, Washington DC, USA. 23-26 June 2009. Oral presentation
 83. Fusaro A, Monne I, Bertolotti L, Salviato A, Cattoli G, Joannis T, L. H. Lombin, Capua I. At least four separate introductions of H5N1 in Nigeria between 2006 and 2008. IMED, 13-16/02/2009
 84. Monne I, Fusaro A, Salviato A, Capua I, Cattoli G. Mutation of public health relevance in contemporary H5N1 viruses isolated in Africa and the Middle East. IMED, 13-16/02/2009
 85. Fusaro A, Joannis T, Bertolotti L, Monne I, Salviato A, Olaleye F, Capua I, Cattoli G. Genetic evolution of H5N1 Avian Influenza A Virus in Nigeria (2006-2008). 7th International symposium on Avian Influenza: Avian Influenza in Poultry and Wild Bird. Athens, Georgia, USA, 5-8 April 2009
 86. Śmietanka K, Fusaro A, Domańska-Blicharz K, Minta Z, Salviato A, Monne I, Dundon

- WG, Cattoli G. Full-length genome sequencing of the Polish HPAI H5N1 viruses suggests separate introductions in 2006 and 2007. Athens, Georgia, USA, 5-8 April 2009
87. Fusaro A, Monne I, Salviato A, Capua I, Cattoli G. An optimized protocol for the complete genome sequencing of H5N1 highly pathogenic avian influenza (HPAI) virus. 2nd Annual meeting of Epizone. Brescia, Italy, 4-6/06/2008
 88. Sturm-Ramirez K, Cattoli G, Fusaro A, Monne I, Holmes E. The dynamics of HPAI H5N1 virus migration and evolution in Africa (2006-2007)-Implications for control strategies in the field. The Third European Influenza Conference. Villamoura, Portugal, 14-17/09/2008
 89. De Benedictis P, Sow A, Fusaro A, Veggiato C, Talbi C, Kaborè A, Dundon W.D, Bourhy H, Capua I. Phylogenetic analysis of rabies virus from Burkina Faso suggest novel incursions from neighboring countries. Accepted for Oral presentation at the 9th Southern Eastern African Rabies Group (SEARG) meeting. Gaborone, Botswana, 25-28/08/2008
 90. De Benedictis P, Sow A, Fusaro A, Veggiato C, Talbi C, Kaborè A, Dundon W.D, Bourhy H, Capua I. Phylogenetic analysis of rabies virus from Burkina Faso suggest novel incursions from neighboring countries. Accepted for Oral presentation at the 9th Southern Eastern African Rabies Group (SEARG) meeting. Gaborone, Botswana, 25-28/08/2008
 91. Cattoli G, Monne I, Fusaro A, De Benedictis P, Mehrez Aly M, Couacy-Hymann E, Joannis TM, Boussini H, S. Salzberg, Capua I (2007). Phylogeny and molecular changes of H5N1 HPAI viruses circulating in african poultry. 13th NRL meeting, 24th May, 2007.
 92. G Cattoli, Monne I, Fusaro A, P De Benedictis, M Mehrez Aly, E Couacy-Hyman, TM Joannis, H Boussini, S Salzberg, I Capua (2007). Phylogeny and Molecular Changes of H5N1 HPAI Viruses Circulating in African Poultry. Options for the Control of Influenza, VI June 17-23, 2007 Toronto, Ontario Canada
 93. Monne I, Cattoli G, Fusaro A, De Benedictis P, C. Terregino, Capua I (2007). Genetic analysis of H5N1 HPAI viruses isolated in Africa between 2006 and 2007. The 15th Congress & Exhibition of the World Veterinary Poultry Association, 2007 Beijing China
 94. De Benedictis P, Monne I, Fusaro A, Mehrez Aly M, Couacy-Hymann E, Joannis T, Boussini H, Salzberg SL, Capua I, Cattoli G (2007). Analisi molecolare dei virus influenzali H5N1 isolati in Africa, 2006-2007. 8th Workshop nazionale di virologia veterinaria, diagnostica ed epidemiologia delle infezioni virali degli animali. Università degli Studi di Bologna, Ozzano Emilia (BO), 7-8 June 2007.
 95. Monne I, Fusaro A, Mehrez Aly M, De Benedictis P, Couacy-Hymann E, T. M. Joannis, Boussini H, Salzberg SL, Capua I, Cattoli G (2007). Analisi epidemiologica-molecolare dei virus influenzali H5N1 isolati in Africa nel periodo 2006-2007. Workshop nazionale di virologia veterinaria. Epidemiologia veterinaria: nuovi strumenti per lo studio delle malattie. Abano Terme, 13-14 September 2007

Data

26-07-2019

Luogo

Noale