Jianfa Bai, M.S., Ph.D.

Professor and Director of Molecular Research and Development

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**PROFESSIONAL PREPARATION**

Northwest A&F University, Yangling, China B.S. 1982

University of the Philippines, Los Baños, the Philippines M.S. 1990

Kansas State University Ph.D. 2000

Kansas State University PostDoc 2000-2003

**APPOINTMENTS**

Clinical Professor (2019), Director of Molecular Research and Development 2019-present

Kansas State Veterinary Diagnostic Laboratory, Department of Diagnostic

Medicine/Pathobiology, Kansas State University

Clinical Associate Professor, Director of Molecular Research and Development, 2015-2019

Kansas State Veterinary Diagnostic Laboratory, Department of Diagnostic

Medicine/Pathobiology, Kansas State University

Assistant Professor, Kansas State Veterinary Diagnostic Laboratory 2007-2015

Department of Diagnostic Medicine/Pathobiology, Kansas State University

Research Assistant Professor, Director of Gene Expression Facility, 2003-2007

Department of Plant Pathology, Kansas State University

**WORKING EXPERIENCES**

**June 2019-present: Professor**

**June 2015—May 2019: Associate Professor**

**Aug 2007—May 2015: Assistant Professor**

**Director of Molecular Research and Development**

**Kansas State Veterinary Diagnostic Laboratory**

**Dept. of Diagnostic Medicine/Pathobiology,**

**Kansas State University**

**1800 Denison Avenue**

**Manhattan, KS 66506-5606**

**Assistant Professor (2007), Associate Professor (2015) and Professor (2019), Director of Molecular Research and Development.**

I am currently a clinical professor in the Kansas State Veterinary Diagnostic Laboratory (KSVDL), Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University. I have 50% service and 50% research appointment, and I am in charge of new molecular assay development, un-routine diagnostic services, routine PCR-based services during the assay validation stage and sequencing services. My service and research activities focus on the development, improvement, and validation of molecular diagnostic methods for the detection, quantification and characterization of animal, zoonotic and foodborne pathogens using molecular approaches including PCR-based (regular, multiplex, RT, and real-time and in combinations), digital PCR, MassTag, Luminex, microarray and sequencing-based (Sanger and next-generation sequencing) technologies. During this period, I have developed and improved **62** molecular diagnostic protocols to meet diagnostic service and research needs (publications 7, 8, 18, 23, 26, 30, 33, 39, 40, 46, 48, 49, 50, 53, 54, 111, 119-138, 140, 142-145, 147-152, 155, 156, 159, 161, 166, 171, 174, 176, 177, 179, 181-187, 191, 193, 195-198, 202,203, 206-209, 213, 215, 216, 234, 235, 239, 241-244, 246, 251-253). Many of these are incorporated into the routine diagnostic operations in the Veterinary Diagnostic Laboratory, and my lab has been continuously developing new assays as needed.

In recent years, we have put the effort in building real-time PCR panel assays that include bovine respiratory disease panel, bovine neonatal diarrhea disease panel, bovine/ruminant abortion panel, bovine keratoconjunctivitis (IBK, also known as pinkeye) panel, canine diarrhea disease panel, canine respiratory disease panel (re-develop), canine blood donor disease panel, swine comprehensive diarrhea disease panels for suckling, weaned and growing pig groups, feline upper respiratory disease panel, equine respiratory disease panel, and equine diarrhea disease panel. We have also been including an internal control into each new PCR assay we develop, to enhance assay’s quality by reducing false negative detections. Please refer to **Appendix 1** in the end of this document for a complete list of my contributions in this period.

In collaboration with Dr. T. G. Nagaraja, I have led the effort for the development of several detection and quantification methods for different Shiga toxin producing *Escherichia coli* (STEC) serogroups. We have developed a 6-gene multiplex PCR test detecting *eae*, *stx*1, *stx*2 and *hly*A, the four major virulence genes and O157 (*rfb*E) and H7 (*fli*C) antigens in *E. coli* O157:H7 strains (publications 53, 251, 253). A 7-gene multiplex PCR method has been established to detect and differentiate seven major *E. coli* serogroups that are important to human infections (publications 50, 239, 244). These serogroups including *E. coli* O26, O45, O103, O111, O121, O145, and O157 are the ones that USDA-FSIS has declared as “adulterants”, and are the major targeted serogroups listed in the USDA-AFRI grant that we have been working on. An 11-gene multiplex PCR to detect the four major virulence genes, at the same time to detect and differentiate the seven major O-groups was developed in our labs (publications 50, 224,234). We have previously developed a 3-gene real-time PCR for *E. coli* O157 (*rfb*E-O157), and two Shiga toxin genes (*stx*1, and *stx*2, publications 49 & 243), now we have added another virulence gene, the *eae* gene (codes for intimin) into the test, to make it a 4-plex real-time PCR assay to identify and quantify O157 STEC strains and major virulence genes (publications 40, 196, 198, 202). We have also developed two more triplex real-time PCR assays, each detects three of the six major non-O157 STEC serogroups (publications 39, 193, 197). With the three sets of real-time PCR assays, we can detect, differentiate, and quantify the seven major STEC O-serogroups and affiliated major virulence genes, *stx*1 and *stx*2, and *eae*.

Recently we have been working on application of digital PCR for culture-independent STEC detection (detailed below); a microarray platform for *Salmonella* serotyping; Application of Luminex and MassTag (kindly shared by CEEZAD, BRD panel in validation) systems for potential disease panel testing, as these systems have higher multiplexing capabilities.

A major issue of PCR-based detection of STEC in beef pre-harvest and post-harvest samples is their inability to associate major virulence genes to a given *E. coli* serogroup, as the virulence genes can be carried by an non-adulterant *E. coli* strain in the sample that may not causing human infections. Currently only top-7 serogroups (O26, O45, O103, O111, O121, O145, and O157) are declared adulterants to human health by USDA Food Safety and Inspection Services (FSIS). It will take at least a week to identify and confirm an adulterant STEC strain by USDA-FSIS recommended procedure, due to the requirement of culture isolation. Using digital PCR technology, we successfully associated key virulence genes, *stx*1, *stx*2 and *eae* with each of the top-7 adulterant STEC O-groups mentioned above without culture isolation (publications 147, 149, 150, 159, 161). Our culture-independent digital PCR method of STEC detection can get result in 24 hours, which significantly reduces the turnaround time. A patent was filled for this application.

Since 2007, I have been serving as a PI for **eight** extramural grants and **two** intramural grants and received a sum of **$497,674**; I have been also serving as a co-PI for **16** extramural grants with total funding of **$11,492,725** during 2007-2018. I have published **65** articles in peer-reviewed journals; **8** articles in Kansas Agricultural Experiment Station Research Reports, and **124** oral or poster presentations in national or international conferences, and I am an invited/guest speaker of **27** seminars/workshops/symposia, during the same period of time.