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王春仁个人简介

王春仁,教授,博士,博士研究生导师,中共党员,黑龙江省教学名师,农垦总局模范教师。现为黑龙江八一农垦大学生命科学技术学院院长,兼任中国畜牧兽医学会兽医寄生虫学分会常务理事,黑龙江省畜牧兽医学会常务理事,黑龙江省畜牧兽医学会家畜寄生虫学分会副理事长,黑龙江省动物学会寄生虫学分会副理事长,《黑龙江省畜牧兽医》编委,《Veterinary Parasitology》、《Gene》等SCI收录杂志审稿人,主要从事动物疫病病原分子分类与遗传变异研究。

教育经历: 1984.9-1989.7 东北农学院 攻读学士学位
2000.9-2003.7 东北农业大学 攻读硕士学位
2009.9-2013.6 吉林农业大学 攻读博士学位
工作经历: 1989.7-2003.9 黑龙江省兽医科学研究所
2003.9-至今 黑龙江八一农垦大学

著作:

1. 动物寄生虫线粒体基因组, 东北林业大学出版社, 2017. 5

科研论文:

1. Sequence variability in four mitochondrial genes among pinworm *Aspicularis tetraptera* isolates from laboratory mice in four provinces in China. *Mitochondrial DNA*. 2015, 26(3), 431-434.
2. The complete mitochondrial genome sequence of *Eimeria magna* (Apicomplexa: Coccidia). *Mitochondrial DNA*. 2015, 26(5), 714-715.
3. Comparative analyses of the complete mitochondrial genomes of the two ruminant hookworms *Bunostomum trigonocephalum* and *B. phlebotomum*. *Gene*. 2014, 541, 92-100.
4. Genetic variability among *Syphacia obvelata* isolates from laboratory mice in four provinces geographical locations of China revealed by sequence analyses of five mitochondrial genes. *Mitochondrial DNA*. 2015, 26(2), 213-216.4
5. Zhu X.Q.* Prevalence of *Clonorchis sinensis* metacercariae in freshwater fishes in northeastern China. *Veterinary Parasitology*. 2014, 204(3-4), 209-213.
6. Characterization analysis of complete nuclear ribosomal DNA sequences (18S, ITS1, 5.8S, ITS2, and 28S rDNA) of *Paramphistomum cervi*. *The scientific world Journal*. 2014. (Article ID: 751907, 11 Page 2014.7.21 published <http://dx.doi.org/10.1155/2014/751907>)
7. Complete Mitochondrial genome of an equine intestinal parasite, *Triodontophorus brevicauda* (Chromadorea: Strongylidae): the first characterization within the genus. *Parasitology International*. 2015, 64(5), 429-434.
8. The complete mitochondrial genome of *Strongylus equinus* (Chromadorea: Strongylidae): comparison with other closely related species and phylogenetic analyses. *Experimental parasitology*. 2015, 159, 94-99.
9. The complete mitochondrial genome of *Oxyuris equi*: Comparison with other closely related species and phylogenetic implications. *Experimental parasitology*. 2015, 159, 215-212. (2014.8.12 *Parasitology Research*, Deny. 2015.03.12 submitted to *Exp. Parasitol*, Submitted, 2015.09.24 Accepted) (10月)
10. Complete Mitochondrial Genome of *Echinostoma hortense* (Digenea: Echinostomatidae). *The Korean journal of parasitology*. 2016, 54(2), 173-179.
11. The complete mitochondrial genome of *Metorchis orientalis* (Trematoda: Opisthorchiidae): comparison with other closely related species and phylogenetic implications. *Infection, Genetics and Evolution*. 2016, 39, 45-50.
12. .Sequence variation in three mitochondrial genes among *Gasterophilus intestinalis* isolates from two distinct regions in China. *mtDNA. Mitochondrial DNA Part A*. 2017, 28(1):37-40.
13. Complete mitochondrial genomes of *Dermacentor silvarum* and comparative analyses with another hard tick *Dermacentor nitens*. *Experimental Parasitology*. 2016, 169, 22-27.
14. Genetic variation analysis of *Triodontophorus brevicauda* and *Triodontophorus nipponicus*, based on mtDNA and rDNA gene sequences. *Mitochondrial DNA Part A*. 2017, 28:4, 570-574
15. Comparative analyses of the complete mitochondrial genomes of two mice pinworms *Aspicularis tetraptera* and *Syphacia obvelata*. *Gene*. 2016, 585(1), 71-75
16. Complete mitochondrial genome of *Cylicocyclus nassatus* and comparative analyses with *Cylicocyclus insigne*. *Exp Parasitol*. 2017,(1)18-22.
17. Complete mitochondrial genomes of *Triodontophorus serratus* and *Triodontophorus nipponicus*, and their comparison with *Triodontophorus brevicauda*. *Exp Parasitol*. 2017,181(10):88-93.
18. Mitochondrial DNA evidence supports the hypothesis that *Triodontophorus* species belongs to the Cyathostominae. *Frontiers in Microbiology*. 2017, 8: 1444.

科研项目:

- 1.黑龙江省集约化养殖奶牛寄生虫病综合防控技术体系的建立与应用, 黑龙江省科技厅, 2013.11-2016.11, GZ13B001.
- 2.东方次睾吸虫病诊断和疫苗候选基因的筛选与鉴定, 黑龙江省自然科学基金, 2017.10-2020.10, C2017048
- 3.国家重点研发项目“畜禽重要人兽共患寄生虫病源头防控与阻断技术研究”, 课题“血吸虫等诊断与疫苗产品研发及产业化工艺研究”子课题2017.7-2020.12. (2017YFD0501306)
- 4.国家重点研发项目“严重危害畜禽的寄生虫病诊断、检测与防控新技术项目”, 课题“反刍动物肝片吸虫病早期诊断与控制技术研究”子课题2017.7-2020.12. (2017YFD0501202)

科研获奖:

重要人兽共患寄生虫病原学、分子遗传学及功能基因组学的研究。教育部自然科学一等奖, 2011年。
黑龙江省牛羊主要寄生虫病原学、诊断技术及功能基因的研究。黑龙江省自然科学三等奖, 2011年。

3.奶牛乳房炎综合防治技术研究与应用。黑龙江省科技进步二等奖, 2012年。

最后更新 (2018-02-25 10:33)