Molecular Detection of Avian Pathogens in Poultry Red Mite (*Dermanyssus gallinae*) Collected in Chicken Farms

Chu Thi Thanh HUONG1), Takako MURANO2), Yukiko UNO1), Tatsufumi USUI1,3) and Tsuyoshi YAMAGUCHI1,3)*

1)Laboratory of Veterinary Hygiene, Department of Veterinary Medicine, Faculty of Agriculture, Tottori University, Koyama Minami 4–101, Tottori 680-8553, Japan
2)Chiba Prefectural Livestock Research Center, He 16–1 Yachimata, Yachimata, Chiba 289-1113, Japan
3)Avian Zoonosis Research Center, Faculty of Agriculture, Tottori University, Koyama Minami 4–101, Tottori 680-8553, Japan

(Received 15 May 2014/Accepted 13 August 2014/Published online in J-STAGE 8 September 2014)

**ABSTRACT.** Poultry red mite (PRM, *Dermanyssus gallinae*) is a blood-sucking ectoparasite as well as a possible vector of several avian pathogens. In this study, to define the role of PRM in the prevalence of avian infectious agents, we used polymerase chain reaction (PCR) to check for the presence of seven pathogens: Avipox virus (APV), Fowl Adenovirus (FAdV), Marek’s disease virus (MDV), *Erysipelothrix rhusiopathiae* (ER), *Salmonella enterica* (SE), *Mycoplasma synoviae* (MS) and *Mycoplasma gallisepticum* (MG). A total of 159 PRM samples collected between 2004 and 2012 from 142 chicken farms in 38 prefectures in Japan were examined. APV DNA was detected in 22 samples (13.8%), 19 of which were wild-type APV. 16S ribosomal RNA (16S rRNA) of MS was detected in 15 samples (9.4%), and the mge2 gene of MG was detected in 2 samples (1.3%). Eight of 15 MS 16S rRNA sequences differed from the vaccine sequence, indicating they were wild-type strains, while both of the MG mge2 gene sequences detected were identical to the vaccine sequences. Of these avian pathogen-positive mite samples, three were positive for both wild-types of APV and MS. On the other hand, the DNAs of ER, SE, FAdV and MDV were not detected in any samples. These findings indicated that PRM can harbor the wild-type pathogens and might play a role as a vector in spreading these diseases in farms.

**KEY WORDS:** avian pathogens, *Dermanyssus gallinae*, DNA detection, poultry red mite

**DISCUSSION.**

*Dermanyssus gallinae* (Acari, Mesostigmata, Dermanyssoidae), poultry red mite (PRM), is an obligatory blood-sucking parasite of both domestic and wild birds. The mite has been reported to parasitize at least 28 avian species [15] and is considered one of the major problems in poultry farms in the United States [7], Europe [2] and Japan [14]. The infestation of PRM in poultry results in stress, decreasing egg production, anemia and even mortality due to exsanguination.

PRMs carry and are potential vectors of several pathogens including *Salmonella enterica* (SE) [9, 25], *Erysipelothrix rhusiopathiae* (ER) [4] and Avipox virus (APV) [3, 18]. The mites can also be sites of *Salmonella Enteritidis* multiplication [24]. However, the prevalence of avian microbial pathogens in PRM over a wide region has not been studied.

In the present study, to define the role of PRM in transmitting and maintaining avian pathogens in poultry farms, PRMs were collected from chicken farms throughout Japan and examined for DNAs of APV, ER and SE. We also examined PRM for the presence of four other pathogens that are frequently detected in chicken habitats, but that so far have not been detected in PRM: *Mycoplasma synoviae* (MS), *Mycoplasma gallisepticum* (MG), Fowl Adenovirus (FAdV) and Marek’s disease virus (MDV).

**MATERIALS AND METHODS**

*Avian Pathology.* A total of 159 samples (at least 50 for each sample) were obtained from 142 chicken farms in 38 prefectures throughout Japan from 2004 to 2012. In all of the farms, the chickens appeared healthy. Each sample was stored in 99.5% ethanol at room temperature until use.

**DNA preparation:** Mite DNA samples used in this study were obtained from 10 pooled adult mites. The mites were homogenized with zirconia beads using TissueLyser II (Qiagen Inc., Chatsworth, CA, U.S.A.) in 20 µl of buffer 1 provided by a Ten Minute DNA Release Kit +1 (Jacksun Easy Biotech Inc., New York, NY, U.S.A.), and the DNA samples were prepared according to the manufacturer’s instructions. When a sample was found to be positive for one of the seven pathogens, another DNA sample was prepared as described below to estimate whether the pathogens exist on surface or internal side of the PRM. Ten mites prepared from the sample that was positive for any pathogens were washed out before the DNA preparation to remove the microorganisms on the surface of the mites as previously described [8]. Briefly, ten mites taken from the 99.5% ethanol were rinsed three times in 500 µl of sterile ultrapure water with vigorous shaking. Then, the washed mites were used for DNA preparation. If the PCRs using the DNA samples prepared from the washed mites were positive, it was speculated that...
the pathogens existed internal side of PRM. DNA samples of commercial vaccines were also prepared with the same DNA extraction kit as a control. The DNA samples prepared were stored at −30°C until use.

**PCR for detection of avian pathogens:** The DNA samples were screened for seven avian pathogens including ER, MS, MG, SE, APV, FAdV and MDV by PCR as described below.

The target genes and their PCR primers are shown in Table 1.

For detection of APV DNA, primers P1x and P2 were used to amplify part of the 4b core protein gene [10]. Primer P1x was designed based on the sequence of primer P1 [10] by adding one more T nucleotide to the 5′ end to improve the sensitivity (our unpublished data). If the gene coding for the 4b core protein was detected, the viral DNA was further examined to determine whether it was derived from the wild type APV or commercial vaccine strain. Because the wild type APV genome includes an intact reticuloendotheliosis (RE) provirus and the genome of the vaccine virus includes only the truncated LTR sequence of RE provirus [6], to detect the insertion of intact RE provirus sequence in APV genome, PCR using heterologous primer set that anneals to env gene of RE provirus (REVenv7F primer) [6] and FPV ORF 203 (FPV203 3R primer) [6] was conducted as semi-nested first PCR. When this PCR was negative, semi-nested second PCR using primers REVenv7F and TR2 [19] that anneals to the internal region flanking to FPV203 3R primer annealing site was conducted. When the first or second PCRs were positive, we concluded that intact RE provirus insertion, that was specifically found in wild type APV, was positive. Each primer sequence, target genes and expected length of the PCR products are shown in Table 1. DNAs prepared from the commercial vaccines used in Japan were used as negative controls for the presence of RE provirus.

Primers MSL1 and MSL2 [12] (Table 1) were used to detect the MS 16S rRNA sequence. Subsequently, the nucleotide sequences of PCR products were compared with the sequence derived from the MS-H vaccine strain used in Japan to differentiate between the MS wild type and the vaccine strain [1].

Primers Mgc2 2F and Mgc2 2R were used to detect the MG mgc2 gene [5]. The obtained nucleotide sequences were used to differentiate MG from 5 commercial live vaccine strains used in Japan (ts-11, 6/85, MGS, G210 and K5831-B19) following a previous report [11].

PCRs were performed in a total volume of 25 μl containing 2 μl of DNA template (or 0.5 μl of the first PCR product in semi-nested second PCR) prepared as described above, 1 μl of forward and reverse primer mixture (final concentration was 0.5 μM each) and 12.5 μl of GoTaq Green Master Mix, 2X (Promega, Madison, WI, U.S.A.). The PCR conditions for each pair of primers were employed according to the previous reports listed in Table 1. Amplification products were confirmed by electrophoresis using 1.2% (w/v) agarose gels, stained with 0.1% Gel Red (Biotium, Inc., Hayward, CA, U.S.A.) and visualized with a UV transilluminator. To confirm the specificity of the PCR, nucleotide sequence of the PCR products was determined by Applied Biosystems 3130 Genetic Analyzer (Applied Biosystems, Carlsbad, CA, U.S.A.) with the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems).

**RESULTS**

Twenty-five (15.7%) of the 159 DNA samples prepared from the mites without washing prior to the DNA preparation were positive for a single pathogen, either APV or MS, while the DNAs of ER, SE, FAdV and MDV were not detected (Table 2). Fifteen of these 25 samples were positive only for APV, and 9 samples and 1 sample were positive only for MS and MG, respectively. In addition, seven samples (4.4%) without washing were multiple pathogens positive. Of the seven DNA samples, six were positive for both APV and MS, and another was positive for both APV and MG. In total, 32 (20.1%) of the 159 DNA samples, 25 for single pathogen and 7 for multiple pathogens, were positive in PCRs conducted in this study. APV, MS and MG positive samples were detected from 12, 12 and 2 prefectures, respectively. Apparent geographical bias was not found in distribution of the positive samples.

The APV gene was totally detected in 22 of the 159 PRM DNA samples (13.8%) prepared from the mites without washing. Furthermore, 4 of the 22 DNA samples prepared from the mites after washing were also positive for APV. Nineteen samples positive for APV were also positive in PCR for REV env to FPV ORF 203 region.

In total, fifteen of the 159 DNA samples (9.4%) prepared from the mites after washing were positive for the MS 16S rRNA. In addition, two of the 15 DNA samples prepared from the mites after washing were positive for the rRNA. Of the fifteen positive samples, seven of these sequences were identical to the sequence of the vaccine MS-H used in Japan. The eight other sequences differed by at least 1 nucleotide from the sequence of MS-H vaccine. Two of these 8 sequences were identical to each other and differed by 2 nucleotides from the MS-H sequence. These two sequences were detected from different chicken houses in the same farm.

Two of the 159 DNA samples (1.3%) prepared from the unwashed mites were positive for the MG mgc2 gene (Table 2). However, when the two DNA samples were prepared from the washed mites, no DNA samples were positive for the mgc2 gene. Of the two positive DNA samples, one sequence was identical to that of vaccine strain G210, and the other was identical to that of vaccine strain K5831-B19.

Of the six samples positive for both APV and MS, 5 samples were positive in PCR for REV env to FPV ORF 203 region. In addition, MS 16S rRNA sequences detected from 3 of these 5 samples were different from the sequence of MS-H vaccine. In the case of another multiple pathogens positive sample, which was positive for both APV and MG, PCR for REV env to FPV ORF 203 region was positive, and the sequence of MG mgc2 gene detected was identical to that of vaccine strain K5831-B19.
In the present study, APV, MS and MG DNAs were detected in 22, 15 and 2 DNA samples prepared from the unwashed mites, respectively. Of the total, 25 samples were single pathogen positive, and 7 samples were multiple pathogens positive. These results indicate the possibility that the poultry red mite can transfer APV, MS and MG. In addition, 4 and 2 of 32 DNA samples prepared from the mites after washing were positive for APV and MS, respectively. Although the positive number decreased after washing, APV or MS was detected even after 3 times washing in the mites. Because the washing step is expected to remove microorganisms on the surface of the mites, this result implied that poultry red mite can harbor APV and MS both externally and internally.

Of the 22 DNA samples positive for APV, 19 were also positive for REV env to FPV ORF 203 region. This finding shows that the 19 samples have intact RE provirus reported as a virulence marker for wild-type APV [20]. In Japan, almost all chickens are vaccinated for APV infection, and only a few outbreaks of avian pox are reported each year. However, this finding raises the possibility that PRM can transmit MS among chickens, further studies, such as experimental infection of MS to chicken through a PRM, may be needed to confirm it. Moreover, the finding of two identical wild-type MS sequences in different chicken houses in the same farm implied that PRM can spread MS among chicken houses in a farm. To our knowledge, this is the first report to show the presence of a mycoplasma in PRM.

Of the six mite samples positive for both APV and MS, three samples were positive in PCR for REV env to FPV ORF 203 region, and the MS 16S rRNA sequences detected were different from the sequence of vaccine strain. These results indicate that both of the APV and MS detected from the 3 samples were wild-type (Table 2). These findings suggest that the mite can harbor and transmit more than one avian pathogen in poultry farms. This is the first report to show the presence of multiple pathogens in PRMs.

In European countries, ER was found in PRM collected from infected farms [4], and SE was found in mites collected from apparently healthy farms [9]. The infections of SE and ER among some chickens have been reported in Japan [17, 22]. However, these bacteria were not detected in any of the present mite samples. Furthermore, although FAdV and MDV are ubiquitous pathogens in chicken farms [13,
Table 2. Sample numbers and the distribution of the mite samples which showed positive in PCR for detection of avian pathogen DNAs from the mite samples without washing

| Prefectures | Sample number | APV<sup>1</sup> | MS<sup>2</sup> | MG<sup>3</sup> | Subtotal<sup>4</sup> | APV Wild<sup>5</sup> | APV Vac<sup>6</sup> | MS Wild<sup>5</sup> | MS Vac<sup>6</sup> | MG Wild<sup>5</sup> | MG Vac<sup>6</sup> | Subtotal<sup>4</sup> | All negative<sup>6</sup> |
|-------------|---------------|----------------|-------------|-------------|-----------------|----------------|-------------|----------------|-------------|----------------|-------------|----------------|----------------|
| Akita       | 1             | 1 (100)       | 0           | 0           | 0               | 1 (100)        | 0           | 0             | 0           | 0             | 0           | 1 (100)        | 0             |
| Aomori      | 2             | 0             | 0           | 1 (50.0)    | 0               | 1 (50.0)       | 0           | 0             | 0           | 0             | 0           | 1 (50.0)       | 0             |
| Chiba       | 44            | 5 (11.4)      | 0           | 1 (2.3)     | 0               | 7 (15.9)       | 1 (2.3)     | 0             | 0           | 0             | 1 (2.3)     | 36 (18.1)      | 0             |
| Fukui       | 2             | 0             | 0           | 0           | 0               | 0             | 0           | 1 (50.0)     | 0           | 0             | 1 (50.0)    | 1 (50.0)       | 0             |
| Gunma       | 6             | 1 (16.7)      | 0           | 0           | 0               | 1 (16.7)       | 0           | 0             | 0           | 0             | 0           | 5 (83.3)       | 0             |
| Hokkaido    | 1             | 0             | 0           | 0           | 0               | 0             | 1 (100)     | 0             | 0           | 1 (100)       | 0           | 0             | 0             |
| Hyogo       | 11            | 2 (18.2)      | 0           | 1 (9.1)     | 0               | 3 (27.3)       | 0           | 1 (9.1)      | 0           | 1 (9.1)       | 7 (63.6)    | 4 (36.0)       | 0             |
| Ibaraki     | 6             | 1 (16.7)      | 0           | 0           | 0               | 0             | 1 (16.7)    | 1 (16.7)     | 0           | 0             | 0           | 1 (16.7)       | 4 (66.7)      |
| Iwate       | 7             | 1            | 1 (14.3)    | 0           | 0               | 1 (14.3)       | 0           | 0             | 0           | 0             | 0           | 6 (85.7)       | 0             |
| Kanagawa    | 3             | 1 (33.3)      | 0           | 1 (33.3)    | 1 (33.3)       | 3 (100)       | 0           | 0             | 0           | 0             | 0           | 0             | 0             |
| Mie         | 12            | 1 (8.3)       | 0           | 0           | 0               | 1 (8.3)       | 0           | 1 (8.3)      | 0           | 1 (8.3)       | 2 (16.7)    | 9 (75.0)       | 0             |
| Nagasaki    | 6             | 0           | 1 (16.7)    | 0           | 1 (16.7)       | 2 (33.3)      | 0           | 0             | 0           | 0             | 0           | 4 (66.7)       | 0             |
| Okayama     | 8             | 0           | 1 (12.5)    | 0           | 1 (12.5)       | 2 (25.0)      | 2           | 0             | 0           | 0             | 0           | 6 (75.0)       | 0             |
| Shizuoka    | 3             | 1 (33.3)      | 0           | 0           | 0               | 0             | 1 (33.3)    | 0           | 0             | 0             | 0           | 2 (66.7)       | 0             |
| Tochigi     | 3             | 0           | 0           | 1 (33.3)    | 0               | 1 (33.3)      | 0           | 0             | 0           | 0             | 0           | 2 (66.7)       | 0             |
| Other 23 prefectures<sup>4</sup> | 44 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 44 (100) |

Total 159 13 (8.2) 2 (1.3) 3 (1.9) 1 (0.6) 25 (15.7) 2 (1.3) 3 (1.9) 1 (0.6) 1 (0.6) 7 (4.4) 127 (79.9)

Erysipelothrix rhusiopathiae, Salmonella enterica, Fowl Adenovirus and Mareks’ disease virus were not detected. a) If the intact RE provirus integration was detected, such samples were considered as wild type. If the intact RE provirus integration was not detected, such samples were considered as vaccine. b) If 16S RNA detected was different from the sequence of vaccine used in Japan, such samples were considered as wild type. If 16S RNA detected was identical to the sequence of vaccine used in Japan, such samples were considered as vaccine. c) If mgc2 sequence detected was different from the sequence of vaccine used in Japan, such samples were considered as wild type. If mgc2 sequence detected was identical to the sequence of vaccine used in Japan, such samples were considered as vaccine. d) Vac: vaccine. e) Other 23 prefectures: Aichi, Ehime, Fukushima, Gifu, Hiroshima, Ishikawa, Kagoshima, Kumamoto, Kyoto, Miyagi, Miyazaki, Nara, Niigata, Oita, Saga, Saitama, Tokushima, Tottori, Toyama, Wakayama, Yamagata, Yamaguchi and Yamanashi.

These pathogens were not detected in any samples in this study. Although the reason why these pathogens were not detected in this study was not clear, because the PRM samples used in this study were stored in ethanol until use, some organisms could be lysed by ethanol and it may affect the results. Alternatively, PRMs may be rarely associated with the spread of these pathogens in Japan. To define the actual distribution of these organisms in PRMs, further studies using PRM without fixation may be needed.

This study demonstrated that APV, MS and MG including wild type strains are prevalent in PRMs. Although further studies about the actual transmission activity of the mites for these pathogens are needed, these findings suggest that PRM may transfer these pathogens among chickens. The present results suggest that eradication of PRM will not only reduce the negative effects of blood-sucking but also decrease the transmission of these pathogens in poultry farms.

ACKNOWLEDGMENTS. This work was supported by JSPS, KAKENHI Grant Number 23580423. The authors also thank the Ministry of Education, Sports, Science and Technology, Japan (MEXT) for the doctoral scholarship (CTTH).

REFERENCES

1. Buim, M. R., Buzinhanii, M., Yamaguti, M., Oliveira, R. C., Mettigoo, E., Timenetsky, J. and Ferreirae, A. J. 2010. Intraspecific variation in 16S rRNA gene of Mycoplasma synoviae determined by DNA sequencing. Comp. Immunol. Microbiol. Infect. Dis. 33: 15–23. [Medline] [CrossRef]

2. Chauve, C. 1998. The poultry red mite Dermatophagoides gallinae (De Geer, 1778): current situation and future prospects for control. Vet. Parasitol. 79: 239–245. [Medline] [CrossRef]

3. Chikuba, T., Itou, H., Sakakibara, H. and Inoue, D. 2008. Detection of fowlpox virus from red mite (Dermatophagoides gallinae) at a layer farm occurring cutaneous fowlpox. J. Jpn. Soc. Poult. Dis. 44: 113–117.

4. Chirico, J., Eriksson, H., Fossom, O. and Jansson, D. 2003. The poultry red mite, Dermatophagoides gallinae, a potential vector of Erysipelothrix rhusiopathiae causing erysipelas in hens. Med. Vet. Entomol. 17: 232–243. [Medline] [CrossRef]

5. García, M., Ikuta, N., Levisohn, S. and Kleven, S. H. 2005. Evaluation and comparison of various PCR methods for detection of Mycoplasma gallisepticum infection in chickens. Avian Dis. 49: 125–132. [Medline] [CrossRef]

6. García, M., Narang, N., Reed, W. M. and Fadly, A. M. 2003. Molecular characterization of reticuloendotheliosis virus insertion in the genome of field and vaccine strains of fowl poxvirus. Avian Dis. 47: 343–354. [Medline] [CrossRef]

7. Gary, R. M. and Barry, M. O. 2009. Mites (Acari). pp. 433–492.
8. Schabereiter-Gurtner, C., Lubitz, W. and Rölleke, S. 2003. Application of broad-range 16S rRNA PCR amplification and DGGE fingerprinting for detection of tick-infecting bacteria. J. Microbiol. Methods 52: 251–260. [Medline] [CrossRef]

9. Hamidi, A., Sherifi, K., Muji, S., Behluli, B., Latifi, F., Robaj, A., Postoli, R., Hess, C., Hess, M. and Sparagano, O. 2011. Dermanyssus gallinae in layer farms in Kosovo: a high risk for Salmonella prevalence. Parasit. Vectors 4: 136. [Medline] [CrossRef]

10. Huw Lee, L. and Hwa Lee, K. 1997. Application of the polymerase chain reaction for the diagnosis of fowl poxvirus infection. J. Virol. Methods 63: 113–119. [Medline] [CrossRef]

11. Lysnyansky, I., Garcia, M. and Levisohn, S. 2005. Use of mgc2-polymerase chain reaction-restriction fragment length polymorphism for rapid differentiation between field isolates and vaccine strains of Mycoplasma gallisepticum in Israel. Avian Dis. 49: 238–245. [Medline] [CrossRef]

12. Marois, C., Dufour-Gesbert, F. and Kempf, I. 2000. Detection of Mycoplasma synoviae in poultry environment samples by culture and polymerase chain reaction. Vet. Microbiol. 73: 311–318. [Medline] [CrossRef]

13. McG Ferran, J. B. and Smyth, J. A. 2000. Avian adenoviruses. Rev. - Off. Int. Epizoot. 19: 589–601. [Medline]

14. Murano, T. 2006. Red mite, Dermanyssus gallinae; Ecology and Lastest problems in Japan. J. Jpn. Soc. Poult. Dis 42: 127–136.

15. Oines, O. and Brännström, S. 2011. Molecular investigations of cytochrome c oxidase subunit I (COI) and the internal transcribed spacer (ITS) in the poultry red mite, Dermanyssus gallinae, in northern Europe and implications for its transmission between laying poultry farms. Med. Vet. Entomol. 25: 402–412. [Medline] [CrossRef]

16. Raja, A., Dhinakar Raj, G., Bhuvaneswari, P., Balachandran, C. and Kumanan, K. 2009. Detection of virulent Marek’s disease virus in poultry in India. Acta Virol. 53: 255–260. [Medline] [CrossRef]

17. Sasaki, Y., Murakami, M., Maruyama, N., Tsujiyama, Y., Kuskawa, M., Asai, T. and Yamada, Y. 2012. Risk factors for Salmonella prevalence in laying-hen farms in Japan. Epidemiol. Infect. 140: 982–990. [Medline] [CrossRef]

18. Shirinov, F. B., Ibragimova, A. I. and Misirov, Z. G. 1972. [Spread of the fowl pox virus by D. gallinae ticks]. Veterinaria 4: 48–49. [Medline]

19. Singh, P., Schnitzlein, W. M. and Tripathy, D. N. 2003. Reticuloendotheliosis virus sequences within the genomes of field strains of fowlpox virus display variability. J. Virol. 77: 5855–5862. [Medline] [CrossRef]

20. Singh, P., Schnitzlein, W. M. and Tripathy, D. N. 2005. Construction and characterization of a fowlpox virus field isolate whose genome lacks reticuloendotheliosis provirus nucleotide sequences. Avian Dis. 49: 401–408. [Medline] [CrossRef]