

Identification of *Varroa* mites (Acari: Varroidae) infesting *Apis cerana* and *Apis mellifera* in China

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Abstract – A total of 24 *Varroa* mite samples were collected from *A. mellifera* and *A. cerana* colonies in 17 Provinces in China and subjected to DNA or restriction enzyme analyses. All *Varroa* mites from *A. mellifera* were identified as the Korean genotype of *Varroa destructor* Anderson and Trueman, confirming earlier finding that *V. jacobsoni* is not present in China, and a single genotype of *Varroa* is infecting the *A. mellifera* bees. Mites collected from *A. cerana* colonies at 2 locations in Guangdong Province were the China genotype of *V. destructor*. Mites collected from *A. cerana* colonies in 3 apiaries at Dayao County, Yunnan Province, and from 5 colonies at Mongzi County, Yunnan Province, were a new genotype, which was named the China 2 genotype of *V. destructor*. Mites collected from *A. cerana* colonies in 4 apiaries at Xishuangbanna, Yunnan Province, were the Vietnam genotype of *V. destructor*. These results should help future mite control and bee quarantine efforts in China.

Apis mellifera / *Apis cerana* / China 2 genotype of *Varroa destructor* / *Varroa* spp. / population genetics

1. INTRODUCTION

Information gathered during the past five years has revolutionised our understanding of *Varroa* mite taxonomy, genetic diversity, host-relationships and epidemiology (Delaplane, 2001). As it currently stands, there are four distinct species of *Varroa*; *Varroa jacobsoni* Oudemans, *V. destructor* Anderson and Trueman, *V. underwoodi* Delfinado-Baker and Aggarwal and *V. rindereri* De Guzman and Delfinado-Baker. The taxonomic status of three other *Varroa* genotypes has yet to be resolved (Anderson & Trueman, 2000). Each of these species and

genotypes have been found to be natural ectoparasites on Asian honey bee species; *V. jacobsoni* on *Apis cerana* Fabricius mostly in India, southern mainland Asia and South-East Asia (Oudemans, 1904; Anderson & Trueman, 2000; Anderson, 2002; Warrit and Smith, unpublished data), *V. destructor* on *A. cerana* mostly in the western and northern regions of mainland Asia (Anderson & Trueman, 2000; Anderson, unpublished data), *V. underwoodi* on *A. cerana* throughout Asia (Delfinado-Baker & Aggarwal, 1987; Woo, 1992; Anderson et al., 1997), *V. rindereri* on *A. koschevnikovi* v. Buttel-Reepen in Borneo (De Guzman & Delfinado-Baker,

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1996; Koeniger et al., 2002) and the three unresolved genotypes on *A. cerana* in the Philippines (Anderson & Trueman, 2000).

The level of genetic variation among *V. underwoodi*, *V. rindereri* and the three unresolved Philippine genotypes has yet to be determined. However, a great deal of genetic variation has been reported among *V. jacobsoni* and *V. destructor* infesting Asian bees. To date, 15 different genotypes (or haplotypes – mites with distinct mtDNA CO-I gene sequences) of *V. jacobsoni* and eight of *V. destructor* have been reported, each only found on a specific geographic population of an Asian bee and each therefore named after the location (usually a country or island) from which it was first discovered on its natural Asian bee host (Anderson, 2000; Anderson & Trueman, 2000; Anderson, unpublished data; Warrit and Smith, unpublished data). Hence, the Borneo genotype of *V. jacobsoni* was first discovered on *A. cerana* in Borneo in the 1990's by Anderson and Trueman (2000), while the Borneo 2 genotype was found in Borneo some time later by Koeniger et al. (2002). All known genotypes of *V. jacobsoni* and *V. destructor* are listed in Table I.

Even though much genetic variation has been found in *V. jacobsoni* and *V. destructor*, each genotype of these species show great consistency in the way it reproduces on its particular bee host. To reproduce, the adult female mites enter drone (male) and worker (sterile female) bee brood cells just prior to the cells being capped, preferring drone cells far more than worker cells. They then proceed to produce offspring on the drone but not on the worker brood. This inability to reproduce on worker brood is mostly responsible for rendering the mites relatively harmless to their natural host's colonies, because the adult worker bees, which perform most of the myriad of diverse colony tasks, such as collecting food and feeding young, remain largely undamaged during their developmental phase. On the other hand, drones that have been infested with, and damaged by, reproducing mites as brood, develop into behaviourally impaired adults. This however is not catastrophic to bee colonies, because drones, whose sole task is to mate with new queens, are produced by the colonies only when needed and usually in large quantities, much of which escapes parasitism by mites (Koeniger et al.,

Table I. Details of all known genotypes of *V. jacobsoni* (VJ) and *V. destructor* (VD). These genotypes exist naturally on specific populations of *A. cerana* in Asia and have been named after the location (country or island) in which they were first discovered on *A. cerana*.

<i>Varroa</i> species (genotype)	Genbank accession number	Reference
VJ (Ambon)	AF106908	Anderson & Trueman (2000)
VJ (Bali)	AF106909	Anderson & Trueman (2000)
VJ (Borneo)	AF106907	Anderson & Trueman (2000)
VJ (Borneo 2)	AY037890	Koeniger et al. (2002)
VJ (Flores)	AF106902	Anderson & Trueman (2000)
VJ (India)	NA	Anderson (unpublished data)
VJ (Java)	AF106910	Anderson & Trueman (2000)
VJ (Laos)	NA	Anderson (unpublished data)
VJ (Lombok)	AF106904	Anderson & Trueman (2000)
VJ (Malaysia)	AF106906	Anderson & Trueman (2000)
VJ (North Thailand 1)	NA	Warrit & Smith (2004)
VJ (North Thailand 2)	NA	Warrit & Smith (2004)
VJ (Sumatra)	AF106905	Anderson & Trueman (2000)
VJ (Sumbawa)	AF106903	Anderson & Trueman (2000)
VJ (Samui 1)	NA	Warrit & Smith (2004)
VD (China)	AF106900	Anderson & Trueman (2000)
VD (China 2)	AY372063	Current study
VD (Japan)	AF106897	Anderson & Trueman (2000)
VD (Korea)	AF106899	Anderson & Trueman (2000)
VD (Nepal)	AF106898	Anderson & Trueman (2000)
VD (Pakistan)	NA	Anderson (unpublished data)
VD (Sri Lanka)*	AF106896	Anderson & Trueman (2000)
VD (Vietnam)	AF106901	Anderson & Trueman (2000)

* Tentative member of VD (pending further data).

NA: accession number not available.

1981; Koeniger et al., 1983; Anderson, 1994; Rath, 1999; Anderson, 2000).

Only two *Varroa* genotypes from the large pool of genotypes present on Asian bees have been found capable of utilizing the European honey bee (*A. mellifera* L.) as an alternative host, following the introduction of this bee into Asia during the early 1900's. These are the Korea and Japan genotypes of *V. destructor*, so-called because they are natural parasites of *A. cerana* in Korea and Japan respectively (until recently the Japan mite was referred to as the Japan/Thailand genotype, but now is known simply as the Japan genotype). On their newly-found bee host, the Korea and Japan genotypes become capable of reproducing on both drone and worker broods, a trait which has led to their current status as the most serious pests ever of *A. mellifera*. Of the two genotypes, the Korea genotype is the most common, being found on *A. mellifera* almost worldwide (Anderson & Trueman, 2000; Garrido et al., 2003), even recently on *A. mellifera* in New Zealand (Zhang, 2000).

In China the identity of *Varroa* mites infesting *A. cerana* and *A. mellifera* has been poorly studied. This is despite the fact that *Varroa* mites were first noticed in China about 1957 (Chen, 1993) and that some of the first *Varroa* mites collected from *A. mellifera* came from China (Akratanakul & Burgett, 1975). Initially, the mites detected on *A. mellifera* in China were thought to be *V. jacobsoni*, but Anderson and Trueman (2000) showed that *V. jacobsoni* was a species-complex and worldwide, only the Korea or Japan genotypes of *V. destructor* were causing damage to *A. mellifera*. Anderson and Trueman (2000) also found that mites collected from *A. mellifera* in China in 1996 were the Korea genotype of *V. destructor*, while other *Varroa* mites collected from *A. cerana* in Guangdong Province (Guangzhou) at the same time were a unique genotype, the China genotype of *V. destructor*. The pilot study by Anderson and Trueman (2000) not only suggested that the mites infesting *A. mellifera* and *A. cerana* in China were different but that they might also be genetically isolated from one another. The current study was carried out to clarify the incidence and taxonomic status of mites infesting *A. cerana* and *A. mellifera* in China.

2. MATERIALS AND METHODS

2.1. Collection of bees and mites in China

Samples of adult female *Varroa* mites were collected from hived *A. mellifera* and *A. cerana* colonies from the locations described in Table II and shown in Figure 1. In all hived *A. cerana* colonies and in most of the hived *A. mellifera* colonies, mites were collected live from the bodies of adult worker or drone bees or from capped worker or drone brood cells. However, in some hived *A. mellifera* colonies (samples 1–4, 9, 16, and 20), mites were also collected from the hive bottom boards within 24 hours following the placement of plastic strips impregnated with acaricide between brood frames.

Mites collected from live bees, brood cells and the bottom boards of hives were placed into small labelled glass vials containing 70% alcohol and transported to CSIRO Entomology laboratories in Canberra, Australia, where they were immediately stored at -20°C until needed for DNA analyses.

We surveyed many colonies for *Varroa* mites in *A. cerana* colonies. In Hebei Province outside Beijing, we examined 200 capped drone and 200 worker cells in five colonies; in Hubei Province, we examined 2 500 capped drone and 2 500 worker cells in five *A. cerana* apiaries; and in Fuzhou City and Nanjing County in Fujian Province, the main *A. cerana* beekeeping districts of China, we examined 11 000 capped drone cells and 8 000 capped worker cells among 268 colonies. However, we failed to find *Varroa* mites at these locations in *A. cerana*. All mite samples on *A. cerana* were found in South China, mostly in Yunnan Province and some in Guangdong Province. In general *Varroa* mites caused much damage to *A. mellifera* colonies but few beekeepers observed their presence on *A. cerana*.

2.2. Identification of mites

The identities of *Varroa* mites collected from 17 of the 24 locations described in Table II and shown in Figure 1 were determined after they were removed from storage, washed twice in 70% alcohol, dried, their DNA extracted and parts of the mtDNA amplified by PCR and sequenced, and the sequences compared with known sequences of other *Varroa* mites following the methods described by Anderson and Fuchs (1998) and Anderson et al. (1998). The identities of mites from the remaining seven locations (all collected from *A. mellifera* colonies) were determined by restriction enzyme analyses. These latter analyses were also carried out on varying numbers of mites from each of the 24 locations to confirm whether their mtDNA sequences were invariant

Table II. Details of the *Varroa* mite samples examined and their identity (genotype), based on mtDNA sequences and restriction enzyme analyses.

Sample No.	Collection Sites ¹	Bee Host ² (No. of colonies/ apiaries sampled)	Sampling Dates: Month/ Year	No. of mites sequenced /examined by RE ³	Genotype ⁴
1	Yuci, Shanxi Prov.	Am (10/2)	6,11/2001	2/5	VD (Korea)
2	Nanjin, Xuzhou, Liuhe Co., Jiangsu Prov.	Am (43/3)	6,7,12/2001	2/8	VD (Korea)
3	Fuzhou, Nanjing Co., Fujian Prov.	Am (18/2)	4,11/2001	0/9	VD (Korea)
4	Fengman, Lishu Co., Changchun, Jilin Prov.	Am (50/3)	9/2000 5,11/2001	2/9	VD (Korea)
5	Chifeng, Inner Mongolia	Am (20/1)	9/2000	0/3	VD (Korea)
6	Xishuangbann, Yunnan Prov.	Am (5/1)	5/2001	0/2	VD (Korea)
7	Xishuangbann, Yunnan Prov.	Ac (4/1)	5/2001	2/2	VD (Vietnam)
8	Institute of Apic Res., Beijing	Am (4/4)	8/2000	0/10	VD (Korea)
9	Hangzhou, Yiwu, Dongyang Co., Zhejiang Prov.	Am (47/3)	7,11/2001	0/8	VD (Korea)
10	Huangshan, Anhui Prov.	Am (5/1)	7/2001	2/3	VD (Korea)
11	Ji'an Co., Jiangxi Prov.	Am (7/1)	7/2001	3/4	VD (Korea)
12	Heilongjiang Prov.	Am (12/1)	9/2001	3/3	VD (Korea)
13	Guiyang, Guizhou Prov.	Am (23/1)	9/2001	2/4	VD (Korea)
14	Mianzhu Co., Sichuan Prov.	Am (21/1)	9/2001	3/2	VD (Korea)
15	Zhuhai, Guangdong Prov.	Ac (17/1)	11/2001	3/3	VD (China)
16	Gangu Co., Gansu Prov.	Am (7/1)	11/2001	3/4	VD (Korea)
17	Zhongshan, Guangdong Prov.	Am (15/1)	11/2001	0/3	VD (Korea)
18	Dayao Co., Yunnan Prov.	Ac (97/3)	4/2002	6/6	VD (China 2)
19	Xishuangbanna, Yunnan Prov.	Ac (67/3)	4,5/2002	6/10	VD (Vietnam)
20	Yuanjiang, Hunan Prov.	Am (5/1)	1/2002	0/5	VD (Korea)
21	Xinjiang Autonomous Region.	Am (7/1)	6/2002	2/4	VD (Korea)
22	Zhongshan, Guangdong Prov.	Ac (3/1)	4/2002	3/4	VD (China)
23	Mongzi Co., Yunnan Prov.	Ac (5/1)	5/2002	10/25	VD (China 2)
24	Mongzi Co., Yunnan Prov.	Am (2/1)	5/2002	4/20	VD (Korea)

¹ Co. = County, which is rural. If a place is not followed by Co., it designates the name of a city or town. Prov. = Province.

² Am = *Apis mellifera*; Ac = *Apis cerana*.

³ RE = Restriction enzyme analyses.

⁴ VD = *Varroa destructor* (genotype is in parentheses).

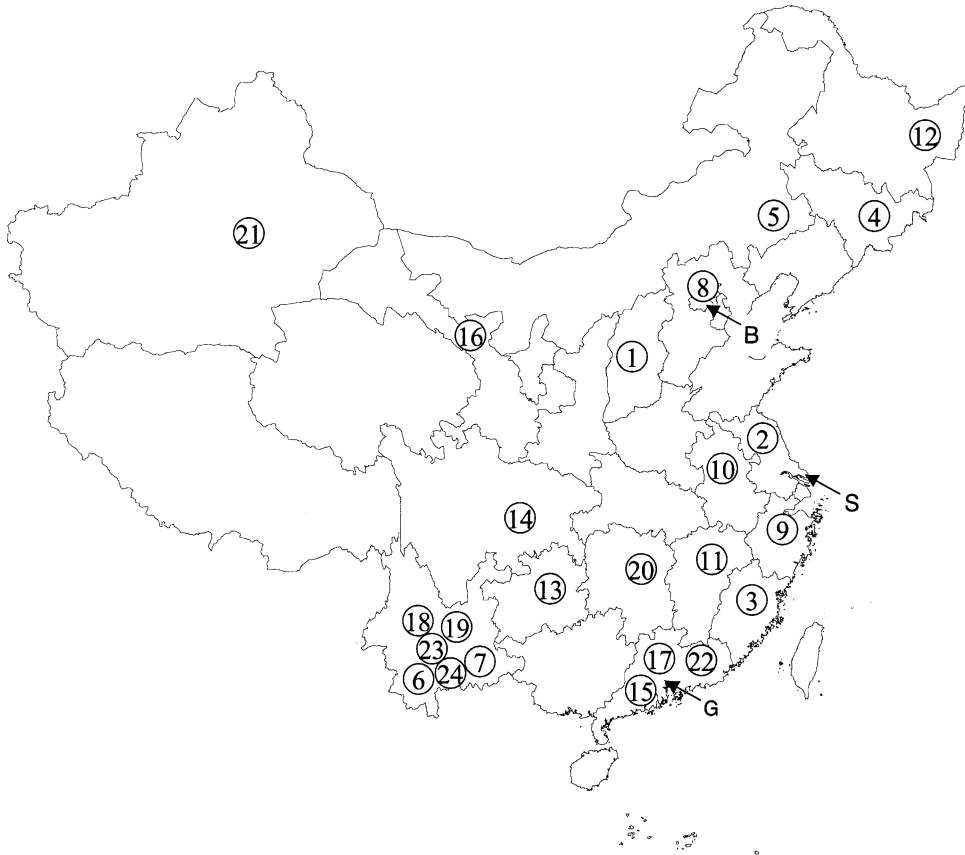


Figure 1. Locations of the sites in China from which *Varroa* mites were collected. Numbers correspond to sample sites in Table II. Beijing, Shanghai and Guangzhou are indicated by the end of arrows of the letters B, S and G respectively.

(Tab. II). Not all mites samples were sequenced because enzyme analysis was less costly and provided information on genotype also, although at a more crude level.

3. RESULTS

The identities of the mites collected, as determined from their mtDNA sequences or from restriction enzyme analyses, are summarized in Table II.

3.1. *Varroa* mites collected from *Apis mellifera*

In many of the samples, when conditions allowed, reproductive status of *Varroa* mites

were determined in worker brood of *Apis mellifera*, and all were found capable of reproduction. MtDNA sequences obtained from all 17 *Varroa* samples collected from *A. mellifera* were identical to that of the Korean genotype of *V. destructor* described by Anderson and Trueman (2000) (GenBank accession number AF106899). Restriction enzyme analyses on varying numbers of mites from each location confirmed that mite samples from the different locations were invariant (see Fig. 2). Identification of mites was based on sequence data which showed that the mtDNA of the Korea genotype *V. destructor* has a *Xho*I but not a *Sac*I site, while the mtDNA of the Japan genotype of *V. destructor* has a *Sac*I but not a *Xho*I site while the mtDNAs of the China and China 2 genotypes of *V. destructor* have both a *Sac*I

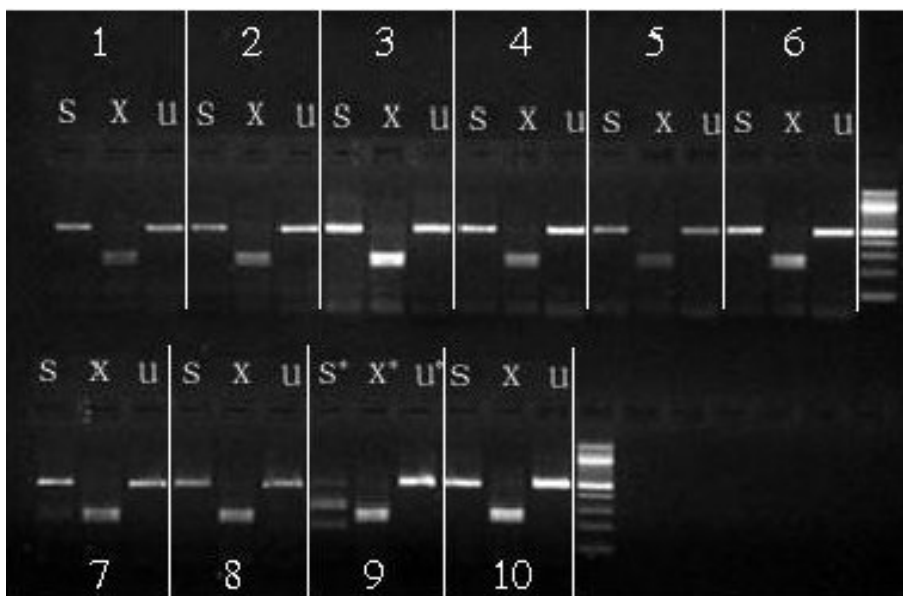


Figure 2. A representative gel of a restriction enzyme analysis carried out on *Varroa* mite isolates from China. Each of the 10 samples has been treated with the *Sac*I enzyme (S), the *Xho*I enzyme (X) or untreated (U). The wells to the right of Samples 6 and 10 contained molecular size markers. All the samples, except sample 9, were only cut with *Xho*I and hence are the Korea genotype of *V. destructor*. Sample 9 (marked as S*X*U*) has been cut with both *Sac*I and *Xho*I and hence is either the China or China 2 genotype of *V. destructor*.

and a *Xho*I site. Mite samples collected from bottom boards (after knockdown by acaricides) showed similar DNA yield and quality compared to those collected live from the brood cells.

3.2. *Varroa* mites collected from *Apis cerana*

None of the *Varroa* mite samples were observed to reproduce on worker brood in *Apis cerana*. MtDNA sequences obtained from *Varroa* mites collected from *A. cerana* colonies at 2 different locations in Guangdong Province were identical to that of the China genotype of *V. destructor* described by Anderson and Trueman (2000) (GenBank accession number AF106900).

MtDNA sequences obtained from *Varroa* mites collected from five *A. cerana* colonies at Mongzi County, Yunnan Province, and from *A. cerana* colonies in three apiaries at Dayao County, Yunnan Province, were identical to

each other but different from any previously recorded genotype. The mtDNA sequences of these mites were similar to that of the China genotype described by Anderson and Trueman (2000) but differed from that sequence by four base pairs. As this is the second *Varroa* genotype to be found on *A. cerana* in China we assign it as the China 2 genotype (or haplotype) of *V. destructor*. Its mtDNA sequence has been placed in the GenBank database under the accession number AY372063. The sequence is compared with that of the original China genotype of *V. destructor* in Figure 3.

The mtDNA sequences of mites collected from *A. cerana* colonies in four apiaries at Xishuangbanna, Yunnan Province, were identical to those of the Vietnam genotype of *V. destructor*, described by Anderson and Trueman (2000).

Again, restriction enzyme analyses on varying numbers of mites from each location confirmed that mite samples from the different locations were invariant (Fig. 2).

1	ATTTATTTTGATTTTTTGGACACCCAGAAGTTTATATTTTAATTTGCCT	50	China
1	ATTTATTTTGATTTTTTGGACACCCAGAAGTTTATATTTTAATTTGCCT	50	China 2
51	GGTTTGGTATTATTCTCATGTAATTTGTATACAGAGAGGGAAGAAGCA	100	China
51	GGTTTGGTATTATTCTCATGTAATTTGTATACAAAGAGGGAAGAAGCA	100	China 2
101	GCCTTTTGGAAATTTAGGGATAATTTACGCTATAATAACTATTGGTATTT	150	China
101	GCCTTTTGGAAATTTAGGGATAATTTACGCTATAATAACTATCGGTATTT	150	China 2
151	TAGGTTTTATTGTATGAGCTCATCATATTTACAGTAGGAATAGATATT	200	China
151	TAGGTTTTATTGTATGAGCTCATCATATTTACAGTAGGAATAGATATT	200	China 2
201	GATACTCGAGCATATTTTACTGCAGCTACAATAATTATGCGGTTCTCTAC	250	China
201	GATACTCGAGCATATTTTACTGCAGCTACAATAATTATGCGGTTCTCTAC	250	China 2
251	TGGTATTAAAATTTTTCTTGATTAGCAACAATTCATGGTTCTATAGTTA	300	China
251	TGGTATTAAAATTTTTCTTGATTAGCAACAATTCATGGTTCTATAGTTA	300	China 2
301	AATTAGATGTCCCAATAATTTGATCTTTAGGTTTTATTTTTTTATTACT	350	China
301	AATTAGATGTCCCGATAATTTGATCTTTAGGTTTTATTTTTTTATTACT	350	China 2
351	TTAGGGGGTATTACTGGTGTAATTTAGCTAATTCCTTCTATTGATATTGT	400	China
351	TTAGGGGGTATTACTGGTGTAATTTAGCTAATTCCTTCTATTGATATTGT	400	China 2
401	TTTACATGATACTTATTATGTAGTAGCACATTTTCACTATGTATTAAGAA	450	China
401	TTTACATGATACTTATTATGTAGTAGCGCATTTTCACTATGTATTAAGAA	450	China 2
451	TAGGGGCT	458	China
451	TAGGGGCT	458	China 2

Figure 3. MtDNA sequences of the original China genotype of *V. destructor* and the China 2 genotype of *V. destructor*. Differences in base-pairs are highlighted in bold and by a gap.

4. DISCUSSION

Our results have helped clarify the taxonomic status of *Varroa* mites infesting European and Asian honey bees in China.

Among the *Varroa* mites we examined from *A. mellifera*, only one mite genotype, the Korea genotype of *V. destructor*, was detected. This result confirms a similar finding by Anderson and Trueman (2000). We did not detect the

Japan genotype of *V. destructor* nor any genotypes of *V. jacobsoni*. Because we and previous researchers have failed to find the Korea genotype of *V. destructor* on *A. cerana* in China, which hosts its own particular genotypes, it is almost certain that the Korea genotype was introduced to China on *A. mellifera*, probably shortly before 1957 when *Varroa* were first noticed causing problems to *A. mellifera* (Chen, 1993).

In our studies, we detected three different *Varroa* genotypes on *A. cerana* in China; the China and Vietnam genotypes of *V. destructor*, and a new genotype which we named the China 2 genotype of *V. destructor*. Our detection of the China genotype from two locations in Guangdong Province confirms the first report of this mite in Guangdong Province, at Guangzhou in 1996, by Anderson and Trueman (2000). Prior to our study, the Vietnam genotype of *V. destructor* had been found on *A. cerana* in Vietnam in 1996 (Anderson and Trueman, 2000), and then in 2002 on *A. cerana* in Thailand (Warrit and Smith, unpublished data). Our detection of this genotype at Xishuangbanna, Yunnan Province, which lies to the north of Vietnam, further extends its geographical range past the official borders of Vietnam.

Our results suggest that there is natural genetic isolation between the different *Varroa* genotypes infesting *A. cerana* and *A. mellifera* colonies in China. If this were not the case, then the different genotypes in China should be readily found on either bee. Clearly, we found that this was not the case. Natural genetic isolation between sympatric populations of different *Varroa* genotypes (those infesting *A. mellifera* and those infesting *A. cerana*) has now been reported from many locations in Asia (Anderson and Trueman, 2000; Fuchs et al., 2000) with the best studied example being in Java, Indonesia. There, the introduced *A. mellifera* are infested with the introduced Korea genotype of *V. destructor* and the native *A. cerana* are infested with the Java genotype of *V. jacobsoni* (Anderson and Sukarsih, 1996). Genetic separation between the two mite genotypes is partly maintained by the inability of the Java genotype of *V. jacobsoni* to reproduce on *A. mellifera* (Anderson, 1994; Anderson and Trueman, 2000), while the introduced Korea genotype of *V. destructor* has never been detected in the *A. cerana* colonies (Anderson

and Trueman, 2000). The reasons for the lack of 'drift' of the Korea genotype are unclear but may reflect a more vigorous grooming response of the *A. cerana* to a foreign (and physically larger) mite genotype (the Korea genotype of *V. destructor*), as suggested by Peng et al. (1987). Further studies on the mechanism responsible for maintaining genetic isolation between sympatric *Varroa* genotypes in Asia would be useful because its determination could lead to the development of new control methods for the *Varroa* genotypes that are so destructive to *A. mellifera*.

In previous studies aimed at identifying *Varroa* mites from their DNA sequences, mites have been collected live and preserved immediately in 70% alcohol. This collection method, while ensuring that the mite DNA is not damaged, is time consuming, because many capped bee brood cells need to be opened in order to find live mites. To find an easier collection method, we collected some dead mites from the bottom boards of some hives within 24 hours following the application of miticide, placed them immediately into 70% alcohol and then treated them similarly to those mites that had been collected live. We experienced no difficulties in obtaining DNA from mites collected this way nor in determining their identification from PCR amplified DNA. This collection method will therefore be useful in future studies.

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Résumé – Identification des acariens *Varroa* (Acari : Varroidae), parasites d'*Apis cerana* et d'*Apis mellifera* en Chine. On connaît très peu de choses concernant le statut taxonomique des acariens *Varroa* qui infestent les abeilles domestiques européennes introduites (*Apis mellifera* L.) et les

abeillen asiatischen indigènes (*Apis cerana* Fabricius) in China. Dans cet article nous résumons d'abord l'état actuel des génotypes connus de *Varroa destructor* Anderson und Trueman et de *V. jacobsoni* Oudemans (Tab. I), puis nous donnons les résultats d'une étude pour laquelle nous avons prélevé 24 échantillons d'acariens *Varroa* dans 17 régions de Chine (Fig. 1 ; Tab. II) et utilisé le séquençage de l'ADN conjointement avec des digestions par des enzymes de restriction (Fig. 2) afin d'identifier les acariens qui infestent en Chine les deux espèces d'abeilles.

Tous les acariens prélevés dans les colonies d'*A. mellifera* ont été identifiés comme étant du génotype coréen de *V. destructor*, ce qui confirme les résultats similaires obtenus dans des études antérieures. Les acariens prélevés dans des colonies d'*A. cerana* dans deux localités de la province de Guangdong étaient du génotype chinois de *V. destructor*, confirmant aussi les résultats d'études antérieures. Les acariens prélevés dans les colonies d'*A. cerana* dans trois ruchers du comté de Dayao, province de Yunnan et dans cinq colonies du comté de Mongzi, province de Yunnan appartenaient à un nouveau génotype de *V. destructor*, que nous avons nommé génotype chinois 2 (Fig. 3). Les acariens prélevés dans les colonies d'*A. cerana* dans quatre ruchers à Xishuangbanna, province de Yunnan, région située au nord du Vietnam, étaient du génotype vietnamien de *V. destructor*, ce qui étend la zone de répartition géographique de cet acarien.

Nos résultats sont applicables aux futurs efforts de lutte contre cet acarien et de mise en quarantaine des abeilles en Chine. Nous avons montré que *V. jacobsoni* n'est pas présent en Chine et que les acariens *Varroa* qui infestent *A. mellifera* appartiennent à un seul génotype (le génotype coréen de *V. destructor*), génotype qui parasite *A. mellifera* dans la plupart des régions du globe. Ce génotype a été probablement introduit pour la première fois en Chine dans les années 1900 à la suite d'importation d'*A. mellifera*. Nos études montrent aussi qu'il existe un isolement génétique naturel entre les génotypes de *Varroa* qui infestent *A. cerana* et *A. mellifera*, phénomène qui a été mentionné maintenant dans de nombreux autres endroits d'Asie.

***Apis mellifera* / *Apis cerana* / *Varroa* spp. / génotype chinois 2 / génétique populations**

Zusammenfassung – Identifikation von *Varroa* Milben auf *Apis cerana* und *Apis mellifera* in China (Acari: Varroidae). Über den taxonomischen Status der *Varroa* Milben (Acari: Varroidae), die die nach China eingeführten Völker der europäischen Honigbienen sowie die einheimischen asiatischen Honigbienen (*Apis cerana* F.) befallen, ist wenig bekannt. In diesem ersten Artikel fassen wir zunächst den derzeitigen Stand der bekannten Genotypen von *Varroa destructor* und *V. jacobsoni* zusammen (Tab. I) und berichten dann über die

Ergebnisse einer Studie, in der wir 24 Proben von Varroamilben von den 2 Bienenarten aus 17 Provinzen über ganz China gesammelt (Abb. 1, Tab. II) und mit DNA-Sequenzierung in Verbindung mit Restriktionsenzymverdauung (Abb. 2) identifiziert haben.

Alle von *A. mellifera* Völkern stammenden Milben wurden als der koreanische Genotyp von *Varroa destructor* Anderson und Trueman bestimmt. Die von *A. cerana* Völkern an zwei verschiedenen Orten in der Guangdong Provinz gesammelten Milben waren der chinesische Genotyp von *V. destructor*. Dies bestätigte die Ergebnisse von früheren Studien. Die aus *A. cerana* Völkern in 3 Bienenständen in Dayao County, Yunnan Provinz, und von 5 Völkern in Mongzi County, Yunnan Provinz gesammelten Milben waren ein neuer Genotyp, den wir den China 2 Genotyp (Abb. 3) von *V. destructor* nannten. Die aus *A. cerana* Völkern von 4 Bienenständen in dem nördlich von Vietnam gelegenen Xishuangbanna, Yunnan Provinz, gesammelten Milben waren der vietnamesische Genotyp von *V. destructor*, wodurch das geographische Verbreitungsgebiet dieser Milbe erweitert wird.

Unsere Ergebnisse sind für die zukünftige Milbenbekämpfung und Quarantäne-Bemühungen in China von Bedeutung. Wir haben gezeigt, dass *V. jacobsoni* nicht in China vorkommt, und dass die zur Zeit die *A. mellifera* Völker in China befallenden Milben einem einzigen Genotyp, dem koreanische Genotyp von *V. destructor* angehören, dem gleichen der *A. mellifera* in den meisten Ländern der Welt befällt. Dieser Genotyp wurde vermutlich erstmalig im 20. Jahrhundert mit nach China importierten *A. mellifera* Völkern eingeführt. Unsere Studien weisen darüber hinaus darauf hin, dass zwischen *A. cerana* und *A. mellifera* infizierenden Milben eine natürliche Isolation besteht. Über diese Erscheinung ist bereits aus vielen anderen Orten in Asien berichtet worden.

***Apis mellifera* / *Apis cerana* / China 2 Genotyp von *Varroa destructor* / *Varroa* spp.**

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