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Original article

Effect of environmental heavy metals on the expression of detoxification-related genes in honey bee *Apis mellifera*

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Abstract – Air pollutants and agricultural pesticides can be environmental stressors to pollinators. In this study, to investigate the expression of detoxification-related genes and heavy metal concentrations in honey bees and honey possibly exposed to environmental stresses, we collected samples from apiaries located in mountainous, agricultural, and urban areas. Compared with the mountainous and agricultural areas, the mercury and lead concentrations were highest in honey and bees collected from urban areas. In addition, the expression levels of *CYP9Q1*, *CYP9Q2*, *CYP9Q3*, and genes encoding catalase and superoxide dismutase were markedly higher in urban bees than those from agricultural and mountainous areas, discreetly indicating that the notable induction of the detoxification metabolism in urban bees might be because of heavy metal pollutant exposure. Our study suggests that honey bees actively respond to environmental stressors, such as heavy metals derived from urban areas.

Apis mellifera **/ enzyme / detoxification / environmental stressor / heavy metal**

1. INTRODUCTION

The honey bee (*Apis mellifera* L.) plays a major role in sustaining food security and maintaining biodiversity, providing critical pollination services to natural ecosystems and crop production (Leonhardt et al. 2013). Over the last decade, colony collapse disorder (CCD), a syndrome describing the large-scale depletion of honey bee colonies, has been reported worldwide, especially in Europe (Potts et al. 2010) and North America (Hu et al. 2017). Some of the major causes of CCD include parasites, pathogens (Alaux et al. 2010; Cornman et al. 2012), metal and metalloid contaminants (Han et al. 2002), exposure to pesticides (Henry et al. 2012), pathogen–pesticide interactions (Pettis et al. 2012), and interactions between chemical pollutants and natural stressors (Holmstrup et al. 2010).

Anthropogenic activities associated with the accelerated growth of urbanization and industrialization over the past century have created localized and regional pollution problems (Molina and Molina 2004). Exposure to metal and metalloids in polluted areas can impair insect behavior, ultimately, for some insects, reducing species fitness, population numbers, and species diversity (Mogren and Trumble 2010). According to the Agency for Toxic Substances and Disease Registry (ATSDR 2007), arsenic, lead (Pb), cadmium, and mercury (Hg) are some of the common heavy metal pollutants with serious health implications (Gupta et al. 2015).

In insects, including honey bees, the immune and detoxification systems respond quickly to chemical

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and biological stresses (Lemaitre and Hoffmann 2007), and metabolic resistance is the principal mechanism to escape the adverse effects of both natural and synthetic toxins. Cytochrome P450 monooxygenases (P450s) have a fundamental role in metabolic detoxification of pyrethroids, which constitute the majority of commercial insecticides (Mao et al. 2009). The *CYP9Q* genes contribute to mediating acaricide—tau-fluvalinate and coumaphos—detoxification in honey bees (Mao et al. 2011), while *CYP6AS3* is involved in the detoxification of quercetin, a flavonoid present in pollen and numerous floral nectars that constitute the honey bee diet, and a potent enzyme inhibitor (Mao et al. 2009). In addition, antioxidant enzymes mediate the intracellular reactive oxygen species (ROS) balance essential for cell survival. An increase in oxidative stress is associated with the upregulation of antioxidant genes, such as superoxide dismutase (*SOD*) and catalase (*CAT*), to prevent ROS-mediated damage (Corona and Robinson 2006).

Considering that urban and agricultural areas are possibly contaminated with metal/metalloid and pesticide pollutants, respectively, an investigation of the expression of detoxification-related genes in honey bees in different environmental situations can aid the understanding of the physiological responses of the honey bees toward different environmental stressors. From this perspective, we collected honey bees from three locations (mountainous, agricultural, and urban) with diverging human activity and interference to compare the expression trends of genes involved in the detoxification mechanism (*CYP9Q* members) and antioxidant pathway (*CAT* and *SOD*) in honey bees from the various locations. In addition, we measured the Hg and Pb concentrations in honey and honey bees, as suitable bioindicators of environmental pollution (Oroian et al. 2016), to distinguish the anthropogenic activities associated with each location.

2. MATERIALS AND METHODS

2.1. Study area and sampling

The three landscapes (mountainous, agricultural, and urban) were systematically selected. The urban site was located in a large city in South Korea close to an industrial zone and residence area. It has a high human influence/interference and high emission of chemical substances from industries (Figure 1a). The agricultural land site was near farming fields with rice and vegetable production activities (Figure 1b). The mountainous site was surrounded by mountains, with limited agricultural activity and human interference compared with the urban and agricultural areas (Figure 1c). The maps were captured from Google satellite maps and colored with Windows Paint (Windows 10, Microsoft Software, London, UK). Three different colonies of beehives were randomly selected from each apiary site. From each beehive, we collected 20 honey bees and 30 mL of honey on July 25, 2017. All bee samples are considered to be nurses because we collected honey bees from the hives during the daytime. The collected honey bees and honey were frozen directly with liquid nitrogen and stored at − 70 °C until RNA extraction and heavy metal analysis.

2.2. Total RNA preparation and cDNA synthesis

Considering that the midgut is the major organ involved in detoxification and protection from oxidative stress in insects (Arrese and Soulages 2010), the abdomens were separated from the whole body of three nurses and pooled as a single replication. RNA samples were prepared from three technical replicates. Abdomen samples were completely homogenized with TRI reagent (Molecular Research Center, Inc., Cincinnati, OH), and total RNA was extracted using Direct-zol™ RNA Miniprep Plus (Zymo Research, Irvine, CA). DNase I digestion occurred during the RNA extraction procedure to eliminate genomic DNA contamination (Moon et al. 2018). The purity and quantity of the extracted RNAs were measured using a SpectraMax® QuickDrop™ spectrophotometer (Molecular Devices, Sunnyvale, CA).

2.3. Quantitative reverse transcription PCR

Sequence information of five genes (*SOD1*, *CAT*, *CYP9Q1*, *CYP9Q2*, and *CYP9Q3*) was obtained from the NCBI database (Table I). Their primers were accurately designed using Oligo Calc software (http://biotools.nubic.

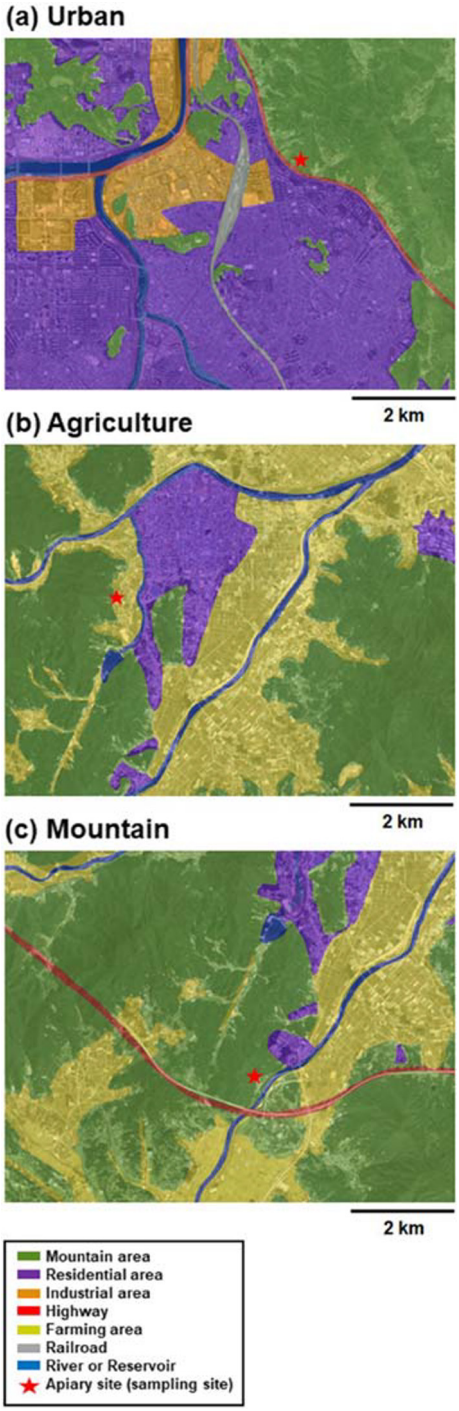

Figure 1. Map showing area land cover of the three landscapes: urban (**a**), agriculture (**b**), and mountain (**c**) where the three apiary sites are located. The maps were captured from Google satellite map and colored with Windows Paint (Windows 10).

northwestern.edu/OligoCalc.html) to ensure similar properties of each primer and amplicon (Table I). *GAPDH* (glyceraldehyde 3-phosphate dehydrogenase) and *RPS18* (ribosomal protein S18) were selected as the reference genes to normalize the gene expression levels (Moon et al. 2018). The PCR specificities and amplification efficiency were verified (Table I) before conducting quantitative reverse transcription PCR (qPCR).

To analyze the expression levels of the five target genes in the abdomen of honey bees collected from three different locations, qPCR was performed using RNA-direct™ SYBR Green Real-time PCR Master Mix (Toyobo, Osaka, Japan). Each sample was analyzed in triplicate (technical replicate) in a total reaction volume of 20 μL, containing 100 ng of the prepared RNA sample. Quantification cycle (C_q) values of the five target genes and reference genes were obtained from the same sample of each location. The relative expression of genes was normalized against the mean C_q values of *GAPDH* and *RPS18* and analyzed by the relative quantification method modified from the original concept of $2^{-\Delta\Delta Cq}$ (Pfaffl 2001).

2.4. Heavy metal concentration in honey and honey bees

To determine the environmental stressor in each location, we measured the concentration of two heavy metals (Hg and Pb) in honey bees and honey samples using the Association of Official Analytical Chemists method (AOAC 1990). Accordingly, after adding HNO_3 to 10 g of the sample, the mixture was allowed to stand at room temperature for 12 h and heated at 100 °C for at least 24 h. HNO_3 was added again, and the reaction was repeated until the acid was completely evaporated in order to remove the organic matter. Afterward, 20 mL of 0.2 N HNO_3 solution was added, and the sample solution was re-eluted for 24 h. After filtration through a 0.45-μm membrane filter, the solution was adjusted to 50 mL in a volumetric flask. Hg and Pb were analyzed using an inductively coupled plasma optical emission spectrometer (IRIS Intrepid, Thermo Elemental Co., Winsford, UK) at $A_{184.950(482)}$ and

Table I. Primer and amplicon information of target and reference genes for qPCR used in this study

Gene			Primer					Amplicon			
Symbol	Full gene name	Accession no.		Sequence (5′ → 3′)	Size (bp)	GC (%)	T_m (°C)	Size (bp)	GC (%)	Efficiency (%)	R^2
CYP9Q1	Cytochrome P450 9Q1	XM_006562301	For.	ACCTGTCCACGAGG AATCAC	20	55	60.5	234	57.3	96.73	0.999
			Rev.	CCTTCACCCCGATC GTCTTT	20	55	60.5				
CYP9Q2	Cytochrome P450 9Q2	XM_392000	For.	ACCTGATCAAGACC ATCACGAT	22	45	60.1	170	54.1	92.47	0.999
			Rev.	GATCTTGCTCGAGG TGAAGG	20	55	60.5				
CYP9Q3	Cytochrome P450 9Q3	XM_006562300	For.	TACGTGGGCATTTA CGAGTTCA	22	45	60.1	249	53.4	83.69	0.9996
			Rev.	CTCGGTCATCAGCT TGAACATA	22	45	60.1				
SOD1	Superoxide dismutase 1	NM_001178027	For	GCGTTCTTCAGGGT GAAGTC	20	55	60.5	203	41.9	91.77	0.9996
			Rev	ATCAGGTCCACCAT GATCCTTT	22	45	60.1				
CAT	Catalase	NM_001178069	For.	CTTGGCCCAAACAA TCTGCAAT	22	45	60.3	151	37.7	98.43	0.9995
			Rev.	GACATTCTCTAGGC CCACCA	20	55	60.5				
RPS18 [a]	ribosomal protein s18	XM_625101	For.	GATTCCCGATTGGT TTTTGAATAG	24	38	60.3	152	35.5	107.56	0.999
			Rev	AACCCCAATAATGA CGCAAACC	22	45	60.1				
GAPDH[a]	Glyceraldehyde-3-phosphate dehydrogenase	XM_393605	For.	CACCTTCTGCAAAA TTATGGCG	22	45	60.1	188	43.1	95.5	0.997
			Rev.	ACCTTTGCCAAGTC TAACTGTTAA	24	38	60.3				

$A_{220.353(453)}$, respectively, operating at an RF power of 1150 W, analysis pump rate of 100 rpm, nebulizer pressure of 20 psi, and observation height of 15 mm.

2.5. Statistical analyses

Data were analyzed using SAS version 9.4 (SAS Institute, Inc., Cary, NC) at the significance level of $P < 0.05$. One-way ANOVA, followed by the Tukey–Kramer multiple comparison post hoc test, was performed to compare the expression levels of genes between different locations. Results are given as mean ± standard error.

3. RESULTS

3.1. Antioxidant protection (*SOD1* and *CAT* expression)

In this study, we compared the expression levels of *SOD1* and *CAT* involved in the antioxidant protection processes in the honey bees from three different geographical locations. qPCR revealed that *SOD1* and *CAT* were more abundantly transcribed in urban bee ($P < 0.05$), whereas their expression levels between mountainous and agricultural regions were not statistically different ($P > 0.05$; Figure 2). This result implies that honey bees in an urban area might have increased exposure to oxidative stressors compared with those in mountainous and agricultural environments.

3.2. Detoxification (expression of *CYP9Q* genes)

A comparison of the expression levels of the major detoxification genes (*CYP9Q1*, *CYP9Q2*, *CYP9Q3*) showed that the expression levels were dramatically higher in urban bees than bees from mountainous or agricultural regions ($P < 0.05$; Figure 3). Urban bees expressed higher ($P < 0.05$) levels of *CYP9Q1* (Figure 3a), *CYP9Q2* (Figure 3b), and *CYP9Q3* (Figure 3c), followed by the bees in the agricultural region, which had marginally but not significantly higher expression levels than those from bees located in the

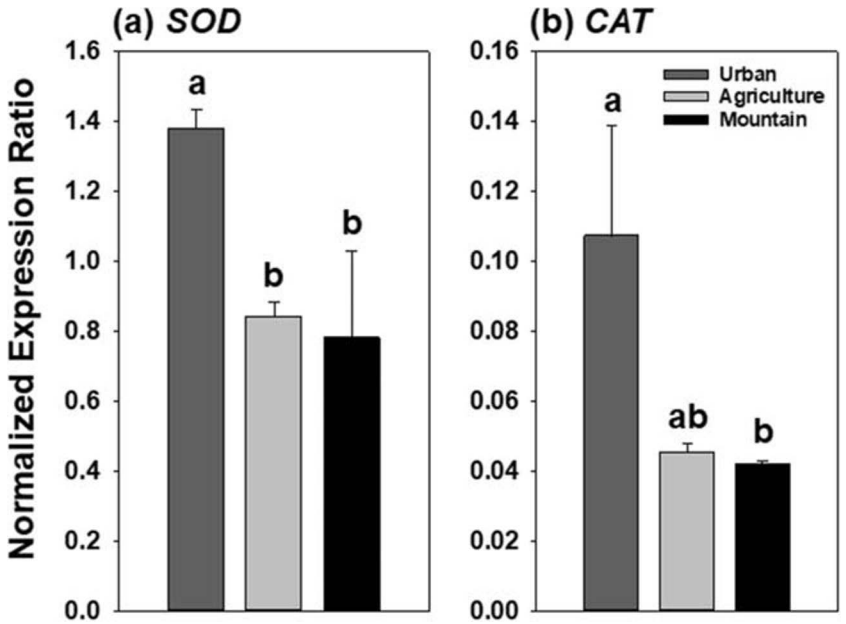

Figure 2. Expression levels of superoxide dismutase 1 (*SOD1*) (**a**) and catalase (*CAT*) (**b**) in the abdomen tissue of honey bees collected from thee different locations: urban, agricultural, and mountainous. The mRNA expression of *the genes* was quantified and normalized. Vertical bars represent the mean ± SE ($n = 3$). *Different letters above the bar* indicate significant differences at $P < 0.05$.

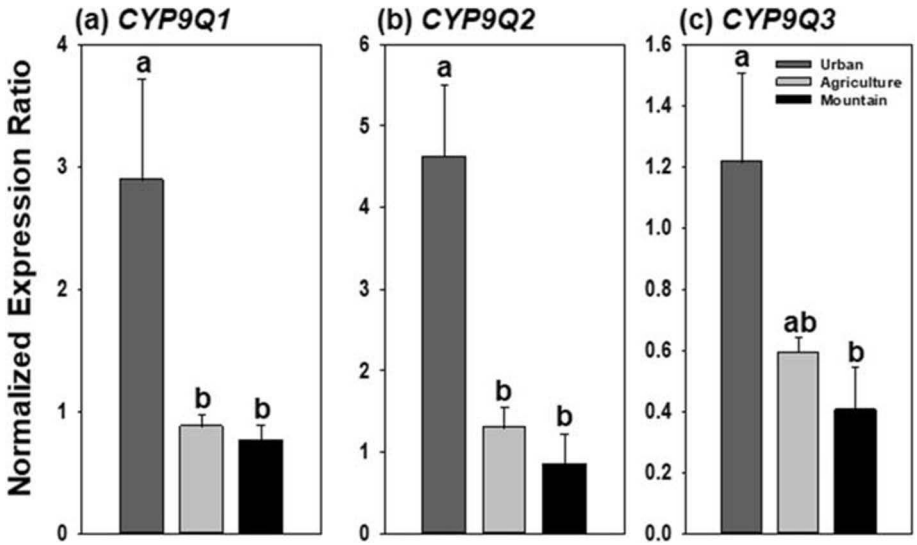

Figure 3. Expression levels of *CYP9Q1* (**a**), *CYP9Q2* (**b**), and *CYP9Q3* (**c**) in the abdomen tissue of honey bees collected from three different locations: urban, agricultural, and mountainous. The mRNA expression of *the genes* was quantified and normalized. Vertical bars represent the mean ± SE ($n = 3$). *Different letters above the bar* indicate significant differences at $P < 0.05$.

mountainous region ($P > 0.05$). The noticeably higher expression level of *CYP9Q* genes in urban bees was suggestive of honey bee responses to the environmental xenobiotics generated by industrial activity in the city.

3.3. Heavy metal concentration in honey and honey bees

The Hg and Pb concentrations were measured in honey (Hg: 0.665, 1.009, and 3.249 mg/kg; Pb: 0.130, 0.131, and 0.238 mg/kg; Figure 4a) and honey bees (Hg: not detected, and 0.039 and 0.051 mg/kg; Pb: 0.258, 0.363, and 0.489 mg/kg; Figure 4b) collected from mountainous, agricultural, and urban areas, respectively. In all instances, except for Hg in the honey bees, the urban environment had the highest levels of both heavy metals ($P < 0.05$). There was also a trend of increased concentrations of Pb and Hg in agricultural samples (both honey and honey bees) than that in mountainous samples, but this was only significant for Hg in honey and Pb in honey bees ($P < 0.05$). According to the provisional tolerable weekly intake (PTWI) value established by a joint WHO/FAO expert consultation, the PTWI (μg/kg (body weight)/week) of Hg and Pb by humans are 5 and 25 μg/kg/week, respectively (WHO/FAO 2015). Considering the weekly amount of honey consumption, the concentrations of Hg and Pb detected in the present study seem to be safe for humans.

4. DISCUSSION

Contamination of agricultural and urban environments with pesticides and industrial pollutants, respectively (Borrego et al. 2006; Satoh 2006), can expose honey bees to environmental stresses, triggering physiological responses to the stressors. In particular, several industrial activities contribute to air pollution experienced by many urban regions (Borrego et al. 2006). In the present study, we detected higher Hg and Pb concentrations in urban samples of both honey and honey bees compared with the corresponding samples from agricultural and mountainous areas (Figure 4). Several previous studies detected various amounts of heavy metals in different geographical locations and areas associated with anthropogenic development. Compared with the Pb concentration detected in honey bees from mountainous (0.258

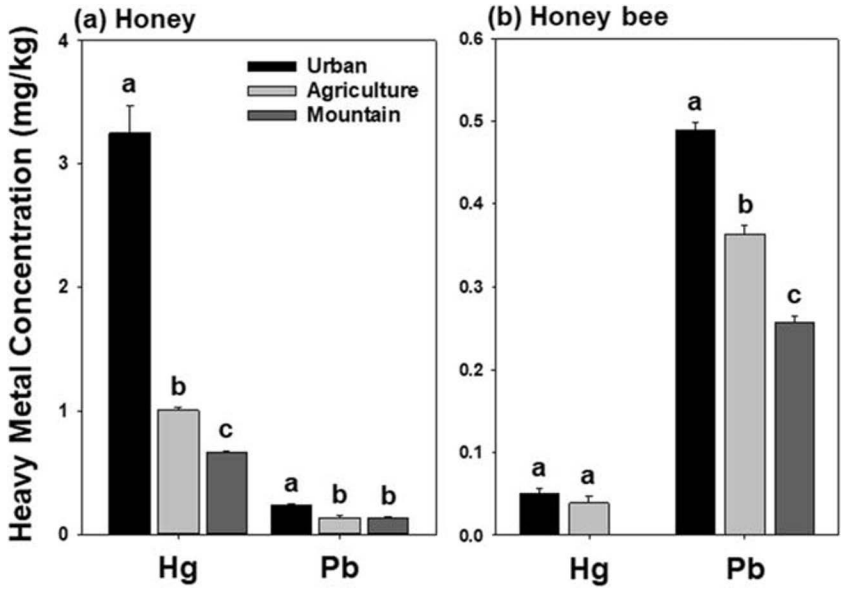

Figure 4. Concentrations of heavy metal (mg/kg) residues in honey (**a**) and honey bee (**b**) samples collected from apiaries in different locations: urban, agricultural, and mountainous. (Hg, mercury; Pb, lead). Vertical bars represent the mean ± SE ($n = 3$). Different letters above the bar indicate significant differences at $P < 0.05$.

mg/kg) and agricultural (0.363 mg/kg) areas in our study (Figure 4b), Conti and Botrè (2001) found a higher mean value of Pb (0.52–1.00 mg/kg), while Porrini et al. (2002) showed a similar amount of Pb in a national park (0.15–0.55 mg/kg). In urban bees, we detected 0.489 kg/ml Pb (Figure 4b), while Roman (2010) measured 0.64–1.25 mg/kg Pb. In addition, Velemínský et al. (1990) noted a high concentration of Hg (3.68–9.28 mg/kg) in bees collected from industrial areas relative to that indicated in our study (0.051 mg/kg; Figure 4b). Contradictory to the low amounts of Hg (0.001–0.145 mg/kg) commonly reported in honey sampled from mountainous areas, villages, and cities (Bilandžić et al. 2012; Carrero et al. 2013), the concentration range of Hg in our honey samples was 0.665–3.249 kg/mg (Figure 4a). However, the maximal 3.249 mg/kg of Hg we detected in our honey samples is comparable to the mean Hg content of 3.030 mg/kg in honey collected from Iran (Akbari et al. 2012). Data obtained from the literature and our study infer that honey and honey bees are environmentally exposed to heavy metals originating from industrial activity. In this study, only 1.4 km separated the apiary site from the industrial zone in the urban area (Figure 1a), and there were two large highways in front of the apiary site. This scenario possibly contributed to the heavy metal contamination in the urban environment, which could explain the higher Hg and Pb concentrations in honey from the urban area relative to the other two locations (Figure 4a). It should also be noted that honey bees are sequentially exposed to heavy metal–contaminated honey in the beehive, supporting the predominant detection of Hg and Pb in the urban honey bees, too (Figure 4b). Although heavy metal concentrations in the agricultural region were less than those in the urban area, they were generally higher than those in the mountainous region (Figure 4), indicating that there must be a pollutant source in the agricultural field studied. Fertilizers, pesticides, and organic manure are the main sources of heavy metals in agricultural soils (Nicholson et al. 2003; Mirsal 2004; Zhang 2006), as supported by our results, showing a trend of higher Hg and Pb concentrations in the agricultural region than that in the mountainous area (Figure4). Moreover, Hg was not detected in honey bees from the mountainous region, indicating that the mountain environment remains relatively low in pollutant

contamination. In the comparison of heavy metal concentrations between honey and honey bees (Figure 4), Hg concentrations were higher in honey than those in honey bees, whereas Pb showed the opposite trend. In humans, the in vivo half-lives of Hg and Pb differ because of distinctly different tissues and pathways mainly contributing to heavy metal metabolism (reviewed by Brodkin et al. 2007). Although the pathways of Hg and Pb metabolism in honey bees have not yet been fully elucidated, the differences between the amounts of Hg and Pb detected in honey and the honey bees could imply that this insect has distinct mechanisms of efficiency of absorption and excretion of these two heavy metals.

According to the expression levels of *SOD1*, *CAT*, and the three *CYP9Q* members, honey bees physiologically respond to pollutants (Figure 2 and Figure 3) because their expression trends between different apiary sites were highly correlated with the differences in Hg and Pb concentrations among the three areas ($R^2 > 0.95$; Fig. S1). Considering that SOD and CAT are representative antioxidative enzymes, urban bees may be exposed to oxidative stresses. Heavy metals are known to induce oxidative stress (Puppel et al. 2015) that is accompanied by an upregulation of antioxidant enzymes, such as SOD and CAT (Corona and Robinson 2006). Previous work suggested CAT activity as a biomarker of exposure to oxidative stress because of its key role in combating ROS in honey bees (Mamidala et al. 2011). This enzyme contributes to antioxidant protection (Collins et al. 2004), and was elevated in *A. mellifera* exposed to xenobiotic compounds in a laboratory (Badiou-Bénéteau et al., 2012). There were equally higher expression levels of antioxidant enzyme genes, such as *SOD1* and *CAT*, in honey bees collected from urban and industrial regions in which the Pb concentration in bees was also higher relative to that in bees from mountainous regions, suggesting adaptation of honey bees to oxidative stress (Nikolić et al. 2015). These earlier studies support that the induction of *SOD1* and *CAT* in the present study is a physiological response of honey bees exposed to environmental pollutants, including Hg and Pb, in the urban area (Figures 2 and 4). Besides *SOD1* and *CAT*, three *CYP9Q* genes were highly induced in the bees from the urban area when compared with the mountainous and agricultural regions (Figure 3). P450s are associated with environmental stressors, catalyzing diverse reactions that contribute to the detoxification of natural and synthetic xenobiotics in insects (Feyereisen 1999). The *CYP450* genes have a functional role in enhancing tolerance to environmental stress in a range of organisms (Guttikonda et al. 2010) and have been indicated as potential biomarkers of pollution (*Široká* and Drastichová 2004). In *Apis cerana*, *CYP450* genes were induced by several stresses, including heavy metals (Zhang et al. 2018). In this context, the strong environmental effect of the urban area on the expression level of the target genes (*CYP9Q1*, *CYP9Q2*, and *CYP9Q3*) observed in this study could be caused by pollutants, including heavy metals, emitted from the industries. While it suggests that heavy metals are contributory stress factors in the urban area, this remains to be verified, and further studies are required to determine whether heavy metals promote a negative effect on the urban bees.

It is well recognized that *CYP* genes, including *CYP9Q1*, *CYP9Q2*, and *CYP9Q3*, contribute to pesticide detoxification in honey bees (De Smet et al. 2017), and insecticides can cause oxidative stress, thereby increasing the abundance of antioxidants (Weirich et al. 2002). On this basis, we expected higher expression levels of the three *CYP* genes in the agricultural area induced by exposure to high concentrations of pesticides because of a high frequency of pesticide application. In contrast to our expectation, the expression levels of the *CYP9Q* genes were much lower in the bees from this region when compared with those in the urban area (Figures 2 and 3), implying that heavy metals mostly act as environmental stresses and induce the genes involved in detoxification mechanisms in the honey bees.

In summary, we detected high concentrations of the heavy metals Hg and Pb (Figure 4), and greater expression levels of detoxification-related genes, *SOD1*, *CAT*, *CYP9Q1*, *CYP9Q2*, and *CYP9Q3* (Figures 2 and 3), in the bees and honey samples from the urban area compared with those in the agricultural and mountainous areas. Furthermore, the gene expression patterns were positively correlated with the concentration of heavy

metals (Fig. S1) in all three environments, suggesting a physiological response of honey bees to environmental stressors, which could be associated with differences in land use in the urban area. Global environmental pollution is increasing because of continuous and intense industrial and technological development in the world, with toxic metals regarded as one of the major harmful pollutants (Alley et al. 1998). Honey bees have been considered to be excellent bioindicators of heavy metals in the environment (Zarić et al. 2016), as also observed in this study. However, a broad range of studies investigating the correlation between various environmental stresses and the expression trends of detoxification-related genes is required to generalize the physiological response of honey bees toward environmental stresses, and honey bees as bioindicators.

GENERAL SUMMARY

Environmental stressors, including parasites, pathogens, and exposure to pesticides, metals, and metalloid pollutants, have been implicated as detrimental to cellular homeostasis and physiological function, and as potential causes of CCD. These factors alter both the detoxification gene expression pathways and immune responses in honey bees. To investigate the expression of detoxification-related genes in honey bees possibly exposed to environmental stresses, we collected honey bees from apiaries located in mountainous, agricultural, and urban (with industrial zone) areas and compared the expression trends of genes involved in the detoxification mechanism (*CYP9Q* members) and antioxidant pathway (*CAT* and *SOD1*) in honey bees from the three locations. In addition, we collected honey samples from the same areas, and measured the Hg and Pb contents in honey and honey bees to distinguish anthropogenic activities in each location.

For gene analysis, RNA samples were prepared from the abdomen, and qPCR was performed. For heavy metal analysis, the Hg and Pb concentrations in honey bees and honey samples were measured using the AOAC method. Data were statistically analyzed to compare the expression levels of genes and the concentration of heavy metals among the locations.

In this study, qPCR revealed dramatically increased expression levels of *SOD1* and *CAT* in urban bees (Figure 2), indicating a greater exposure of the honey bees to oxidative stressors in the urban areas compared with the other two locations. Similarly, the *CYP9Q1*, *CYP9Q2*, and *CYP9Q3* levels were increased noticeably in urban bees relative to their mountainous and agricultural land counterparts (Figure 3), suggesting that honey bee responses to the environmental xenobiotics resulted from industrial activity in the urban area. In addition, heavy metal analysis showed a marked increase in the Hg and Pb concentrations in the honey sample, and in the level of Pb in honey bees sampled from the urban area (Figure 4), inferring that urban areas expose honey bees to greater pollution by heavy metals in comparison with mountainous and agricultural regions. This implication was supported by a strong and positive correlation of the *CYP9Q1–3*, *SOD1*, and *CAT* expression patterns with the concentration of heavy metals (Fig. S1).

Heavy metals induce oxidative stress, and antioxidant enzymes, such as SOD and CAT, regulate the intracellular ROS balance. Likewise, the CYP9Q subfamily has been reported to catalyze various reactions that contribute to the detoxification of natural and synthetic xenobiotics in insects. Therefore, the strong environmental effect of the urban area on the transcript accumulation of *CYP9Q1*, *CYP9Q2*, *CYP9Q3*, *CAT*, and *SOD1* observed in this study could be caused by pollutants, including heavy metals, that were emitted from the industries in the urban area. However, it remains to be verified and warrants further investigation.

AUTHORS' CONTRIBUTION

GG, YHK, and JKP conceived this research and designed experiments; GG, KM, YK, and JBC performed experiments and analysis; GG and YHK wrote the paper. All authors read and approved the final manuscript.

FUNDING INFORMATION

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COMPLIANCE WITH ETHICAL STANDARDS

Conflict of interest The authors declare that they have no conflict of interest.

Effet des métaux lourds de l'environnement sur l'expression des gènes liés à la détoxification chez l'abeille, *Apis mellifera*.

***Apis mellifera* / enzyme / détoxification / facteur de stress environnemental / métal lourd.**

Der Effekt von Schwermetallbelastungen auf die Expression von Detox-Genen bei der Honigbiene *Apis mellifera*.

***Apis mellifera* / Enzyme / Detoxifikation / Umweltstressoren/ Schwermetall**.

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