Estimating Geographic Range Shifts of *Vespa simillima* after *Vespa velutina* (Hymenoptera: Vespidae) Invasion in South Korea

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Abstract

In South Korea, there are six native and an invasive (*Vespa velutina nigritorax*) species of hornets. This invasive species was first observed and recorded in the southern parts of South Korea in 2003. After the first observation, it has spread to higher latitudes at a rate of 10–20 km per year. Some studies consider this species as a serious competitor for the native species of *V. simillima* with the possibilities of occupying the native niches of *V. simillima*. Because *V. velutina* spread throughout Korea between 2003 and 2015, we aimed to estimate the geographical range shift in *V. simillima* distribution after the invasion of *V. velutina* in South Korea. For this purpose, we used species distribution models and the GBIF database to create distribution maps of the species for two periods before and after 2012. Our results showed that there is a significant difference in the geographical distribution of *V. simillima* in the periods of 1999–2011 and 2012–2022, so that between 1999 and 2011, this species mostly occupied the eastern and southern parts. However, between 2012 and 2022, the distribution of this species shifted towards the central and western parts. Considering that *V. velutina* occupies most of the southern parts of South Korea, it seems that it has caused the *V. simillima* populations to decrease in these areas.

INTRODUCTION

In South Korea, there are six native species of hornets that include *Vespa analis*, *V. mandarinia*, *V. simillima*, *V. crabro*, *V. ducalis*, and *V. dybowskii* (Choi *et al*., 2012). Hornets belong to the genus *Vespa* and the subfamily *Vespinae*, which has 22 species globally (Perrard *et al*., 2013). Recently, there has been a growing concern regarding the increase in hornet populations throughout Korea as these species are considered a challenge to the beekeeping industry in Korea. These species, along with the non-native species called yellow-legged hornet (*Vespa velutina nigritorax*), which was recorded in Korea in 2003 (Kim *et al*., 2006), have caused damage to beekeepers by attacking beehives. For example, the annual economic loss of hornets to the beekeeping industry in Korea is estimated at 100–170 billion Korean won (Jung,

2012; Jung and Cho, 2015). In Europe, *V. velutina* has damaged 18 to 50% of honey beehives (Laurino *et al*., 2019). Therefore, this concern has increased the need to study the distribution of hornets in South Korea (Kwon and Choi, 2020; Zhu *et al*., 2020) and has led to more studies to identify the threats of hornets and to estimate the effects of the invasion of *V. velutina* on pollinators and other hornets.

In addition to affecting honeybees and damaging beekeepers, hornets also create disturbances as competing species. For example, Choi *et al*. (2012) reported that *V. velutina* became the most abundant species of hornet in South Korea and could occupy habitats of native hornets such as *V. simillima*. This species has a high ability to occupy different environments beyond the borders of its native niche (Verdasca *et al*., 2022). Kwon and Choi (2020) compared the aggressive behaviors and body size

of *V. velutina* with five native hornet species to iden-
tify the interspecific hierarchies that influence the rate
of spread of this species. Their results showed that *V. velutina* was superior to *V. simillima* but it was weaker
against other hornets. To test this claim, it is necessary to
map the distribution of *V. simillima* before and after the
invasion of *V. velutina* throughout South Korea. Choi
et al. (2012) reported that *V. velutina* had a significant
expansion in Korea between 2003 and 2015. Species
distribution models (SDMs) are among the tools that can
help us to investigate the competitive effects caused by
the invasion of *V. velutina* on *V. simillima*. In this method,
according to the correlation between the climatic vari-
ables and their presence points, we can determine the
areas that are potentially suitable for species of interest
(Rahimi *et al.*, 2021).

Recently, there was a study to develop SDMs to deter-
mine high-risk areas according to the presence of hornet
species in the world Kim *et al.* (2021). In this study, they
attempted to determine the geographic ranges of *V. velu-
ina* at a global scale. In their study, the most suitable
areas for *V. velutina* in Korea were the southern areas.
According to the above background, the main objective
of this study is 1- to determine the geographic range of
V. simillima before and after the invasion of *V. velutina*
in South Korea. For this purpose, by using occurrence
points of *V. simillima* in different years, distribution maps
of this species are prepared at the country level, and by

comparing these maps, distribution changes due to the
introduction of *V. velutina* are determined.

METHODS

To prepare species distribution maps using species
distribution models, we need two general types of data,
presence data and predictive data (Zurell *et al.*, 2020). To
determine the geographic range of *V. simillima*, we used
presence data (300 points) (Fig. 1) of this species between
the years 1999 and 2022 freely available at www.gbif.
org. We divided occurrence data into two groups before
and after 2011. The number of these points was 150 for
the year 1999−2011 and 150 for the year 2012−2022.

Bioclimatic variables were also used as predictors
of distribution. These data were downloaded from the
WorldClim database (www.worldclim.org). To reduce
Multicollinearity among climatic variables, we removed
variables that correlated higher than 0.8 (Rahimi *et al.*,
2021). Finally, in this study, layers such as Bio 3, Bio 7,
Bio 8, Bio 12, and Bio 17 were used in the modeling
process. In the present study, we used the SDM package
(Naimi *et al.*, 2016) in R software to model the distribu-
tion of the studied species. For this purpose, we used the
MaxEnt algorithm to prepare habitat suitability maps
based on the presence and climate data. We used 10 runs
of subsampling replications to evaluate the model and
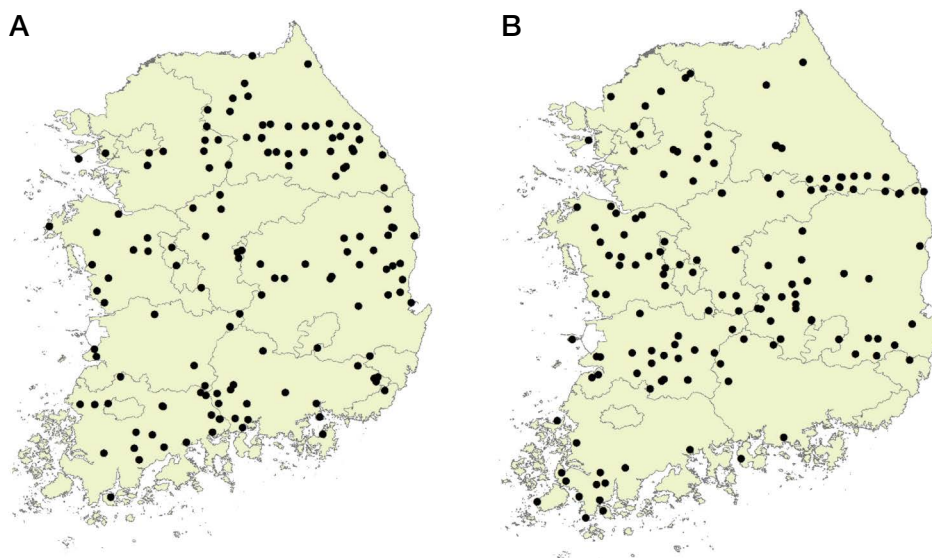
Fig. 1. Occurrence data of *V. simillima* during 1999−2011 (A) and 2012−2022 (B).

considered 70% of the presence data as training data and the remaining 30% as a test. Also, to evaluate the effectiveness of the results obtained from the MaxEnt model, we used two statistics of True skill statistic (TSS) and the area under the ROC curve (AUC). The value range of habitat suitability maps is between 0 and 1, where the number 1 represents the maximum suitability. To estimate the changes in the distribution maps, we divided the maps into three classes with low (0−0.3), moderate (0.3−0.6) and high suitability (>0.6).

RESULTS

1. Model assessment

The TSS and AUC values for *V. simillima* indicated the developed models in this study were reliable (Table 1). The AUC values between 0.7 and 0.9 indicate acceptable results and values greater than 0.9 mean excellent prediction (Valavi *et al*., 2020). TSS values are between −1 and +1, where 1 indicates complete and correct prediction, while values between 0.4 and 0.6 indicate moderate prediction.

2. Variable importance

For the period 1999−2011, precipitation seasonality is the most important variable in determining the geographical distribution of *V. simillima*, and precipitation of driest month has the least effect on the distribution of this species (Table 2). However, for the period 2012−2022, precipitation of driest month is the most important variable that determines the distribution of this species, and precipitation of warmest quarter has the least effect on predicting the distribution of *V. simillima* (Table 2).

3. Geographic distribution

The distribution of *V. simillima* between 1999 and 2011 is more limited to the eastern and southern parts of

Table 1. Model validation metrics including TSS and AUC for *V.simillima*

	AUC	TSS
1999−2011	0.73	0.44
2012−2022	0.79	0.46

South Korea (Fig. 1). However, between the years 2012 and 2022, the distribution of this species has expanded towards the central and western parts (Fig. 2).

4. Change detection

Each of these classes in the period of 1999−2011 has almost the same area as in the period of 2012−2022. The overlap column also shows the degree of overlap of each of these classes with each other (Table 3). The overlap between the class with high suitability between 2012−2022 with its previous period is only 24% (Table 3). This result shows that in recent years, the suitable areas for *V. simillima* have had a significant shift to the central and western regions of South Korea (Fig. 2).

DISCUSSION

Our results showed that between the years 2012 and 2022, the geographical range of *V. simillima* has significant change compared to the previous years. The difference in the geographical distribution of this species in the present study can be related to two main reasons: (1) the presence of the competing species, i.e. *V. velutina*, and (2) the uncertainty associated with the presence of data obtained from the GBIF database. This study showed

Table 2. Importance of different climatic variables used in the models

Variable importance	1999−2011	2012−2022
Bio2 (Mean diurnal range)	18.6%	8.5%
Bio3 (Isothermality)	16.2%	2.8%
Bio5 (Max temperature of warmest month)	17.1%	11.9%
Bio12 (Annual precipitation)	2.8%	2.3%
Bio14 (Precipitation of driest month)	0.9%	20.1%
Bio15 (Precipitation seasonality)	34.5%	4.1%
Bio18 (Precipitation of warmest quarter)	1%	0.2%

Table 3. Changes of suitable habitats (Ha) by the suitability classes during 1999−2000 and 2012−2022, and their overlapping percentage (%) of *V. simillima* in Korea

Class	1999−2011	2012−2022	Overlap (%)
Low	3712.2	3501.2	50.86
Moderate	4534.4	4881	51.11
High	2339.1	2203.5	24.61
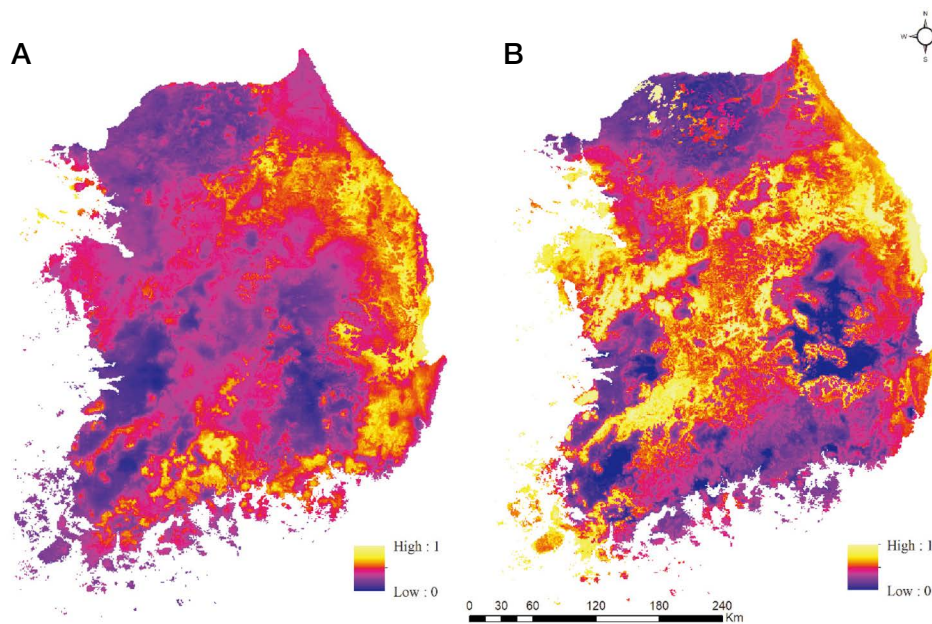
Fig. 2. Habitat suitability maps of *V. simillima* during 1999−2011 (A) and 2012−2022 (B). Light colors show high suitability (values close to 1), and dark colors (values close to 0) show low suitability. Therefore, in values close to 1, we have a higher probability and expectation for the presence of *V. simillima*.

that *V. simillima* distribution has completely disappeared from the southern parts and this species has shifted to higher latitudes. This phenomenon could be explained by the increase of the habitat of *V. velutina*. Choi *et al*. (2012) found that this species occupies most of the southern parts of South Korea. Kim *et al*. (2021) also showed that the most suitable areas for *V. velutina* are the southern parts of South Korea. Another hypothesis is that the populations of *V. velutina* as an invasive species could decrease due to competition with native hornets or the development of defensive mechanisms in European honey bees. Although testing this hypothesis is beyond the scope of this study, the findings of other studies further confirm the hypothesis of the expansion of the population of *V. velutina* and the decrease of the population of competing species in South Korea (Choi *et al*., 2012). In addition, the development of defensive mechanisms in the European honey bee as a non-native species is likely to be less efficient than in native honeybee (*A. cerena*) (Kwon and Choi, 2020; Cappa *et al*., 2021).

Southern parts of Korea (Busan) have a subtropical climate, while the rest of South Korea has a hot and humid continental climate (Peel *et al*., 2007), meaning that the subtropical climate can be the favorite climate for *V. velutina*. Other studies have also shown that climate is an important factor in determining the geographical distribution of this species (Bessa *et al*., 2016). In Europe, the spread of this non-native species is expanding, which means that it has a high ability to occupy the niches of competing species. For example, Keeling *et al*. (2017) claimed that, without control, *V. velutina* could occupy the British mainland rapidly, depending on how the hornet responds to the colder climate in Britain compared to France. Therefore, the difference in the geographical distribution of *V. simillima* in the present study may be related to the role and presence of *V. velutina*. However, to further investigate this hypothesis, more studies are needed in this field. Future studies can compare the relative abundance of *V. simillima* and *V. velutina* species by trapping in the southern parts of Korea. If *V. velutina* has occupied *V. simillima* niches in these areas, we expect *V. simillima* abundance to show a significant decrease in these areas.

CONCLUSION

Using species distribution models, we tried to estimate the geographic range shift of *V. simillima* after the invasion of *V. velutina* in South Korea. These models showed

that the southern regions of Korea that are climatically suitable for *V. velutina*, have been unsuitable for *V. simillima* between 2012 and 2022. This result was obtained using the GBIF database. These data are valid and hundreds of scientific studies have been published based on this database. However, the southern regions of South Korea might not be sampled enough after 2012, and therefore, fewer occurrences of *V. simillima* were recorded in these areas. On the other hand, other studies claim that *V. velutina* is known as an important competitor for *V. simillima* and can occupy the niches of this species. Our study also confirms these findings and shows that it is possible that in the southern parts of South Korea *V. simillima* population has decreased due to the presence of *V. velutina*.

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