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Amitraz resistance in French Varroa destructor populations: geographic distribution, association with N87S, and changes in resistance phenotype after amitraz withdrawal

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Abstract

Varroa destructor remains a major threat to honey bee health, and amitraz is widely used for its control in France. However, increasing treatment failures suggest emerging resistance. This study investigated the spatiotemporal distribution of phenotypic amitraz resistance in French *V. destructor* populations, its association with candidate resistance mutations, and its dynamics following amitraz withdrawal in a longitudinally monitored experimental apiary. Phenotypic resistance was assessed using an *in vitro* bioassay based on corrected mortality at Lethal Concentration 90. From 2018 to 2025, 184 apiaries across France were classified as susceptible, moderately resistant, or strongly resistant. TaqMan assays targeting mutations (N87, Y215, F290) in the β-adrenergic-like octopamine receptor were applied to selected populations (2019–2023). Resistance dynamics were also monitored in the experimental apiary subjected to amitraz treatments (2018–2022) followed by alternative treatments (2023–2025). Susceptible populations predominated in early years, whereas resistant populations became increasingly frequent over time. Among the targeted mutations, only N87S was detected, with frequencies rising across resistance classes (0.03, 0.21, and 0.39 in susceptible, moderately resistant, and strongly resistant populations, respectively). In the experimental apiary, resistance increased under repeated amitraz use and partially declined after withdrawal, without returning to full susceptibility. Overall, these results highlight the widespread nature of amitraz resistance in French *Varroa destructor* populations and suggest that its dynamics could partly reversible following changes in treatment pressure.

INTRODUCTION

Varroa destructor (Anderson & Trueman, 2000) (Mesostigmata: Varroidae) is widely recognized as the most damaging ectoparasite of managed *Apis mellifera (Linnaeus, 1758)* (Hymenoptera: Apidae) colonies and remains one of the major drivers of colony weakening and loss worldwide (Boecking & Genersch, 2008). Following its host shift from *Apis cerana* (*Fabricius, 1793*) (Hymenoptera: Apidae) to *A. mellifera*, this mite spread globally and became a central constraint for modern apiculture (Nazzi & Le Conte, 2016; Oudemans, 1904).

Varroa infestation, or varroosis, reduces colony survival, especially overwinter, and impairs honey production (Emsen et al., 2014). At the individual level, the mite disrupts development and causes morphological and physiological alterations in both brood and adults and it is also vector of viruses (Beaurepaire et al., 2019; Bowen-Walker & Gunn, 2001; Chen et al., 2004; Mondet et al., 2016). As a result, varroosis is considered the most destructive disease affecting honey bee colonies (Boecking & Genersch, 2008). Because unmanaged infestations compromise colony survival, control of *V. destructor* largely depends on chemical acaricides. Despite the availability of alternative Integrated Pest Management (IPM) methods, chemical treatments remain the primary approach in both professional and hobbyist beekeeping (Jack & Ellis, 2021). A recent study conducted in 30 European countries has highlighted that amitraz is one of the most widely used compounds for *V. destructor* control (Brodschneider et al., 2023). This reliance is concerning given the limited number of available active

substances and the widespread resistance already observed to compounds such as pyrethroids and coumaphos, which restricts long-term control options.

Amitraz, a formamidine acaricide, acts primarily through octopamine and tyramine signaling pathways, with the β-adrenergic-like octopamine receptor (Octβ2R) considered a major target site in *V. destructor* (Guo et al., 2021; Hernández-Rodríguez et al., 2021). As in other arthropod pests, repeated exposure to the same active substance is expected to impose sustained selection pressure and may progressively reduce treatment efficacy (Haubruge & Amichot, 1998). In *V. destructor*, amitraz resistance has therefore become a growing concern in recent years, particularly in contexts where amitraz has remained one of the last widely effective synthetic options. Phenotypic bioassays provide a direct way to assess reduced susceptibility under controlled conditions, whereas molecular approaches can help identify markers associated with resistance and ultimately contributed to the development of faster surveillance strategies (Almecija et al., 2020; Bertola & Mutinelli, 2025; Hernández-Rodríguez et al., 2022).

Recent molecular studies have substantially advanced the understanding of amitraz resistance in *V. destructor*, but they also suggest that the underlying mechanisms are more heterogeneous than initially assumed. In French and U.S. populations, amino acid substitutions N87S and Y215H in Octβ2R were associated with amitraz resistance and treatment failure, respectively (Hernández-Rodríguez et al., 2022; Rinkevich et al., 2023). More recently, a third mutation, F290L, was reported in Spanish populations, further supporting the idea that target-site resistance to amitraz may evolve through distinct substitutions in different geographic backgrounds (Hernández-Rodríguez et al., 2025). Evidence from French and U.S. populations indicates that amitraz resistance is associated with Octβ2R substitutions, N87S and Y215H respectively, which are linked to reduced treatment success (Hernández-Rodríguez et al., 2022; Rinkevich et al., 2023). More recently, additional mutations such as F290L in Spain (Hernández-Rodríguez et al., 2025), T115N in South Korea (Lee et al., 2025) and Y337F in Turkey (Inak et al., 2024) have been reported, further highlighting the diversification and ongoing evolution of resistance mechanisms. In parallel, recent work has emphasized that amitraz resistance in French populations may not always be fully explained by a single nucleotide change alone, suggesting that additional genetic or physiological factors may contribute to the resistant phenotype (Marsky et al., 2024). Taken together, these studies indicate that molecular diagnostics are highly promising, but that genotype–phenotype relationships still need to be documented more carefully at population level and across epidemiological contexts.

This need is reinforced by recent syntheses of the literature. A systematic review published in 2025 highlighted substantial heterogeneity among amitraz-resistance studies, including differences in bioassay protocols, mite origin, and environmental conditions, and concluded that robust surveillance should combine field efficacy, laboratory phenotyping, and molecular diagnostics rather than relying on a single approach (Bertola & Mutinelli, 2025). Likewise, resistance-management analyses have underlined that the peculiar life history of *V. destructor* complicates the direct transposition of classical insecticide-resistance management strategies to this parasite. In particular, there is still little published evidence that treatment rotation alone is sufficient to reduce resistance, and data on resistance-associated fitness

costs remain scarce (Lester, 2023). As a result, the dynamics of amitraz resistance after treatment withdrawal remain poorly documented under field conditions, despite their obvious practical relevance.

In France, previous phenotypic work has already shown reduced susceptibility to amitraz in some *V. destructor* populations, indicating that resistance has emerged and requires continued surveillance (Almecija et al., 2020). However, several key questions remain insufficiently resolved. First, the current spatiotemporal distribution of phenotypic resistance across French apiaries is still incompletely documented. Second, the relationship between French resistance phenotypes and candidate molecular markers remains only partially characterized. Third, little is known about how resistance levels may change after discontinuation of amitraz under real beekeeping conditions. These gaps are directly relevant to resistance monitoring and to the design of more sustainable control strategies.

The present study was therefore designed to investigate amitraz resistance in French *V. destructor* populations at both national and local scales. Specifically, we aimed to document the spatiotemporal distribution of phenotypic resistance in field populations collected through a surveillance network, to assess its association with candidate mutations in the octopamine receptor, and to describe changes in resistance phenotype in a longitudinally monitored experimental apiary after amitraz withdrawal.

MATERIALS AND METHODS

Varroa mite sampling

Varroa mites were collected from 2018 to 2025 from 184 apiaries distributed across multiple regions of France (Table 1) through a field surveillance network involving beekeeping associations, veterinarians, and professional beekeepers (see ESM 1). Apiaries were sampled according to field monitoring needs and requests related to varroa control; consequently, sampling did not follow a formal probabilistic design and should be considered surveillance-based rather than nationally representative.

Table 1

Annual number of French apiaries sampled for Varroa destructor collection between 2018 and 2025. Samples were obtained through a national surveillance network involving beekeeping associations, veterinarians, and professional beekeepers.

Year	Number of French apiaries tested
2018	n = 9
2019	n = 24
2020	n = 36
2022	n = 21
2023	n = 31
2024	n = 26
2025	n = 37
Total	**n = 184**

For each apiary, brood fragments (15 × 15 cm) exhibiting high infestation levels (> 5% mites in the dispersal phase) were sampled from one to three colonies within the same apiary. The collected brood was transported *via* express mail to the laboratory and maintained under controlled conditions (relative humidity: 70 ± 5%; temperature: 30 ± 1°C)(Almecija et al., 2020). Phenotypic assays were performed within 1 to 3 days following sample reception.

In the laboratory, mites were removed from the brood frames collected from the different colonies of a given apiary and pooled to constitute a single apiary-level population (Almecija et al., 2020). All phenotypic bioassays were therefore performed at the apiary level, and the apiary was considered the unit of analysis throughout the study.

An experimental apiary in Lagord (France), was monitored by the APINOV research center over an eight-year period. Colonies were maintained at a single site in Lagord (France), and the same colonies were followed throughout the study period. From 2018 to 2022, colonies received an annual amitraz-based treatment (APIVAR®) applied for ten weeks starting in July, in accordance with the Summary of Product Characteristics (SPC). A complementary winter treatment with oxalic acid was administered under broodless conditions (December) to reduce Varroa infestation levels. From 2023 to 2025, the treatment protocol was modified: colonies were treated annually with thymol-based treatment (APIGUARD®) for four weeks in July, again following the SPC, with the same winter oxalic acid treatment applied under broodless conditions.

In Lagord apiary, resistance bioassays were conducted prior to the summer treatment period (July) on three to four colonies exhibiting high infestation levels. One to three phenotypic assays were performed

per year (at different periods), depending on sample availability and technical feasibility. Missing years in the longitudinal dataset were due to internal technical constraints and do not correspond to a planned interruption of the monitoring design.

Evaluation of mite resistance to amitraz in vitro

An amitraz resistance analysis was carried out using an *in vitro* phenotypic test as described by Almecija et al. (2020). Mites were removed from the brood in the laboratory, and only adult females were retained for the assay. One mL of amitraz solution (Sigma Aldrich, St Louis, MO, USA; 0.4 µg/mL in hexane) was added to Petri dishes. According to Almecija et al. (2020), this concentration corresponds to the lethal concentration required to kill 90% of the sensitive mite population in France (LC90). Control dishes were treated with hexane only.

For each apiary-level population, four replicates were performed for the control and four replicates for the LC90 treatment. Fifteen adult female mites were placed in each Petri dish. Petri dishes containing mites were then incubated for 1 h at 30 ± 1°C and 70 ± 5% relative humidity. Subsequently, three pupae were transferred to an uncontaminated Petri dish, and mites were incubated for 24 h at 30 ± 1°C and 70 ± 5% relative humidity.

Twenty-four hours after amitraz exposure, mite mortality (M) was assessed. Following stimulation with forceps, mites were separated into two groups: (1) dead mites, including dead and paralyzed mites, and (2) surviving mites, defined as mites still able to move. Corrected mortality was calculated to account for mortality observed in the control group (Mt). Control mortality reflected the natural mortality of mites due to handling or transportation. Tests were rejected when control mortality exceeded 30%. Corrected mortality was calculated as follows: (M-Mt) / (1-Mt)

After mortality assessment, dead and surviving Varroa mites were separated into Eppendorf tubes for each population and stored dry at − 20°C until molecular analysis.

TaqMan diagnostic assays

A subset of varroa populations sampled between 2019 and 2023 was selected for molecular analysis (see ESM 2). This subset was chosen in order to represent the three phenotypic classes identified by the bioassays, namely susceptible, moderately resistant, and strongly resistant populations.

For detecting amitraz-resistant and susceptible profiles, TaqMan assays described by Hernandez-Rodriguez et al. (2022) and Hernandez-Rodriguez et al. (2025) were performed. Genomic DNA was extracted from individual adult female mites as described by Gonzalez-Cabrera et al. (2013) using an alkaline hydrolysis method. The supernatant containing genomic DNA was recovered and stored at − 20°C until use.

Three TaqMan real-time PCR assays were performed to evaluate the presence of mutations at the N87, Y215, and F290 positions in the Vd_Octβ2R protein. Primers and probes are detailed in Table 2. TaqMan real-time PCR assays were performed as described by Almecija et al. (2022).

Table 2

Primer and probe sequences used in the TaqMan real-time PCR assays targeting three candidate amitraz-resistance mutations in *Varroa destructor*. The table lists the oligonucleotide sequences (5'–3') used to detect mutations at positions N87, Y215, and F290 of the *Vd_Octβ2R* gene. For each target site, the forward and reverse primers, as well as the allele-specific probes designed for the wild-type and mutant alleles, are provided. The corresponding reference publication for each assay is also indicated.

Mutation site	Primers and probe (5'-3')	Reference
N87	Fwd OctR_Vd_N87S_F: CGCCCTGTTCGCGATGA Rev OctR_Vd_N87S_R: ATCCACTTGCCCGAAATGGT Probe Vd_N87S_V (wild type): ACGACGCATTGAATG (YY, MGB-EDQ) Probe Vd_N87S_M (mutant): CGACGCACTGAATG (6FAM, MGB-EDQ)	Hernandez-Rodriguez et al.2022
Y215	Fwd OctR_Vd_Y215H_F: GGATACCGTGCTCAGTAATGCT Rev OctR_Vd_Y215H_R: CTGTCGGGTCGCTTCTAGATAG Probe Vd_Y215H_V (wild type): ATGCGCCAATAAGTGAAT (YY, MGB-EDQ) Probe Vd_Y215H_M (mutant): CGCCAATGAGTG AAT (6FAM, MGB-EDQ)	Hernandez-Rodriguez et al.2022
F290	Fwd OctR_Vd_F290L_F: CAGCCAAAACACTAGGCATAATCAT Rev OctR_Vd_F290L_R: GTTGTCACGTACCACAGAAAGAAC Probe Vd_F290L_V (wild type): CATAGAATGAACGCTCCC (YY, MGB-EDQ) Probe Vd_F290L_M (mutant): TAGAATGAGCGCTCCC (6FAM, MGB-EDQ)	Hernandez-Rodriguez et al. 2025

Statistical analysis

Spatial distribution maps of phenotypic resistance were generated using Tableau software.

For the national phenotypic survey, corrected mortality at LC90 was calculated for each apiary-level population and used to assign populations to one of three phenotypic resistance classes: susceptible, moderately resistant, or strongly resistant. Because the national dataset was derived from surveillance-

based field sampling that varied among years, these data were analysed primarily descriptively to document the geographic distribution of resistance phenotypes.

For the genotyping dataset, the frequency of the homozygous resistant genotype at the N87S locus (RR) was calculated for each analysed population. Because mutant genotypes at positions Y215 and F290 were not detected in the analysed samples, comparative statistical analyses focused on N87S only. Given the distribution of the data and the unbalanced sample sizes among phenotypic classes, non-parametric methods were used. Differences in N87S RR genotype frequency among the three phenotypic resistance classes were evaluated using a Kruskal-Wallis rank-sum test using the *kruskal_test* function from the rstatix package (V0.7.3; Kassambara, 2025). When the overall test was significant, pairwise comparisons were performed using Dunn's post-hoc test with Bonferroni correction using the *dunn_test* function from rstatix.

Genotyping data were visualized using boxplots representing the median, first and third quartiles, and whiskers extending to 1.5 times the interquartile range.

For the Lagord (France) longitudinal dataset, corrected mortality values were analysed descriptively because the monitoring involved a single experimental apiary, included 1 missing year, and was based on a limited number of replicates per year.

All statistical analyses were performed in R (R Core Team, 2024).

RESULTS

Evolution of amitraz-resistance in V. destructor populations in France from 2018 to 2025

To monitor the evolution of amitraz-resistance in *V. destructor* populations across France, phenotypic bioassays have been implemented, measuring the corrected mortality at the LC90, following exposure to the acaricide molecules. Between 2018 and 2025, a total of 184 apiaries were monitored to evaluate resistance to amitraz-based treatments. Results were recorded annually and georeferenced in France to enable spatial analysis of resistance patterns (Fig. 1).

The Fig. 1 illustrates the spatiotemporal evolution of amitraz susceptibility in French *V. destructor* populations. In the earliest sampling years, the monitored apiaries were predominantly classified as susceptible, as indicated by high-corrected mortality at LC90. In subsequent years, apiaries showing lower corrected mortality values, corresponding to moderately resistant and strongly resistant populations, were increasingly detected. These resistant profiles, initially observed in a limited number of locations, were later identified in several regions of France. In the most recent years shown, susceptible and resistant populations co-occurred in different parts of the country, indicating spatial heterogeneity in resistance levels among apiaries. Overall, Fig. 1 indicates a progressive broadening of the geographic distribution of amitraz resistance in France.

Association between resistance phenotypic classes and the frequency of the N87S genotype

Among the three targeted mutations, only N87S was detected in the French *V. destructor* populations sampled between 2019 and 2023. No mutant genotypes were detected at the Y215 or F290 positions in the analysed samples. The Fig. 2 shows that the frequency of the N87S RR genotype increased across phenotypic resistance classes, with the lowest values in susceptible populations, intermediate values in moderately resistant populations, and the highest values in strongly resistant populations. Mean RR genotype frequencies were 0.03, 0.21, and 0.39 in susceptible, moderately resistant, and strongly resistant populations, respectively. Overall, the distributions differed significantly among the three classes (Kruskal-Wallis, $\chi^2(2) = 7.37$, $p = 0.025$; n = 23 populations). Pairwise Dunn tests with Bonferroni correction indicated that sensitive populations were observed to be significantly different from strongly resistant populations (z-value = 2.50, p-adjusted = 0.037). No other differences were statistically significant.

Interannual evolution of amitraz resistance in a monitored Varroa population under annual amitraz treatment followed by amitraz withdrawal

During the period of annual amitraz treatment (2018–2022), the monitored Lagord (France) population showed an overall decline in corrected mortality at LC90, shifting from moderate resistance in 2018 to strong resistance in 2020 and 2022. In 2023, the first year without amitraz treatment, corrected mortality remained in the strong-resistance range and reached its lowest level among the sampled years. In 2024, corrected mortality increased markedly, and the population shifted back to the moderate-resistance range. In 2025, corrected mortality decreased slightly relative to 2024 but remained within the moderate-resistance range and below the susceptibility threshold. No phenotypic data were available for 2019 and 2021.

DISCUSSION

This study provides phenotypic evidence that amitraz resistance of *V. destructor* are now widely detected across several regions in France. At the national scale, the earliest sampling years were dominated by susceptible populations, whereas later surveys more frequently identified moderately and strongly resistant populations in several regions (Almecija et al., 2020; Bertola & Mutinelli, 2025; Hernández-Rodríguez et al., 2022). Rather than indicating a uniform replacement of susceptible populations across France, these results support a progressive geographic expansion of resistant phenotypes together with marked spatial heterogeneity among apiaries. This interpretation is consistent with previous reports of declining amitraz efficacy in France and, more broadly, with the selection pressure generated by repeated use of a single acaricide (Almecija et al., 2020; Brodschneider et al., 2023; Rinkevich et al., 2023).

Among the three targeted mutations screened in this study, only N87S was detected in the French populations analysed between 2019 and 2023. The frequency of the N87S RR genotype increased across phenotypic resistance classes, with the highest values observed in strongly resistant populations. These findings support a potential association between N87S mutation and amitraz resistance in French *V. destructor* populations, in agreement with previous studies identifying mutations in the octopamine receptor as markers of reduced susceptibility to amitraz (Hernández-Rodríguez et al., 2022; Hernández-Rodríguez et al., 2025; Rinkevich et al., 2023). However, the phenotypic pattern was not fully explained by genotype alone, indicating that N87S should presently be considered an associated marker rather than a complete predictor of resistance status. The absence of Y215 and F290 mutant genotypes in the analysed samples further suggests that the molecular basis of amitraz resistance in France may differ from that reported in other countries. In contrast to our findings, the Y215 mutation plays a key role in amitraz resistance in North America, where it is present in nearly 90% of individuals in some populations (Rinkevich et al., 2023). This high prevalence highlights its strong and robust involvement in resistance, whereas for the N87 mutation, additional mechanisms remain to be elucidated. The first evidence of the F290 mutation in Spanish populations (Hernández-Rodríguez et al., 2025), demonstrated its presence and suggested an association with the amitraz treatment. In an interesting finding, a new investigation on the frequency of the F290 mutation in Spain reported a high prevalence (89%) within the sampled populations. However, its occurrence did not appear to be directly associated with the treatment applied, as no significant differences were observed between colonies treated with oxalic acid and those treated with amitraz (Pérez-Pérez et al., 2026). Various hypotheses have been suggested, highlighting the complexity of the mechanisms underlying this resistance, compared with the better-understood mechanisms of pyrethroid resistance.

The longitudinal monitoring performed in Lagord (France) apiary provides further insight into resistance dynamics under changing treatment pressure. During the period of repeated annual amitraz treatment from 2018 to 2022, corrected mortality at LC90 declined overall, and the monitored population shifted from moderate to strong resistance. After amitraz withdrawal and replacement with a non-amitraz treatment from 2023 onward, corrected mortality increased in 2024 and remained higher in 2025 than in 2023, although it did not return to the susceptible range. Taken together, these observations suggest a partial reduction in resistance after removal of amitraz selection pressure, but also indicate that this process is neither immediate nor complete over the time frame studied.

Several non-exclusive mechanisms may account for this delayed and incomplete response. Resistant mites selected during previous years of amitraz exposure may persist for several generations, particularly if resistance is associated with limited fitness costs under field conditions. In addition, immigration of mites from surrounding colonies, local infestation dynamics, or resistance mechanisms not captured by the N87S assay may contribute to the maintenance of reduced susceptibility. The longitudinal monitoring performed in Lagord apiary dataset should therefore be interpreted as preliminary evidence of partial phenotypic reversion after amitraz withdrawal rather than proof of full recovery of susceptibility.

From an applied perspective, these findings highlight the risk of sustained reliance on amitraz as a single control option. Continued annual use of the same active substance is likely to maintain strong selection for resistant phenotypes, whereas diversification of control strategies may help slow further resistance development. In this context, phenotypic monitoring remains essential, and molecular markers such as N87S may provide useful complementary information for surveillance, although they should not be used as a stand-alone proxy for resistance status. Integrated pest management strategies combining rotation of treatment modes of action with non-chemical approaches should therefore be prioritized to preserve the efficacy of available acaricides (Brodschneider et al., 2023; Jack & Ellis, 2021).

This study also has several limitations that should be acknowledged. First, the national survey was based on field sampling that varied among years, so the maps primarily document the geographic expansion of detected resistance rather than exact annual prevalence at the national scale. Second, the genotyping analysis was performed on a limited number of populations and targeted only three candidate mutations. Third, the reversion analysis relied on a single experimental apiary, with missing phenotypic data for some years and a limited number of replicates. Additional longitudinal studies will be required to determine the reproducibility, duration, and magnitude of amitraz-resistance reversion under field conditions.

Declarations

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AUTHOR CONTRIBUTION

Conceptualization : Benjamin Poirot, Véronique Duquesne ; **Methodology** : Benjamin Poirot, Precillia Cochard, Véronique Duquesne ; **Lab analysis** : Alix Constant, Victoria Camilli, Aurélie Del Cont, Amandine Tison, Véronique Duquesne; **Formal analysis and investigation** : Benjamin Poirot, Théa Missud, Jules Pomart, Claire Gay ; **Writing - original draft preparatio**n : Benjamin Poirot ; **Writing - review and editing** : Precillia Cochard, Théa Missud, Jules Pomart, Véronique Duquesne; **Resources** : Robin Azemar, Victoria Camilli.

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Conflict of interest

The authors declare that there is no conflict of interest in this study.

Data availability statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Figures

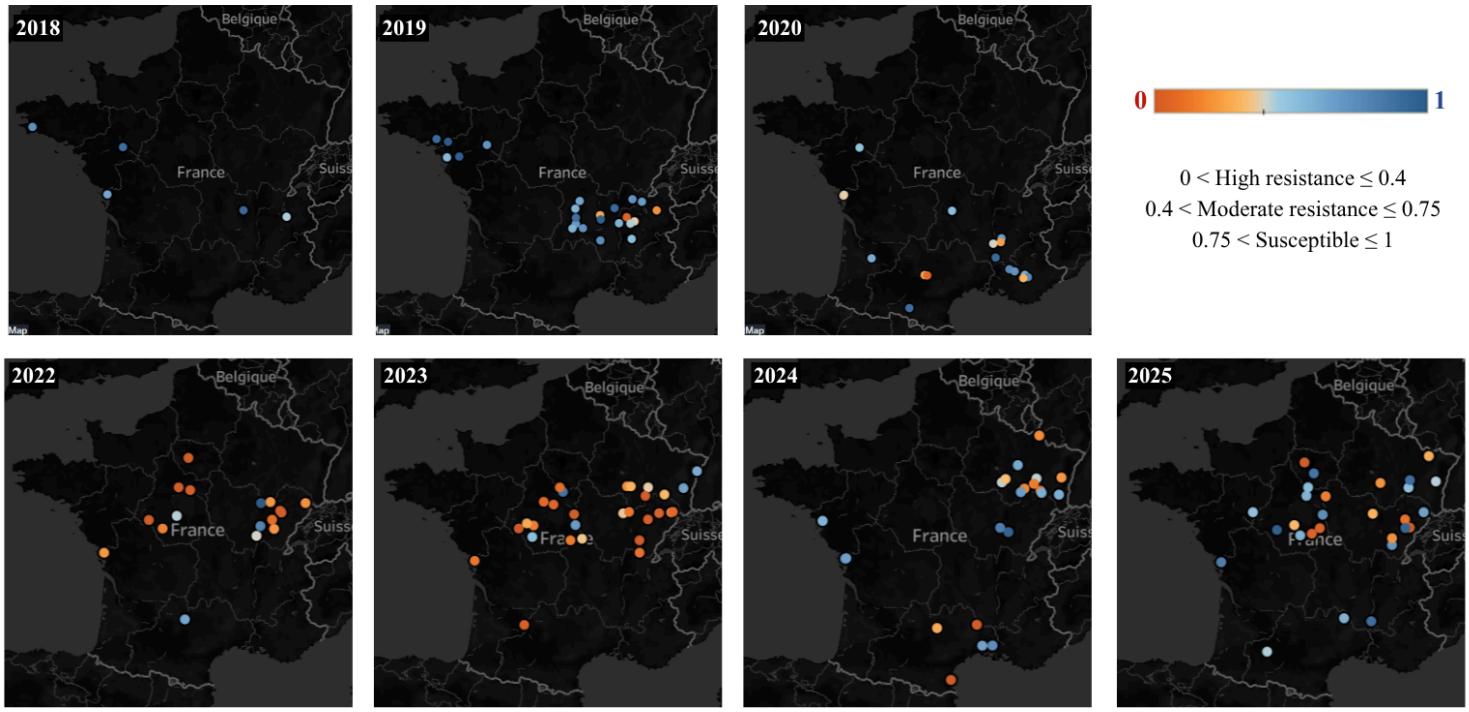

Figure 1

Spatiotemporal distribution of phenotypic amitraz resistance in French *Varroa destructor* populations. The maps represent the geographic location (postcode) of apiaries sampled in France from 2018 to 2025, excluding 2021. Several apiaries may share the same postcode. For each apiary, mites collected from one to three colonies were pooled to constitute a single apiary-level population, which was phenotypically characterized using an in vitro amitraz bioassay at LC90. According to corrected mortality, populations were classified as susceptible, moderately resistant, or strongly resistant. The figure shows the annual geographic distribution of the phenotypic classes detected during the survey period.

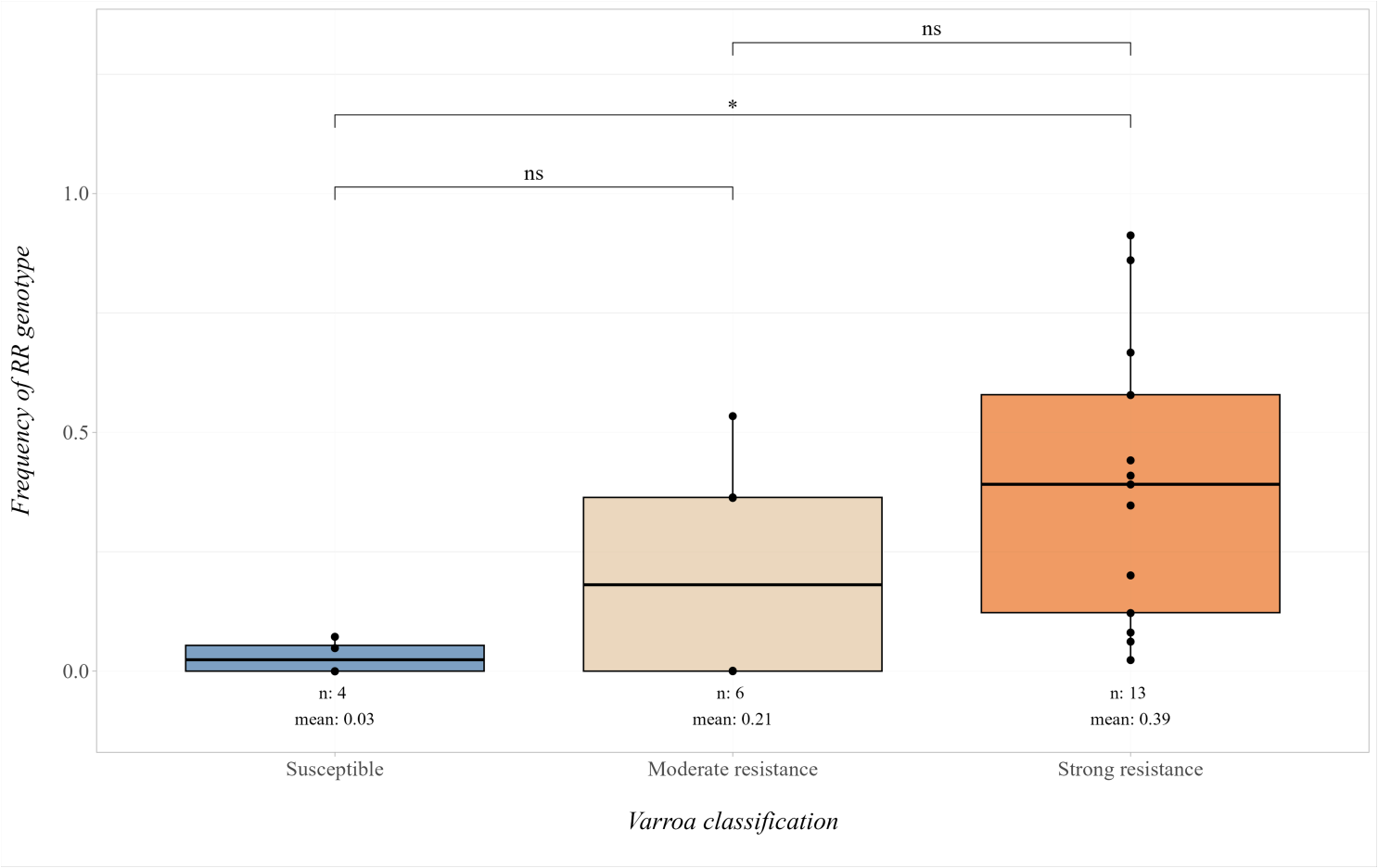

Figure 2

Frequency of the N87S RR genotype in French *Varroa destructor* populations sampled between 2019 and 2023, according to phenotypic resistance class (susceptible, moderate resistance, strong resistance). The boxplots represent the data distribution (median, 1st and 3rd quartiles, and whiskers extended to 1.5 times the inter-quartile range; no outliers or extreme outliers detected). Kruskal-Wallis statistical tests and Dunn post-hoc tests (with Bonferroni correction): if p-value < 0.001 then ***; if 0.001 ≤ p-value < 0.01 then **; if 0.01 ≤ p-value < 0.05 then *; if 0.05 ≤ p-value < 0.1 then '.'; otherwise 'ns'.

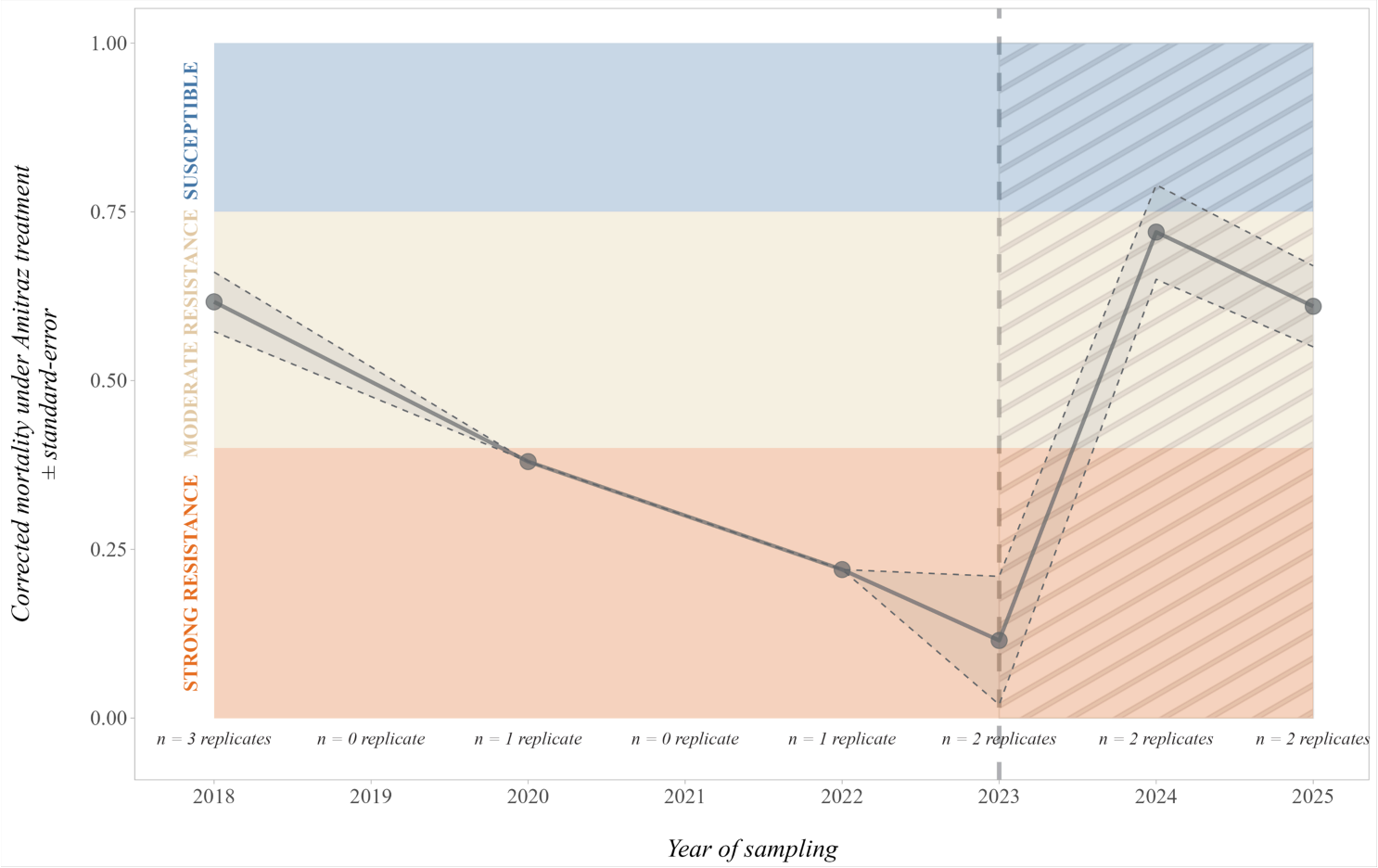

Figure 3

Annual monitoring of the level of amitraz resistance (phenotypic assay at LC90) in the Lagord (France) experimental apiary (2018–2025). Colonies were treated once per year with APIVAR® (10 weeks) from 2018 to 2022, and with APIGUARD® (non-amitraz treatment) from 2023 to 2025.

Supplementary Files

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