

Novel PCR-based genotyping approach allowed to detect spreading of pyrethroid resistance in *Aedes albopictus* across Italy

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INTRODUCTION. The highly invasive mosquito species *Aedes albopictus* has become a major health concern in Italy and other temperate regions due to its capacity to transmit arboviruses such as Dengue and Chikungunya. Pyrethroid insecticides are fundamental tools to counteract autochthonous arbovirus transmission, but extensive use of these compounds to control mosquito nuisance is selecting insecticide resistance in mosquito populations worldwide. Phenotypic signature of resistance to pyrethroids (PyR) has been already highlighted in *Ae. albopictus* populations from the native range and in invasive populations from temperate regions (Italy, Spain and US). Among pyrethroid target-site resistance mechanisms, a mutation in position 1016 (V1016G) of the voltage-sensitive sodium channel has been shown to confer the highest levels of PyR in *Ae. albopictus* populations from Vietnam and Italy.

MATERIALS AND METHODS. We genotyped 516 *Ae. albopictus* specimens collected from 2017 to 2019 in 37 sites in Trentino, Veneto, Emilia Romagna, Toscana, Lazio and Puglia regions by an AS-PCR assay we developed to genotype the V1016G allele and to allow large scale monitoring of the occurrence and spread of this mutation in wild populations.

RESULTS AND CONCLUSIONS. The mutated 1016G allele was detected in almost all examined sites (i.e. 31/37) and in all regions, except Trentino. Highest frequencies (between 20–45%) of 1016G allele were observed in coastal touristic sites of Emilia Romagna and Lazio regions, where pyrethroid treatments are extensively implemented, mostly for mosquito nuisance reduction. The widespread presence of this mutation in Italian *Ae. albopictus* populations should serve as a warning bell, advocating for increased monitoring and management of a phenomenon which risks neutralizing the only weapon today available to counteract (risks of) arbovirus outbreaks.