Molecular identification of *Hyalesthes* and *Reptalus* species (Hemiptera: Cixiidae) allows monitoring of vector species throughout the year

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There is a growing interest in *Hyalesthes* and *Reptalus* species (Hemiptera: Cixiidae) because of their role as vectors of stolbur phytoplasmas (16SrXII-A group). *Hyalesthes obsoletus* (Signoret) is the vector of grapevine bois noir (BN), *Reptalus panzeri* (Löw) transmits stolbur to maize and it is suspected, along with *Reptalus quinquecostatus* (Dufour), to be an alternative vector of BN.

To date, cixiid vectors recognition is based on morphological characters and it is restricted to few specialist entomologists. Furthermore, the main taxonomic characters concern male genitalia, thus hampering the identification of nymphs and adult females. DNA-based approaches can offer valuable support to the traditional taxonomic methods.

PCR and PCR-RFLP assays carried out on the mitochondrial cytochrome oxidase I gene (COI) and on a ribosomal internal transcribed spacer region (ITS2) provided species-specific profiles for four common *Reptalus* species: *R. quinquecostatus*, *R. cuspidatus* (Fieber), *R. panzeri* and *R. melanochaetus* (Fieber). Similarly ITS2 amplicon length and RFLP assays performed after COI amplification allowed the unambiguous identification of three *Hyalesthes* species: *H. obsoletus*, *H. scotti* (Ferrari) and *H. luteipes* (Fieber). Our molecular identification assays have been tested on a large number of samples collected on different host-plants in several European regions.

Both COI and ITS2 sequences proved to be fast and reliable tools for the correct cixiid identification and, making feasible the species identification of females and nymphs, greatly extend the vector monitoring period.