

The *Colomerus vitis* (Eriophyidae) identity crisis: genetic evidence of highly diverged groups not associated with plant symptoms*

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The worldwide grapevine pest, *Colomerus vitis* (Trombidiformes: Eriophyidae), comprises three strains recognised by different plant symptoms: bud, erineum, and leaf curl strains. It has been hypothesised that these may represent different cryptic species, each causing a specific symptom.

We approached this long-standing conundrum by using complementary genetic and morphological methods to investigate the diversity and symptom association of *C. vitis* (Saccaggi *et al.* 2022). COI sequences of *Colomerus* grapevine mites worldwide showed five distinct phylogenetic groups (G1 to G5), with clear separation between groups and low genetic divergence within groups, suggesting the presence of distinct species. Three of these groups (G1, G2 and G3) were found in South Africa, and were further investigated on a site- and symptom-specific scale.

A novel multiplex PCR method was developed to identify mite genetic groups recovered from grapevine tissue. All groups could be found in bud and erineum samples, while only G1 and G2 were amplified from leaf curl samples. The three groups were frequently co-present in the same plant sample (48% of samples with genetic mixtures). G1 was more often associated with erineum and G3 with buds, but not exclusively so, and not at all sites sampled.

We imaged 30 specimens from buds and erineum from a single sample site using cryo-SEM. This technique showed variation in the prodorsal shield pattern (Fig 1), number of empodial rays and microtubercle shape. Prodorsal shield pattern and empodial rays were significantly, but not exclusively, associated with plant niche.

Mites from buds exclusively showed a smooth prodorsal shield and six-rayed empodia in specimens where this could be observed. Mites from erineum were more variable, with 80% showing a strongly patterned prodorsal shield and 70% with five-rayed empodia. Microtubercle shape showed a gradient from sharply pointed through oval to rounded, and could not be linked to either plant niche.

These results suggest that what is currently recognised as *C. vitis* should instead be viewed as a complex of species occurring in the same niches. Considering the non-exclusive association of some genetic and morphological groups with specific plant niches, we tentatively propose two possible ecological scenarios. Firstly, different groups

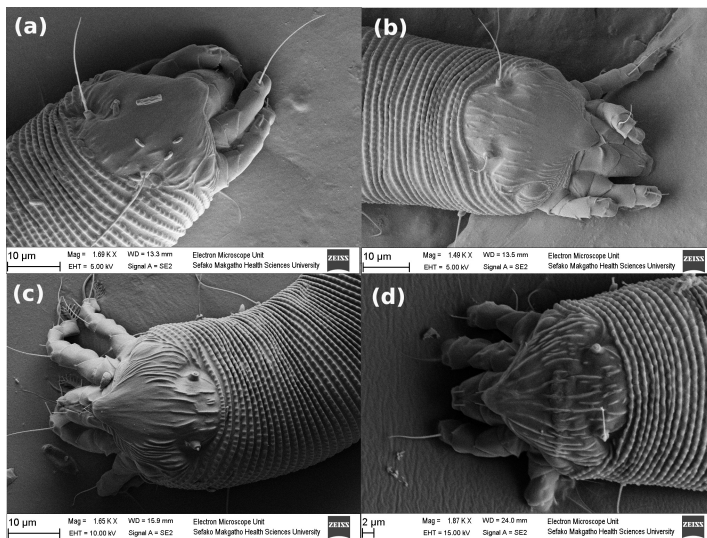


FIGURE 1. (from Fig 6, Saccaggi *et al.* 2022; Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>)): Prodorsal shield ornamentation in *Colomerus* specimens, showing gradation from smooth to strongly patterned.

may be responsible, separately, for bud and erinea symptoms on grapevine (*e.g.* G1 and G3); but these groups are not restricted to the buds or erinea where they cause damage and may often be found as inquiline species in other niches. In this scenario, there may be additional groups which cause the same symptoms or do not cause symptoms at all, but merely occur in that plant niche (*e.g.* G2). Alternatively, all five genetic groups found worldwide are associated with all grapevine symptoms with no causal association between any one group and symptom. Further investigation would be needed to elucidate this relationship.

Reference

Saccaggi, D. L., Maboei, P., Powell, C., Ngubane-Ndhlovu, N.P., Allsopp, E., Wesley-Smith, J. & van Asch, B. (2022) Towards solving the “*Colomerus vitis* conundrum”: Genetic evidence reveals a complex of highly diverged groups with little morphological differentiation. *Diversity*, 14, 1–19.
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