CURRENT TRENDS OF RESEARCH ON FANLEAF, FLECK AND OTHER VIRUSES WITH SPHERICAL PARTICLES

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Reference databases, such as ISI Web of Science or CABI, can easily been accessed through the Internet to search for publications on particular topics on grapevine viruses or related subjects. It is, however, not easy to get a meaningful classified and simple output that would set a trend of research about fanleaf, fleck and other viruses with spherical particles. A manual sorting was therefore still necessary for this compilation. From the ISI and CABI databases, I retained 81 papers on the subject that were published from 2003 to 2005 (1 - 83). I attributed to each of them one ore more topics from the list in figure 1 according to their main content or objectives. The frequency is given by the bars of figure 1.

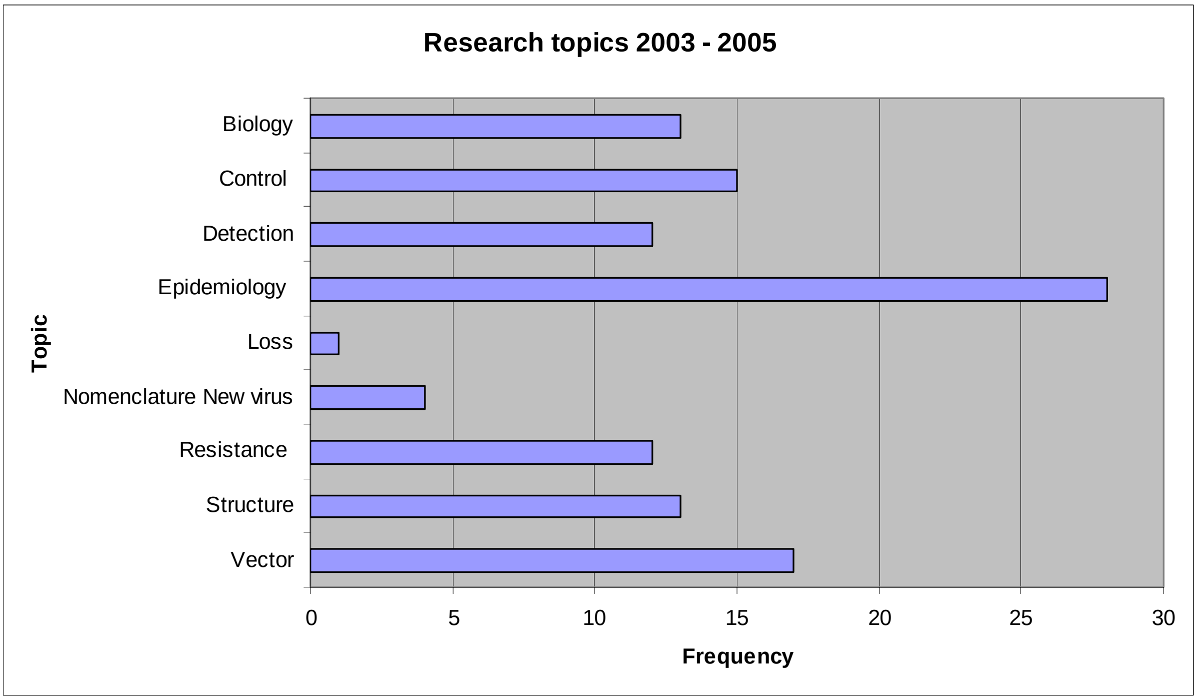

Fig. 1. Research topics on fanleaf, fleck and other viruses with spherical particles cited in the ISI and CABI database from 2003 to 2005.

Papers covering epidemiological aspects, including first observations of known and new viruses, appear to be very trendy whereas new studies on the economical incidences are the less numerous. Reports on grapevine virus vectors are also very frequent, followed by publications focusing on the control of grapevine virus diseases by sanitary selection and vector control. Studies on the molecular structure and organization of viral genes, their evolution and on the biological interactions between viruses and their host and vector are numerous and more accurate thanks to modern technology. The improvement of virus detection methods also remains an important subject. The development of virus resistance by genetic transformation is continued. New viruses are regularly described and appropriate nomenclature is still requested.

Epidemiology
28 out of the 81 references treat epidemiological aspects of grapevine viruses (4, 5, 6, 10, 16, 18, 19, 25, 27, 32, 35, 37, 44, 46, 50, 51, 54, 55, 56, 57, 58, 60, 61, 64, 72, 75, 76, 79). A comprehensive review on *Grapevine fanleaf virus* (GFLV) states the importance of a major nepovirus of grapevine (5). Epidemiology in the field is now efficiently assisted by refined molecular tools. A remarkable study from

France improves the understanding of the population structure and surprising genetic diversity of GFLV and gives herewith a better insight in epidemiological processes (72). The results show first that isolates are made up of populations of genetically related variants and that multiple infection and recombination events (73) are responsible of genetic diversity within and between isolates of GFLV from a single vineyard. Similar results have been obtained in studies made with samples from northern Tunisian vineyards (22). This could contribute to explain the great natural biological variability, i.e. symptom bearing and symptomless vines observed in some heavily infested vineyards. This impedes the probability to find true virus tolerant or resistant vines. On the other hand, the results could also lead to new strategies to control GFLV. Genetic diversity is also revealed by the regular finding of related new nepoviruses such as *Grapevine deformation virus* (GDefV) (16). Newly identified host plants, such as the Bermuda grass (32) bypass older views on the narrow natural host range of GFLV as well as the believed exclusion of graminae species to host nepoviruses.

Vector

17 out of the 81 references deal with vectors of grapevine virus (1, 5, 9, 14, 17, 18, 23, 29, 30, 31, 36, 40, 44, 48, 66, 76, 78). Molecular tools are also of great use in the study of virus vector interactions and vector identification. Thus, elegant mutational analysis allowed to show that the coat protein of GFLV is the sole viral determinant for the specific transmission of this virus by *Xiphinema index* (6, 48). Much hope comes from the isolation of microsatellites from genomic libraries and the development of ribosomal primers for the specific and highly sensitive molecular identification of virus vectors extracted from soil samples (29, 31, 78). One target nematode could be picked up in a sample of over a hundred non-related nematodes. This progress is particularly welcome in a time where traditional taxonomists in nematology are becoming rare. *X. vuittenezi* has been reported for the first time in Australia (76). The association of longidorid nematodes with wild vine *Vitis vinifera spp.sylvestris* has been studied in eastern Austria (66).

Control

15 out of the 81 references have as objective the prevention of grapevine virus diseases (1, 8, 9, 11, 12, 13, 18, 26, 37, 43, 49, 53, 63, 67, 80). Alellopathy and biofumigation find increased interest since the use of nematicides is prohibited in a number of viticultural countries. Nematode-antagonistic plants are evaluated as green manure to control *X. index* (1). Results from greenhouse experiments will however not be transposable to deep field soil conditions. Biofumigation with animal manure appears to be more promising than short fallow periods (1 year) or solarization (9), especially on shallow soils, down to 60 cm where the roots normally develop in the beginning of reestablishment of vines. A combination of biofumigation and fallow is suggested. This fits with results obtained while studying the long term survival, up to 4 years, of viruliferous *X. index* in soil samples in the absence of host plants (18). Indeed, a 2 to 8-fold decrease of the population, regardless of the temperature (7 and 20 ^{o}C), leaves still enough surviving and viruliferous nematodes behind. The incidence of virus infected grapevine stocks in various regions can be improved by applying efficient sanitary selection programs (37, 53). Sole visual selection eliminates only partially infected stock (67).

Structure

13 out of the 81 references focus primarily or secondarily on structural features of grapevine viruses (2, 3, 7, 19, 20, 21, 22, 39, 58, 65, 72, 74, 81). Partial or complete nucleotide sequences have been established for a number of viruses: GDefV and *Grapevine Anatolian ringspot virus* (GARSV) (2, 3, 16, 27), *Grapevine fleck virus* (GFkV) and GFkV-like viruses (2, 65), GFLV (7, 72, 74), a particular isolate of *Arabis mosaic virus* (ArMV) (81) and the cherry isolate of *Raspberry ringspot virus* (RpRSV-ch) from grapevine (20). Frequent sequence variants of GFKV are unraveled (65). Questions of virus taxonomy, epidemiology and biology are addressed. The results also steadily improve virus detection and therefore sanitary selection of healthy grapevine.

Biology

13 out of the 81 references (5, 6, 19, 24, 47, 48, 59, 62, 68, 69, 70, 71, 73) concentrate on virus biology in relation with transmission by specific vectors (6, 48), cellular infection and defense mechanisms (24, 59, 62, 71), experimental conditions (69, 70) and risk assessment of transformed plants (73). One comprehensive review summarizes very well historic and most recent knowledge on GFLV (5). An other review treats virus movement between plant cells, gene silencing and engineered resistance studies with soil-borne viruses such as grapevine nepoviruses (71).

Detection

12 out of the 81 references address virus detection (4, 7, 15, 17, 22, 23, 38, 40, 45, 46, 52, 53). ELISA is often used but developments deal with molecular tests that are set up, evaluated, adapted or further improved. Numerous sequence variants of viral genes are obtained and deposited in gene data banks

(7). Reliable detection of viruses in vectors is particularly useful in epidemiological studies (17,23, 40). GFLV is detected with surprising sensitivity in one viruliferous out of 3000 aviruliferous nematodes (17). Two real-time PCR procedures have been evaluated for the detection of GFLV in the vector *X. index* (23). They do not only allow quantitative studies but also single base sensitive detection. The presence of 2 molecules of RNA-2 in the B-particles must nevertheless be considered in quantitative analysis. Despite of the progress on laboratory tests, there is still interest in improving tests for large scale testing using green-grafting procedure (53).

Resistance

12 out of the 81 references discuss resistance to grapevine viruses, mainly the potential of transgenic resistance (11, 12, 13, 24, 28, 33, 34, 41, 59, 69, 71, 73). Although viral genes have now successfully been inserted into *V. vinifera*, potential resistance still needs to be validated in the field (24, 73). Complex cascades of events are suggested to occur, both locally and distant, within the grapevine plant and cause sequential defense responses after the exposure to methyl jasmonate (59) or simply to biolistic inoculation of GFLV on to grapevine (23).

New virus / Nomenclature

4 out of the 81 references focus on new viruses (2, 3, 16, 27). Increased consideration of the health status of grapevine in some old viticultural regions leads to the discovery of further new viruses or variants, such as some new nepoviruses: GDefV and GARSV (3). The classification is derived from the molecular, biological, physico-chemical, serological and ultrastructural characteristics. Though the novel *Grapevine rupestris vein feathering virus* (2) found in Greece is proposed for a new putative species in the genus *Marafivirus*. The work deepens our understanding of GFkV-like viruses that are omnipresent in grapevine, but symptomatically distinct on *V. rupestris* used as biological indicator.

Loss

Most references mention the economical incidence of virus diseases but little new agronomic evaluation is reported (5).

Conclusion

A wealth of results has been published since the last meeting of ICVG. The selected references indicate a trend of research with direct or indirect epidemiological implications. Molecular technology assists not only very efficiently basic research on GFLV, GFkV and other viruses with spherical particles but also applications, particularly in the field of epidemiology, diagnosis and control of grapevine virus diseases. Sanitary selection remains the only efficient control strategy. New approaches are however urgently needed in premium vineyards that are contaminated with soil-borne viruses.

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