

Distribution and intraspecific variation of Beet yellows virus (BYV) in Switzerland

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INTRODUCTION

Virus yellows (VY) of sugar beets are caused by five distinct viruses: Beet yellows virus (BYV), Beet mild yellowing virus (BMYV), Beet chlorosis virus (BChV), Beet western yellows virus (BWYV) and the Beet mosaic virus (BtMV). Following the ban of neonicotinoid pesticides controlling its aphid vectors in 2019, the reemergence of these viruses has become agronomically and economically important with heavily diseased areas experiencing up to 50% sugar yield losses in 2020.

1. Flight of virus yellows vectors in 2020

The main vectors of VY in sugar beet are *Myzus persicae* and *Aphis fabae*. Flight dynamic of both vectors in Agroscope Changins (VD) was monitored using a suction trap. In comparison to the average of the last 20 years, aphid flights occurred earlier and more massively in 2020, probably due to the mild spring of that year. This is consistent with reports from UK for the same period (Dewar et al. 2021).

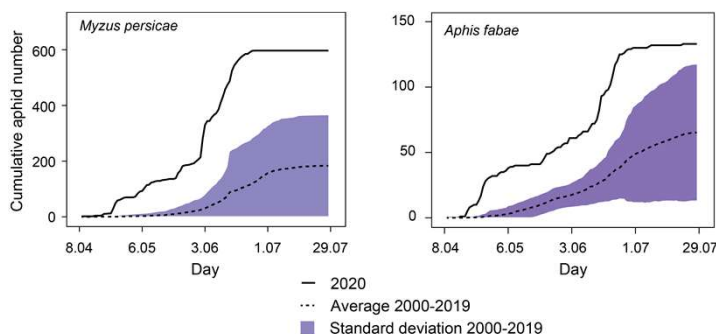


Figure 1. Flights of *M. persicae* and *A. fabae* during the period 2000-2020. Number and identity of aphids were recorded daily from insect caught in the suction trap in Changins (VD).

2. Distribution of yellows viruses in Switzerland in 2020

Sampling was performed across the regions growing sugar beet in Switzerland to get a better overview of the distribution of yellows viruses species. BYV and BChV were the most common species detected, followed by BMYV. In contrast, BtMV and BWYV were not detected. Interestingly, mixed infections (2 or 3 viruses) were present in half of the sites. A similar situation was observed in other European countries (Hossain et al. 2020).

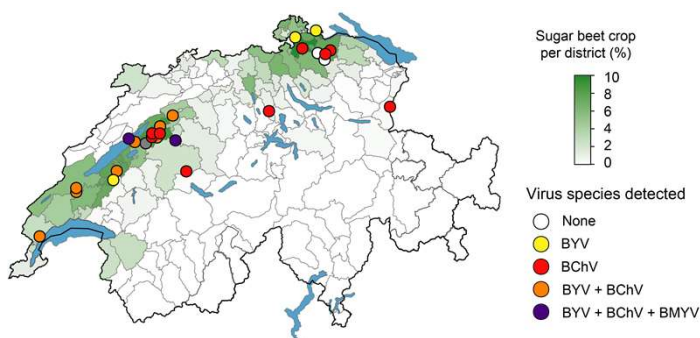


Figure 2. Distribution of yellows virus of sugar beets in Switzerland during the 2020 season. Circles indicate the location of sampling and are colored according to the virus species detected. Swiss districts were colored according to the proportion of sugar beet grown as compared to other crops (source: OFS)

3. Widespread distribution of BYV haplotypes

Based on a short fragment from 50 sites, we found that overall diversity was rather low, with most samples belonging to 3 haplotypes. In addition, our data indicate that haplotype identity is not linked to the geographical origin of the sample.

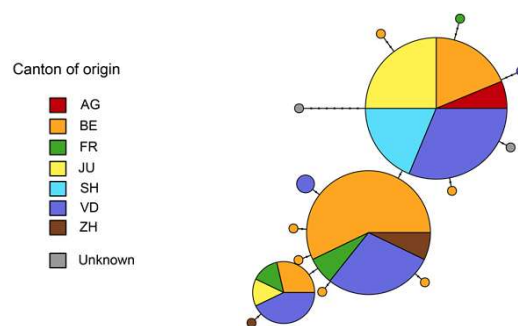


Figure 3. Haplotype network of BYV populations. A ~600bp fragment from BYV was sequenced in 50 random sites. The number of sequences belonging to a given haplotype is shown. Circle size indicate the number of sequences belonging to a given haplotype. Colors show the Canton of origin of the different sequences. The number of mutations separating two haplotypes is displayed as ticks on the connecting lines.

4. Intraspecific diversity of Swiss BYV isolates

In order to get a better view of the diversity of BYV genomes, we generated full-length sequences of 5 swiss isolates. We found that overall diversity (Fig. 1B) and the amount of non-synonymous variants (Fig. 1C) were low in these isolates. Interestingly, the relative amount of non-synonymous variants were highest in p6 and p20 two genes involved in cell to cell and systemic transport, and in p21, which is described as an RNA silencing suppressor. This suggests that non-housekeeping genes may be subjected to diversifying selection in swiss isolates.

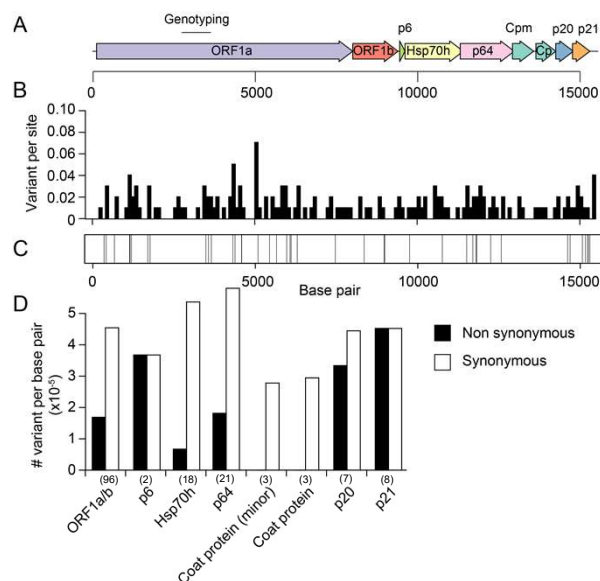


Figure 4. Analysis of diversity in 5 BYV genomes from Switzerland. A. BYV genome organization. The fragment used for the analysis in Fig. 3 is shown. B. Sliding window analysis of the number of variant per site across the BYV genomes. Window and step size are 100bp. C. Location of non-synonymous mutations in the BYV genomes. Each line represents a single variant. D. Number of synonymous and non-synonymous mutations in BYV genomes in individual viral genes. To allow for comparison between genes, the number of variants was normalized to gene size. The number below the bars indicate the total number of variants in each gene.

Conclusions and perspectives

- Vector pressure was record-breaking in 2020
- Presence of three main haplotypes with ubiquitous distribution in the sampled area
- Most variation within swiss BYV isolates occur in non-housekeeping genes
- Future work is needed to identify the role of this variation during infection

References

Dewar A, Qi A. (2021) The Virus Yellows Epidemic in Sugar Beet in the UK in 2020 and the Adverse Effect of the EU Ban on Neonicotinoids on Sugar Beet Production. *Outlooks on Pest Management* 32-2, 53-59

Hossain, R, Menzel, W, Lachmann, C, Varrelmann, M. (2021) New insights into virus yellows distribution in Europe and effects of beet yellows virus, beet mild yellowing virus, and beet chlorosis virus on sugar beet yield following field inoculation. *Plant Pathol.* 2021; 70: 584–593.