Objectives and Rationale

A previous research project (A-15-USP-PM20) suggested that conidia, in addition to ascospores, of the apple scab (fusi) pathogen, *Venturia inaequalis*, may be an important source of primary inoculum during dry and warm autumns. RIMpro is a disease forecasting model that can assist in the management of fusi if predictions are accurate. The objectives of the study are to (i) use a population genetics approach to investigate the role of conidia as primary inoculum source, (ii) develop a pre-bud break ascospore assessment method and (iii) evaluate RIMpro.

Methods

Fusi lesions were collected from trap- and orchard trees in two seasons for a population genetic study using published simple sequence repeat (SSR) markers.
Pre-bud break evaluation of ascospore production was conducted by overwintering fusi leaves in orchards in 2019 and 2020. At set times during late winter, leaves were moved to the laboratory to accelerate ascospore formation and maturation.
RIMpro was evaluated in two seasons using spore samplers and trap trees. Fusi leaves were overwintered in autumn to determine the biofix.

Key Results

Population genetic analysis of trap tree lesions suggested that all populations were ascospore derived, whereas conidia served as an additional primary inoculum source in only one orchard. Orchard populations have not been genotyped.
Pre-bud break analysis in the 2019/20 season was unsuccessful including the positive control. In the 2018/19 season, in the Grabouw region, RIMpro was accurate based on spore trap data, but trap tree data showed the contrary. In the Koue Bokkeveld data could not be collected successfully. In the 2019/20 season spore sampler and trap tree data supported the accuracy of RIMpro. The biofix could not be determined in both seasons.

Conclusion and Discussion

Techniques have been optimized for evaluating RIMpro, but not pre-bud break analysis. Evaluating RIMpro in the 2020/21 season will be useful to assess the accuracy of RIMpro.