Genomic Tools to Enable Epidemiological Monitoring of Eukaryotic Pests

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Original thinking... applied

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BACKGROUND AND RATIONALE

- Epidemiological comparative genomic techniques are more difficult to deploy on the larger more complex genomes of eukaryotic organisms
- Larger scale single nucleotide polymorphism (SNP) typing on Next Generation Sequencing (NGS) platforms have the potential to improve the discriminatory power when differentiating between individuals (Andrews 2018)
- *Vespa velutina* (Asian hornet) and *Meloidogyne fallax* (false Columbia root knot nematode) are pest species that are of particular interest in the world of plant health
- Asian hornets are non-native pest species to the UK and consume native pollinators such as honeybees. There have been 23 confirmed sightings since 2016 (Jones 2020)
- *M. fallax* cause external galling and internal necrosis on crops such as potatoes, carrots and leaks affecting the yield, marketability, and quality of the crops (DEFRA 2021)

Fig 1. *Vespa velutina* (Asian Hornet). Copyright Fera Science Ltd. 2017

Fig 2. *Vespa velutina* (Asian Hornet) with 1cm size indicator included. Copyright Fera Science Ltd. 2016

AIMS AND OBJECTIVES

The main aim of the project is to develop genotyping panels for *Meloidogyne fallax* and *Vespa velutina* that can be used on outbreaks and incursions:

- Identification of highly informative single nucleotide polymorphism (SNP) panels in both study species
- Design primers to optimise highly multiplex PCR as part of genotyping in thousands sequencing (GT-seq) assays
- How rapidly can a generalisable GT-seq assay workflow be applied to other species

Fig 3. *Meloidogyne fallax* outbreak on organic leak crops. Top leak is a healthy crop and bottom two leaks have been infested with *M. fallax*. Copyright Fera Science Ltd. 2013

METHODOLOGY

- Comparison of sequencing technologies for suitability for the project., e.g., Oxford Nanopore, PacBio and Illumina. Genome assembly and analysis of various resequencing data samples of *Meloidogyne fallax* and *Vespa velutina*.
- Identification of single nucleotide polymorphism (SNP) panels to establish relatedness and origins of outbreaks and incursions
- Design primers to optimise highly multiplex PCR as a part of the GT-seq assay and apply assay to samples of *V. velutina* and *M. fallax*
- Extract DNA and sequence any samples from new outbreaks or incursions
- Apply the GT-seq assay methodology to any other pest species of interest to plant health to assess the generalisability of the technique, e.g., *Meloidogyne chitwoodi* (close relative of *M. fallax*)

Fig 4. *Meloidogyne fallax*. Photograph taken from AFBI and Queens University Belfast, Northern Ireland 2017 (Hainon-McDowell 2017)

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Figure 2. Meloidogyne fallax. Photograph taken from AFBI and Queens University Belfast, Northern Ireland 2017 (Hainon McDowell, 2017)

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Aims and **Objectives**

The main aim of the project is to develop genotyping panels for *Meloidogyne fallax* and *Vespa velutina* that can be used on outbreaks and incursions:

- ✓ Identification of highly informative single nucleotide polymorphism (SNP) panels in both study species
- ✓ Design primers to optimise highly multiplex PCR as part of genotyping in thousands sequencing (GT-seq) assays
- ✓ How rapidly can a generalisable GT-seq assay workflow be applied to other species

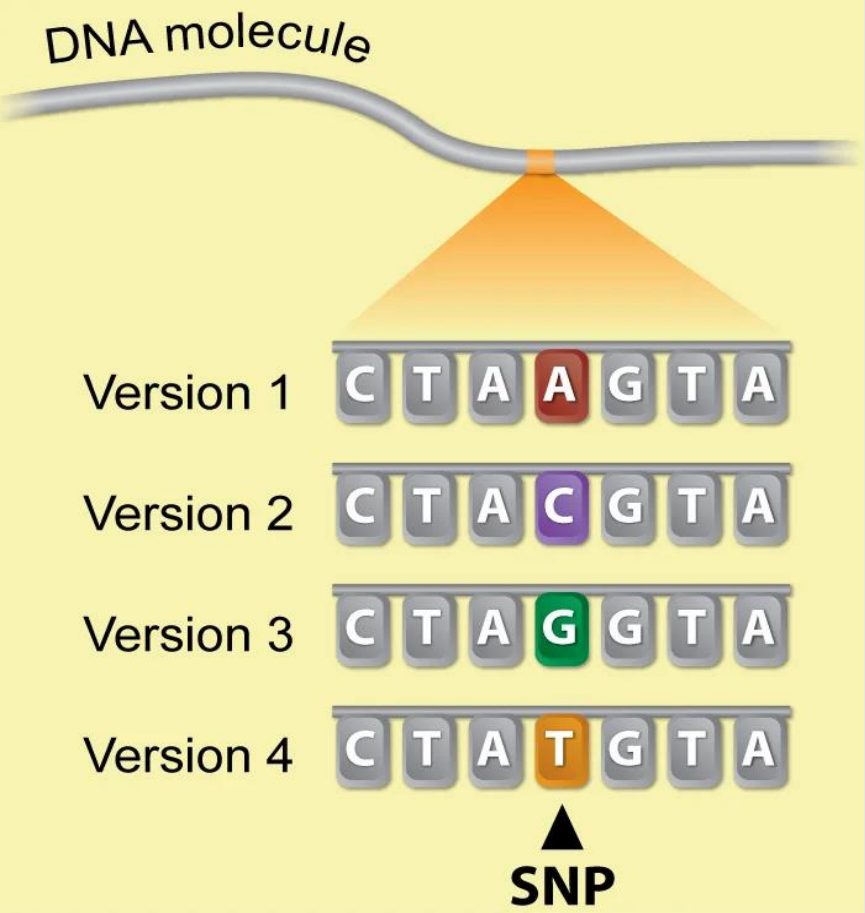

Figure 4. A schematic representation of single nucleotide polymorphisms (SNPs) (University of Utah, 2023)

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References

- Andrews, K. R., Adams, Jennifer R., Cassirer, E. Frances., Plowright, Raina K., Gardner, Colby., Dwire, Maggie., Hohenlohe, Paul A., Waits, Lisette P. (2018). “A bioinformatic pipeline for identifying informative SNP panels for parentage assignment from RADseq data.” Molecular Ecology Resources 18(6): 1263-1281.
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- University of Utah (2023). Making SNPs Make Sense

Thank You for Listening

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