Portable, In-field, Multispectral Imaging Sensor for Real-time Detection of Insect Viral-Vectors

DOI:

[10.1109/ICSENS.2017.8234206](https://doi.org/10.1109/ICSENS.2017.8234206)

Document Version

Final published version

[Link to publication record in Manchester Research Explorer](#)

Citation for published version (APA):

Grieve, B., Veys, C., Jose, D., Colvin, J., & Nwezeobi, J. (2017). *Portable, In-field, Multispectral Imaging Sensor for Real-time Detection of Insect Viral-Vectors*. 990-992. Paper presented at IEEE Sensors 2017 Conference, Glasgow, United Kingdom. <https://doi.org/10.1109/ICSENS.2017.8234206>

Citing this paper

Please note that where the full-text provided on Manchester Research Explorer is the Author Accepted Manuscript or Proof version this may differ from the final Published version. If citing, it is advised that you check and use the publisher's definitive version.

General rights

Copyright and moral rights for the publications made accessible in the Research Explorer are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

Takedown policy

If you believe that this document breaches copyright please refer to the University of Manchester's Takedown Procedures [<http://man.ac.uk/04Y6Bo>] or contact uml.scholarlycommunications@manchester.ac.uk providing relevant details, so we can investigate your claim.

Portable, In-field, Multispectral Imaging Sensor for Real-time Detection of Insect Viral-Vectors

Bruce Grieve, Charles Veys, Jose Dingle
School of Electrical & Electronic Engineering
The University of Manchester
Oxford Road, Manchester, M13 9PL, UK
bruce.grieve@manchester.ac.uk

John Colvin, Joachim Nwezeobi,
Natural Resources Institute, University of Greenwich
Central Avenue, Chatham Maritime, Kent, ME4 4TB, UK
j.colvin@greenwich.ac.uk

Abstract — The paper introduces a multispectral imaging system and data-processing approach for speciation of the insect viral vectors (whitefly) responsible for the transmission of Mosaic and Brown Streak viruses in Sub-Saharan African cassava. The trial results for four species of whitefly, on two plant leaf types (cassava & aubergine), are reported as well as the methodology applied. This indicates that a correct classification could be achieved in 85-95% of cases. The engineering design for an in-field, handheld, variant of the technology is discussed alongside the learning gained from this initial study.

Keywords — multispectral; MSI; hyperspectral; real-time; imaging; virus; brown streak disease; mosaic virus; insect; whitefly; cassava; *Bemisia tabaci*; begomoviruses;

I. INTRODUCTION

This paper presents a novel technique for autonomously identifying the *species and number* of whitefly (*Bemisia tabaci*) insects on a leaf surface, or similar environment. It has been specifically designed and demonstrated to address the detection of potential virus vectors for Cassava Mosaic Disease (CMD) and Cassava Brown Streak Disease (CBSD) viruses in African cassava (*Manihot esculenta*), however the underlying technical approach may be extended under future study to insect viral vectors for a broad range of crop, livestock and human diseases. This technology will also have applications in whitefly research generally and will, for instance, make the rearing of colonies of pure species for experimentation much less labour-intensive and expensive. As such, it is a technology that is highly appropriate for adoption in Development Assistance Committee (DAC) listed countries.

A. Importance of *B. Tabaci* to Cassava & Global Development

Cassava is a uniquely important food-security crop for one third of the world's low-income, food deficit countries and is the world's third largest source of calories in the human diet [1]. After 15 years of global increases, however, cassava production is predicted to fall due to droughts and diseases. Cassava mosaic begomoviruses and cassava brown streak virus, in particular, destroy an estimated 35 million tonnes of African cassava annually (FAOSTAT, 2010). *B. tabaci*, and the greater than 200 plant-viruses it transmits, have an undeniable impact on the world's food security, directly affecting a broad range of staple crops such as cassava, common bean and sweet potato. In Africa, over 200 million people obtain close to 50% of their daily food intake from cassava.

B. Disease Management Programmes for *B. Tabaci*

Once the viral vectors are identified within a region management programs may be implemented to control the spread of begomoviruses. For example, in the 1990s a CMD pandemic caused widespread famine in East Africa and this was driven by unusually high *B. tabaci* populations which were generated, in part, by a virus-vector-host plant interaction that

increased *B. tabaci* fecundity on CMD infected cassava, thus boosting vector numbers and driving disease spread [2]. The disease was contained through developing and distributing distributing CMV-resistant cassava varieties to farmers and the variety TMS 30572 (Migyeria) was adopted rapidly and more than 11,338 ha were being grown by 1996 [3]. However, in more recent years resistant strains of the virus have resulted in a continued spread of CMD and CBSD across Africa [4] requiring further containment and eradication programs to be instigated.

C. Motivation Behind Sensor Development for In-Field Viral Vector Identification

B. tabaci is not a single species [5], but consists of a group of more than 34 closely-related cryptic species. At present, these can only be identified using molecular markers. Although Africa is the evolutionary origin of *B. tabaci*, its diversity there remains poorly studied and so the number of species will continue to increase as more are identified. Several African *B. tabaci* species feed on cassava and the rapid spread of CMD and CBSD has been associated with high whitefly populations of the species now called, SSA1 and SSA2. As well as *B. tabaci*, other whitefly species such as *B. afer* also colonise cassava and due to their similar size, they can be confused easily with *B. tabaci*.

Current survey and epidemiological research in sub-Saharan Africa focussed on *B. tabaci* borne viruses relies on destructive sampling of the subjects followed by a multi-step molecular sequencing technique, of partial mtCO1 sequences, to identify the whitefly species present. The costs and time taken to undertake the necessary steps for this diagnostic method are often prohibitive, when thousands of individual whitefly need to be typed accurately. The complexity of the analysis also necessitates that it is undertaken within centralised laboratory facilities using comparatively expensive instrumentation, with the corresponding delays in analytical lead times and the requirements for servicing and support infrastructure.

As a consequence, with existing technology, it is not possible to do detailed landscape ecological research in cassava-based agro-ecosystems, because of the magnitude of the species identification problem. The delivery of the real-time, portable and non-destructive sensor system, as introduced within this paper, would enable the spread of insect viral vectors to be mapped in a reliable and timely manner. This may be achieved by exploiting the sensor data alongside the accurate positional and time data as derived from a linked smartphone handset and then using the latter to relay just the relevant extracted information to a central data-base, so minimising bandwidth usage. Furthermore, the approach proposed may be undertaken rapidly by semi-skilled field operatives, as it requires no pre-treatment of the leaf or insect samples. Such a tool offers the potential for virologists and breeders to deliver a

paradigm shift in the eradication of Cassava Mosaic Virus and Brown Streak Disease, through targeted control measures and introduction of new varieties, with the consequent impact on cassava production in Africa and broader implications for deploying variants of the technology-platform for viral disease control elsewhere.

D. Prior Research for Rapid Assessment of Viral Vectors

Previous research has been undertaken to identify the symptoms of CMD and CMBD, on cassava leaves, through visual imaging algorithms that are compatible with the modest processing power within mobile phone handsets [6, 7]. More recently it has been reported that similar approaches have been adapted to count the numbers of *B.tabaci* on the underside of cassava leaves (Mwebaze, E., Makerere University, Kampala, Uganda; unpublished) but, due to the morphological similarity of the species, such techniques have not viable for identifying the potential viral vectors from the visual images of *B.tabaci*. An additional problem in getting accurate population counts of African cassava *B.tabaci* nymphs arises in the field, because they are pale and silvery in colour and so do not stand out against the green leaf background.

Similarly, near to mid-infrared linear models (1.4 to 2.1 μ m wavelength) have been developed for autonomous species identification of the age and / or species in entomology, such as: mosquitos [8]. These models have been developed using single-point conventional laboratory spectrometers, which provide a composite measure of the infrared-active organic functional groups within the beam of the spectrometer, e.g. the C-H, N-H, O-H, C-C or S-H atomic bonds within the molecular groups on the surface of the pests. However, such instrumentation requires comparatively exotic semiconductor materials, tending to be based upon Indium Gallium Arsenide (InGaAs) detectors, as proprietary, low-cost, silicon detectors are limited to a wavelength upper limit of 1,125nm, due to the bandgap of silicon. Semiconductor silicon detectors and sources offer significant opportunities in terms of their costs and availability of sensitive, high spatial-resolution imaging sensor components, by virtue of the digital camera industry.

E. Rationale for Undertaking the Research

As minor pigment variations between the whitefly species have been observed under laboratory conditions the hypothesis was that detection of species differences could be automated using a miniaturised Multispectral Imaging (MSI) systems, combined with morphological and spectral processing of the data. The resulting system could then be exploited in the field to autonomously identify and count, in real-time and non-destructively, known viral-vectors from their non-virus-carrying neighbours.

The ability to use whole image rather than gross single-point spectral measurements also opens up the possibility of greater discrimination accuracy, without the need for skilled preparation of the insect samples. The latter is by virtue of being able to use combined image and spectral feature extraction to automatically extract the insect features from the background, correct for insect orientation and then use parts of the structure of the insect, as opposed to the whole body, to provide specific species identifier markers.

II. EQUIPMENT

An existing prototype MSI instrument (the 'Bravo' unit), which was developed primarily for the commercial arable agricultural industry [9] was adapted for the whitefly duty. This system utilises active, close proximity, MSI based on

proprietary components from the consumer electronics industry. This is based upon narrowband Light Emitting Diodes (LEDs) which are then integrated with modified colour silicon-CMOS imaging detectors, such that their spectral range is extended from the visible (Vis) region (400-700nm wavelengths) out into the near infrared (NIR), up to the bandgap of silicon (wavelengths up to 1125nm). Such an approach offers the potential to deliver cellular / wireless network-connected handheld sensors for in-field use at US\$10-100's as opposed to the non-portable laboratory near to mid-infrared equipment used in the previous entomological speciation work which cost in excess of US\$30,000.

The reported results were collected from a 63 waveband, 380-940nm wavelength, bench-top 'Bravo' MSI unit from the earlier crop related research (Fig. 1a) which was then enhanced by the addition of a macro lens (Fig. 1b), so as to image the relatively small whitefly features (c.1-2mm in length) versus the larger supporting leaf structure. This system also enabled the much smaller nymphs (c.500 μ m) and eggs (c.100 μ m) to be imaged. The latter are extremely challenging to identify by eye within the fibrous texture of cassava leaves even with the aid of a lab microscope.

Fig. 1. [a] External overview of prototype MSI instrument, [b] Internal details of prototype MSI instrument showing LED array and camera with macro lens assembly

The Light Emitting Diodes (LEDs) within the unit were conventional sources providing non-coherent light across wavelength range of 365-940nm at 5-10nm Full Width Half Maximum (FWHM) resolution, in a virtually continuous coverage of the spectra with the exception of the 530-585nm bands. The latter was due to the lack of availability of suitable LEDs at the time. Subsequently this range, as well as that from 940-1050nm, has been included within the prototype unit, but such systems post-date the trials reported within this paper. LED control and image capture was achieved through a proprietary single board computer (Raspberry PI Model 2, Raspberry PI Foundation, UK), interfaced to a bespoke driver card. The approach provided a cost-effective and flexible platform, for initial proof-of-concept studies, prior to developing a more optimised portable dedicated unit for rapid in-field measurements. The spectral output and illumination power of each of the LEDs was characterised using a laboratory spectrometer (Ocean Optic USB4000, Ocean Optics Inc., USA) and the intensity balanced, across the wavelength range, using Pulse Width Modulation of the drive signals. A barium sulphate reference tile was used to calibrate the spectral intensity of the light output from each of the LEDs.

III. METHODS & RESULTS

This first phase of the study comprised of ten whole leaf samples of cassava and aubergine (eggplant), with 30-70

whitefly on each leaf. These had been removed from healthy plants that had previously been exposed to isolated colonies of four species of African *B. tabaci*, reference: SSA1-SG1, SSA2, SSA3 and MED, the first three being CMV insect vectors and the last is not. After removal the leaves were chilled, so as to partially immobilise the insects. This was necessary for these preliminary studies as the 'Bravo' instrument was not optimised for rapid image capture and so required around 2-5 minutes, per leaf, to accumulate the necessary spectral images and then store them to memory.

The raw multispectral image data, as illustrated in Fig. 2a, were processed using the Optimised Soil Adjusted Vegetative Index approach [10] to mask-out the background supporting leaf structure, to provide results as exemplified by Fig. 2b. The MSI data was then further processed to exclude the smaller items (speckles) which were predominantly a consequence of specular reflectance errors.

Fig. 2. (a) 540nm whitefly image, (b) Spectral extraction of whitefly

The resulting multispectral data-set was then auto-scaled (mean centred and each variable scaled to unit standard deviation) and processed using the supervised multivariate classification technique, Partial Least Squares Discriminative Analysis (PLS-DA), by using 20 randomly selected samples of each species of whitefly as the training set. This, and the pre-conditioning of the data, was undertaken using custom code written within the MatLab environment (MatLab R2015a, Mathworks, USA). The resulting classification model is illustrated in Fig. 3, where each point within the clusters corresponds to a classification of an individual whitefly whereas the full set represents the population of the four insect species across separate individual leaves.

Fig. 3. MED species discrimination exemplar

IV. CONCLUSIONS AND DISCUSSION

This initial study indicates that an 85 to 95% correct classification for whitefly species may be achieved for the four species studied, with respect to the others, using just 11 of the available 63 wavebands. The chosen wavelengths were selected

on the basis of their loadings (relative contribution to the model) so as to achieve the highest classification accuracy for the data-set without including additional noise from non-contributing wavebands.

This initial trial was limited to adult whitefly all of a similar age and which had all been cultivated under controlled laboratory conditions with similar diets and environments. A significantly larger study is now underway which incorporates a larger range of insect species all and a variation in diets, so as to address concerns over the effects of the insects environment on their spectral features. As the orientation and exposed surface topology of the insects is highly variable within a leaf sample, during this first study the research team manually selected wing or body structures upon which to base the classification and so reduce potential variability due to inconsistent sampling. Automated extraction of these features and / or other ones that may prove more relevant in the future, i.e. for smaller body parts within the adult whiteflies or for the eggs or nymphs, has since been developed within the custom MatLab code and forms part of a second phase of the trials.

Similarly, the reliance on chilling of the insects to reduce their mobility and potential for reorientation during multispectral imaging has been reduced within the design for the next generation of the 'Bravo' unit. This exploits a dedicated FPGA, based on the Altera Cyclone IV family of processors, and custom electronics for high-speed data processing and interfacing to a large-format (16mm square) full-frame image capture sensors (Sony Pregius IMX250). Additionally significantly higher intensity and homogeneous lighting is achieved using a combination of an optical integrating hemisphere with appropriately located LEDs driven by high power current sources, run at very short duty-cycle to prevent overheating of the sources. The resulting system reduces the capture time for a typical 32 waveband multispectral dataset to less than a second, whilst achieving a resolution of 2048 by 2048 pixels for each wavelength image.

REFERENCES

1. Patil, B.L. and C.M. Fauquet, *Cassava mosaic geminiviruses: actual knowledge and perspectives*. Molecular Plant Pathology, 2009. **10**(5): p. 685-701.
2. Colvin, J., et al., *Host-Plant Viral Infection Effects on Arthropod-Vector Population Growth, Development and Behaviour: Management and Epidemiological Implications*. Advances in virus research, 2006. **67**: p. 419-452.
3. Otim-Nape, G., et al., *The current pandemic of cassava mosaic virus disease in East Africa and its control*. Natural Resources Institute, Chatham, UK, 2000.
4. Legg, J.P. and C.M. Fauquet, *Cassava mosaic geminiviruses in Africa*. Plant molecular biology, 2004. **56**(4): p. 585-599.
5. Maruthi, M., et al., *Reproductive incompatibility and cytochrome oxidase I gene sequence variability amongst host-adapted and geographically separate Bemisia tabaci populations (Hemiptera: Aleyrodidae)*. Systematic Entomology, 2004. **29**(4): p. 560-568.
6. Aduwo, J.R., E. Mwebaze, and J.A. Quinn. *Automated Vision-Based Diagnosis of Cassava Mosaic Disease*. in *Industrial Conference on Data Mining-Workshops*. 2010.
7. Tuhaie, J., J.A. Quinn, and E. Mwebaze, *Pixel Classification Methods for Automatic Symptom Measurement of Cassava Brown Streak Disease*.
8. Mayagaya, V.S., et al., *Non-destructive determination of age and species of Anopheles gambiae sl using near-infrared spectroscopy*. The American journal of tropical medicine and hygiene, 2009. **81**(4): p. 622-630.
9. Grieve, B., et al. *Localized multispectral crop imaging sensors: Engineering & validation of a cost effective plant stress and disease sensor*. in *Sensors Applications Symposium (SAS), 2015 IEEE*. 2015. IEEE.
10. Rondeaux, G., M. Steven, and F. Baret, *Optimization of soil-adjusted vegetation indices*. Remote sensing of environment, 1996. **55**(2): p. 95-107.