Scientia Africana, Vol. 20 (No. 2), August, 2021. Pp 87-98 *https://dx.doi.org/10.4314/sa.v20i2.8*
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

GENETIC VARIABILITY OF SPIRALLING WHITEFLY *ALEURODICUS DISPERSUS* RUSSELL ON *CITRUS AURANTIFOLIA* CHRISTM AND *OCIMUM GRATISSIMUM* L.

***Adeleke, Mistura Temitope[1]., Adekunle, Oladunni Nimota[1]., Feyisola, Roseline Tolulope[2] Owagboriaye, Folarin Ojo[1]., Arowosegbe, Olayemi Tope[1]., and Lawal, Olusegun Adebayo[1].**

[1]Department of Zoology and Environmental Biology, Olabisi Onabanjo University, Ago-Iwoye, Ogun State, Nigeria
[2]Department of Plant Science, Olabisi Onabanjo University, Ago-Iwoye, Ogun State, Nigeria
*Corresponding author: adeleke.mistura@oouagoiwoye.edu.ng

Received: 17-04-2021
Accepted: 24-05-2021

ABSTRACT

The spiralling whitefly, Aleurodicus dispersus Russell (Hemiptera: Aleyrodidae), has a wide range of anatomy, physiology, behaviour, and ecology depending on the host plant. This research looked at the genetic variations between A. dispersus populations on two separate host plants (Citrus aurantifolia and Ocimum gratissimum). The existence of host-related genetic variation in A. dispersus populations was determined using Rapid Amplification of Polymorphic DNA (RAPD) markers. Our findings revealed that the A. dispersus populations on the two host plants had a considerable amount of genetic divergence. The spiralling whiteflies on the adaxial part of Citrus aurantifolia were genetically distinct from those on the abaxial part of the same plants. Various population genetic parameters such as heterozygosity, Nei's genetic gap, and fixation indices (FST) revealed that spiralling whitefly populations vary genetically, which may be attributable to spiralling whitefly populations originating from multiple sources. These findings also have consequences for the invasive pest's quarantine safety strategy.

Key words: *Aleurodicus dispersus*, Hemiptera, Aleyrodidae, genetic diversity, host plants, RAPD markers, polymorphism

INTRODUCTION

Citrus is one of the world's most essential fruit crops, with widespread abundance and popularity, adding to human diets as a rich source of fibre, carbohydrates, vitamins, and minerals that are essentially important for the maintenance of human health and growth. Citrus fruits are eaten fresh or refined into citrus by-products such as flavourings all over the world (Yano *et al.* 1999); jams, sorbets, pickles, jellies, and candies (Okwu, 2008) and Citrus fruit peel oils are used to flavour beverages and sweets, as well as medications, soaps, perfumes, hair cream, body oil, and other cosmetics, as well as cleaning products. (Ferguson, 1990). Citrus fruits are cultivated in more than 140 countries around the world, mainly in the tropics and subtropics. Oranges, lemons, limes, grapefruit, and tangerines are the most well-known commercial citrus fruits.

C. aurantifolia is a native of southwest Asia and is known as Lime (Nigeria), Key lime, Mexican lime, Sour lime, Dayap, bilolo, Indian lime, and Egyptian lime (Burkill, 1997). The plant belongs to the

Phylum: Magnoliophyta; Class: Magnoliopsida; Order: Sapindales; Family: Rutaceae; Genus: Citrus and Species: Citrus aurantifolia (Sethpakdee, 1992). On an estimated 3 million hectares of land in Nigeria, around 930,000 tons of citrus fruits are produced annually (FAO, 2007), with production coming from Benue, Nassarawa, Kogi, Ogun, Oyo, Ebonyi, Kaduna, Taraba, Ekiti, Imo, Kwara, Edo, and Delta. (Taiwo, 2005).

Lime is a spiny shrubby or small tree with a single or several stems and irregular branches covered in smooth brown to grey bark that grows up to 6 meters tall (Aprioku and Obianime, 2014). The fruits are 3 to 5cm in diameter and have a juicy, greenish-yellow flesh that turns yellow when they mature. They also have a few white, pointed seeds that are around 1cm long (Katz and Weaver, 2003).

The pericarp (rind) of *C. aurantifolia* contains 7% essential oil, with key constituents such as citral, limonene, and fenchon, as well as terpineol, bisabolene, and other terpenoids including terpineol, bisabolene, and other terpenoids (Bruneton, 1999). Its main applications include food seasoning, refreshing beverages, delectable desserts, and seasoning foods, fruits, salads, sauces, and casseroles (Katzer, 2002). lime is used to treat a huge number of ailments (Burkill, 1997), such as colon cancer, cardiovascular diseases, obesity, kidney stones, gout, arthritis, to relieve flu by taking tea prepared from juice, fruit rind or leaves as an expectorant (Rafter, 2002). The juice and peels of fruits are mixed with vinegar to create a disinfectant; polish brass; bleach cloth; remove ink, rusty, and mineral stains from cloths; whiten tannin shoes; and soften fabrics (Ferguson, 1990). Citrus fruit peel pulp is used as a cereal substitute in ruminant feeds because of its high energy content and ruminant digestibility (Heuzé *et al.*, 2012).

Vulnerability of *C. aurantifolia* to pests and diseases is high just like other citrus trees, pests include; citrus snow scale (*Unaspis citri*), spiralling whitefly (Manner *et al.* 2006), citrus leafminer (*Phyllocnistis citrella*), citricola scale (*Coccus psuedomagnoliarum*), citrus leafroller (*Archips argyrospila*) and aphids (Weinblatt, 2007).

Ocimum gratissimum (African basil or Basil fever plant or tea bush) is an herbaceous plant food (vegetables) in developing countries, especially Nigeria that makes a significant contribution to local diets and ethnomedicine (Okigbo and Ogbonna, 2006). It is an aromatic, perennial plant native to Africa, Madagascar and southern Asia (USDA, 2013). *O. gratissimum* contains an essential oil, alkaloids, glycosides, tannins, and other chemical constituents (Pandey *et al.* 2014). Food flavoring, biological activity such as antidiabetic antiseptics, antitussive, anthelmintic, antispasmodic, and antimicrobial are just a few of the health benefits (Gbolade, 2009). It has also been proved to induce abortion (Nikolajsen *et al.* 2011), facilitate childbirth (Attah *et al.* 2012), manage diabetes (Ejike *et al.* 2013) and alleviate headache as well as fever (Nweze, 2009).

Aleurodicus dispersus Russell (Spiralling Whitefly) is a major pest devouring agricultural crops as it spread with extraordinary speed across tropics (plate 1). Spiralling whitefly develops as colonies of individuals on the underside of the

Scientia Africana, Vol. 20 (No. 2), August, 2021. Pp 87-98 https://dx.doi.org/10.4314/sa.v20i2.8
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

leaves where by the nymphs and adult suck the sap from the leaves. The polyphagy of the white spiralling whitefly is the major reason it is able to spread quickly from one crop to another across the tropics (Inbar and Gerling, 2008). Furthermore, this whitefly is a threat to many plants which includes; banana (*Musa sapientum*) *Citrus spp*, coconut (*Cocos nocifera*) guava (*Psidium quajava*), tomato *(Lycopersicon esculentum*), pawpaw (*Carica papaya*), and African basil (*Ocimum gratissimum)* (Okolle *et al.* 2010; Sundararaj and Selvaraj, 2017; Kapantaidaki *et al.* 2019).

Plate 1: Sooty mould of *A. dispersus* infestation on *O. gratissimum* (**A**) and *C. aurantifolia* (**B)**

Direct feeding damage is also caused by immature and adult stages of whiteflies piercing and sucking sap from foliage (Boopathi *et al*. 2013). When feeding, dense populations of this polyphagous pest cause premature leaf drop and abundant honeydew, which serves as a substrate for the growth of sooty fungus, causing cassava fields to be abandoned (Akinlosotu *et al*. 1993). Understanding the invasion process requires knowledge of the genetic makeup of invading insect populations (Kreiser *et al.* 2000; Cristescu *et al.* 2001; Patti and Gambi, 2001), since significant genetic variability is expected to favour adaptation and, as a result, the successful establishment of introduced populations (Lee, 2002; Kolbe *et al.* 2004; Facon *et al.* 2006; Lavergne and Molofsky, 2007).

Genetic variability is a measure of individual genotypes in a population in order to determine if the population differ from one another (Sousa *et al.* 2011). This is distinct from genetic diversity, which refers to the amount of variation found in a population (Ehrich and Per Erik, 2005). Variability is an important factor in evolution because it influences an individual's reaction to stress in the environment, resulting in differential survival and natural selection of the fittest variants. (Linhart and Janet, 2003).

Genetic markers such as RAPD, Amplified Fragment Length Polymorphism (AFLP), have been an efficient tool to differentiate geographically and genetically population (Subodh *et al.* 2010). Analysis of microsatellite and allozyme markers on plant pest indicates the existence of genetically different individuals on the various plants (Simon *et al.* 2003). It's been used to test the genetic diversity of insect pests like the sweet potato whitefly (*Bemisia tabaci*) in Indian (Moya *et al.*

2001; Sharma *et al.* 2008), grain aphids Sitobion avenae (Lushai *et al.* 2002), Russian wheat aphid *Diuraphis noxia* (Shufran *et al.* 1997), whitefly *Aleurocanthus spiniferus*) in Greece (Kapantaidaki *et al.* 2019) and giant whitefly *Aleurodicus dugesii* in Indonesia (Hidayat *et al.* 2020) However, considering its economic value, little is known about *A. dispersus*' genetic variability level and pattern. Moreover, the level of genetic divergence among host plant specific *A. dispersus* populations is uncertain because in earlier studies the populations were analysed using markers with different resolutions. As a result, we examined the extent of genetic differentiation between *A. dispersus* populations on two host plants in this study.

METHODS

Two hundred (200) insect samples (active spiralling whiteflies) were collected from various parts of leaves of *Citrus aurantifolia* (adaxial and abaxial surface) and *Ocimum gratissimum* (abaxial surface) early in the morning (7am) with improvised pooter into sterile bottles.The plants and insects species were identified at the herbarium and Entomology laboratory in Plant and Applied Zoology of Olabisi Onabanjo University, Ago-Iwoye, Ogun State. The samples were then preserved in the refrigerator for 24hours for further analysis at the Animal Science Laboratory of Federal University of Agriculture, Abeokuta, Ogun state.

The extraction of the genomic DNA of *A. dispersus* was done using CTAB (Cetyl trimethyl ammonium bromide antiseptic agent) extraction buffer method (Cortes *et al.* 2010). Purity and quantity of extracted DNA were tested using a spectrophotometer, and purity was checked using a 1% agarose gel electrophoresis, which was visualized using an ultraviolet light transmitter and stored at -20°C.

DNA AMPLIFICATION: Five (5) RAPD markers namely OPAD 09, OPAE 04, OPAE 05, OPAE 09 and OPAF 07 (Table 1) were used to amplify the DNA samples that had been collected. PCR was performed according to Solignac *et al.* (2003). Electrophoresis in a 6.0 % polyacrylamide gel with 1.0 X TBE buffer was used to overcome the amplification materials. Gels were stained with ethidium bromide solution after electrophoresis.

Table 1: List of primers used and their sequences

S/N	Primer Name	Sequence	Fragment size
1	OPAD 09	TCGCTTCTCC	200bp - 2500bp
2	OPAE 04	CCAGCACTTC	200bp - 2500bp
3	OPAE 05	CCTGTCAGTG	250bp - 2500bp
4	OPAE 09	TGCCACGAGG	250bp - 3000bp
5	OPAF 07	GGAAAGCGTC	250bp - 3500bp

Scientia Africana, Vol. 20 (No. 2), August, 2021. Pp 87-98 *https://dx.doi.org/10.4314/sa.v20i2.8*
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

DATA ANALYSIS

For RAPD studies, polymorphic bands were scored as present (1) or absent (0). Shannon's knowledge indices (I), observed heterozygozity (Ho), gene diversity (He) (Nei, 1973), and percent of polymorphic bands (Lewontin, 1972) were calculated using the following equation:

$I = -\Sigma pi \ln pi$

where pi denotes the population proportion of the ith allele.

The binary value was transferred into software for constructing the UPGMA tree based on the original distance PAST v.4.0.3 (Miller, 1997)

RESULTS

All amplification products were consistent and reproducible in the RAPD analysis. This revealed genetic diversity among the spiralling whitefly populations collected from the two (2) host plants. In the RAPD amplifications, a total of twenty alleles were detected from the two host plants however, only ten were polymorphic and were used in the analysis (Table 2).

Table 2: Observed number of bands, percentage of polymorphic bands, observed heterozygosity (Ho), Gene diversity (H_e) and Shannon's information index (*I*) values for populations studied.

LOCUS	Observed	% Polymorphic	Ho	Gene diversity (He)	I
OPAD 09	10	50	0.02	0.34	1.089
OPAE 04	12	60	0.02	0.36	1.099
OPAE 05	3	15	0.01	0.19	0.637
OPAE 09	7	35	0.02	0.3	1.079
OPAF 07	9	45	0.02	0.33	0.965
Mean			**0.018**	**0.304**	**0.762**

Per locus, the number of alleles ranged from 0 to 4, with 2 alleles per locus on average. The percentage polymorphism ranged between 15% (OPAE 05) and 60% (OPAE 04). The observed heterozygosity (H_o), Gene diversity (H_e) and Shannon's information index (*I*) ranged from 0.01 to 0.02 (mean = 0.018), 0.19 to 0.36 (mean = 0.304) and 0.64 to 1.10 (mean = 0.76), respectively. It is noteworthy that the observed heterozygosity is much lower than the expected heterozygosity.

The most informative primers were OPAD 09 and OPAE 04, they have the highest number of expressed bands (10 and 12 respectively) in 20 loci. The organisms with highest number of polymorphic expressions were those obtained from *O. gratissimum* (16 bands) and *C. aurantifolia* (adaxial) (13 bands).

The neighbour joining dendrogram of *A. dispersus* populations from the two host plants based on Nei's genetic distances revealed two major clusters (Figure 1). The mean genetic distance coefficient based on

four markers is 0.99. Spiralling whitefly populations on the *C. aurantifolia* (adaxial) is of same origin with those found in *O. gratissimum* host plants forming a major cluster. The second cluster consists of *C. aurantifolia* (abaxial).

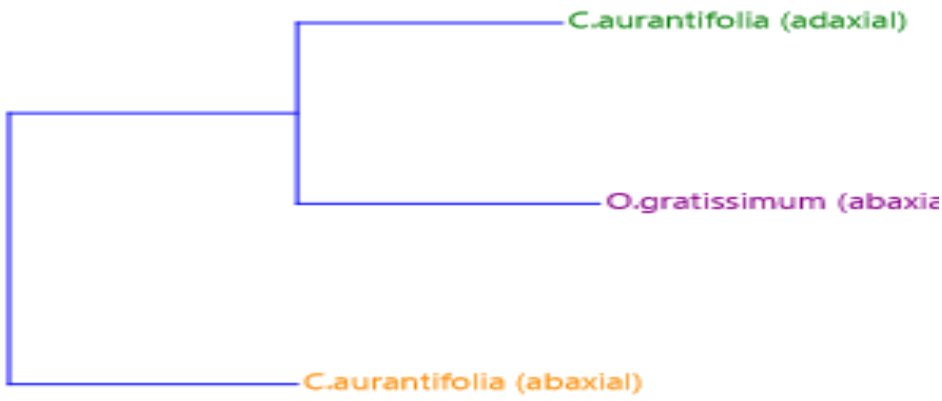

Figure 1: Neighbour joining dendrogram for populations of *Aleurodicus dispersus* collected from two host plants based on Nei's (1973) genetic distances generated using PAST 4.03.

Pairwise F_{ST}, which estimates the correlation of alleles among hypothetical populations of spiralling whiteflies, indicated that population *C. aurantifolia* (adaxial) is genetically closer to *O. gratissimum* (abaxial) than the other population (Table 3).

Table 3: Pairwise F_{ST} correlation matrix for spiralling whitefly populations based on the clusters identified by the PAST analysis.

Host Plant	*C.aurantifolia* (adaxial)	*C.aurantifolia* (abaxial)	*O. gratissimum* (abaxial)
C.aurantifolia (adaxial)	1		
C.aurantifolia (abaxial)	0.778	1	
O. gratissimum (abaxial)	0.9649	0.6447	1

DISCUSSION

The first step toward a deeper understanding of insect ecology at the molecular level is to define, validate, and apply molecular markers. This study has revealed spiralling whitefly colonising abaxial surface of leaves of *O. gratissimum* and both the abaxial surface and adaxial surface of leaves of *C. aurantifolia* are widely infested in acceptance with Chin *et al.* (2006) that reported spiralling whitefly colonization of both the underside and upper (adaxial) surface of leaves. Despite the fact that there is no morphological variation between the insect populations on the adaxial and abaxial surfaces of the

Scientia Africana, Vol. 20 (No. 2), August, 2021. Pp 87-98 https://dx.doi.org/10.4314/sa.v20i2.8
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

leaves, the size of the insect population on *O. gratissimum* is smaller.

The RAPD analysis clearly demonstrated a substantial level of polymorphism among the populations of spiralling whiteflies. Twenty multiple alleles were generated from *C. aurantifolia* (adaxial surface and abaxial surface) five alleles being polymorphic and ten alleles expressing polymorphism between *C. aurantifolia* and *O. gratissimum*, this indicates clear differentiation between the samples collected from *C. aurantifolia* (abaxial and adaxial) and *O. gratissimum* (abaxial) surface of leaves. Following the analysis of this study, it was revealed that the similarity coefficient of *A. dispersus* colonising the adaxial and abxial leaf surface of *C. aurantifolia* is 78% similar in their genetic makeup and 96% between *C. aurantifolia* and *O. gratissimum*

. This is in line with an analysis of host-associated genetic variation in *Bemisia tabaci* in India, which found a high degree of genetic relatedness (72% to 85%) among the whitefly types studied and the lineage of their origin from the common type (Sharma *et al.* 2008; Boopathi *et al.* 2019). Furthermore, in an analysis of genetic trends in *A. dispersus* populations from the Canary Islands, no variations in RAPD patterns were found, but there was a high degree of genetic similarity and low genetic variability among populations (Callejas *et al.* 2005). Oyelade and Ayansola (2015) have justified that this outcome can be aided by the favourable conditions and nutrient availability for the pest.

The use of ten markers in the genetic variability analysis of whitefly populations revealed substantial variability among whitefly populations, with an observed mean heterozygosity (H_o) of 0.018 and average expected heterozygosity (H_e) of 0.304. In contrast, Ma *et al.* (2011) reported using microsatellite markers, a higher level of heterozygosity in populations of spiralling whiteflies in the Hainan and Canary Islands, which may be due to differences in the environment, population behaviour or shorter distances between samples. Expected heterozygosity is a prediction based on the assumption that the population is in Hardy-Weinberg equilibrium (HWE). Lower H_o than H_e indicated that the populations of spiralling whiteflies are smaller in size or have undergone a severe bottleneck in recent times. Another reason for this may be that the populations often do not outcross, which may vary from species to species. Substantial divergence among the populations of *A. dispersus* might be due to parallel multiple introductions of already diverged populations of the species from different sources and further divergence due to preferences for different host species (Boopathi *et al.* 2019).

From the Neighbour Joining clustering pattern it was evident that the genetic distances between *A. dispersus* populations do not correlate with the taxonomic relations of their host plants. There was an exception; where *A. dispersus* populations from *C. aurantifolia* (adaxial) and *O. gratissimum* were in the same clusters while populations from *C. aurantifolia* (abaxial) formed another cluster on its own despite being the plant belonging to the same family. This could have been due to the coexistence of flies from two distinct populations on a single host species as genetic and mixture resulting from inter-crossing is not expected to occur.

A high degree of gene diversity and a low level of reported heterozygosity (expected heterozygosity) indicated that the populations were not in HWE, which may be due to a high incidence of inbreeding and low incidence of intercrossing between individuals of distinct populations. This could be attributed to the result of sexual preferences between host plant specific populations and host plant-whitefly interactions.

The genetic data presented here, as well as the biological data on success and feeding behaviour presented in studies (Banjo, 2010; Oyelade and Ayansola, 2015; Boopathi *et al.* 2014) demonstrate that the genetical divergence of *A. dispersus* is associated with differences in the host plants.

Spiralling whitefly host specialization may have occurred before their introduction into any plant population, according to this research. Further research into the genetic relationships between and within *A. dispersus* host plants in various Nigerian geographical zones is required to decide if host specialization evolved once or many times.

CONCLUSION

The present study also utilized RAPD markers for identifying host correlated genetic variability amongst populations of *A. dispersus*. This research demonstrates unequivocally that *A. dispersus* on the two host plants differ substantially genetically and there is a minimum of intercrossing between these populations. In order to shed light on the host-race creation process in *A. dispersus*, it is essential to conduct phylogeographic study. More studies on molecular tools such as Restriction Fragment Length Polymorphism, AFLP, Simple-Sequence Repeats, Single Nucleotide Polymorphisms as used by Boopathi *et al.* (2019) and Elfekih *et al.* (2018) respectively, and molecular sequences (mitochondrial and nuclear genomes) can be of great help to reinvestigate the genetic variability of *Aleurodicus dispersus* in Nigeria.

ACKNOWLEDGEMENTS

The authors would like to express their gratitude to the administration of Olabisi Onabanjo University in Ago-Iwoye for approving this study.

REFERENCES

Akinlosotu T.A., Jackai L.E.N., Ntonifor N.N., Hassan A.T., Agyakwa C.W., Odebiyi J.A., Akingbohungbe A.E. and Rossel H.W. (1993) Spiralling whitefly *Aleurodicus dispersus* in Nigeria. *FAO Plant Protection Bulletin*, 41: 127–129.

Aprioku, J. S. and Obianime, A. W. (2014) Evaluation of the effects of Citrus aurantifolia (lime) juice in lead-induced hematological and testicular toxicity in rats. *Pharmacologia, 5*(1): 36-41.

Attah, A. F., O'brien, M., Koehbach, J., Sonibare, M. A., Moody, J. O., Smith, T. J. and Gruber, C. W. (2012) Uterine contractility of plants used to facilitate childbirth in Nigerian ethnomedicine. *Journal of Ethnopharmacology, 143*(1): 377-382.

Banjo, A.D. (2010) A review on Aleurodicus dispersus Russell. (spiraling whitefly) (Hemiptera: Aleyrodidae) in Nigeria. *Journal of*

Scientia Africana, Vol. 20 (No. 2), August, 2021. Pp 87-98 https://dx.doi.org/10.4314/sa.v20i2.8
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

Entomology and Nematology 2(1): 001-006.

Boopathi T., Karuppuchamy P., Kalyanasundaram M., Mohankumar, S. and Ravi M. (2013) Pathogenicity, ovicidal action, and median lethal concentrations (LC50) of entomopathogenic fungi against exotic spiralling whitefly, *Aleurodicus dispersus* Russell. — *Journal of Pathogens*, 393787: 7 pp.

Boopathi, T., Mohankumar, S., Kalyanasundaram, M.P., Singh, S.B., Aravindraj, R., Preetha, B., Meena, K.S. and Chandrasekar, K. (2019) Host-based genetic divergence in populations of an exotic spiralling whitefly, Aleurodicus dispersus (Hemiptera: Aleyrodidae). *European Journal of Entomology*, *116*: 221-228.

Boopathi, T., Mohankumar, S., Karuppuchamy, P., Kalyanasundaram, M., Ravi, M., Preetha, B. and Aravintharaj, R. (2014) Genetic evidence for diversity of spiralling whitefly, *Aleurodicus dispersus* (Hemiptera: Aleyrodidae) populations in India. *Florida Entomologist, 97*(3): 1115-1122.

Bruneton, J. (1999) Toxic plants dangerous to human and animals. *Lavoiscer publisher*, Paris. 545pp.

Burkill, H.M. (1997) The useful plants of west Trophical Africa. *Royal Botanic Gardens kew*, UK 4: 969 pp.

Callejas, C., Beitia F.J., Gobbi A., Velasco, A. and Ochando, M.D. (2005) The use of RAPD markers to detect genetic patterns in *Aleurodicus dispersus* (Hemiptera: Aleyrodidae) population from Canary Island. *Europe Journal Entomology*, 102: 289-291.

Chin, D., Brown, H., Wallace, H., Neal, M., Zhang, L. and Thistleton, B.M. (2006) Biology and management of the spiralling whitefly. *Northern Territory Department of Primary Industry, Fisheries, and Mines*, Technical Annual Report.

Cortes, N.C., Quesada, M., Camacho, H.C. and Paramo, G.Z, (2010) A simple and rapid method for DNA isolation from xylophagous insects. *International Journal Molecular Science* 11 (*12*): 5056 – 5064.

Cristescu, M. E., Hebert, P. D., Witt, J. D., MacIsaac, H. J. and Grigorovich, I. A. (2001) An invasion history for Cercopagis pengoi based on mitochondrial gene sequences. *Limnology and Oceanography, 46*(2): 224-229.

Ehrich, D. and Per Erik, J. (2005) High genetic variability despite high amplitude population cycles in Lemmings. *Journal of Mammalogy*, 86: 380-385.

Ejike, C. E., Awazie, S. O., Nwangozi, P. A. and Godwin, C. D. (2013) Synergistic postprandial blood glucose modulatory properties of Vernonia amygdalina (Del.), Gongronema latifolium (Benth.) and Occimum gratissimum (Linn.) aqueous decoctions. *Journal of Ethnopharmacology, 149*(1): 111-116.

Elfekih, S., Tay, W. T., Gordon, K., Court, L. N. and De Barro, P. J. (2018) Standardized molecular diagnostic tool for the identification of cryptic species within the Bemisia tabaci

complex. *Pest management science 74*(1): 170-173.

Facon, B., Genton, B. J., Shykoff, J., Jarne, P., Estoup, A. and David, P. (2006) A general eco-evolutionary framework for understanding bioinvasions. *Trends in Ecology & Evolution, 21*(3): 130-135.

FAO (2007) Citrus production. Retrieved from FAO Statistical data base.

Ferguson, U. (1990) Citrus fruits processing. Horticultural Science, *Florida* 23:117-118.

Gbolade, A. A. (2009) Inventory of antidiabetic plants in selected districts of Lagos State, Nigeria. *Journal of Ethnopharmacology*, *121*(1): 135-139.

Heuzé, V., Tran, G. and Hassoun P. (2012) Citrus pulp, dried. A programme by INRA, CIRAD, AFZ and FAO 2012. Retrieved from: http://www.feedipedia.org/node/680.

Hidayat, P., Maryana, E., Kusumah, Y. M. and Nurulaila, L. (2020) Host range and population density of the giant whitefly Aleurodicus dugesii Cockerell (Hemiptera: Aleyrodidae) on horticultural crops in Cipanas-Cianjur, West Java, Indonesia. In *IOP Conference Series: Earth and Environmental Science, 468*(1): 012008.

Inbar, M., and Gerling, D. (2008). Plant-mediated interactions between whiteflies, herbivores, and natural enemies. *Annual Review of Entomology*, *53*, 431-448.

Kapantaidaki, D. E., Antonatos, S., Kontodimas, D., Milonas, P. and Papachristos, D. P. (2019) Presence of the invasive whitefly Aleurocanthus spiniferus (Hemiptera: Aleyrodidae) in Greece. *EPPO Bulletin, 49*(1): 127-131.

Katz, S.H. and Weaver, W.W. (2003) Encylopedia of food and culture. 1st Edition *Schribner*, New york. 861pp.

Katzer, G. (2002) Lime (*Citrus aurantifolia* Christian et Panz) Gernet Katzer's spice pages http://www.aug.kfunigrazc.at/~katzer/engl/citraur .html. p4.

Kolbe, J. J., Glor, R. E., Schettino, L. R., Lara, A. C., Larson, A. and Losos, J. B. (2004) Genetic variation increases during biological invasion by a Cuban lizard. *Nature, 431*(7005): 177-181.

Kreiser, B. R., Mitton, J. B. and Woodling, J. D. (2000) Single versus multiple sources of introduced populations identified with molecular markers: a case study of a freshwater fish. *Biological Invasions, 2*(4): 295-304.

Lavergne, S. and Molofsky, J. (2007) Increased genetic variation and evolutionary potential drive the success of an invasive grass. *Proceedings of the National Academy of Sciences, 104*(10): 3883-3888.

Lee, C. E. (2002) Evolutionary genetics of invasive species. *Trends in Ecology* and *Evolution 17*(8): 386-39.

Lewontin, R.C. (1972) The apportionment of human diversity. *Evolutionary Biology*, 6: 381-398.

Linhart, Y. B. and Gehring, J. L. (2003) Genetic variability and its ecological implications in the clonal plant Carex scopulorum Holm. in Colorado

Scientia Africana, Vol. 20 (No. 2), August, 2021. Pp 87-98 https://dx.doi.org/10.4314/sa.v20i2.8
© Faculty of Science, University of Port Harcourt, Printed in Nigeria *ISSN 1118 – 1931*

tundra. *Arctic, Antarctic, and Alpine Research, 35*(4): 429-433.

Lushai, G., Markovitch, O. and Loxdale, H. D. (2002) Host-based genotype variation in insects revisited. *Bulletin of Entomological Research, 92*(2): 159-164.

Ma, G. C., Wu, X., Ma, C. L., Wu, H. L., Hu, H. Y., Niu, L. M. and Fu, Y. G. (2011) Isolation and characterization of polymorphic microsatellite loci in *Aleurodicus dispersus* (Hemiptera, Aleyrodidae). *Genetics and Molecular Research, 10*(4): 2523-2526.

Manner, H., Buker, R., Smith, V. and Elevitch, C. (2006) Citrus species (citrus) in: Species profiles for pacific island agroforestry. *Permanent Agriculture Resources (PAR) Hawaii*, pp. 1-35.

Miller, M.P. (1997) Tools for population genetic analyses (TFPGA) 1.3: A Windows program for the analysis of allozyme and molecular population genetic data. Computer software distributed by the author. Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ.

Moya, A., Guirao, P., Cifuentes, D., Beitia, F. and Cenis, J. (2001) Genetic diversity of Iberian population of Bemsia tabaci (Hemiptera: Aleyrodidae) based on random amplified polymorphic DNA-polymerase chain reaction. *Molecular Ecology*, 10: 891-897.

Nei, M. (1973) Analysis of gene diversity in subdivided populations. *Proceedings of the National Academy of Sciences*, 70: 3321-3323.

Nikolajsen, T., Nielsen, F., Rasch, V., Sørensen, P. H., Ismail, F., Kristiansen, U. and Jäger, A. K. (2011) Uterine contraction induced by Tanzanian plants used to induce abortion. *Journal of ethnopharmacology 137*(1): 921-925.

Nweze, E. I. and Eze, E. E. (2009) Justification for the use of *Ocimum gratissimum* L in herbal medicine and its interaction with disc antibiotics. *BMC complementary and alternative medicine, 9*(1): 1-6.

Okigbo, R.N. and Ogbonna, U.O. (2006) Antifungal effects of two tropical plant leaf extracts (*Ocimum gratissimum* and *Aframomum melegueta*) on postharvest yam (Dioscorea spp.) rot. *African Journal of biotechnology, 5*(9): 727-731.

Okolle, J. N., Abu Hassan, A., Mashhor, M., and Tripathi, L. (2010). Bioecology and management of the banana skipper (Erionota thrax). *Tree and Forestry Science and Biotechnology, 4*(1): 22-31.

Okwu, D. E. (2008) Citrus fruits: a rich source of phytochemicals and their roles in human health: a review. *International Journal of Chemical Science*, 6(2):451-471.

Oyelade, O. J. and Ayansola, A. A. (2015) Diversity and distribution of whiteflies in south-western Nigeria. *African Crop Science Journal, 23*(2): 135-149.

Pandey, A. K., Singh, P. and Tripathi, N. N. (2014) Chemistry and bioactivities of essential oils of some Ocimum species: an overview. *Asian Pacific Journal of Tropical Biomedicine, 4*(9): 682-694.

Patti, F. P. and Gambi, M. C. (2001) Phylogeography of the invasive polychaete Sabella spallanzanii

(Sabellidae) based on the nucleotide sequence of internal transcribed spacer 2 (ITS2) of nuclear rDNA. *Marine Ecology Progress Series, 215*: 169-177.

Rafter, J. J. (2002) Scientific basis of biomarkers and benefits of functional foods for reduction of disease risk: cancer. *British Journal of Nutrition,88*(2): S219-S224.

Sethpakdee, R. (1992) *Citrus aurantifolia* (Christm. and Panzer) Swingle. *Plant Resources of South-East Asia. Edible fruits and nuts. Prosea Foundation, Bogor, Indonesia 2*: 126-128.

Sharma, R., Gupta, V., Jinda, J. and Dilawari, V. (2008) Host associated genetic variation in whitefly Bemisia tabaci (Genn). *Indian Journal of Biotechnology,* 7: 366-370.

Shufran, K.A., Burd, J.D. and Webster, J.A (1997) Biotypic status of Russian wheat aphid (Homoptera: aphididae) populations in the United States. *Journal of Economy Entomology,* 90: 1684 – 1689.

Simon, J. C., Carre, S., Boutin, M., Prunier–Leterme, N., Sabater–Muñoz, B., Latorre, A. and Bournoville, R. (2003) Host–based divergence in populations of the pea aphid: insights from nuclear markers and the prevalence of facultative symbionts. *Proceedings of the Royal Society of London. Series B: Biological Sciences, 270*(1525): 1703-1712.

Solignac, M., Vautrin, D., Loiseau, A., Mougel, F. and Baudry, E. (2003) Five hundred and fifty microsatellite markers for the study of the honey bee (*Apis mellifera L.*) genome. *Molecular Ecology Notes,* 3: 307–311.

Sousa, P., Froufe, E., Harris, D. J., Alves, P. C. and Van der Meijden, A. (2011) Genetic diversity of Maghrebian Hottentotta (Scorpiones: Buthidae) scorpions based on CO1: new insights on the genus phylogeny and distribution. *African Invertebrates, 52*(1): 135-143.

Subodh, K., Bharat, N., Divya, P. and Kalpana, J. (2010) RAPD markers system in insect study: A review. *Indian Journal of Biotechnology,* 9: 7-12.

Sundararaj, R., and Selvaraj, K. (2017). Invasion of rugose spiraling whitefly, Aleurodicus rugioperculatus Martin (Hemiptera: Aleyrodidae): a potential threat to coconut in India. *Phytoparasitica, 45*(1): 71-74.

Taiwo, T.A. (2005) Production of Fruits, Vegetables, Grains, Legumes. Root crops in Nigeria; Problems and Prospects. *University Press* 1:9.

USDA (2013) Agricultural Research Service, United States Department of Agriculture. National Nutrient Database for Standard Reference, Release 26 Software v.1.3.1.

Weinblatt, V. (2007) Pest of regulatory significance for California citrus. *University of California at riverside.*

Yano, M., Kawaii, S., Tomono, Y., Katase, E. and Ogawa, K. (1999) Quantification of Flavonoid Constituent in Citrus Fruits. *Journal of Agricultural Food Chemistry,* 47:3565 - 3571.