Journal of Entomological Research

Volume 13, Issue 3, pages: 68-79

Islamic Azad University, Arak Branch
ISSN 2008-4668
http://jer.iau-arak.ac.ir

Review article

INSECT GENOME STUDIES FOR PEST MANAGEMENT: A GUIDE FOR ENTHUSIASTIC STUDENTS

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Abstract

Insects, especially *Drosophila* are used for genetic, immune system, and histochemical studies. Insect genome studies have resolved epigenomic, metabolomics, physionomics, transcriptomics, evolution and many other biological problems. Differences in gene and alleles within the population of one insect species can produce variations in characters or different genotypes. Genomic studies can be used for solving some of the insect pest population variation problems. This article intends to describe general applications of insect genomic studies with an example of its application to solve insect pest management (IPM) problems.

KEY WORDS: Genomic, IPM, Marker, Stress, Insect

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Received: 8 Mar. 2021 – Accepted: 10 Jun. 2021

INTRODUCTION

Insect genomes contain components of usual animal cells. The nuclear complement of the genome consists of chromosomes with DNA wound around histone proteins, resulting in a coiled, compact, linear structure. A gene in a chromosomal region is capable of making a functional transcript. The DNA containes non coding regions called introns and the coding gene part are called exons. Different versions of the same gene are called alleles. Genes can have two or more possible alleles that can determine individual traits. Heterochromatin has specific histone modifications, such as H3K9me2, H3K9me3, and H3K27me3 and it can form attachments between chromosomes and the nuclear envelope. Chromatin regions marked with H3K27me3 can mediate intra-and inter-chromosomal interactions in the nucleus. Heterochromatin has been associated with several functions, from gene regulation to the protection of chromosome integrity. Some of these roles can be attributed to the dense packing of DNA, which makes it less accessible to protein factors that usually bind DNA or its associated factors. Genome methylation can be silenced by DNA sequences that might be hazardous to the organism. Heterochromatin can silence these regions with repetitive nucleotide sequence. In the process of gene silencing transcriptome have an important role in DNA methylation associated with citochrome residue (Madlung and Comai, 2004).

Each nucleotide or genes with four aminio acids C-G and A-T with active alignment are related to chromatin and attachment of methyl to CG and cNG that with asymmetric methylation of nucleotide it may change genome function (Glastad et al, 2019). Environmental stress regulates gene functions. Loss of DNA methylation or transposon activation through transposable elements (TE) may change genome structure. It suppress motor element and can influence evolutionary riddle (Fedoroff, 1999; Li F, et al, 2019). Adaptation to environmental conditions through genetic drift and selection for resistant forms while declining the source population produce new trait in insect population. Neutral genetic markers and adaptive traits via microsatellites effects increase the resistance to stress (Lexer and Fay, 2005). Meta – analyses in response of insect to environmental stress may result in fluctuating asymmetry indicate the presence of variations in traits of many insect pests (Leftwich et al, 2021).

Insects have evolved with a variety of genetic responses to stress. The reaction to toxic materials in their body is caused by genetic, epigenetic or physiological pathways. Biological reaction to metal toxic concentrations may be directly damaging DNA or producing oxidative stress. Oxidative stress (OS) and anti-oxidant enzymes have major roles in insect metal response (Isaksson et al, 2011; Merritt and Bewick , 2017). Fluctuating asymmetry (FA) of insect pest that is imposed by stressful effects on plants is changed to the normal shape of leaves for the next generation in *Betula.* The insect pests such as leaf roller (*Deporaus betulae*), leaf miners and other defoliators can cause the changes in symmetry and leaf shapes(Kozlov et al, 2018). The number of *Acyrthosiphon pisum* on *Pisum sativum* host were three times higher than plants cultivated in full light (Dancewicz and Markunas, 2018).

So far about 5000 species of insects have sequenced genomes. About 155 genomes in insects are concisely annotated. About hundred sequences of insects are published in various reviews. Contigs or scaffolds of genome sequences of many other species are presented by many graphs or software programs. Genome assembly for beneficial, migratory, agricultural pests or invasive and disease vectors are also available in publications (Li F, et al, 2019).

Pest invasions are considered to have increased by global climatic changes. Advances with molecular genomic techniques resulted in choosing effective genetic traits of natural insect pest enemies in the laboratory. Population genomics and adaptive evolution are key studies for biological control. The ecological conditions and the sustainability in agroecosystems are related to the population genomics of insect pests and their natural enemies. Various factors are involved in these types of studies and are reviewed by Sethuraman et al (2020).

In this review the outlines of research results related to insect genome in relation to efforts for solving IPM problems are described by giving one successful result related to sketches showing genomic and IPM research results for a few African countries and general description of pathways of information from genes to transcriptome and genome that may be used to solve insect pest problems.

IPM-OMICS:

Genomics and many other words that in English are ended in "-omics" such as. epigenomic, metabolomics, physionomics, transcriptomics are referred to factors affecting genomic studies. Agunbiade et al (2012) published an article in the "Proceedings of the Fifth World Cowpea Conference" by showing the field application of their basic genomic research results that can be applied in IPM strategies for cowpea pest control. As an example of genomic research application in pest management their explicit results in five figures are represented (Figs 1-5).

BIOGENIC AMINES, NEUROHORMONES AND STRESS

The environmental conditions such as heat or starvation, is marked on genes by epigenetic, and transcription of gene code for proteins. Biogenic amines such as octopamin (OA) or dopamine (DA) and Tyramine (TA) by neurotransmitters or hormones modulate physiological or behavioral characters in insects (Meng et al, 2019; Li Yo, et al 2016). Transcription factors are directing some population of species to resist to environmental stress. *Drosophila* becomes resistant to starvation by changing its metabolic processes and producing another genotype in its population (Hofmann et a, 2016; Li Yo, et al, 2016). The main factors that are involved in starvation resistance are neurohormones and OA or other biogenic proteins signaled by genes or translated by transcriptome. In this process it appears that transcription factor regulate the gene expression changing the functioning of the organism (Meng et al, 2019). Orthologous transcription factors focus on evolving new resistant population to stressful conditions. In *Drosophila* Hox-like expression of genes along the anterior-posterior axis of the body has the role of segmentation in the embryo. Evolution of Hox 3/Zen/ Bed protein motifs and function in phylogenetic divergence between Zen the orthologous factors separated *Drosophila* from *Megagaselia*. The differences in homologous and orthologous recombination of proteins are described by Hsia and McGinnis (2003). Transcriptome analysis of cotton pests of Uzbakestan show that *Aphis gossypii* was changed to resistant form to thametoxan poison by decreasing gene expression to cytochrome oxide and P450 gene groups (Ayubov and Abdurakhmanov, 2018). DNA markers such as mtDNA, RAPD, AFLP, microsatellites and ESTs have been used as popular marker systems in insect genetics research. Mitochondrial DNA is used for marker analyses largely because of their maternal inheritance, haploid status, and high rate of evolution. The biological roots of signals from genome to behavioral genetics change path through a conceptual path through routes indicating individual genes role in shaping insect behavior (Hoffmann 2003) (Fig. 6).

GENE EXPRESSION AND STRESS

Genome, epigenome and transcriptome are marked for next generation through molecular marker as a result of environmental effects. The hypothetical pathways are schematically described by (Ekblom and Galindo (2011). Gene expression signals are passed between transcriptome and phenotype (Harrison et al, 2012). Gene ontology process is to determine the relation of genes to body organs through transcriptome via nervous system. Transcriptomics can compare instinctive and learned or reward-based change of behavior. They receive signals for mating, flights and time to start or finish training the foraging workers(Naeger and Robinson, 2016).

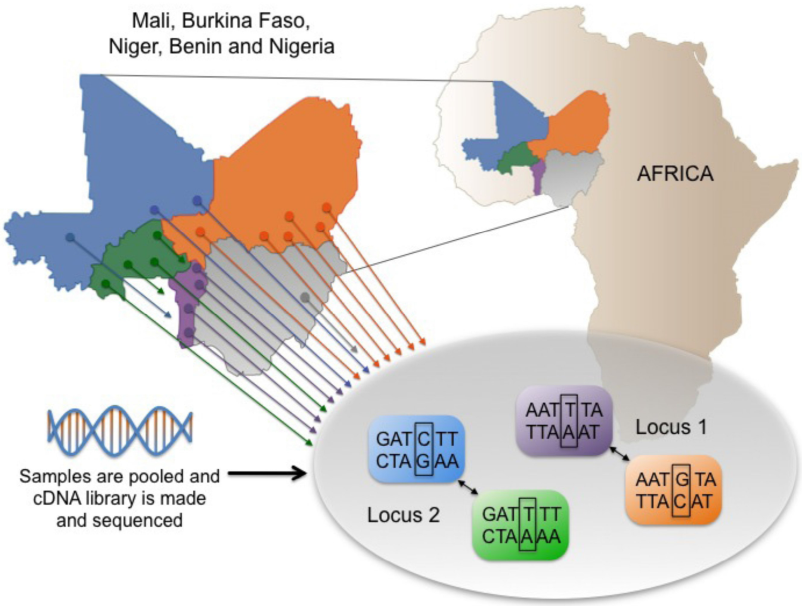
GENOME AND INSIGHT TO PEST CONTROL

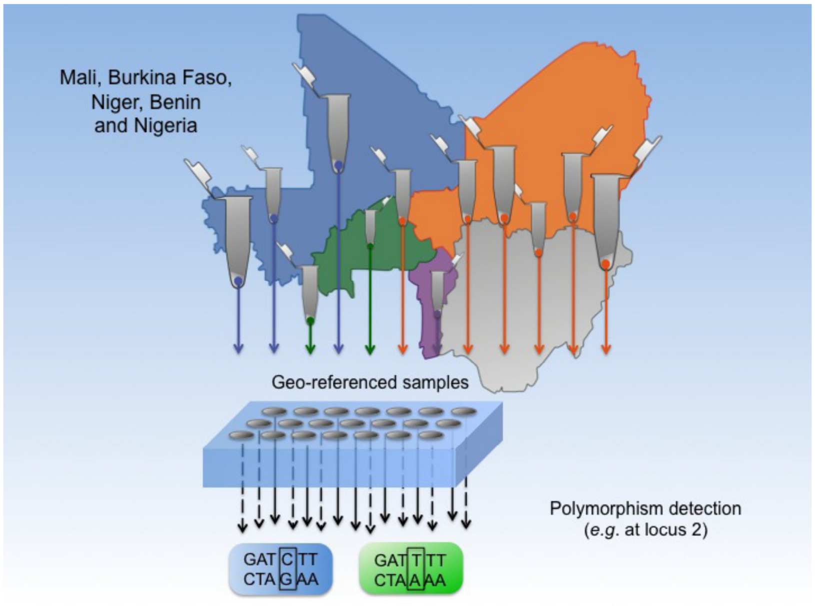
High genetic diversity is associated with the potential for rapid pest invasions. The mechanism of pest resistance to pesticides and pathways of diverse genotypic population of insect to adopt feeding on available regional crops can be traced by molecular and genomic studies and genetic markers. Neutral molecular markers can identify histories of pest invasions. Neutral markers are not associated with genes. It gives some information about evolution processes such as genetic drift. Molecular markers used in association with pest outbreaks areCO1 COII CytB and SSR (Kirk et al, 2013).

STRESS EFFECTS IN INSECT PESTS

Ecological speciation and response of insect pests to climate warming facilitate acclimatization (Wandsworth and Dopman, 2015). The effects of ambient and optimal temperatures on 31 species of insect pests have been compared by Lehmann *et al*. (2020). North Europe, South America and Australia had less outbreaks of these pests compared to Asia and Africa. Repeated insecticide treatments without considering the importance of natural enemies can cause pest outbreak. At present, the locust outbreaks are occasionally reported only after a rainy winters and revival of natural pastures in Iran. Some pest species such as *Eurygaster intericeps* Put*, Bemisia tabaci*, *Chilo suppressalis* (Walker) and occasionally other insect pests of crops and fruit tree need a continuous survey (Davatchi, 1954). However, locust phase polymorphism, phenotypic plasticity, including various mechanisms responsible for insurgence of aggressive biotypes, or resistance to insecticides are the main factors behind the pest control problems (Augustyniak et al, 2016; Sgro *et al*., 2016; Lehmann *et al*.,2020; Hodjat, 1968; Hodjat and Saboori, 2021; Hodjat and Soleymannejadian, 2021) (Fig, 7).

Figs: 1-3


Mali, Burkina Faso,
Niger, Benin and Nigeria
AFRICA
Samples are pooled and
cDNA library is made
and sequenced
AAT T TA
TTA A AT
Locus 1
GAT C TT
CTA G AA
AAT G TA
TTA C AT
Locus 2
GAT T TT
CTA A AA


Mali, Burkina Faso,
Niger, Benin
and Nigeria
Geo-referenced samples
Polymorphism detection
(e.g. at locus 2)
GAT C TT
CTA G AA
GAT T TT
CTA A AA

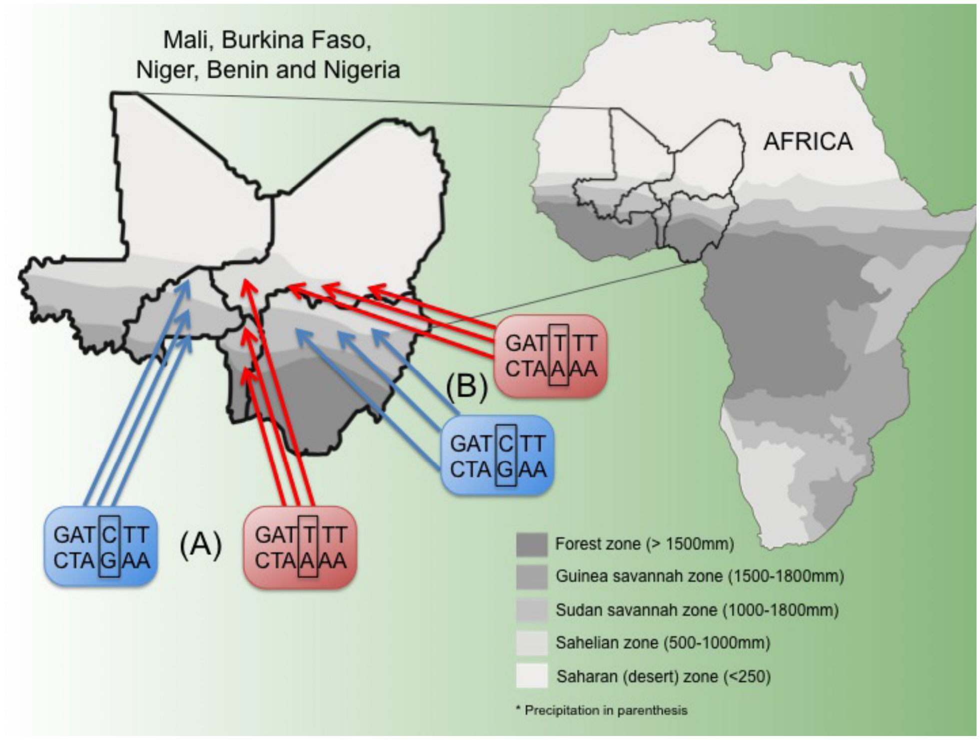
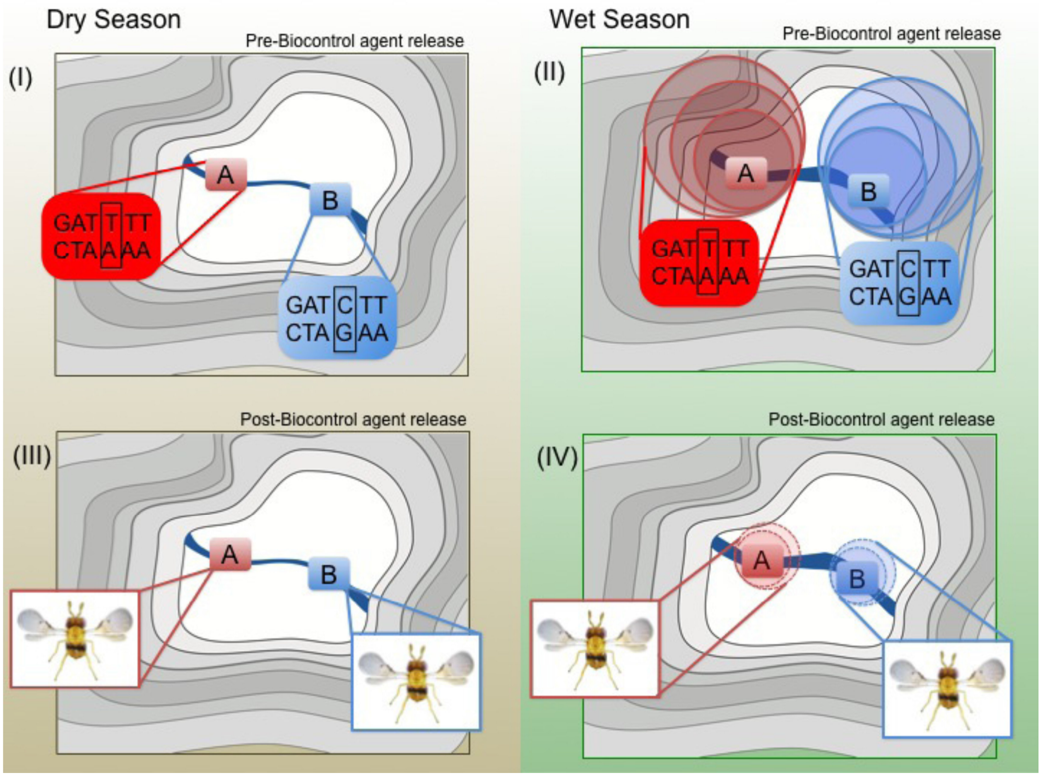

Mali, Burkina Faso,
Niger, Benin and Nigeria
AFRICA
GAT T TT
CTA A AA
(B)
GAT C TT
CTA G AA
GAT C TT
CTA G AA
(A)
GAT T TT
CTA A AA
Forest zone (> 1500mm)
Guinea savannah zone (1500-1800mm)
Sudan savannah zone (1000-1800mm)
Sahelian zone (500-1000mm)
Saharan (desert) zone (<250)
* Precipitation in parenthesis

Fig. 4


Dry Season
Pre-Biocontrol agent release
(I)
A
B
GAT T TT
CTA A AA
GAT C TT
CTA G AA
Wet Season
Pre-Biocontrol agent release
(II)
A
B
GAT T TT
CTA A AA
GAT C TT
CTA G AA
Post-Biocontrol agent release
(III)
A
B
Post-Biocontrol agent release
(IV)
A
B

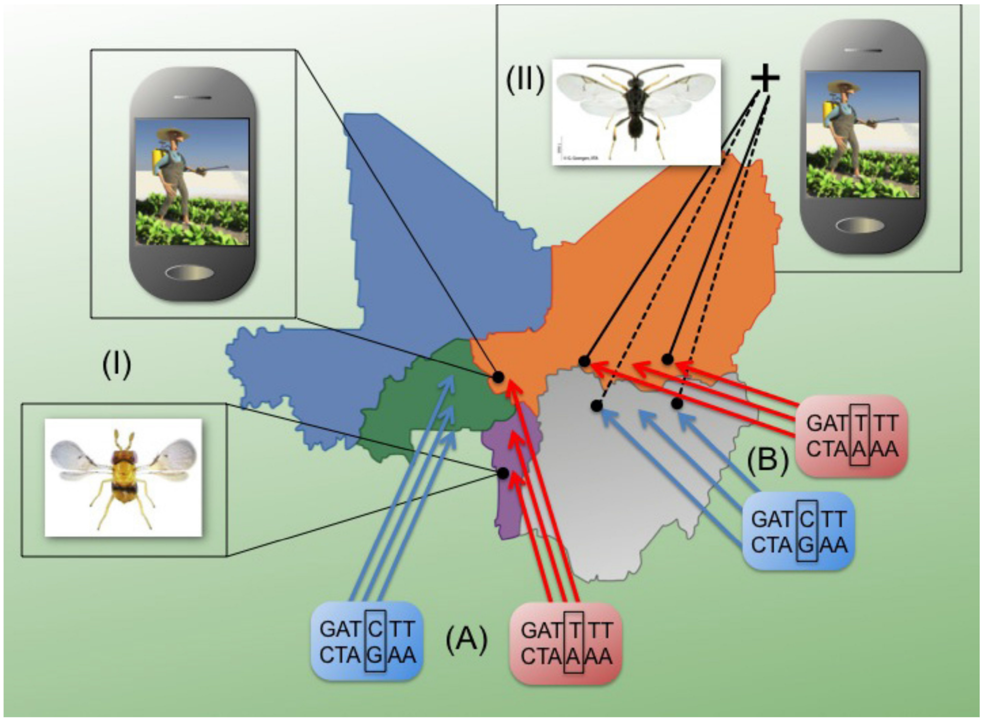

(I)
(II)
GAT C TT
CTA G AA
(A)
GAT T TT
CTA A AA
(B)
GAT T TT
CTA A AA
GAT C TT
CTA G AA

Fig. 5

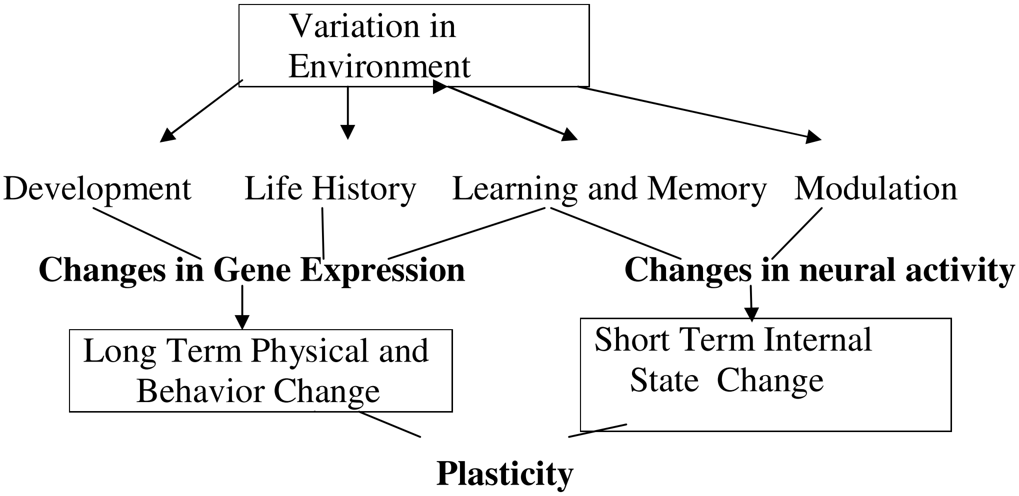

Variation in Environment
Development
Life History
Learning and Memory
Modulation
Changes in Gene Expression
Changes in neural activity
Long Term Physical and Behavior Change
Short Term Internal State Change
Plasticity

Fig. 6

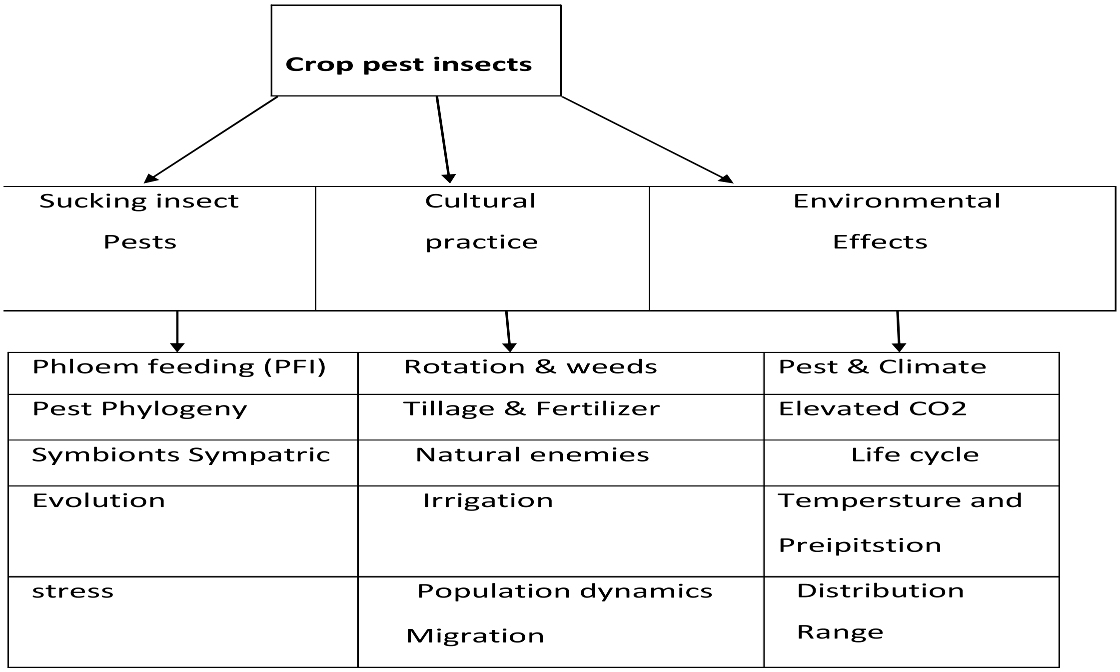


Fig. 7

Glossary

AFLP-PCR or just AFLP: is a PCR-based tool used in genetics research, DNA fingerprinting, and in the practice of genetic engineering.

cDNA library: A collection of cloned DNA sequences that are complementary to the mRNA that was extracted from an organism or tissue (the 'c' in cDNA stands for 'complementary').

DNA Profiling: is the process of determining an individual's DNA characteristics. DNA analysis intended to identify a species, rather than an individual which is called isolation by distance.

Homologous recombination: A type of genetic recombination that occurs during meiosis (the formation of egg and sperm cells). Paired chromosomes from the male and female parent align so that similar DNA sequences from the paired chromosomes cross over each other.

Hox Transcription: Transcription that specify where different morphological factors will develop on the head-tail axix of embryos (Hsia and McGinnes, 2003).

Isolation by distance :IBD is a term used to refer to the accrual of local genetic variation under geographically limited dispersal. Isolation by distance is usually the simplest model for the cause of genetic isolation between populations.

SSRs: Simple sequence repeats, also referred to as **microsatellites**, represent a PCR-based marker system that has been described in mammalian and plant genomes in recent years. In self-pollinating crop plants they have been shown to be superior to other DNA markers with respect to their level of polymorphism.This marker is used to find the history of outbreaks by a few aphid species such as *Acyrthosiphon pisum* and other pests such as *Grapholita molesta* (Kirk, 2013).

Motif: A distinctive repeating feature or idea; often, it helps develop other narrative aspects such as theme or mood. A narrative motif can be created through the use of imagery, structural components, language, and other elements throughout literature.

Orthologous: Homologous genes where a gene diverges after a speciation event, but the gene and its main function are conserved. If a gene is duplicated in a species, the resulting duplicated genes are paralogs of each other, even though over time they might become different in sequence composition and function

Transcriptome: Transcription factor regulate thr spatio-temporal expression of thousands of genes, ensuring the proper development and functioning of the organism (Hsia and McGinnis, 2003).

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DESCRIPTION OF FIGURES

Supplement 1: Figs 1-5 from Agunbiade et al, 2012. Cowpea (*Vinga anguiculata*) pest genome analysis. DNA library recorded from pest in Mali.
Experimental method shown in Fig. 1.

- mRNA is pooled and cDNA library is sequence and arranged.
- Alignment of subsequent DNA sequence form a set of expressed sequences tag (EST) or alleles at locus.
- Polymorphisms among alleles or SNPs (Single Nucleotide Polymorphism) are those adapted genotype individuals.

Fig.2 Supplent 2: Samples of genomes from the pest in five countries

- Insect samples were used to differenciate genotypes and investigate geography / genotype correlation.
- Genetic Polymorphism were detected between individual insects.
- Differences in C/G and T/A detected for two locus.

Fig. 3, Supplement 1: Polymorphisms detected in different agroecological zones.

- Differences between C/G and T/A for nucleotides are shown at the sides of the figure(A) and (B).

Fig. 4, Supplement 1: Use of molecular marker for the study of local pest population structures.

- Dry season (1)
- Wet season (II)
- Biocontrol for endemic pests (A) and (B).
- Short DNA marker sequences of (A) and (B) in blue and red.
- Populations are endemic (III)
- Suppressing the pest population in wet season:

-
- The pest population during the wet season expands without biocontrol:
- Population expansion is shown by red and blue rings around source population A and B.
- In wet season (IV) the biocontrol reduced the pest population level.

Fig. 5, Supplement 1: Genomic studies of pest population show how to use the information for decision making in IPM strategies.

- In rainy season pest moves from the south to the north. For effective control biological control agents (Release of *Trichograma* or *Apantheles*) or parasithoids should be released before pest population migration.
- **The pest is endemic in both regions without migration.** Biocontrol as well as spray is needed with regard to preservation of parasithoids.

Fig.6

Variation in environment affect the genome by gene expression and DNA metylation and by transciptome various proteins are producing biogenic amines that in long short terms affect insect neurotransmission and neurohormones as Octopamine and Dopamine. Brain and nervous systems are important producing important metabolic changes in insects such as Juvenile Hormones and ecdysteroids. The changes of internal body system regulate life cycles and causes plasticity in response to variable environments. References to the plasticity in grasshoppers are given by Hodjat and Saboori (2021). Gene expression effects in pest biology and fixed by transcriptom and epigenetic (Hofmann, 2003).

Fig. 7

Schematic relationships for describing complex interplay between soil, plant and microbe and the effect of drought stress on aphids, crop yield and symbionts. They are important factors that affect IPM strategies and need explaining (Leybourne et al, 2020; Sudakaran et al, 2015). The influence of Malpighian tubules (MT) and insect endosymbionts in defending insects, soil rhizosphere, and climate conditions on crop genotype and their development are also important factors for measuring the effects of drought stress on soils bacterial communities and plant physiology. The stress effects of drought on bacterial communities can lead to selection of various traits in microbiome symbionts and affecting insect pests (Naylor and Coleman, 2017, from Hodjat, in press).