



SFR QUASAV

PhD Students' Day

13TH EDITION

PhD students' work presentation seminar

Tuesday, the Novembre 10th
Virtual seminar
08h45-13h00



Planning of the SFR QUASAV PhD students' day

8h45 : Opening of the doctoral students' day

8h50 : Introduction

First session

9h00 : Erwan CHAVONET – Apple agglutinins, resistance markers to *Erwinia amylovora*?

9h08 : Guillaume CHESNEAU – Dynamics of seed microbiota assembly: from mother plant to mature seed.

9h16 : Souleymane MBALLO – Quantification and modelling of the climatic services provided by trees in a canyon street.

9h24 : Question session

Second session

9h39 : Sekhou CISSE - Development of an alternative in vivo for molecular screening.

9h47 : Julie MALLET - Role of the microRNAs in the photo-control of bud burst in *Rosa 'Radrazz'*.

9h55 : Thibault BARRIT - Role of nitrogen in the plant-fungal pathogen interaction during seedling establishment.

10h03: Question session

Third session

10h18 : Toky RAMANANJATAVO - Characterization and modelling of lettuce growth in apple tree lettuce intercropping.

10h26 : Eva REVOYRON - Transitions towards diversified cropping systems : examples and lessons from farms of the Vendée department.

10h34 : Question session

10h44 : Pause

Fourth session

11h00 : Alexandre PILON - Functional and molecular characterization of *Anopheles gambiae* muscarinic receptors.

11h08 : Jean-Baptiste DOMERGUE - Isotopic and metabolic biomarkers of seed quality.

11h16 : Stéphane PERRIER - Compensation mechanisms resulting from the resistance-associated mutations in *Anopheles gambiae* AcerKis and KdrKis strains.

11h24 : Question session

Fifth session

11h39 : Laure BOEGLIN - Effect of *R. leguminosarum* on *P. sativum*'s root system architecture in response to nitrate signal at seedling establishment.

11h47: Xabi CAZENAVE - Exploiting favourable alleles in apple genetic resources using genomic selection.

11h55 : Question session

Deliberation

12h05 : start of deliberations

13h00 : Announcements of the deliberations and end of the PhD students' day

Video abstracts

You will find all the video abstracts of the PhD students on the following links :

Week 1 : https://youtu.be/kB61o5_c_GM.

- Erwann CHAVONET (ResPom, IRHS) : Apple agglutinins, resistance markers to *Erwinia amylovora* ?
- Guillaume CHESNEAU (EmerSys, IRHS) : Dynamics of seed microbiota assembly : from mother plant to mature seed.
- Souleymane MBALLO (EPHor, Institut Agro) : Quantification and modelling of the climatic services by trees in a canyon street.

Week 2 : <https://youtu.be/BvljFiEXtRI>.

- Sekhou CISSE (SONAS, Nor-Feed) : Development of an alternative in vivo for molecular screening.
- Julie MALLET (STRAGENE et STREMO) : Role of the microRNAs in the photo-control of bud burst in Rosa 'Radrazz'.
- Thibault BARRIT (SMS et FUNGISEM) : Role of nitrogen in the plant-fungal pathogen interaction during seedling establishment.

Week 3 : <https://youtu.be/PbW-A1KzKhk>

- Toky RAMANANJATOVO (EPHor - Institut Agro). Characterization and modelling of lettuce growth in apple tree lettuce intercropping.
- Eva REVOYRON (LEVA, IRHS). Transitions towards diversified cropping systems : examples and lessons from farms of the Vendée department.
- Alexandre PILON (SifCir, UA). Functional and molecular characterization of *Anopheles gambiae* muscarinic receptors.

Week 4 : <https://youtu.be/AyJUY4f9-ok>

- Jean-Baptiste DOMERGUE (SMS, IRHS). Isotopic and metabolic biomarkers of seed quality.
- Stéphane PERRIER (SiFCiR, UA). Compensation mechanisms resulting from the resistance-associated mutations in *Anopheles gambiae* AcerKis and KdrKis strains.
- Laure BOEGLIN (LEVA et SMS, IRHS). Effect of *R. leguminosarum* on *P. sativum*'s root system architecture in response to nitrate signal at seedling establishment.
- Xabi CAZENAVE (ResPom, IRHS). Exploiting favourable alleles in apple genetic resources using genomic selection.

Apple agglutinins, resistance markers to *Erwinia amylovora* ?

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Fire blight is a destructive apple (*Malus domestica*) disease with progressive necrosis caused by the colonization of *E. amylovora* in apoplast. The two essential pathogenicity factors of this bacterium are its exopolysaccharides (EPS), a capsular layer allows *E. amylovora* to progress in tissues, and its type III secretion system (T3SS) involved in host cell death by injecting protein effectors (Vanneste *et al.*, 2000). Susceptible varieties can be protected by eliciting their defence by spraying acibenzolar-S-methyl (ASM) (Brisset *et al.*, 2000), a functional analogue of salicylic acid (Oostendorp *et al.*, 2001). Recently, a global analysis of the transcriptome determined a new ASM-induced agglutinins (*MdAGGs*) (Warneys *et al.*, 2018). Agglutinins are proteins referenced in plant defence to aggregate bacterial cells by binding to their extracellular carbohydrate (Peumans & Van Damme, 1995). The structural model of *MdAGGs* suggested that agglutinin forms homodimers with carbohydrate binding site on both sides (Warneys *et al.*, 2018). Our research revealed that *MdAGGs* were excellent resistance markers such as the fact that the induction and accumulation of *MdAGGs* were correlated with the protective persistence provided by ASM against *E. amylovora*. Using bacterial mutants, we suggested that *E. amylovora* were able to repress *MdAGGs* induction in susceptible apple genotype by direct intervention of these effectors or indirect/direct intervention of EPS. We established the agglutination ability of *MdAGGs* by mixing purified recombinant proteins with *E. amylovora* suspensions. Only the unencapsulated mutant formed aggregates in the mixture but the addition of EPS inhibited bacterial agglutination as well as mix with a wild-type strain, showing the saturating role of EPS. We hypothesized that ASM induce agglutinins quickly to prevent fire blight colonization before bacteria feeds on the necroses sufficiently to secrete enough EPS and inhibit agglutination.

Keywords : Fire blight, Apple, Agglutinin, Induced resistance, PRI

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Dynamics of seed microbiota assembly: from mother plant to mature seed.

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Seed microbiota contributes to the improvement of seed vigor and the development of healthy seedling. Members of the seed microbiota are derived from three main pathways: systemic, floral and external. To date, the relative importance of these pathways and the order and timing of microbial taxa immigration during seed microbiota assembly are unknown. In this study, we investigated the dynamic of seed microbiota assembly of bean (*Phaseolus vulgaris*).

We estimated the structure of bean ($n=600$) individual seed bacterial communities during four seed developmental stages. We assessed the relative contribution of stochastic and deterministic processes with null community model. Finally, to evaluate the bacterial seed transmission routes, other habitats (flowers, stems, and atmosphere) were also sampled.

According to this estimation, an average of four bacterial taxa were detected per individual seed, with a single dominant taxon per seed representing between 75 to 100% of all reads. Variation of seed bacterial community structure was not only important between plants but also within the same plant whatever the stage of development considered. B-null deviation measure indicated that stochastic processes were driving seed bacterial communities structure at each seed developmental stage. Most of the seed-associated bacterial taxa were detected in the atmosphere, which suggested that these taxa were acquired from the external pathway.

In conclusion, seeds are endowed with a single dominant bacterial taxon, whose phylogenetic identity is highly variable, confirming the « primary symbiont hypothesis ». We are currently demonstrating the impact of this variation in community structure on seedling fitness.

Keywords : Bacterial transmission, Neutral processes, *Phaseolus vulgaris*, Seed microbiota

Quantification and modeling of the climatic services provided by trees in a canyon street

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Abstract - Growing urbanization makes the city an increasingly vulnerable area to heat. In addition to the anthropogenic cause and to the urban form that influences the wind speed and the absorption and reflection phenomena of incident solar radiation, the reduction in the proportion of vegetation is one of the main causes of urban overheating. Among the consequences of urbanization on the urban microclimate, the most known is the Urban Heat Island (UHI) phenomenon, which is a kind of heat accumulation phenomenon within urban area due to urban construction and human activities (Yang et al., 2016). UHI is considered as one of the major problems in the 21st century posed to human beings as a result of urbanization and industrialization of human civilization (Rizwan et al., 2008). Extensive studies of the characteristics of UHI effect carried out in recent decades by authors such as (Arnfield, 2003; Rizwan et al., 2008) have shown that the UHI effect is closely related to urban heat release, surface properties and structure, vegetation coverage, population density and weather conditions (Yang et al., 2016). Vegetation plays an increasingly important role in urban planning policies because it helps reduce temperature peaks in cities during heat waves. Studies such as those of (Aboelata, 2020; Andreou, 2014) have been carried out on urban canyons, and others on urban areas as those of (Gebert et al., 2019; Gillner et al., 2015) to study the impact of vegetation. Many studies on the impact of vegetation on the urban microclimate have been undertaken in recent decades, but few have been carried out on tree-covered canyon streets. Canyon streets are representative places of the urban environment. The objective of my thesis is to quantify and analyze the climatic services provided by trees in urban areas and to study the impact of environmental conditions and water restrictions on these services. We carry out measurement campaigns on a canyon street on a scale of 1/5th and we also conduct numerical simulations using the ANSYS FLUENT software. A study to transpose the results into real scale will also be undertaken.

Keywords: *urbanization, microclimate, tree, numerical modeling, canyon street, climatic services*

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Development of an alternative *in vivo* model for molecular screening

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For a long time, antibiotics have been used as growth promoters for preventing diseases and improving zootechnical performances of animals. Nevertheless, due to the development of resistance to antimicrobials, this application has been banned in Europe, giving way to alternative options. Among these solutions, citrus extracts are particularly interesting. Indeed, a recent trial conducted by Nor-Feed has shown significant effects of a citrus extract on broiler chicken growth performance. The objective here is to evaluate the influence of this citrus extract major component on zootechnical performances and on microbiota of animals. To do that, the development of an *in vivo* molecular screening model is crucial, due to the high number of compounds present inside the citrus extract. The work presented here are about the development of this model. The insect model *Tenebrio molitor* have been chosen because of its simplicity and rapidity, in addition to the many common point with monogastric animals. Two aspects are evaluated: The growth parameters and the intestinal microbiota evolves. Regarding the growth parameters, first results showed that under controlled environmental conditions, the growth of the insect model is standard and similar to a linear model. Nonetheless, conversely to the observation made in monogastric, the addition of additive didn't show any significant effect on growth parameters of the insect model, probably due to the optimal growth condition. The growth of the insect model was therefore evaluated under stress condition. Preliminary results show a significant and repeatable effect of light stress and dietary stress on the growth of the insect model. However, temperature stress didn't show any effect. Concerning the evolution of microbiota, feed supplementations have been performed on the insect model, in order to bring it as close as possible to the microbiota of monogastric. The different tested group were respectively fed with poultry faeces, bacteria of a standardized intestinal microbiota of chicken and one or more strains of lactic bacteria. The first results showed no effect of the supplementations on the microbiota of the insect model, which remains more than 90% composed by *Spiroplasma*. One of the hypotheses to explain these results concerned the period of fasting implemented between the end of supplementation and sequencing. Other studies are needed to confirm these hypotheses.

To conclude, studies concerning the development of this alternative model are still ongoing. Supplementation tests with citrus extract are programmed on the insect model under stress. Others experiments are also being studied about the intestinal microbiota

Keywords : *alternative model, Tenebrio, intestinal microbiota, growth parameters*

Role of the microRNAs in the photo-control of bud burst in Rosa 'Radrazz'

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Shoot branching is highly determinant in plant architecture elaboration, and its control in production ensures high productivity and visual quality, in order to meet consumer expectations while taking production constraints into account. This process is highly dependent of environmental factors, especially light, which is a major determinant in this process (Leduc et al., 2014). The main objective of our team aims to tackle the complexity of the hormone (SL, IAA, GA, CK, ABA) and nutrient (sugar, nitrogen) regulatory network behind the branching process in response to environment (i.e. light). Our teamwork, focused on the rosebush as an important plant in ornamental horticulture, demonstrated the absolute requirement of light to trigger bud burst in Rosa 'Radrazz' (Girault et al., 2008). At the molecular level, while a great progress has been made in terms of transcriptional regulation into this network, in contrast, little is known on the role of post-transcriptional regulation in control of bud growth in response to this environmental signal (Barbier et al., 2015, Azri et al., 2015, Henry et al., 2011). In this context, my thesis aims to provide new insights in post-transcriptional mechanisms underlying the control of bud outgrowth via elucidating the role of microRNAs. Combined high throughput sequencing of small RNAs and mRNA (from RNA extracted from axillary buds) approach was used to identify novel and conserved microRNAs and their potentially targeted transcripts involved in the light regulation of bud outgrowth.

A set of known and novel microRNAs were identified (about 110 novels microRNAs and 160 conserved) in the axillary buds and selected candidates are based on their differential expression in dormant (dark condition) versus outgrowing buds (light condition) and on their potentially involvement in metabolic and hormonal regulatory pathways. Their target genes were predicted by bioinformatics analysis by complementary sequence analysis.

Expression patterns of these pairs of candidates (microRNAs and target genes) will be validated by qRT-PCR and their biological function investigated *in planta*. In order to confirm the microRNAs / target gene interactions, co-infiltrations on tobacco leaves are carried out with GFP fluorescence analysis.

Keywords: *Bud outgrowth, Rosa, microRNAs, Light, Post-transcriptional regulation, Sequencing*

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Role of nitrogen in the plant-fungal pathogen interaction during seedling establishment

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Seed germination and seedling development are critical steps for successful crop establishment. These steps are very sensitive to environmental factors such as nitrogen availability in the soil or the presence of fungi. Because of the development of an agriculture at the same time sustainable and efficient, the control of these factors is becoming less precise, creating a real interest in the study of the effect of nitrogen fertilization on plant-fungal pathogen interactions during seedling establishment. Indeed, nitrogen plays a central role in plant-pathogen interactions, not only as an essential nutrient for the development of plants and fungi, but also as a constituent of many plant defense molecules. It is important to note that the impact of nitrogen on plant-fungus interactions is complex and cannot be generalized. It can, depending on the pathosystem and the forms it takes (ammonium, nitrate, amino acids), favor either the plant or the fungus. In addition, the role of nitrogen in these interactions has never been studied during the seed germination and development of seedlings, for which there are specificities to underline. Indeed, the seedling stage is distinguished from the adult stage by its access to two sources of nitrogen: an endogenous source originating from the mobilization of the seed reserves and an exogenous source originating from the absorption of nitrogen present in the medium by the roots (mainly in the form of nitrate). Nitrate is also a signal molecule, involved in the growth of the primary root, in the metabolism and in the defense responses of the plant. It is in this context that this work on the role of nitrogen on the interaction between *Arabidopsis thaliana* and *Alternaria brassicicola*, a necrotrophic fungus transmitted to and by the seed, was undertaken. The effect of different concentrations and forms of nitrogen (ammonium or nitrate) on the course of both germination and seedling development, and on the development of the fungus and symptoms on the plant, is characterized on a panel of genotypes resistant and sensitive to the fungus. For this, a new *in vitro* pathosystem was developed, allowing the study and the phenotyping of the early stages under the studied conditions. It allowed, in particular, to show that the seedlings grown in nitrate condition seem more resistant to the fungus than those cultivated in ammonium condition. Secondly, in order to explain the differences observed in the different conditions (genotypes or nitrogen), a study of the primary metabolism of nitrogen (determination of nitrate by HPLC, of amino acids by GC-MS, study of the expression of the genes of the plant and the fungus linked to the absorption of nitrate and its metabolism by qPCR) will be carried out. In this objective, defense pathways and metabolites (dosage of plant defense compounds in collaboration with the PHYTO platform of the SFR Quasav, study of the expression of plant defense genes by qPCR) as well as pathogenetic factors (study of the expression of genes linked to pathogenicity of the fungus by qPCR) will also be studied.

Keywords: *Arabidopsis thaliana*, *Alternaria brassicicola*, plant-pathogen interactions, nitrogen, pathosystem.

Characterization and modelling of lettuce growth in apple tree-lettuce intercropping

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Agroforestry systems are amongst the most sustainable approaches to ensure a high production through the tree-crop complementarity in terms of land and resources use (Dupraz and Liagre, 2008). Garden-Orchards are agroforestry-based fruit and vegetable production system in which intercropping between various vegetables with fruit trees has been implemented. Despite the multiple advantages of these cropping systems (Ouma and Jeruto, 2010), no scientific studies have been carried out to quantify their efficiency in terms of resource use. This study aims at characterizing an association of 20-year old apple trees (*Malus x domestica* Borkh) with a drip-irrigated lettuce crop (*Lactuca sativa* L., var. Olana) by experimental and modelling approaches. We studied the apple tree-induced microclimate and its effects on lettuce growth. Leaf area and biomass dynamics of lettuce as well as soil mineral nitrogen and soil water content were monitored on five lettuce beds located at a distance of 1.5 to 5 m from the apple trees during one growing season. Furthermore, nitrate in soil solution was monitored at 30 and 90 cm depth using ceramic suction lysimeters. All datasets were then used to calibrate growth of lettuce in the STICS crop model (Brisson et al., 2009). Shading improved climatic conditions in summer by lowering air temperature, which increased the lettuce's growth rate. During a heat spell on a sunny summer day, the measured temperature difference between the lettuce beds closest to the apple trees and those situated 5 m from the row was 2°C. Nitrate in soil solution was very low for all lettuce beds (under 8 mg NO₃-N.L⁻¹). Calibration of lettuce in STICS was satisfactory. Both variables related to plant growth and those related to soil were generally well simulated. Validation of the lettuce parametrization in STICS will be done by means of a second lettuce culture currently in progress. Finally, the modelling of the spatiotemporal dynamics of C, N and water in the system will be performed later with the Hi-sAFe model (Dupraz et al., 2019), which consists in coupling the STICS crop model to a tree model.

Keywords: Garden-Orchard system, nitrogen, microclimate, soil moisture, STICS

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Transitions towards diversified cropping systems: examples and lessons from farms of the Vendée department

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Diversified cropping systems are a fundamental component of resilient farming systems. However, the trend in Europe for the past 50 years has rather been a simplification of these cropping systems, leading to lock-in effects around a few major crops. A range of barriers preventing the development of minor crops have been identified along value-chains, from seed production to farming to processing and distribution. The pathways of change through which actors from agrifood systems could overcome these barriers are less well known. We studied the case of the French department of Vendée where, apart from the main crops (wheat and maize), around 15 different cash crops are grown on areas ranging from 1 to 5% of the total annual crops' area. In-depth surveys were carried out with farmers growing one or several of these crops, to understand why and how they had changed their practices towards crop diversification. Our first results show that there are contrasted dynamics of transition to more crop diversity depending on the farms: some farmers will progressively add new crops to their systems, while others will completely change their cropping systems from one year to the next, and then adjust the species and their respective shares in the crop rotation. Most farmers in the "progressive" dynamic initially diversify their cropping systems to solve technical or economic issues encountered on their major crops, while for the farmers who evolve more rapidly crop diversification is often part of a more global transformation of the farm. The resources that farmers mobilize in order to take charge of the specificities of the introduced minor crops are also strongly correlated to the type of diversification dynamic. Farmers in the "progressive" dynamic usually have marketing strategies oriented towards security, through annual production contracts that are locally available on a limited number of crops (e.g. hemp, lentil, linseed). This type of outlet grants them access to productive resources (equipment, workforce) external to their farm when necessary, and to specific advisory services associated with the contracts. On the other hand, farmers in the "transformation" dynamic are looking for more flexibility or autonomy in their strategies, at the cost of more unsecure outlets and resources. They often try to manage without external equipment or workforce. To compensate for the lack of local examples and references on the diversification crops, they strongly rely on references and shared experiences from web resources, and on their own experience.

A complementary analysis on crop diversification processes in different regions and contexts in Europe will enable us to compare these results with varied situations and to identify more generic levers and local specificities for crop diversification.

Functional and molecular characterization of *Anopheles gambiae* muscarinic receptors

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Agriculture has to face a great challenge: it must be ensured that enough high-quality food is available to meet the needs of a continuously growing population. Even if chemical pesticides such as insecticides have been used successfully in controlling a number of pest insects, their widespread uses during several decades has led to environmental and health concerns. It is then necessary to develop new strategies in order to reduce the use of pesticides in accordance with the Ecophyto 2+ program.

The strategies developed in the laboratory are based on the intracellular calcium increase which modulates the sensitivity of insecticide targets. Indeed, it has been shown on *Periplaneta americana* neurones that intracellular calcium increase *via* muscarinic receptors (mAChRs) activation elicited by repellent leads to increase the insecticide neuronal target sensitivity¹. Muscarinic receptors could then be good candidates to develop a strategy leading to enhancement of the efficiency of insecticide treatment which can be used in pest control as well as in vector borne disease control. In this study, we propose to characterize mAChRs of mosquitoes *Anopheles gambiae*, known as the main malaria vector.

Insects mAChRs are known only in a few species and their molecular characterization remains to be explored. In drosophila *Drosophila melanogaster*, three types of mAChRs named mAChR-A, mAChR-B and mAChR-C have been found. Whereas the mAChR-A and mAChR-C are coupled to calcium signalling across G $\alpha_{q/11}$ protein activation, the mAChR-B is linked to AMPc signalling across G $\alpha_{i/o}$ protein activation^{2,3,4}.

Based on these knowledges, our study consists in the molecular, functional and pharmacological characterization of *An. gambiae* mAChRs. Using a bioinformatic approach we shown the existence of a mAChR-A, two variants of mAChR-B named mAChR-B1 and mAChR-B2, and a mAChR-C in the anopheles which are homologous to their drosophila counterpart. To explore the signalling pathway of mAChR-A and its pharmacology, this receptor was expressed in Sf9 cell line. Using calcium imaging we shown that mAChR-A is activated by acetylcholine, muscarine and oxotremorine and blocked by atropine. By using proteins inhibitors, we demonstrated that mAChR-A activation leads to an increase of intracellular calcium induced by the activation of the phosphoinositide pathway. Thus, in this study, we demonstrate that as the activation of anopheles mAChR-A induces the increase of cytoplasmique calcium, this receptor could be considered as a key element in a strategy to enhance insecticide treatment while reducing doses.

Keywords: Muscarinic receptors, *Anopheles gambiae*, heterologous expression, calcium imaging

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Isotopic and metabolic biomarkers of seed quality

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Seed quality plays a major role in modern agriculture. The term "quality" is broad and includes varietal or specific purity of seeds lots, phytosanitary quality, germinative vigor and resistance to ageing, stress and diseases. Having seeds of sufficient quality is therefore essential for crop production (yield) and food industry. As such, it has been suggested that "good quality seeds are the basic source of a secure food supply" (Wimalasekera, 2015). Understandably, many research projects are devoted to molecular and genetic determinants of seed quality in crops. However, despite the importance of metabolism in germination (energy generation and reserve remobilization) and seedling establishment (anabolism and development of autotrophy), little is known on metabolic determinants of seed quality. To address this question, this thesis involves two research topics: the use of mutants affected in germination performance in *Arabidopsis* and *Nicotiana sylvestris*, and the use of natural variability (in germination performance and velocity of seedling establishment) in barrel clover (*Medicago truncatula*). The first part takes advantage of my work initiated during my Master 2, and exploits respiratory mutants affected in the mitochondrial complex I, which have a germination phenotype (low germination rate, and slow post-germinative development). Two likely causes for this phenotype are examined: First, a purely metabolic effect, whereby the mutation impacts on lipid metabolism. This involves analyses by lipidomics, absolute lipid quantification and nuclear magnetic resonance for phospholipid quantitation; Second, a metabolic signaling effect, whereby amino acid homeostasis and the regulation of translation are impacted by mitochondrial metabolism during germination. The second part of the thesis exploits a "core collection" of *M. truncatula* to study the natural variability in metabolic parameters (metabolite content, natural isotope abundance) and how it relates to quality indicators. I will be using techniques such as GC-MS, EA-IRMS and GC-C-IRMS, i.e. mass spectrometry techniques allowing metabolomics profiling and measurements of natural isotope abundance (delta values). The use of isotopes is an important objective of this thesis, because we might be able to find simple relationships between quality of seeds and delta values, while delta values are easy to measure and therefore have a significant potential for agronomic application.

Keywords: isotopes, metabolism, metabolomics, lipidomics, seed quality, vigor, germination.

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Compensation mechanisms resulting from the resistance-associated mutations in *Anopheles gambiae* AcerKis and KdrKis strains

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Malaria is mostly transmitted by *Anopheles gambiae* mosquitoes. It accounts for a total of about 405,000 deaths and 228 million contamination cases each year (WHO, 2019). Malaria transmission is controlled via the use of insecticide-treated bed nets (ITNs) integrated in insecticide-based mosquito control. However, insecticide resistance arises massively in vector mosquitoes, causing control failure and resurgence of malaria (Ranson and Lissenden, 2016). Previous studies highlighted that these resistance mechanisms are very complex since they induce unexpected compensation mechanism that strengthen mutation-altered physiological functions. Compensatory mechanisms obviously impact the effectiveness of Insect Resistance Management (IRM) and insecticide-based strategies. As silent point mutations are the most common resistance phenomenon, we investigated the compensatory neuronal mechanisms following the development of resistance-associated point mutations in two strains of *Anopheles gambiae* resistant to two distinct class of insecticides : 1) Acerkis strain, resistant to organophosphates and carbamates (Ace-1_R, G119S substitution in acetylcholinesterase 1) and 2) KdrKis strain, resistant to pyrethroids (kdr, L1014F substitution in voltage-gated sodium-channels). We use RT-qPCR, electrophysiological and calcium imaging approaches adapted to isolated *Anopheles gambiae* neurons (Laviaille-Defaix et al., 2011) to characterize changes in the expression and pharmacological profile of neuronal nicotinic acetylcholine receptors (nAChR) following the mutations G119S in AcerKis strain and L1014F in KdrKis strain compared to the laboratory reference *Anopheles gambiae* Kis strain. We report that 1) higher nAChR density associated with reduced AChE1 activity is observed in AcerKis strain, and 2) modification of biophysical properties of the voltage-gated sodium current impacts nAChR sensitivity to acetylcholine, the most abundant endogenous excitatory neurotransmitter. These physiological modifications act as compensatory mechanism in the cholinergic system upon resistance-associated mutation appearance. They need to be taken into account to adapt vector control strategies as they deeply influence insecticide efficacy.

Keywords: Mosquitoes, *Anopheles gambiae*, Vector control, Insecticide resistance, Compensation mechanisms

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Effect of *R. leguminosarum* on *P. sativum*'s root system architecture in response to nitrate signal at seedling establishment

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Effectiveness of weed control during intercrop establishment, such as legume-rapeseed intercrops, is strongly related to the ability of the two-companion species to run for soil resources, especially for mineral nitrogen N (Corre-Hellou *et al*, 2011). Mineral N is indeed a key driver of competition between plants; however, legumes are known to be poorly competitive for soil N uptake (Hauggaard-Nielsen *et al*, 2001). Dayoub *et al* (2017) demonstrated that competitiveness for mineral N absorption is highly correlated to lateral root -LR- development. But in the particular case of legumes, LR formation -induced by nitrate signal- is in competition with nodule formation, which is under control of nodulation factors secreted by Rhizobia (Herrbach *et al*, 2014).

In order to explore the early trade-offs between LR and nodule formation as a function of soil nitrate concentration, we phenotyped in the first instance the root system architecture of young pea (*Pisum sativum*) under various nitrate concentration in the presence or absence of *Rhizobium leguminosarum*. Our objectives were: (i) to determine patterns and threshold values around which the root architecture is highly contrasted (ii) to study how the presence of *Rhizobium* influences phenotypically the root architecture in interaction with exogenous nitrate concentration. In a second step, the expression of genes specific to nitrate signal and to the symbiosis will be studied at the early stage of pea establishment. This particular observation window allowed us to cut up the complexity governing the early morphological development of roots.

Keywords: *pea, root, seedling establishment, nitrate signal, biological nitrogen fixation, symbiosis*

References: Corre-Hellou *et al*. 2011. *Field Crops Res* 122: 264-272; Dayoub *et al*. 2017. *Heliyon* 3(2); Hauggaard-Nielsen *et al*. *Field Crops Research* 70:101–109; Herrbach *et al*. *Journal of Plant Physiology*, 171: 301– 310

Exploiting favourable alleles in apple genetic resources using genomic selection

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Although more than 10.000 apple cultivars have been documented worldwide, modern commercial apple production is dominated by only a few cultivars. Broadening the genetic diversity used in breeding programs thus appears as a necessity in order to reduce the vulnerability resulting from genetic uniformity¹. In this context, the identification of genetic resources that contain favourable alleles absent or rare in elite material is of primary importance for breeders. Harnessing this genetic diversity will probably require several generations of crosses starting from genetic resources, so that parents carrying the identified favourable alleles are ready to be used in breeding programs. In order to efficiently transfer these alleles, we propose to use genomic selection, a breeding approach that aims to estimate the breeding value of selection candidates using only genetic markers information².

To do so, apple genetic resources (i.e. old varieties), elite material and hybrids between them have been genotyped and phenotyped so that prediction equations can be developed in order to evaluate the potential of genetic resources. As a preliminary step, these equations were built using data from either elite material or genetic resources and prediction accuracies were assessed and compared. To further improve the choice of the individuals used to build the model, various optimisation algorithms were also used before estimating these accuracies³. Given the differences in allele frequencies and linkage disequilibrium patterns between the two datasets, the predictive ability of these models is expected to differ. One way to account for the differences is to combine these datasets and to use models that allow the estimation of population-specific effects⁴. We will discuss the assets of such an approach and how it could be effective to evaluate selection candidates. Overall, the obtained results should help us identify breeding strategies intended to efficiently transfer interesting alleles from genetic resources into elite material.

Keywords : genetic diversity, genomic selection, apple breeding, training set, population combination

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