Brussels, 24 October 2016

COST 106/16

DECISION

Subject: **Memorandum of Understanding for the implementation of the COST Action "EuroXanth: Integrating science on Xanthomonadaceae for integrated plant disease management in Europe" (EuroXanth) CA16107**

The COST Member Countries and/or the COST Cooperating State will find attached the Memorandum of Understanding for the COST Action EuroXanth: Integrating science on Xanthomonadaceae for integrated plant disease management in Europe approved by the Committee of Senior Officials through written procedure on 24 October 2016.

MEMORANDUM OF UNDERSTANDING

For the implementation of a COST Action designated as

COST Action CA16107
EUROXANTH: INTEGRATING SCIENCE ON XANTHOMONADACEAE FOR INTEGRATED PLANT DISEASE MANAGEMENT IN EUROPE (EuroXanth)

The COST Member Countries and/or the COST Cooperating State, accepting the present Memorandum of Understanding (MoU) wish to undertake joint activities of mutual interest and declare their common intention to participate in the COST Action (the Action), referred to above and described in the Technical Annex of this MoU.

The Action will be carried out in accordance with the set of COST Implementation Rules approved by the Committee of Senior Officials (CSO), or any new document amending or replacing them:

a. "Rules for Participation in and Implementation of COST Activities" (COST 132/14);
b. "COST Action Proposal Submission, Evaluation, Selection and Approval" (COST 133/14);
c. "COST Action Management, Monitoring and Final Assessment" (COST 134/14);
d. "COST International Cooperation and Specific Organisations Participation" (COST 135/14).

The main aim and objective of the Action is to Present, emerging or re-emerging plant diseases due to infection by bacteria of the Xanthomonadaceae family are continually challenging food security and cause significant losses to the EU economy each year, thus demanding for concerted R&D actions at the international level, which will be supported by the COST Action networking instruments.. This will be achieved through the specific objectives detailed in the Technical Annex.

The economic dimension of the activities carried out under the Action has been estimated, on the basis of information available during the planning of the Action, at EUR 68 million in 2016.

The MoU will enter into force once at least five (5) COST Member Countries and/or COST Cooperating State have accepted it, and the corresponding Management Committee Members have been appointed, as described in the CSO Decision COST 134/14.

The COST Action will start from the date of the first Management Committee meeting and shall be implemented for a period of four (4) years, unless an extension is approved by the CSO following the procedure described in the CSO Decision COST 134/14.

OVERVIEW

Summary
Bacteria of the family *Xanthomonadaceae*, including species of *Xanthomonas* and *Xylella fastidiosa*, belong to the most devastating plant pathogens continually challenging food security. Many of the pathogens are listed as quarantine organisms in the EU and their study is of uttermost importance. The concerned pathogens infect all kinds of crop plants, such as cereals, forage crops for ruminant feed, vegetables, fruits, shrubs and trees.

This COST Action will bring together some of the brightest and best minds to join in an interdisciplinary network to develop strategies for sustainably protecting plants and significantly reducing yield losses. Specifically, this initiative will address several key aspects of the pathogen-vector-host interactions from the cellular to the population level. A better insight into population structures and virulence mechanisms of the pathogens, together with the exploration of the molecular mechanisms underlying disease resistance to the pathogen, will enable development of durably resistant plant cultivars and exploitation of bio-control schemes tailored to population and pathogen.

This Action will generate a platform that gathers experts from different disciplines, such as molecular diagnostics, molecular host-microbe interactions, plant resistance breeding, and applied microbiology. Joining their efforts will help to develop and implement effective plant protection schemes, be it via resistant crop cultivars or via other control mechanisms. This goal will be achieved by mobilizing and training scientists from major European institutions, regulatory bodies and commercial companies working on the various aspects of this complex of problems.

Areas of Expertise Relevant for the Action	**Keywords**
● Agriculture, Forestry, and Fisheries: Microbiology ● Agriculture, Forestry, and Fisheries: Sustainable Agriculture ● Agriculture, Forestry, and Fisheries: Agriculture related to crop production, soil biology and cultivation, applied plant biology, crop protection ● Agriculture, Forestry, and Fisheries: Ecology (theoretical, community, population, microbial, evolutionary ecology) ● Agricultural biotechnology: Genetic engineering, transgenic organisms, recombinant proteins, biosensors for agricultural biotechnology, animal biotechnology	● Genetic Diversity ● Molecular Plant-Pathogen Interaction ● Resistance Gene ● Xanthomonas ● Xylella fastidiosa

Specific Objectives
To achieve the main objective described in this MoU, the following specific objectives shall be accomplished:

Research Coordination
● To develop, implement, compare and standardize methods of pathogen detection by coordinating research on molecular diagnostics of plant-pathogenic Xanthomonadaceae (WG1)
● To estimate the risk of epidemics and outbreaks by coordinating research on the genetic diversity and population structure of plant-associated Xanthomonadaceae (WG1).
● To develop, distribute and valorize bioinformatics tools for data analysis by coordinating research and development in the field of epidemiology and population genetics (WG1).
● To identify key bacterial factors in the microbe-eukaryote interaction at different steps of the infection/dissemination cycle by coordinating research on the pathogen's biology (WG2).
● To identify elicitors of plant defense responses as targets for resistance breeding by coordinating research on pathogen-associated molecular patterns and effector-triggered immunity (WG2).

● To discover novel resistance traits by coordinating research on QTL mapping, genome-wide association studies, comparative genomics and transcriptome analyses (WG3).
● To generate durably resistant crop cultivars by coordinating research and development in the field of breeding, transgenesis and genome editing of resistance traits (WG3).
● To evaluate and establish disease control measurements by coordinating research on the impact of biological products/microorganisms to control xanthomonads and X. fastidiosa and to prevent the spread of infections (WG4).
● To evaluate and compare approaches to eliminate or reduce vector populations by coordinating research on adapted agronomic practices, effects of volatile compounds, and trapping systems (WG4).

Capacity Building
● Continued education of European investigators and linking them with most relevant stakeholders (e.g. EPPO, national regulatory authorities and companies active in the fields of crop breeding, biocontrol or development of diagnostic tools) by annual general conferences covering topics of all four working groups.
● Target-oriented training of European investigators by specific workshops that will introduce the concepts of new technologies, methods and tools, along with hands-on training to foster familiarity with these techniques.
● Mentoring of early-career European investigators by a training school that will be dedicated to skills required by early-career investigators to develop a successful career in the field.
● On-site training of European investigators, mainly at the early-career stage, by inter-laboratory exchange of personnel in the frame of Short-Term Scientific Missions (STSM).
● Lower entrance hurdles for young scientists and newcomers in the field by collecting, drafting, and making available guidelines for experimental approaches to avoid time-consuming, erroneous investments.

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COST Association, International not-for-profit organisation/Association internationale sans but lucratif Register of legal Entities Brussels: 0829090573
COST Association
Avenue Louise 149 I 1050 Brussels, Belgium
t: +32 (0)2 533 3800 I f: +32 (0)2 533 3890
office@cost.eu I www.cost.eu

TECHNICAL ANNEX

1. S&T EXCELLENCE

1.1. Challenge

1.1.1. Description of the Challenge (Main Aim)

Food security is of key importance for the welfare of individuals and communities, and is defined as where “all people at all times have access to sufficient, safe, nutritious food to maintain a healthy and active life” (World Food Summit, 1996). Yet, food supply is always at risk due to various challenges, with plant pathogens as a major cause of severe losses. At the same time, “safe food” requires limiting the use of pesticides as a means to counteract pathogens because of its detrimental effects on humans and ecosystems, which led to the formulation of the EU directive 2009/128/EC on a European Community action to achieve the sustainable use of pesticides. Pressure on food security may even increase in the future due to disadvantageous climatic conditions, concomitantly leading to economic and social problems. Pressure on food security is even more relevant in the current climate change that is likely to favor conditions for pathogen development and higher/faster migration and adaptation potential in pathogens and pathogen vectors. In addition, climate change scenarios predict an increase in epidemic severity and a northwards geographic expansion of pathogen distribution in Western Europe. Finally, accelerated human migration, including refugees, and international trade bear an addition risk for the emergence of disease epidemics.

The bacterial genera Xanthomonas and Xylella, both belonging to the family Xanthomonadaceae, harbour some of the most devastating plant pathogens continually challenging food security. Collectively, strains of these taxa can infect a plethora of plants found in agriculture, forest or unmanaged ecosystems. Notably, four of the top10 plant pathogenic bacteria in plant pathology belong to these two genera: Xanthomonas axonopodis pathovars, Xanthomonas campestris pathovars, Xanthomonas oryzae pv. oryzae, and Xylella fastidiosa[1]. In this COST Action, we will bring together some of the brightest and best minds to join in an interdisciplinary network to develop strategies for sustainably protecting plants and significantly reducing yield losses. Specifically, this initiative will address several key aspects of the pathogen-vector-host interactions from the cellular to the population level. A better insight into population structures and virulence mechanisms of the pathogens, together with the exploration of the molecular mechanisms underlying disease resistance to the pathogen, will enable development of durably resistant plant cultivars and exploitation of bio-control schemes tailored to population and pathogen.

1.1.2. Relevance and timeliness

As a universal threat to food security, yield loss due to plant diseases causes losses of billions of Euros to the EU economy each year. The use of disease resistant crop varieties constitutes an economically and ecologically sustainable strategy in plant disease control. Unfortunately, the efficacy of resistance genes is continually challenged by the emergence of new pathogenic strains, necessitating isolation and exploitation of new sources of broad-spectrum resistance and to pyramiding them in order to increase efficacy and durability[2]. Breakdown of resistance can occur after only a few cropping seasons and durability of resistance genes cannot be reliably predicted without knowledge of the underlying molecular mechanisms and the evolutionary potential of the

[1] Mansfield J, et al. (2012). Top 10 plant pathogenic bacteria in molecular plant pathology. Mol. Plant Pathol. **13**: 614-629.

[2] Kumar Joshi R & Nayak S (2010). Gene pyramiding - a broad spectrum technique for developing durable stress resistance in crops. Biotechnol. Mol. Biol. Rev. **5**: 51-60.

pathogen population. Obviously, breeding of ever more disease resistance traits into crop varieties by trial and error is a slow and costly endeavour. As an alternative to plant breeding, plant-pathogenic bacteria can be defeated using antimicrobial substances or competing microorganisms. For instance, application of bacteriophages is a re-emerging strategy to combat bacteria, both in human health and crop protection[3].

This COST Action will focus on major pathogens in the bacterial genera Xanthomonas and Xylella, which, as closely related members of the same taxonomic family, share several features enabling synergies in the study of plant-pathogen interactions. Many of these pathogens are listed as quarantine organisms in the EU and their study is of uttermost importance. These pathogens affect all kinds of crop plants, such as cereals (e.g. wheat, barley), forage crops grown for ruminant feed (e.g. ryegrasses, fescues), vegetables (e.g. haricot bean, cabbage, onion, pepper, tomato), fruits (e.g. apricot, cherry, peach, plum, strawberry), shrubs and trees (e.g. almond, citrus, grape-vine, nuts, olives).

The European research community occupies a leading position in the field of molecular plant pathology, including genomics, diagnostics, plant breeding and bio-control. Furthermore, national, multinational and EU-funded projects were and are key in the acquisition and exploitation of molecular insight into the most important plant pathogens, including Xanthomonas and Xylella. Yet, a major problem is that research teams in the EU often focus on specific plant-pathogen models (pathosystems) using distinct approaches (diagnostics, molecular mechanisms, bio-control) and often lack an integrated view extending from the population structure to the biotech application. Hence, gathering researchers and linking them with potential users of their research under the umbrella of a COST Action will bring substantial benefits to European breeding companies, biotechnology companies, regulatory authorities and the European research community.

1.2. Objectives

1.2.1. Research Coordination Objectives

This COST Action will provide a platform to coordinate the various national and institutional research activities that are related to plant-pathogenic Xanthomonadaceae, including diagnostics, epidemiology, resistance breeding and bio-control measurements. The following activities will be implemented:

- Generate standardized, platform-independent methods for detection & diversity analysis of bacterial plant pathogens (inter-laboratory ring tests);
- Develop and evaluate protocols for resistance and pathogenicity screening of the most important crop species and bacterial strains, respectively;
- Organize international test performance study (validation of test performance in terms of accuracy, analytical specificity, analytical sensitivity, repeatability, and reproducibility as defined by European Plant Protection Organization [EPPO] standard PM7/98);
- Adopt appropriate methods for molecular strain typing, depending on the scale of analysis;
- Share data with partners and disseminate them using internet-accessible databases;
- Enable a multidisciplinary exchange of knowledge and resources among scientists from different areas (microbiology, molecular genetics, plant pathology, evolutionary ecology, agronomy) and working on various host-pathogen systems;
- Update and improve the comprehensive website on Xanthomonas/Xylella virulence factors (see http://www.xanthomonas.org);
- Facilitate exchange of plant germplasm (carrying specific resistance traits) and bacterial isolates for research as well as for the development of novel plant germplasm.

1.2.2. Capacity-building Objectives

[3] Gross M (2014). Phage therapies for plants and people. Curr. Biol. **24**: R541-R544.

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COST Association
Avenue Louise 149 I 1050 Brussels, Belgium
t: +32 (0)2 533 3800 I f: +32 (0)2 533 3890
office@cost.eu I www.cost.eu

This COST Action will contribute to capacity building by the organization of **annual general Conferences**, where top-level senior scientists will present their work and concepts to a broad audience, including Early Career Investigators (post-docs, PhD and master's students), breeders and regulatory authorities. At the same time, Early Career Investigators are encouraged to discuss their ideas and experimental work with a multidisciplinary audience.

Specific Workshops and **Training Schools** will introduce the concepts of new technologies, methods and tools, along with hands-on training to foster familiarity with these techniques. Topics will cover, among others:

- VNTR typing and MLVA schemes: from prediction to database searches (WG1);
- Genomics-based prediction and evaluation of bacterial pathogenicity factors and their potential as targets for resistance breeding (WG2);
- Comparative genomics of bacterial plant pathogens (WGs 1&2);
- Metabolomic profiling as a discovery tool to combat pathogens (WG2);
- From virulence factors to resistance genes (WGs 2&3);
- Genome-wide association studies (GWAS) as a promising approach to uncover new sources of resistance (WG3);
- Prospects and limits of disease control using bacteriophages (WG4);
- Targeted genome editing and vector control (WGs 2&4).

One particular Workshop will be dedicated to skills required by Early Career Investigators to develop a successful career in the field. Capacity building will also be facilitated by inter-laboratory exchange of personnel, mainly at the early-career stage, via **Short-Term Scientific Missions** (STSM). STSM calls will be launched twice a year and applications will be evaluated by the STSM Committee.

A **consortium website** will facilitate the efficient exchange of relevant information, such as step-by-step protocols and datasheets. The community will be asked to draft comprehensive guidelines for experimental approaches, which will help newcomers in the field to avoid time-consuming, erroneous investments. A recently published paper entitled "Do's and Don'ts of Effectoromics" illustrates well the usefulness of such guidelines[4].

Collectively, these actions will call young scientists' attention to hitherto neglected facets of plant pathology and thus open new avenues of research and development.

1.3. Progress beyond the state-of-the-art and Innovation Potential

1.3.1. Description of the state-of-the-art

OMICs have revolutionized the field of molecular plant pathology. Currently, almost 500 genome sequences are publicly available from Xanthomonas and Xylella strains. Genomics has contributed to a more robust taxonomic framework for plant-pathogenic bacteria[5], and these resources have been used to develop and evaluate new diagnostic (multiplex PCR schemes, loop-mediated isothermal amplification [LAMP] assays) and epidemiological (multilocus sequence typing [MLST], multilocus sequence analysis [MLSA], multiple-locus variable number tandem repeat analysis [MLVA]) tools[6,7]. At the same time, an increasing number of plant resistance genes have been identified for a range of crop species particularly suffering from diseases caused by

[4] Du J & Vleeshouwers VG (2014). The Do's and Don'ts of Effectoromics. Methods Mol. Biol. **1127**: 257-268.
[5] Ryan RP, et al. (2011). Pathogenomics of Xanthomonas: understanding bacterium-plant interactions. Nat. Rev. Microbiol. **9**: 344-355.
[6] Palacio-Bielsa A, et al. (2009). PCR detection and identification of plant-pathogenic bacteria: updated review of protocols (1989-2007). J. Plant Pathol. **91**: 249-297.
[7] Pérez-Losada M, et al. (2013). Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. Infect. Genet. Evol. **16**: 38-53.

Xanthomonadaceae[8,9].

Bacteria of the two Xanthomonadaceae genera Xanthomonas and Xylella are genetically close to each other. Yet, members of both genera are also distinguished by specific features. This combination makes them an ideal pairing to be studied by similar approaches and to be compared with each other. Yet, the communities of scientists working on either Xanthomonas or Xylella are to a large extent split from each other and they interact only occasionally. For instance, despite efforts by the organizers, not a single scientist working on Xylella joined the 5th Xanthomonas Genomics Conference in 2015 (http://xgc2015.uniandes.edu.co). In line with this schism, only a few studies or reviews discussed and compared both genera[10,11,12].

Common themes among Xanthomonas and Xylella include, among others:

- Methods for pathogen detection and studies of the genetic diversity of pathogen populations;
- Regulatory cascades and networks (e.g. quorum sensing, Rpf cell-cell communication system via a diffusible signal factor [DSF]);
- Mechanisms of chemotaxis, motility and attachment to eukaryotic cells and their contribution to pathogenicity;
- Defence cascades employed by the affected host plants.

Specificities of the two research fields include, among others:

- Broad symptomless plant host range (Xylella, yet distinct genetic lineages) versus a generally narrow-host range (Xanthomonas);
- Efficient transmission of Xylella by a variety of widespread and abundant insect vectors while vectoring is only speculative for some clade-I xanthomonads;
- Host-adapted, xylem-restricted, genome-reduced Xylella versus Xanthomonas with an epiphytic phase in its life cycle and colonization of different plant tissues.

1.3.2. Progress beyond the state-of-the-art

This initiative will go beyond the state-of-the-art for several reasons. First, this initiative will bring together the largely separated scientists that either work on Xanthomonas or on Xylella and who hardly ever interact directly. Certainly, they do not work in isolation and they learn from one another but mainly from scientific publications and, occasionally, at scientific conferences. In addition, work on plant disease resistance is often limited to one or few very closely related plant species and the synergies arising from exchange of knowledge, plant germplasm and pathogen strains are by no means sufficiently exploited. This COST Action would thus offer a significant shortcut and accelerate research and development, and it will stimulate new collaborations.

Second, even less interaction is common between academic scientists and researchers at commercial companies. Consequently, timely exchange of new insight into key phenomena in pathogen-host or pathogen-vector interaction will accelerate development and testing of new means that control microorganisms or inhibit their growth. Exchange among participants is also expected to stimulate new ideas and to commercially exploit them in start-up companies.

Due to differing demands from agriculture and due to the specificities of the two bacterial genera, work on Xanthomonas and Xylella has focused on different aspects. A significant proportion of work

[8] Gururani MA, et al. (2012). Plant disease resistance gene: current status and future directions. Mol. Plant Pathol. **78**: 51-65.
[9] Boch J, et al. (2014). TAL effectors – pathogen strategies and plant resistance engineering. New Phytol. **204**: 823-832.
[10] Mhedbi-Hajri N, et al. (2011). Adhesion mechanisms of plant-pathogenic Xanthomonadaceae. Adv. Exp. Med. Biol. **715**: 71-89.
[11] Varani AM, et al. (2013). The role of prophage in plant-pathogenic bacteria. Annu. Rev. Phytopathol. **51**: 429-451.
[12] Castiblanco LF & Sundin GW (2016). New insights on molecular regulation of biofilm formation in plant-associated bacteria. J. Integr. Plant Biol. **58**: 362-372.

on Xylella has focused on diagnostics and some aspects of the host colonization process (quorum sensing, twitching motility), whereas Xanthomonas took off as a model to study diverse virulence mechanisms, plant interactors and (quantitative) disease resistance components. These imbalances are reflected by the number and content of publications over the last 15 years (Table 1) and a special Frontiers research topic on GENOMICS AND EFFECTOMICS OF THE CROP KILLER XANTHOMONAS (http://journal.frontiersin.org/researchtopic/3173/).

	2001-2005	2006-2010	2011-2015
Xanthomonas	615	835	1138
Xylella	131	164	172

Table 1. Number of PubMed-referenced publications.

As an emerging pathogen of great economic interest to the European community, work on Xylella may well profit from intense interactions with researchers in the Xanthomonas field. Conversely, as already shown in the past years, the Xanthomonas community could and will continue to learn from the work on Xylella, which was the first bacterial plant pathogen to be sequenced[13] and for which the first high-resolution molecular typing schemes were established[14] and later adapted for Xanthomonas. This COST Action will reinforce interactions between the Xanthomonas and the Xylella communities, thus generating synergistic effects to the benefit of research and development on two important plant-pathogenic bacterial genera.

1.3.3. Innovation in tackling the challenge

This COST Action will interconnect major European players dealing with or impacted by two important genera of bacterial plant pathogens, Xanthomonas and Xylella. This network addresses research and development in both the academic and the private sector, but also links them to regulatory authorities. It will lead to rapid development, transfer and implementation of modern, high-resolution typing schemes for several bacterial pathogens of high economic interest. This Action will strongly encourage the research community to share these data in internet-accessible databases, such as PAMDB for MLSA/MLST data (http://www.pamdb.org) and MLVAbank for VNTR data (http://www.biopred.net/MLVA/). Harmonization of typing schemes will improve comparability of data and will generate a pan-European view on endemic and emerging diseases. A EU-wide overview about pathogen populations will guide in the choice of model strains for comparative and in-depth analyses of their virulence factors, thus uncovering universal mechanisms and conserved targets for resistance breeding and bio-control agents. The close interaction among scientists working on a broad range of host-pathogen system will further facilitate the development of novel resistance breeding strategies. In-depth understanding of population structures will also help to define optimized strategies for integrated plant protection, thus ultimately lowering the use and negative impact of environmentally questionable control methods (i.e. unnecessary use of pesticides and insecticides) to the benefit of producers, consumers and ecosystems.

All in all, such a highly interconnected European platform dedicated to the comparative study of two important plant-pathogenic genera will strengthen the European research community and help to maintain the high productivity of the European agriculture. In addition, such a collective and interdisciplinary approach will result in novel scientific insights into the emergence of diseases, pathogenicity mechanisms, plant defence responses, durability of resistance genes, mechanisms

[13] Simpson AJ, et al. - The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis (2000). The genome sequence of the plant pathogen Xylella fastidiosa. Nature **406**: 151-159.
[14] Coletta-Filho HD, et al. (2001). Differentiation of strains of Xylella fastidiosa by a variable number of tandem repeat analysis. Appl. Environ. Microbiol. **67**: 4091-4095.

and impact of antimicrobial agents (including chemicals, substances of biological origin, competing microorganisms, bacteriophages), etc. It will also give room to explore new concepts, such as the phytobiome (http://www.phytobiomes.org) or pathobiome[15]. Work resulting from interactions within this network will be published in scientific papers in high-impact journals. In addition, start-up companies may result from this initiative, which can rapidly transfer technologies into products, and commercial companies may benefit from the training of Early Career Investigators.

1.4. Added value of networking

1.4.1. In relation to the Challenge

Integrated, sustainable and efficacious plant protection depends on profound knowledge about population structures, prevalent/predominant pathotypes, conserved major pathogenicity factors, mechanisms of plant defence, efficacy and durability of bio-control agents, etc. This rather complex scenario is rarely considered overall in any research project. Rather, funding typically allows targeting of one or the other aspect and to deciphering some details of a specific problem.

Therefore, we consider COST as THE framework to build an extensive, interconnected network that brings together all the different disciplines with the aim to foster science on agriculturally important traits of pathogens, vectors and host plants. New insight into the complex interplay between pathogens, vectors and host plants at different levels, i.e. from the individual organisms to the population, will allow to develop and implement better disease control means. By coordinating on-going research activities of the participating groups, redundant research activities will be prevented and new collaborations will arise that can tackle the various questions more efficiently.

The network will enable comparative analyses and exchange of material (e.g. bacterial isolates, following the EU guidelines and national quarantine regulations) and techniques before publication and thus accelerate progress and improve competitiveness of the European research landscape. It will also give access to specific facilities and expertise to those academic groups who do not possess them or who have only recently entered this research area. In addition, COST provides an appropriate framework that allows young researchers to visit different laboratories across Europe, thus stimulating the emergence of new, next-generation career networks, increasing their job opportunities and accelerating research and innovation for sustainable crop protection.

The COST framework is also an ideal instrument to build a network between academic research laboratories and commercial entities, such as diagnostics services, seed companies (e.g. breeding of new varieties, importance of pathogen detection for certification of seed material), producers of bio-control agents, etc. This will strengthen the market position of European agriculture-related companies and contributes to the economic development of Europe in general.

Taken together, this COST Action will generate new collaborations, new knowledge, and new products to the benefit of the COST Countries.

1.4.2. In relation to existing efforts at European and/or international level

The COST Action is complementary to and will add value to numerous ongoing national and international programs, such as the French Network on Xanthomonads (http://www.reseau-xantho.org), the Pierce's disease network (http://www.piercesdisease.org), the Euphresco network for phytosanitary research coordination and funding (http://www.euphresco.net), and the POnTE (Pest Organisms Threatening Europe) initiative (http://www.ponteproject.eu). Yet, this specific Action will integrate specific aspects and covered organisms of the other initiatives under a new umbrella, which will allow to better develop the concept of an integrated plant protection based on knowledge about pathogen populations and the biology of the pathosystems.

[15] Vayssier-Taussat M, et al. (2014). Shifting the paradigm from pathogens to pathobiome: new concepts in the light of meta-omics. Front. Cell. Infect. Microbiol. **4**: 29.

Many of the research teams that have expressed their interest in the COST Action have an excellent track record within the field and are often involved in several other national, European and International research projects. They will be encouraged to create links between this COST Action and those projects. Integrating experts from International Partner Countries (IPC) who are active in research on Xanthomonadaceae and/or where diseases caused by Xanthomonadaceae are endemic (e.g. Australia, Brazil, USA) will generate mutual benefits for both sides. Two members of the Management Committee will be appointed to establish and maintain links with other programs and COST Actions. In contact with the Core Group (i.e. Chair, Vice Chair, STSM Coordinator and WG Leaders and Vice Leaders), they will seek out for new inter-program initiatives and they will make propositions for joint Meetings, Workshops and Training Schools.

2. IMPACT

2.1. Expected Impact

2.1.1. Short-term and long-term scientific, technological, and/or socioeconomic impacts

This COST Action will coordinate the various national and institutional research activities that are related to plant-pathogenic Xanthomonadaceae, including diagnostics, epidemiology, resistance breeding and bio-control measurements. Plant diseases and their management can be considered as a warfare where pathogens emerge to break-down natural resistance barriers and overcome human interventions. Hence, studies on the evolution of pathogen populations, on virulence factors and plant defense mechanisms will enable to develop new and better ways to prevent epidemics and substantial yield losses. New diagnostic technologies and rapid and robust molecular typing tools will be disseminated among collaboration partners within this COST Action. Comparative and complementary studies on the two plant-pathogenic genera Xanthomonas and Xylella will generate new insight into the biology of the pathosystems and define targets for resistance breeding and implementation of bio-control measurements.

More efficient and better coordinated Research and Development will contribute to sustainable agriculture in Europe. Even if the importance of agriculture in Europe differs largely among the EU countries, it can contribute to more than 10% of the Gross Domestic Product (GDP) in some countries. Beyond doubt, agriculture is a major activity in some regions of Europe and can generate up to 30% of the total employment[16]. Sustainable agriculture thus contributes to the welfare of the European citizen and ensuring self-sufficiency is considered a major pillar of the stability and strength of the European Community. It is also key to maintain sufficient expertise within the EU for optimal decision-making in cases of pathogen outbreaks.

2.2. Measures to Maximise Impact

2.2.1. Plan for involving the most relevant stakeholders

In preparation of the COST Action, a consortium representing a substantial portion of the European research community working on Xanthomonas and/or Xylella was built. In the next step, targeted invitations will be sent to the EPPO, to national regulatory authorities, to breeders, seed producers, bio-control companies and developers of diagnostic tools. The Management Committee will be responsible to identify the most relevant stakeholders in the participating countries. Two members of the Management Committee will be appointed to generate and maintain links to other programs and COST Actions, as discussed in Section 1.4.2.

2.2.2. Dissemination and/or Exploitation Plan

[16] http://ec.europa.eu/agriculture/statistics/factsheets/index_en.htm.

The Management Committee will appoint a person responsible for managing a dedicated website for the COST Action according to the needs of the COST Action Participants and promoting dissemination of relevant information (dissemination and exploitation of results, factsheets, opinions, etc.). To facilitate the dissemination of information, an email list will be generated and social media will be used to disseminate news. Concise reports will be drafted summarizing the annual Meetings and the activities of the four Working Groups, their specific Conferences and Workshops. These reports will be circulated among all COST Action Participants via the website.

Each Working Group will be asked to contribute at least one collective review (e.g. Annual Reviews, http://www.annualreviews.org/; Current Opinion, http://www.current-opinion.com, or Trends, http://www.cell.com/trends series) or to organize a specific Frontiers Research Topic (http://www.frontiersin.org) during the funding period. In addition, new or reinforced collaborations will result in publication in peer-reviewed scientific journals. All publications will acknowledge the support from COST using a standardized Acknowledgement phrase.

Thanks to the link with the European and Mediterranean Plant Protection Organization, this COST Action will provide expertise and help to update EPPO recommendations, such as Data Sheets on Quarantine Pests, Diagnostic Protocols for Regulated Pests, National Regulatory Control Systems, Phytosanitary Procedures, and Schemes for the Production of Healthy Plants for Planting.

2.3. Potential for Innovation versus Risk Level

2.3.1. Potential for scientific, technological and/or socioeconomic innovation breakthroughs

This COST Action is expected to generate innovation breakthroughs, which will emerge from reinforced collaborations and from exchange of personnel via the STSM (Short Term Scientific Missions) mechanism. As examples, we anticipate the generation of new tools for population studies, new pipelines for data analysis, new bioinformatic tools for genome mining, new temperature-robust resistance genes, and new bio-control formulations. We do not identify any specific risks related to the work plan. Since the COST Action will build on existing, more specific networks, we expect to be operational within a very short time.

3. IMPLEMENTATION

3.1. Description of the Work Plan

3.1.1. Description of Working Groups

The COST consortium will be sub-divided into four Working Groups (WGs), each of which will be coordinated by two members of the Management Committee, both with outstanding expertise in the respective field, one with a focus on Xanthomonas and the other one with a focus on Xylella. Topics of the four WGs are highly connected to each other, as illustrated in Figure 1. For example,

- Knowledge of Population Structure will guide studies of the Pathogen Biology;
- Knowledge of Population Structure and Pathogen Biology will guide the exploitation of Genetic Resistance;
- Knowledge of Pathogen Biology will guide the approaches of Disease Control;
- Exploitation of Genetic Resistance will drive the evolution of pathogens and shape the Population Structure;
- Disease Control (e.g. via antimicrobials) will shape the Population Structure;
- Use of Genetic Resistance and Disease Control complement one another in Integrated Plant Protection.

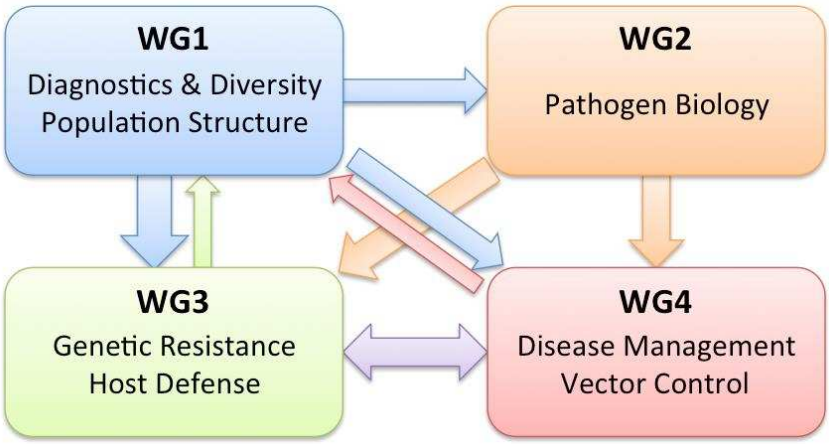

Figure 1. Overview of Working Groups and their interconnections.

Working Group 1 - Diagnostics & Diversity – Population Structure

This Working Group will focus on diagnostics and diversity of plant-pathogenic Xanthomonadaceae. For most species and pathovars, efficient molecular detection tools have been developed over recent years, thanks to the availability of more and more genome sequences. Even if rapid serological assays (e.g. lateral-flow immunoassays) are still in use, there is a clear shift to DNA-based assays for identification of bacterial pathogens[17], such as multiplex-PCR, real-time PCR and loop-mediated isothermal amplification (LAMP) assays[18]. Notably, whole-proteome analyses using matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectroscopy (MS) emerged as a complementary method but requires access to high-end equipment[19]. Driven by the recent outbreaks of X. fastidiosa in Apulia region (southern Italy), which called for the implementation of immediate actions, powerful diagnostic tools have been developed and inter-laboratory ring tests comparing molecular and serological methods for identification of X. fastidiosa have been organized[20]. In contrast, little was invested into similar tests for xanthomonads, including those that are listed as European quarantine organisms. Consequently, this COST Action will enable the transfer of diagnostics expertise generated on X. fastidiosa to the many Xanthomonas species and pathovars of European interest and coordinate surveys of Xanthomonas diseases currently present in the EU.

In addition to early detection of pathogens and disease diagnosis as the basis for effective prevention strategies enabling reduction in the use of pesticides, knowledge about the genetic diversity of pathogens and prevalent pathogen populations is of importance for developing efficient control schemes, be it the use of genetic host resistance (WG3) and/or the implementation of bio-control schemes (WG4). Mini- and microsatellites, also called variable-number of tandem-repeats (VNTR), have emerged as a powerful tool to assess the population structure of bacterial plant pathogens, and several multilocus VNTR analysis (MLVA) schemes have been developed. The COST Action will be used as a platform to familiarize the different players with these new tools and how results can be compared using internet-accessible databases.

Among others, WG1 will address the following epidemiological aspects:

- Genomics-based development of diagnostic tools;

[17] Pérez-Losada M, et al. (2013). Pathogen typing in the genomics era: MLST and the future of molecular epidemiology. Infect. Genet. Evol. **16:** 8-53.
[18] Nezhad AS (2014). Future of portable devices for plant pathogen diagnosis. Lab Chip **14**: 2887-2904.
[19] Ahmad F, et al. (2012). Potential of MALDI-TOF mass spectrometry as a rapid detection technique in plant pathology: identification of plant-associated microorganisms. Anal. Bioanal. Chem. **404**: 1247-1255.
[20] Loconsole G, et al. (2014). Detection of Xylella fastidiosa in olive trees by molecular and serological methods. J. Plant Pathol. **96**: 7-14.

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Avenue Louise 149 I 1050 Brussels, Belgium
t: +32 (0)2 533 3800 I f: +32 (0)2 533 3890
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- Standardization and improvement of molecular detection protocols for distinct genetic taxa of plant-pathogenic Xanthomonadaceae (multiplex PCR protocols, LAMP, padlock probes, microbeads, MALDI-TOF MS);
- Coordination of studies on the genetic diversity of plant-pathogenic bacteria;
- Definition of sets of pathovar reference strains for epidemiological studies and deposition in European strain collections (CIRM-CFBP, BCCM/LMG, NCPPB);
- Adaptation of tools for molecular epidemiology (CRISPR-based spoligotyping, MLST/MLSA, VNTR, MLVA);
- Estimation of parameters in population genetics (e.g. migration rates among populations);
- Modern bioinformatics tools for data analysis (Approximate Bayesian Computation);
- Internet-accessible databases (http://www.pamdb.org/, http://pubmlst.org/xfastidiosa/, http://www.biopred.net/MLVA/).

Working Group 2 - Pathogen Biology

Xanthomonas spp. and X. fastidiosa are Gram-negative plant-associated bacteria that cause numerous plant diseases of economic importance. For instance, xanthomonads can cause bacterial blight (e.g. on aroids, hazelnut, rice), bacterial canker (on citrus), bacterial spot (e.g. on strawberry, pepper, tomato, stone fruit and ornamental trees), and bacterial streak (e.g. on barley, wheat, rice), whereas X. fastidiosa causes Pierce's disease of grapevine, citrus variegated chlorosis, peach phony disease, plum leaf scald, and leaf scorch and dieback of olive trees. Collectively, xanthomonads can cause diseases on over 400 different plant species, but individual strains typically have a very narrow host range. As a whole, X. fastidiosa strains can infect at least 300 plant species from 63 different families, often without detectable symptoms. Yet, members of each of the few X. fastidiosa subspecies described so far have a more restricted host range[21].

X. fastidiosa is obligately vector-transmitted in nature by various xylem sap-feeding insects with generally polyphagous behavior in relation to host plants, so all xylem fluid-feeding insects in Europe are considered to be potential vectors. In contrast, active vector transmission of xanthomonads (i.e. after ingestion of the pathogen) has not been reported yet. Both Xanthomonas and Xylella colonize distinct tissues of the host plant. While X. fastidiosa is restricted to xylem vessels, different pathovars of Xanthomonas can colonize the xylem or the mesophyll.

Most xanthomonads have evolved a specific protein secretion system, the type III secretion system (T3SS), which injects bacterial effector proteins into the plant's cells to the benefit of the pathogen. While some effectors suppress plant defense responses, others help the bacteria to colonize the plant tissue by creating favorable conditions (e.g. making nutrients available). Such mechanisms have not been observed for X. fastidiosa and it is barely understood how these bacteria escape from detection by the plant immune system. This is also the case for some xanthomonads such as the xylem-limited Xanthomonas sacchari.

Overall, WG2 will address several key aspects of the pathogen-host and pathogen-vector interaction, which are cutting-edge subjects with high relevance to the understanding of the molecular pathogenesis mechanisms of these quarantine pests. As a xylem-limited pathogen, the interaction of X. fastidiosa with the host plant is central to its ecology. Several cellular aspects of the infection process have already been unveiled, but more information is required to determine whether this infection process is host-specific, or if ubiquitous strategies are involved. Elucidation of regulatory networks in response to host colonization (e.g. quorum sensing) will be promptly addressed by this WG. It also remains to be answered whether during evolution the interaction between X. fastidiosa and distinct hosts has generated a pool of virulence traits that allows the infection of unrelated plant hosts.

21 EFSA Panel on Plant Health (2015). Scientific Opinion on the risk to plant health posed by Xylella fastidiosa in the EU territory, with the identification and evaluation of risk reduction options. EFSA J. 13: 3989.

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Avenue Louise 149 I 1050 Brussels, Belgium
t: +32 (0)2 533 3800 I f: +32 (0)2 533 3890
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The ability of most pathogens to manipulate host cell processes relies on determinants that differ during the course of the infection process. Hence, another relevant topic to be addressed is understanding the mechanisms underlying microbe-eukaryote interactions, namely chemotaxis, adhesion, motility, etc. OMICs approaches to study bacterial interactions with hosts and vectors (genomics, transcriptomics, proteomics, metabolomics) are state-of-the-art and will be extensively explored in this WG. Comparative genomics and genomics-based prediction of virulence-related effectors will help to identify broadly conserved effector sets as promising targets for resistance breeding, once their critical contribution to the proliferation of the pathogen in the host is demonstrated (meaning that their loss would be associated with a substantial fitness cost). Additionally, dual RNA-seq (i.e. simultaneous transcriptome analyses of both host and microbe) during the infection process will allow the identification of important virulence traits and defense genes, an important step towards generating resistant cultivars through breeding or genome editing, offering the opportunity for the development of new control schemes with high impact on society. Likewise, these results could lead to a better understanding of the host processes that facilitate the survival of these bacteria in different hosts and reveal new information on how basic eukaryotic cellular processes are regulated.

To highlight a few aspects, we will address the following aspects of the pathogen's biology:

- OMICs approaches to study bacterial interactions with hosts and vectors (genomics, transcriptomics, proteomics, metabolomics);
- Mechanistic understanding of microbe-eukaryote interaction at different steps of the infection/dissemination cycle (e.g. chemotaxis, adhesion, motility);
- Deciphering of regulatory networks in response to host colonization (e.g. quorum sensing);
- Identification of pathogen-associated molecular patterns (PAMPs) and conserved effectors as targets for resistance breeding.

Working Group 3 - Genetic Resistance & Host Defense

The primary aim of WG3 is to unite researchers working on disease resistance in different crop species and bring them together with plant breeders to exploit existing knowledge, develop novel tools and strategies for resistance breeding and to transfer this knowledge into practical breeding programs. Effects of temperature increase on the robustness of resistance genes and on the fitness of pathogens will be particularly addressed.

While plant resistance to diseases caused by Xanthomonadaceae has been quite extensively studied in species such as rice, tomato, pepper or citrus, only fragmented information on resistance traits is available for stone fruit trees (e.g. apricot), small-grain cereals (wheat, barley) or forage grasses. The rice – X. oryzae pv. oryzae pathosystem has been particularly well studied and a broad range of resistance genes has been described including typical R genes such as NLR genes[22],which interact with specific virulence genes of the pathogen, as well as broad-spectrum genes conferring quantitative resistance such as zinc finger nucleic acid-binding proteins[23]. This knowledge has been partially transferred into breeding programs and various rice varieties have been developed with resistance to specific X. oryzae pv. oryzae races. However, novel races are continually emerging and qualitative resistances are often overcome by rapidly evolving pathogen populations. The same holds true for other crop species including wheat, brassicas, fruit and forage crops.

Recent advances in the areas of genomics, proteomics and transcriptomics have greatly facilitated the elucidation of the genetic control of disease resistance also in non-model organisms. High-throughput sequencing technologies today enable genome-wide analyses of resistance traits and potentially allow rapid introgression into advanced breeding material. However, so far attempts to

[22] Zhang H & Wang S (2013). Rice versus Xanthomonas oryzae pv. oryzae: a unique pathosystem. Curr. Opin. Plant Biol. **16**: 188-195.

[23] Deng H, et al. (2012). A CCCH-type zinc finger nucleic acid-binding protein quantitatively confers resistance against rice bacterial blight disease. Plant Physiol. **158**: 876-889.

integrate this knowledge have been limited to individual species and synergies arising from interactions of scientists and plant breeders have not been exploited.

In addition to approaches of "classic" transgenesis that turned out to produce plants resistant to Xanthomonas infection[24,25,26], this COST Action will particularly consider non-GMO approaches, such as knowledge-based molecular screens of germplasm[27], and New Breeding Technologies (NBTs)[28], such as genome editing, as a means to generate resistant plants[29].

This Working Group will focus on the following aspects of plant resistance to Xanthomonas and Xylella spp.:

- Development of a comprehensive inventory of plant resistance genes and quantitative trait loci (QTL), made accessible through the COST Action's website;
- Establishment of validated common protocols for phenotypic characterisation of plant resistance;
- Discovery of novel resistance traits through traditional QTL mapping and more powerful genome-wide association studies (GWAS), investigation of potential targets for pathogen virulence factors, comparative genomics and transcriptome analyses;
- Introgression and pyramiding of resistance traits through phenotypic and marker-assisted selection;
- Evaluation of transgenic approaches to achieve protection from pathogen infection;
- TALEN- and CRISPR/Cas9-mediated genome editing, including DNA-free methods[30];
- Discussion on regulatory issues linked to transgenesis, GMOs and NBTs.

Working Group 4 - Disease Management & Vector Control

This Working Group will bring together partners from different countries and disciplines with the central aim to evaluate the impact of biological products/microorganisms to control xanthomonads and X. fastidiosa and to prevent the spread of infections.

So far, little is known about the potential and effectiveness of biological products/microorganisms on the control of symptomatic/asymptomatic infected plants, on the prevention of infection spreading, and on their impact on health of plants and products. Their beneficial activity may promote/induce resistance or directly inhibition the growth/virulence, hypotheses that need to be fully understood before such interventions can be widely applied. Moreover, a balanced risk/benefit analysis of widespread application is needed to guide a safe biological control method development.

A better insight into biology and virulence of the pathogen (WG2) will enable development of different bio-control schemes. For instance, it has been shown that accumulation of a pathogen-produced diffusible signal factor (DSF) regulates the expression of different sets of genes in X. fastidiosa. DSF increases the production of cell surface adhesins and suppresses the expression of extracellular enzymes and, thus, tends to reduce the virulence of X. fastidiosa because these more adherent cells

[24] Horvath DM, et al. (2012). Transgenic resistance confers effective field level control of bacterial spot disease in tomato. PLoS One **7**: e42036.
[25] Tripathi JN, et al. (2014). Transgenic expression of the rice Xa21 pattern-recognition receptor in banana (Musa sp.) confers resistance to Xanthomonas campestris pv. musacearum. Plant Biotechnol. J. **12**: 663-673.
[26] Zeng X, et al. (2015). Genetic engineering of the Xa10 promoter for broad-spectrum and durable resistance to Xanthomonas oryzae pv. oryzae. Plant Biotechnol. J. **13**: 993-1001.
[27] Hutin M, et al. (2015). A knowledge-based molecular screen uncovers a broad-spectrum OsSWEET14 resistance allele to bacterial blight from wild rice. Plant J. **84**: 694-703.
[28]http://ec.europa.eu/food/plant/gmo/legislation/plant_breeding/; http://www.epsoweb.org/agricultural-technologies-wogr; http://www.nbtplatform.org.
[29] Li T, et al. (2012). High-efficiency TALEN-based gene editing produces disease-resistant rice. Nat. Biotechnol. **30**: 390-392.
[30] Woo JW, et al. (2015). DNA-free genome editing in plants with preassembled CRISPR-Cas9 ribonucleoproteins. Nat. Biotechnol. **33**: 1162-1164.

exhibit less movement along and between grapevine xylem vessels[31]. In this regard, a biological control strategy with endophytic bacteria that would grow within plant tissues and produce DSF could be an attractive strategy. Another approach that links this topic to WG3 is the use of transgenic plants that express bacterial genes from the DSF regulon, thus disturbing the balance of biofilm formation and motility and in turn reducing the virulence of Xanthomonas in citrus plants[32].

Other means of bio-control may rely on antimicrobial substances, resistance induced by bio-control microorganisms, promotion of antagonistic endophyte community, and application of bacteriophages as a control means[33], ultimately leading to increased host tolerance, with symptom relief and significant reduction of potential inoculum in affected plants. Since X. fastidiosa is an insect-transmitted pathogen, approaches to eliminate or reduce vector populations will be considered as well, including adapted agronomic practices, effects of volatile compounds, trapping systems, etc.

3.1.2. GANTT Diagram

The COST Action will be implemented for a period of four years. The timetable and GANTT diagram illustrate the implementation of the different activities over this period of time. The culmination of the activities includes an inaugural meeting and a final meeting with all four WGs. Annual meetings will be used to interconnect the different WGs. WG-specific Meetings, Workshops and Training Schools will generally be held once a year per active WG after approval by the MC; yet, if applicable, extra activities will be considered. One particular Workshop will be dedicated to skills required by Early Career Investigators to develop a successful career in the field.

Year 0	Year 1		Year 2		Year 3		Year 4	
	R&D activities		R&D activities		R&D activities		R&D activities	
Inaugural meeting	WG-specific COST activities	Annual meeting & MC meeting	WG-specific COST activities	Annual meeting & MC meeting	Early-career-focused meeting	Annual meeting & MC meeting	WG-specific COST activities	Final meeting & MC meeting

Table 2. Timetable of the COST Action.

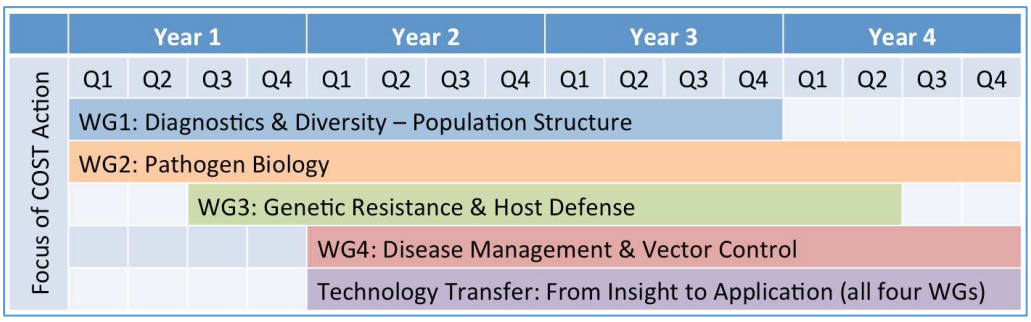

Figure 2. GANTT diagram illustrating WG activities and implementation of tasks.

3.1.3. PERT Chart (optional)

[31] Baccari C, et al. (2014). Diffusible signal factor-repressed extracellular traits enable attachment of Xylella fastidiosa to insect vectors and transmission. Phytopathology **104**: 27-33.
[32] Caserta R, et al. (2014). Expression of Xylella fastidiosa RpfF in citrus disrupts signaling in Xanthomonas citri subsp. citri and thereby its virulence. Mol. Plant Microbe Interact. **27**: 1241-1252.
[33] Balogh B, et al. (2010). Phage therapy for plant disease control. Curr. Pharm. Biotechnol. **11**: 48-57.

3.1.4. Risk and Contingency Plans

Yearly meetings of the Management Committee will ensure that activities will be organized according to the defined objectives of the four Working Groups and the capacity-building objectives, as defined in Section 1.2.2. If rapid action is needed, the Core Group (see Section 3.2) will serve to handle emergent problems using email lists and/or teleconferences.

To ensure a high standard of the COST Action and a well-balanced representation of interacting partners (universities and higher education organisations, research institutes, regulatory authorities, R&D-performing bodies), we aim at appointing an independent Advisory Board, consisting of six deputies (three non-European lead scientists, two representatives from the private sector and one member of the European and Mediterranean Plant Protection Organization [EPPO, http://www.eppo.int/]).

3.2. Management structures and procedures

This COST Action will provide the necessary means to establish and stimulate a European platform for scientists active in control, research and development in the field of bacterial plant pathology. This platform will enable efficient exchange of expertise, staff, material and technologies originating from their on-going research programs. Moreover, this European platform will also stimulate new ideas and allow to rapidly test them, thus helping to develop new strategies of disease control. This Action is based on the concept that knowledge of pathogen population structures and profound insight into the biology of the pathogen (e.g. molecular mechanisms of pathogen-host interactions) is key to the efficient and sustainable control of microbial plant pathogens by several complementary means (genetic resistance, bio-control, etc.).

To achieve these objectives, the Action will be organised in accordance to the “Rules for Participation in and Implementation of COST Actions” (COST 132/14) and four Working Groups will be set up with well-defined objectives (section 3.1.1).

The **Management Committee** (MC) will coordinate and supervise the action. It will be composed of one to two representatives of each country and will meet once a year in conjunction with the annual conference. The MC will have the following responsibilities:

- Election of the Chair and Vice Chair;
- Election of the Grant Holder Institution;
- Election of two Financial Rapporteurs from two different countries;
- Appointment of a **Core Group**, consisting of the Chair, Vice Chair, four Working Group (WG) Leader and Vice Leaders and the STSM Coordinator;
- Appointment of a person responsible for managing a dedicated website for the COST Action according to the needs of the COST Action Participants and promoting dissemination of relevant information (reports, factsheets, opinions, etc.);
- Critical appraisal of progress within each WG towards defined objectives, as outlined in the annual reports;
- Decision on Scientific Meetings, Workshops and Training Schools proposed by WG Leaders;
- Decision on applications for Short-Term Scientific Missions after evaluation by the STSM Committee;
- Appointment of two persons acting as contacts with other programs and COST Actions;
- Ensuring gender balance and substantial involvement of Early Career Investigators (see Section 3.3).

The Core Group will have the following responsibilities:

- Organisation of MC Meetings;
- Drafting of annual reports on the activities of the COST Action based on reports from the four WGs;
- Assessment of applications for Short-Term Scientific Missions;
- Stimulating interactions between the four WGs.

Short-term scientific missions, particularly for Early Career Investigators, will be an important part of the Action. Specialized Meetings, Workshops and Training Schools will be organized for the four WGs under the responsibility of the WG Leader. The WG Leader may delegate the responsibility to a person at the institution that wishes to organize a Meeting or Workshop or Training School. In addition, annual Meetings addressing topics of all four WGs will be organized in order to ensure lively interaction within and among the WGs.

3.3. Network as a whole

Detailed knowledge on population structures and the lifestyle of bacterial pathogens of the Xanthomonadaceae family, i.e. how they are transmitted and adapt to their hosts (crop plants, insect vectors), is key to identify, develop and exploit genetic resistances and/or bio-control measurements in a sustainable manner. Addressing this problem has become more and more feasible over the last years thanks to methodological revolutions in high-throughput OMICs and the development of new assays, molecular typing schemes, functional screens, and so on. However, efficient problem solving needs to bring together a critical mass of people from research and development in the COST Countries. This COST Action will be instrumental in coordinating and increasing the impact of fragmented approaches undertaken as part of various national initiatives in the field of molecular plant pathology.

This Action will generate a **platform** that gathers experts from different disciplines, such as molecular diagnostics, molecular host-microbe interactions, plant resistance breeding, and applied microbiology. Joining their efforts will help to develop and implement effective plant protection schemes, be it via resistant crop cultivars or via other control mechanisms (antimicrobial substances, vector control, etc.). This goal will be achieved by mobilizing and training scientists from major COST Country institutions, regulatory bodies and commercial companies working on the various aspects of this complex of problems. At present, the network includes 53 partners from 17 COST Countries (41% of them classified as “inclusiveness countries”) representing 26 universities, 18 academic research institutions and 9 other partners (bio-control agencies, companies). This network will bring together and stimulate the collaboration between scientists from research and development, aiming to translate knowledge and expertise into field applications.

The Management Committee (MC) will ensure that this COST Action respects an adequate **gender balance** in all its activities, such as COST management, Workshops, Meetings and Short-Term Scientific Missions. The current network of 82 COST Country scientists includes 40% women and 60% men. A similar percentage of women and men was involved in drafting this document.

The COST Action will also stimulate activities by **Early Career Investigators**, be it their representation in the MC, their training in specific Workshops, and their active participation in the WG-specific and annual Meetings. Early Career Investigators will be given priority in Short-Term Scientific Missions to other laboratories. As a matter of fact, both senior scientists and Early Career Investigators contributed substantially to this document in preparation of the COST Action.

It is expected that Early Career Investigators and both men and women will play leading roles in the Management of the Action and the coordination of WGs. Networking within the COST Action will help Early Career Investigators to establish themselves in the field and to create valuable contacts for further career steps. One particular Workshop will focus on the skills required by Early Career Investigators to develop a successful career in this field. Two MC Members (both genders and both senior/junior) will be appointed that will monitor gender balance and appropriate participation of Early Career Investigators in the activities of the COST Action.

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Avenue Louise 149 I 1050 Brussels, Belgium
t: +32 (0)2 533 3800 I f: +32 (0)2 533 3890
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