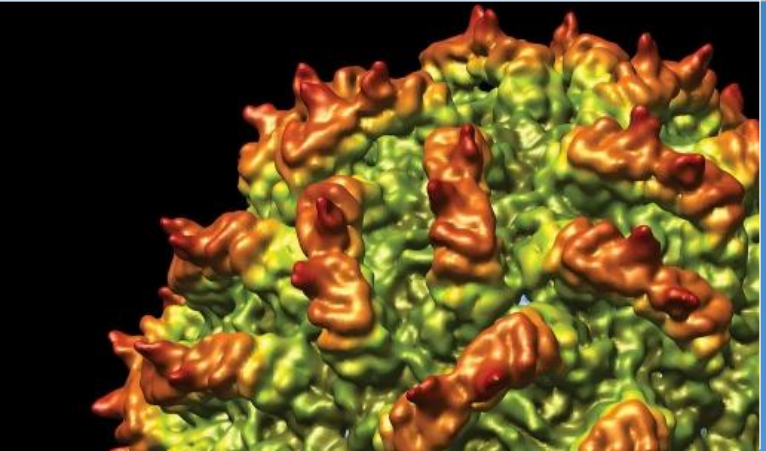
The strategic research and innovation agenda of Infect-ERA

Coordination of European funding for infectious diseases research

ERA-NET



Infect-ERA

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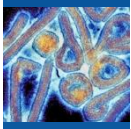


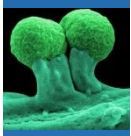
INTRODUCTION

Despite significant scientific, public health and political efforts, infectious diseases remain a key challenge and one of the major causes of death worldwide. Recent epidemics, such as Zika, demonstrate the need of a long-term strategy to combat infectious diseases, to prevent epidemics by a deeper knowledge of the interaction host-pathogen and, in case of viruses, the vectors. Every year in Europe, communicable diseases cause tens of thousands of deaths and represent a crucial societal priority. The threat of emerging infectious diseases, mass migration, global travel and growth of congested urban areas inefficient prevention campaigns, environmental changes, misuse and overuse of antimicrobials and co-infection all contribute to the most recent challenges in infectious diseases.

The Strategic Research and Innovation Agenda of Infect-ERA will be focusing an unexploited field of research and intervention, how to efficiently manage emergent microbial challenges that might cause public health problems.

Networks of transnational scientists funded under Infect-ERA programme focus their research on identifying emerging infectious threats and developing novel diagnostic and therapeutic approaches. The scope of Infect-ERA encompasses different fields including but not limited to bacteria, fungi and virus, but also immunology.

Important challenges in infectious diseases have been identified by the Infect-ERA External Advisory Board members (EAB) and developed at the four EAB workshops with the help of external scientists (Lisbon, June 2013, Vienna in March 2014, Brussels in March 2015 and Madrid in May 2016).

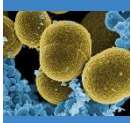


1 CURRENT CHALLENGES IN INFECTIOUS DISEASES

1.1 Host-pathogen relationships during onset and progression of infections

The characterization of the initial events of infections is highly important - particularly with respect to developing prophylactic and therapeutic measures that target the early phases of microorganisms' invasion and propagation or the cellular factors that are crucial for the onset of the infection.

Nevertheless, the progression of established infections should not be neglected because this is the phase that is mainly relevant for treatment, and where diagnostic and prognostic biomarkers can be implemented (see research area 4 and 3, respectively). The concept of personalized medicine and more recently the one of precision medicine emphasizes the importance of patient stratification according to their individual risk and prognostic profile.



The main aspects of the challenge “Host-pathogen relationships during onset and progression of infections” are 1) to study the initial events of infection and the cellular and/or pathogen-related factors involved in progression and 2) to identify the host targets for the immune modulation of the innate inflammatory processes and further specific immune response.

1. Factors that influence host-pathogen interaction

Historically, research has been focused on characterization of either the pathogen or the host. More and more, research projects also characterize the mutual influence of the two actors – an important step that was also reflected in the successful proposals funded through the first three joint calls of Infect-ERA.

The development of new genomic and proteomic tools enables the identification of host factors interacting with pathogens as well of the composition and changes of the host's microbiome prior to, and during the initial phases of infections.

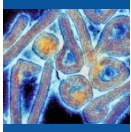
Host genetic background can significantly influence the outcome of infection. Identification of candidate genes for disease susceptibility through genome-wide association studies (GWAS) and linkage analysis tools allowed the identification of genetic variations frequently associated with severity of disease.

Current Challenges:

- Defining and implementing *in vivo* models that reflect the real disease scenario, i.e., using appropriate models for defined questions rather than using a" one for all model": taking into account differences between experimental and clinical settings; this may be achieved for instance by combining *in vivo* experimental models with models based on animal and human cell/tissue cultures.
- Study of mutual host-pathogen interactions not focusing exclusively on pathogen or host, usually not a single pathogen/host relationship (microbiome composition and changes, superinfection).
- Identifying host factors (host genetic background, metabolic diseases, microbiome, etc) that regulate infection and disease progression.
- Tackling the knowledge-gap on the initial molecular-level processes of infection, immune sensing and immune evasion. Identifying determinants of pathogen clearance versus persistence.
- Studying the impact of environmental factors on the infectious agent genome and on the microbiome composition affecting infectivity and the immune response.
- Identifying anti-virulence strategies to allow new diagnostic and therapeutic approaches that target the early steps of pathogen invasion as well as established infections progression (see Challenges 3 and 4).
- Characterization of co-pathogenic polymicrobial infections; most common microbial combinations have to be defined in clinical settings before tackled in model systems.

Potential ways to tackle the challenges and recommendations:

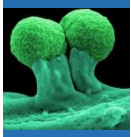
- Develop of experimental capacities, including experiments on animals and alternative *in vivo* models
- Develop and apply innovative methods to identify host susceptibility determinants (genome-wide association study, metabolomics, haploid embryonic stem cell, gene silencing techniques, etc).
- Develop and exploit screening systems to characterize the initial steps of infections and combine unbiased data collection with targeted approaches to define causality.



- Development and application of methodologies to allow whole genome sequencing of pathogens directly from clinical samples without laboratory propagation of strains, in order to understand the *in vivo* host-pathogen "arms-race" that takes place during infection (and eventually during different infection stages that characterize some diseases). This would allow the precise identification of loci that are modified under the pressure of the host (e.g. immune pressure), at specific infected organs, or even the loci involved in the transition from a colonization or a localized infection to a systemic infection.
- Bioinformatics infrastructure for omics data analysis.

2. Personalized treatment

- Personalized medicine uses individual genetic variation to predict disease progression and to tailor more effective treatment dedicated to a subgroup of subjects or even to a specific individual, e.g. IL28 polymorphism used for HCV response to Interferon based therapies, CCR5 homozygosis used to induce resistance to HIV infection
- Pharmacogenetics and pharmacogenomics are used to identify polymorphisms that impact individual response to anti-infective drugs will replace the "one size fits all" approach in medicine prescription (e.g. hypersensitivity to Abacavir related to the HLA-B*5701 allele)
- (i) the protective potential of commensals, e.g. "the nice bug" - Infect-ERA project: faecal microbiota transplantation (*C. difficile*), (ii) clonal pathogen strain differences



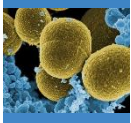
<u>Current challenges</u>:

- Identification of genetic and epigenetic determinants for susceptibility to infections as well as effectiveness of medications
- To transform the knowledge on individual differences into treatment
- To apply personalized medicine in disease prevention and prognosis (e.g. individual differences in response to vaccination or microbiome composition that increase susceptibility to certain infections)

<u>Potential ways to tackle the challenges and recommendations</u>

- Population studies to look at the diversity of response to pathogens, and host-pathogen contacts (e.g. study of the innate immune response to the pathogen in different sets of patients based on clinical diversity in the responses to the pathogen; looking at a broad range of cytokine profiles among individuals with different susceptibilities or clinical expressions of such infections). Improvement of stratification of patients

- Development of holistic approaches employing systems biology, computational biology and bioinformatics capacities for data analysis.
- Establishment of population-based epidemiologic data-base that will enable delineation between individuals according to their susceptibilities to certain infections (i.e. recurrent infections, life threatening infections, infections by specific pathogens, lack of response to certain therapeutic modalities, vaccination coverage, herd immunity etc.).
- Individualized medicine appears most important for infectious diseases, where treatment heavily influences the outcome, e.g. the immunocompromised patient.



1.2 Role of human microbiota in health and infectious diseases

The microbiota or the microbiome refers to the composition of microorganisms (bacteria, fungi, protozoa and viruses) that live within and on animals and human hosts. The advent of high-throughput DNA sequencing has initiated a real revolution in biology, creating the ability to characterize the composition and function of individual microbiome species as well as the complex structure of their communities. The microbiota and the host may present various forms of relationship, including mutualism, parasitism and commensalism. The nature of the host-microbiome relationship is a multifactorial interaction that is highly dependent on the specific context and is shaped by the status of the host's immune system, genetic predisposition, microorganism localization and further conditions yet to be identified. The ability to determine the dynamics and regulation of the microbiome and the expression profile of host genes over time uncover how the microbiota communities interact with the host and how host genetics, nutrition, lifestyle and behavior feedback the microbiota. Nowadays, although the role of the microbiome is well-accepted as a relevant factor in human's disease and health, the field is still dominated by highly descriptive studies and exploratory sequencing approaches. More mechanistic approaches are needed for interpretation of how microbiomes function in a community context, and how they interact within the environments and hosts they inhabit. Future progress in microbiota research is expected to provide a more holistic understanding about diseases and disorders, microbial nature and development of novel therapeutic strategies to treat infectious and inflammatory diseases.

Current challenges:

1. **Role of non-bacterial organisms in altering microbiota**

If the role of bacterial community in the microbiota population has drowned most of the scientific attention so far, the roles of non-bacterial communities such as viruses (including bacteriophages) and protozoa is poorly studied.
It is important:

- to identify the non-bacterial organisms that are part of the microbiome,
- to understand their interaction with the host (directly or via other microbiota species), and
- to understand their role in the microbiome communities, in disease and in health.

2. **Gut is not the only affected system,** microbiota is also known to affect the health and disease in other organs/tissues

It is important:

- to better understand the interaction between the microbiota and the host in other organs and tissues notably in the skin, eyes, oral cavity and the genitals, and
- to understand their role in disease and in health.

3. **The effect of the host-microbiota metabolome on human health and disease**

Although many of the host and microbiota metabolic pathways can occur independently, the host depends on its microbiome for an expanded collection of digestive and metabolic enzymes. For

example, it is known that the gut microbiota yields a highly diverse metabolite repertoire from the anaerobic fermentation of undigested host dietary products, as well as endogenous substrates that are generated by microorganisms. Furthermore, host-driven processes, such as inflammation or secretion of reactive oxygen species have also shown to affect metabolic pathways of the microbiota. Thus, Microbiota-generated metabolites are increasingly being appreciated as a vital component of human physiology.
It is important:

- to create comprehensive understanding of the metabolic pathways net and the production of secondary metabolites given the wealth and diversity of microbiota communities,
- to understand how these compounds affect microbiota communities and the host, and
- to elucidate how microbial products modulate host immune responses Well-established approaches such as Mass spectrometry (MS) in conjunction with new technologies such as metabolic oligosaccharide engineering (MOE) or Bio-orthogonal click chemistry (BCC) may be implemented to uncover the microbiota metabolome and its effect on the host in health and disease.

4. **transition of microbiota from a commensal to a pathogenic state**

A large number of commensal microorganisms that co-exist peacefully with their host may cause a disease under certain circumstances and in a specific context.
It is important to understand the mechanisms and the processes that lead to the transition from a commensal to a pathogen. Mechanisms facilitating this transition are expected to include changes in the immunological status of the host's, regulatory environmental signals, ageing, acquisition of new phenotypes by the microbial species (e.g. via horizontal gene transfer or mutagenesis) or changes in the nutrition or host lifestyle. Illuminating the mechanisms underlying this transition is important for the understanding of the biology and dynamics of opportunistic infections.

Potential ways to tackle the challenges and recommendations:

- **Development of new experimental tools to study microbiota**

Understanding the role of individual species and strains within the microbiome communities, especially uncultured or low-abundance microorganisms are important for a more complete understanding of the function of the microbiota. This need in now limited, by the lack of appropriate experimental tools. Using hybrid capture and single-cell approaches involving the isolation and sequencing of infrequent microbiota species or single microbial cells may facilitate such a need. Additionally, new microbiological techniques that will base on the genomic data of a specific species may be used to formulate appropriate growth media and conditions for culturing. Similarly, development of artificial intestine or other model organs to investigate microbiota function ex-vivo are highly desired.

- **Development of new bioinformatics tools for analysis.**

Although a plethora of metagenomic data analysis tools exists either as standalone software packages or R libraries, no versatile, generic and freely available solution exists for researchers who do not have access to a bioinformatic collaborator. Access to existing microbiome for

comparison or reanalysis purposes is also complicated although public repositories have emerged, e.g. EBI's Metagenomics. As a matter of fact, such web sites only offer basic analytic capabilities which are fully integrated with the repository. Independent tools providing functionalities to access and integrate data from major public databases would allow easy comparison with fresh data or further exploration of already generated data.

Metaproteomics is emerging as a strong complement to metagenomics. Similarly, generic tools amenable to the non-bioinformatics researchers would be very welcome in this direction. Such tools should support metagenome/metaproteome comparisons.

1.3 Advancing Infectious Diseases Diagnostics and Molecular Epidemiology

Diagnostic microbiology is now at the verge of transition from Koch's methods to molecular microbiology in routine diagnostics on a broad scale. This move still requires extensive research to design new technologies to optimally address patients' as well as societal needs.

1. **Bringing infectious diseases diagnostics closer to the patient at the general practitioner's level**

The majority of infections dealt with by the general practitioner are viral respiratory and gastrointestinal diseases. However, there are very few diagnostic tests available for the rapid and sensitive diagnosis of viral infections. In addition, there are currently no tools available to identify changes in the composition of the physiological flora.

Routine diagnostics of bacterial infections and in particular antimicrobial susceptibility testing is still mainly culture-based with a few exceptions including PCR-based molecular testing for Methicillin-resistant Staphylococcus aureus (MRSA) and *Clostridium difficile* as well as for some difficult-to-culture organisms such as *Legionella*, *Chlamydia*, and *Tropheryma*.

The resulting delay until pathogen identification becomes available leads to prolonged empirical broad-spectrum antimicrobial therapy and promotes antimicrobial resistance development.

<u>Potential ways to tackle the challenges and recommendations:</u>

- To develop near-patient diagnostic technologies for common viral and bacterial respiratory tract, gastrointestinal tract and urinary tract infections in the general practitioners' office to better and more rapidly (within an hour) inform on the need for antimicrobial therapy,
- to develop tools or markers for rapid identification of dysbiotic states such as dysbiosis of the gastrointestinal and vaginal tract,
- to further advance early molecular diagnostics for pathogen identification in severe infections, mainly bacterial, both in the laboratory and at the point-of-care to allow for prudent and judicious use of antimicrobials to ultimately eliminate the need for empirical therapy and go directly for targeted therapy,
- to identify or optimize ways to perform whole genome sequencing of pathogens directly from clinical samples without laboratory propagation of strains. This would allow the identification of virulence markers as well as antibiotic resistance markers that could

eventually be lost during laboratory passage (e.g. plasmid loss or mutagenesis), and thus could contribute for a more accurate therapy, and

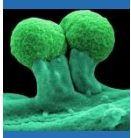
- to advance currently available and to develop novel molecular, mass spectrometry-based, Fourrier Transform Infrared Spectroscopy (FTIR) as well as imaging technologies for use on frequently encountered pathogens including *Streptococcus pneumoniae*, *S. pyogenes*, *Haemophilus influenza*, *Staphylococcus aureus*, *Enterococcus* spp., *Enterobacteriaceae*, *Campylobacter* spp., *Pseudomonas aeruginosa*, pathogens implicated in sexually transmitted diseases, bacterial vaginosis as well viruses implicated in acute respiratory tract and gastrointestinal tract infections that allow for rapid species identification and at the same time detection of the majority of known resistance mechanisms even in a mixed population of bacteria.

2. Enable individualized antimicrobial treatment for infectious diseases at the hospital level

Treatment of bacterial, fungal and viral infections is mainly guideline-driven. In particular, empiric therapy is usually broad-spectrum to cover all potential pathogens including those that are multi-drug resistant.

Antimicrobials are usually dosed in a one-fits-all fashion, not taking into account pathogen kinetics, individual drug pharmacokinetics and pharmocodynamics, patient co-morbidities, co-medication, distribution volumes, renal and hepatic function etc.

Current biomarkers are not capable of response prediction and guiding duration of antimicrobial therapy



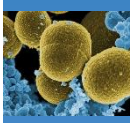
Current challenges:

- To optimize choosing and dosing of an antimicrobial in the individual patient to improve patient outcome and minimize the probability of resistance development

Potential ways to tackle the challenges and recommendations:

- To develop methods for rapidly and accurately determining drug levels and pathogen concentrations at different body sites and in different bodily fluids to optimize antimicrobial therapy – both dosing and dosing intervals – in an individual patient. This will lead to improved patient outcome and also reduce the probability of resistance development,
- to develop and evaluate biomarkers that allow for more accurate response prediction to shorten antimicrobial treatment duration, and
- to correlate drug levels and drug-level guided individualized therapy with outcome in clinical pilot studies.

3. Focusing on pathogen sub-typing for detection of high-risk clones in various infectious diseases



Typing of bacterial, fungal and viral organisms at the subspecies level is mainly done in reference laboratories to confirm or refute a clinical hypothesis of pathogen transmission and the presence of an outbreak and may take up to several weeks.

Small-scale outbreaks often go undetected, however, characterizing the origin and the dynamics of an outbreak of pathogen infections is key to its control.

Molecular characterization of virulence properties is mainly restricted to research projects and usually has no direct impact on patient management as results are available not before several days or even weeks.

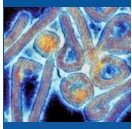
Current challenges:

- To provide strain-specific information at the subspecies level including pathogen strain type, epidemicity and virulence properties (see below) as an integral part of routine diagnostics triggering an alert that would enable optimal patient management as well as rapid institution of appropriate infection control interventions to clinicians, microbiologist, epidemiologists, infection control personnel, and bioinformaticians.

Potential ways to tackle the challenges and recommendations:

- To develop novel, affordable and cost-effective sequencing technology and analysis software for easier interpretation of genomic data for broader use in the diagnostic lab to allow for routinely performing diagnostics at the subspecies level for "relevant" organisms,
- to provide data not only on the resistance genotype and the mechanism of resistance but also on strain-specific characteristics such as epidemicity (basic reproductive number), tenacity, resistance to disinfectants, virulence, and presence of mobile genetic elements of epidemiological and therapeutic importance,
- to exploit genomic data and relate to a web-based database and framework that enables the integration of genomic, epidemiological and patient data to rapidly identify microbial threats such as hyper-virulent or hyper-epidemic "high-risk" clones that can be used to optimize patient management and institute effective control measures to contain their spread, and
- to develop a universal nomenclature for "high-risk" clones that also allows to assess different risk-levels based on genomic, epidemiological and patient-related data

1.4 Development of new treatments



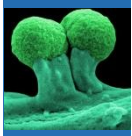
1. **Novel and experimental therapies to fight against emerging microbial challenges, either due to bacteria, viruses, fungi, parasites, and their vectors**

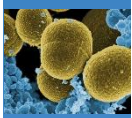
Current challenges:

The field of this multi-level therapeutics and research is wide and need continually and simultaneously research efforts on new anti-microbial compounds.

Potential ways to tackle the challenges and recommendations:

- To develop computational predictive models to analyse the risk health problem that an emergent microbe could provoke in a multi-factorial way,
- to expend the concept of treatment, from the current "treatment of the infection in the individualized patient" to the "treatment of the community of patients and their susceptible contacts" (as "outbreak therapy"),
- to consider the treatment of the "infected" environment, including disinfection procedures, hygiene and sanitation at large, including anti-insect vectors new insecticides, in order to try to reduce the global population size of the offending microbes, and therefore their possibilities to spread and evolve,
- to develop novel treatments including to new biological entities, phages, vaccines and adjuvants and immune system modulators and not to limit it to new chemical entities, anda number of existing therapies could be extended:
    - **Phage therapy**: treating people with phages is a rapid evolving field. Some phages are already in clinical trials and have the positive trait of being strain specific and have a high therapeutic index.
    - **Antibody therapy**: Treating people with antibodies for infectious diseases is evolving as the cost of developing and producing novel antibodies decreases. Being strain-specific, and having a high therapeutic index and being able to recruit an immune response makes antibodies an alternative for resistant strains and severe infections diseases.
    - **Anti-MGE (mobile genetic elements) therapy:** A problem in a number of emerging bacterial diseases is not directly related with the propagation of particular microbial species or clones, but the genes involved in the pathogenic or resistance traits. This spread depends on MGE vectors, which can be targeted by specific drugs, as conjugation inhibitors, recombination inhibitors, maintenance inhibitors (CRISPR-related strategies), restriction-based inhibitors, or negative fitness enhancing agents.
    - **Epigenetics-based therapy:** Many microbial adaptive traits, including virulence, colonization, and antibiotic resistance are deeply influenced by the epigenetic context. The relation between metabolism-resistance-virulence offers plausible new targets. Indeed, that relates with the "nutritional atmosphere" of the target organism, which eventually can be modified by nutritional therapies.
    - **Microbiota-based therapy**: Therapy directed to the decontamination of offending pathogens with microbial communities or "precision probiotics", taking advantage of bacterial competition. An example of this is the transplantation of microbiota to





decontaminate a patient from pathogens or virulent organisms. Cooperations and competitions in the microbial community should still be investigating in order to find the optimal microbiota composition as an alternative treatment

- **Plasma medicine therapy**: Physical plasma (ionized gas) treatment is a promising new technology regarding its antimicrobial effects. Treatment of infected implants, indwelling devices (catheters) or chronic wounds (diabetes) may benefit from a cold plasma treatment, which is an interesting alternative or supplemented approach to current chemical antimicrobial therapies that are restricted by drug resistance or toxicity. To ensure efficacy and a long-term safety of cold plasma applications in medicine and healthcare, the conditions of the treatment (different carrier gases and plasma generation setups, time point of the treatment, pathogen strain specificity, pathogen form (planktonic bacteria or biofilm) and tissue sensitivity) have to be established and a safety (a cytotoxicity effect, a mutagenic capacity) has to be determined. Fulfilment of these tasks will allow finding suitable compositions for highly effective novel antimicrobial treatments in human medicine and healthcare.

2. New antivirals to fight emerging and re-emerging viral infections:

Current challenges:

The increase in human population together with environmental changes and rapid increases in exchanges of goods and people is leading to the emergence of new zoonotic infections that can lead to global health and economic crisis as shown with recent viral infections like SARS-Coronavirus, EBOLA virus, Chikungunya virus, MERS-Coronavirus, Zika virus…

These environmental changes can also lead to expansion of viral infections like dengue and West Nile viruses in countries that were free from these infections. Meanwhile, we remain at high risk of a flu pandemic. Therefore, we need to be better prepared by developing new antivirals ready to be used to fight these pathogens.

Potential ways to tackle the challenges and recommendations:

- To identify the virus interactome
- To develop antivirals, which can directly target viruses or viral gene products
- To develop host-oriented drugs, in particular host factors shared by several viral families.

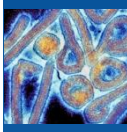
3. Therapy of the pathogenic host response to the microbial challenge.

Current challenges:

In most cases, pathogenic microbes produce the infective clinical phenotype with the necessary collaboration of the host's innate immunological response, leading to widespread inflammation and sepsis. Controlling therapeutically that response, the infection will be controlled. Alternatively, to targeting the pathogenic agent with drugs or pharmaceuticals, therapeutic strategies that are becoming increasingly relevant exploit and regulate the immune system of the host.

The immune system is very powerful in combating most foreign challenges but it is also highly self-regulated. It is usually able to identify the precise antigenic determinants of the aggressor by tailoring specific receptors in lymphocytes, but a desirable immune response may depend on the sub-cellular type where these receptors are induced. A potential way to tackle a given infection

is to acquire **information on the pathogen's responsive antigens** and through different combinatorial strategies that induce the expression of the specific receptors on the most appropriate lymphocyte subpopulations.



Potential ways to tackle the challenges and recommendations:

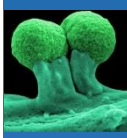
- To develop therapies that can maintain the inflammatory response under control while allowing some level of toleration to the pathogen targeting the inflammatory cells or soluble mediators.

  Potential ways to tackle area are:

  - targeting inflammatory signalling pathways for enzymatic intervention
  - activating/blocking regulatory receptors of leukocytes that are used by the pathogens to subvert immune responses
  - controlling inflammatory cells or soluble mediators to keep inflammation under control;
  - used interferon treatment: explore immunostimulating properties of the newly described interleukines and of other biologically active and human-derived substances.

- To condition the immune responses against the particular pathogen.

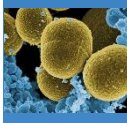
Possible strategies include: 1) vaccination regimens using the microbial antigens with adjuvants that promote the development/selection of the most appropriate lymphocyte sub-populations; and 2) control of regulatory lymphocytes that modulate/prevent the desirable specific immune response



2 VIEW OF INFECT-ERA

To tackle the human infectious diseases challenge, transnational investments, European and beyond, are necessary. Promotion of international collaborations allow joining effort to fight infectious diseases, an international issue. In these arenas, European collaborations are crucial due to existence of common disease in the countries and to limit the propagation of the microbes. It is also necessary that the Europeans Initiatives collaborate with each other and do not duplicate efforts. Infect-ERA should address complementary issues not tackled in the existing European initiatives as for instance JPIAMR or IC PerMed, initiatives on Antimicrobial resistance and personalized Medicine, respectively.

European collaborations enable sharing of data faster, characterizing the mechanisms of microbes' infections and better deciphering of individual differences in proneness and responses to infections. Moreover, development of international collaborations allows access to infrastructures and complementary expertise. Multidisciplinary research is important to build-up of knowledge but also to build on knowledge in a way the research benefits the patients. In addition, human infectious diseases should be tackled as part of the "One World One Health" concept taking into account other disciplines as, among others, domestic animals and wildlife health and environmental changes.



Fostering collaborations between academia and clinicians is a must in the field of infectious diseases. Much of the relevant clinical data as well as unique pathogens strains come from the clinical settings and should be further provided and transferred to the research laboratories in hospitals, universities and research institutes for in-depth studies. In addition, to facilitate the

launch of a novel diagnostic test or therapeutic treatment, based on basic research results, the collaboration between academics-clinicians and the industry sector are necessary from the start of the innovation development.

Interconnected workforces will help a fast development of new results in the field. The use of existing data and infrastructures should be promoted. Funding organizations should contribute to the FAIR[1] principles by promoting research results and data in an open access to the data manner. Open data can reinforce the impact of the results as it allows open scientific inquiry and the combination of different datasets and can encourage new research on topic not envisioned by the initial investigators. In addition, the use of infrastructures as biobanks is essential for collecting, authenticating and preserving human and/or pathogen specimens prior to, during and following treatment, with a comprehensive characterization of the sample donors.

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The External Advisory Board of Infect-ERA:

- *Prof. Fernando Baquero,* research professor in microbial evolution at the department of microbiology of the Ramon y Cajal University Hospital, Madrid, Spain
- *Dr. André Faustino, CEO of Gene Predit, Cantanhede, Portugal*
- *Prof. Arnaud Fontanet, head* of the Emerging Diseases Epidemiology unit at the Institute Pasteur in Paris, France
- *Prof. Luca Guardabassi, Prof. of* Antimicrobial Resistance and Antibiosis *at Ross University School of Veterinary medicine,* West Indies
- *Dr. Hubertus Haas,* Assoc. Prof. in Molecular Microbiology at Innsbruck Medical University, Austria
- *Prof. Waleria Hryniewicz, professor Emerita in Epidemiology and Clinical Microbiology at National Medicines Institute, Warsaw, Poland*
- *Dr. Antonio Parada,* CEO of Fairjourney Biologics, Porto, Portugal
- *Prof. Elisabeth Nagy, Institute of Clinical Microbiology, University of Szeged, Hungary*
- *Dr. Itamar Shalit,* CEO of the Galilee Biomedical Research Administration, Israel
- *Prof. Harald Seifert,* Professor of Medical Microbiology and Hygiene at the Institute for Medical Microbiology, Immunology and Hygiene (IMMIH) at the University of Cologne, Germany
- *Dr. Lieven Stuyver,* Senior Scientific Director and Fellow at Janssen Diagnostics, Beerse, Belgium
- *Dr. Simona Ruta* Professor of Virology, at the Stefan S. Nicolau Institute of Virology Bucharest, Romania

External scientists:

- *Dr. Samuel Alizon, Evolutionary ecologist, National Centre of Scientific Research CNRS, Montpellier, France*
- *Dr. Serge Ankri,* Technion Israel Institute of Technology, Haifa, Israel
- *Dr. Françoise Bachelerie, National Institute of Health and Medical Research, Clamart, France*
- *Dr. Nadia Berkova, National Institute for Agronomic research, Rennes, France*
- *Dr. Alexandre Carmo, Institute for Molecular and Cell Biology, Porto, Portugal*
- *Prof. Luka Cicin-Sain, Helmholtz Centre for Infection, Brunswick, Germany*
- *Dr. Victor Cid, Complutense University, Madrid Spain*
- *Dr. Jaques Colinge, University of Montpellier, France Dr. Maria Teresa Coque,* Ramon y Cajal University Hospital, Madrid, Spain
- *Dr. Jean Dubuisson, National Institute of Health and Medical Research, Lille, France*
- *Dr. Ohad Gal-Mor, heba Medical Center and Tel-Aviv University, Tel-Aviv, Israel*
- *Prof. Guntram Grassl, Hannover Medical School, Hannover, Germany*
- *Dr. Bernhard Hube,* Hans Knöll Institute, Jena, Germany

1 - http://ec.europa.eu/isa/documents/isa_annex_ii_eif_en.pdf

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Contact:

Infect-ERA coordinator: Martine Batoux

martine.batoux@agencerecherche.fr or Infect-eracoord@agencerecherche.fr

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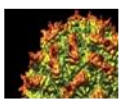
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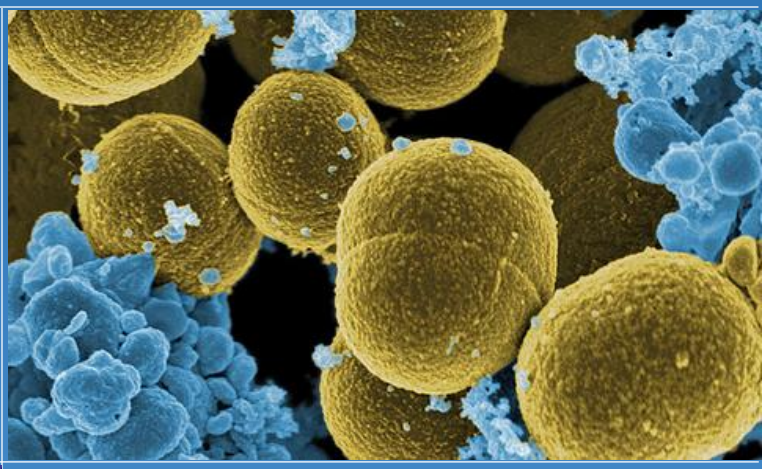

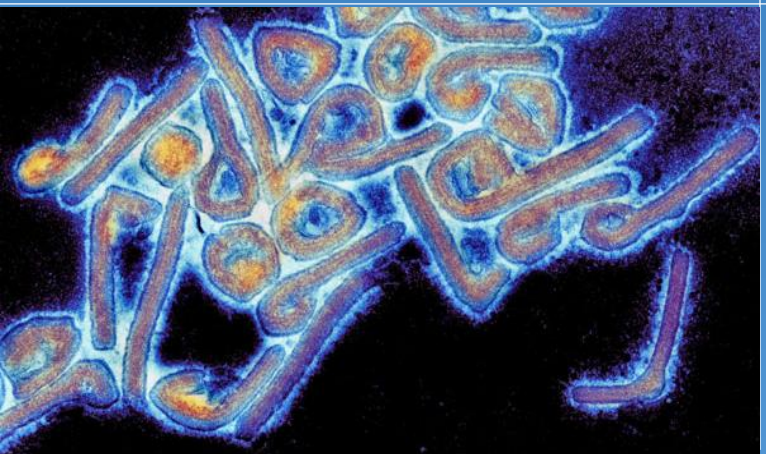

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