

## Fact Sheet

### Acronym

PathoNGen-Trace

### Full Title

Next Generation Genome Based High Resolution Tracing of Pathogens

### Programme

FP7 – Health - Collaborative project

### Contract Number

278864

### Duration

54 months (01/01/2012 – 30/06/2016)

### Project Funding

5.995.267,00 €

### Consortium

- Research Center Borstel, Leibniz Center for Biomedical Research, Germany (PD Dr. Stefan Niemann)
- Genoscreen SAS, France (Caroline Allix-Béguec)
- Applied Maths NV, Belgium (Dr. Bruno Pot)
- Ridom GmbH, Germany (Jörg Rothgänger)
- Westfälische Wilhelms-Universität Münster, Germany (Prof. Dr. Dag Harmsen)
- Piext BV, Netherlands (Ronald Burggrave)
- University of Oxford, Department of Zoology, United Kingdom (Prof. Dr. Martin Maiden)
- European Research and Project Office GmbH, Saarbrücken, Germany (Claudia Schacht)

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**PATH**  **NGenTrace** [patho-ngen-trace.eu](http://patho-ngen-trace.eu)

From base pairs to bedside – The PathoNGen-Trace project aims at enhancing the medical diagnosis of pathogens with Next Generation Sequencing (NGS) in order to pave the way for personalized medicine.

**PATH**  **NGenTrace** [patho-ngen-trace.eu](http://patho-ngen-trace.eu)



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## Next Generation Genome Based High Resolution Tracing of Pathogens

Next Generation Sequencing (NGS) has fundamentally altered genomic research by promising ultra-fast and accurate molecular typing and diagnostics. In addition, the rapid development of this technology is intended to enhance performance and bring down DNA sequencing costs, thus widening the spectrum of possible applications including the medical diagnosis of pathogens. In this context, the EU research project PathoNGen-Trace was launched bringing together an international consortium of leading experts in the field of clinical microbiology and well known enterprises in this area.

The goal of the project is the transition of NGS from a basic research tool to a highly efficient technology for pathogen typing and diagnostics at EU level. This objective will be achieved by establishing a unique European consortium that brings together three small and medium-sized enterprises leading in the fields of “data to knowledge” and “NGS genome research” with foremost experts in the clinical microbiology of three model pathogens of high European and worldwide importance (methicillin-resistant *Staphylococcus aureus*, *Campylobacter* spp., and *M. tuberculosis* complex).

### Main Objectives

- To develop new, completely integrated bioinformatics tools for fast and easy quality-controlled data extraction and interpretation for general diagnostics and public health applications.
- To streamline and implement new internal quality control procedures of the whole NGS process.
- To test and validate the performances of NGS for ultra-sensitive/early diagnostics and monitor the spread of major microbial pathogens in Europe and elsewhere.

PathoNGen-Trace will foster the development of new and widespread applications of NGS in clinical microbiology and disease surveillance, ranging from basic research to medical research, diagnostics, and pathogen genotyping.

Our aim is to develop new applications of NGS for microbial disease surveillance and early warning systems.

### Bio-informatics pipelines for quality-controlled and easy interpretation of NGS data

The project will develop bioinformatics tools that will enable a fast and easy quality-controlled data extraction as well as interpretation for general diagnostic (e.g. drug-resistance) and public health applications (genomics-based molecular epidemiology). Users will be provided with direct information on quality, type and distribution of DNA polymorphisms, antibiotic resistance, or virulence markers. Rule-based expert systems will be implemented for optimizing and facilitating generic use on multiple bacterial species.

Improved protocols for the whole NGS process from sample preparation protocols to final sequence assemblies or mapping will be developed. The Focus will be on the development of new protocols for multiplexing and genome sequencing starting from low amounts of DNA, e.g. from crude DNA extracts, early cultures or directly from clinical samples.

### Dedicated NGS-based pathogen diagnostic kits

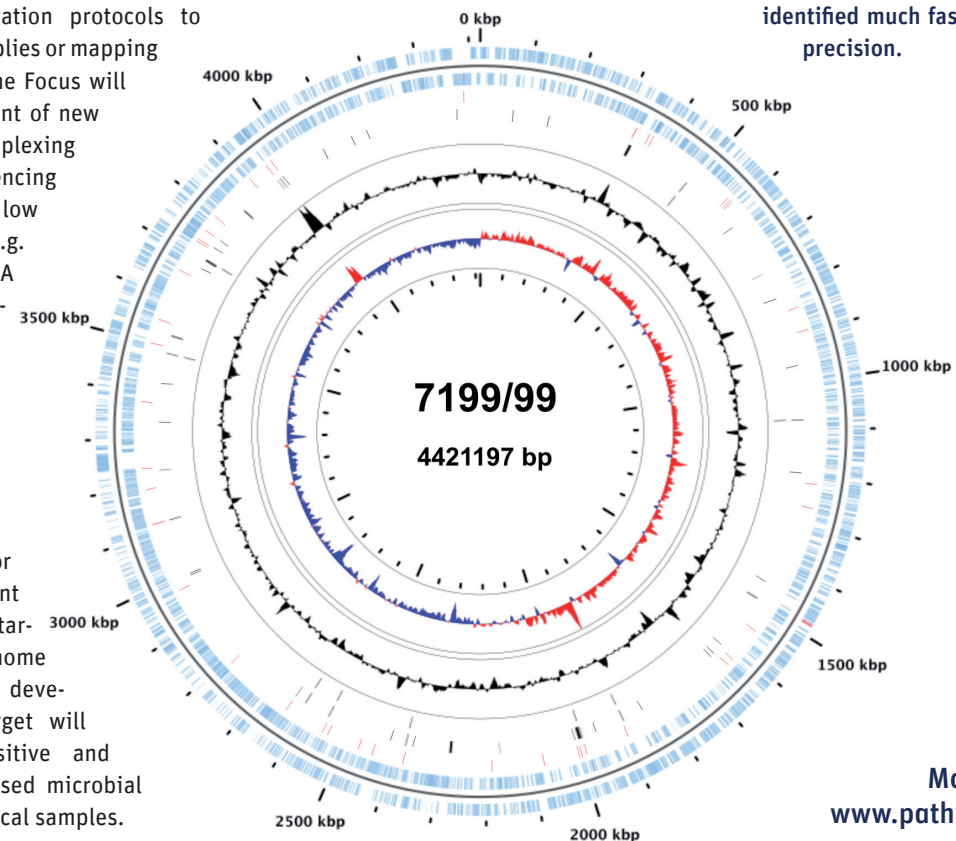
New procedures for target DNA enrichment and special kits for targeted microbial genome sequencing will be developed. The final target will be novel ultra-sensitive and wide-ranging NGS-based microbial diagnostics from clinical samples.

### Expected Results

The proposed new NGS research tools will significantly enhance data generation (e.g. better NGS workflow, new technologies), improve standardization (ontology, API and kits), quality control (algorithms), and analysis (new bio-informatics tools).

The development of new and improved tools/technologies in this SME-targeted project will overcome existing obstacles of NGS and open the door for a wide application of NGS for European scientists and clinical microbiologists, thus fostering competitiveness of Europe in NGS research and medical applications.

Pathogens and their mutations will be identified much faster and with more precision.



More information:  
[www.patho-ngen-trace.eu](http://www.patho-ngen-trace.eu)