Phylogenetics and population genetics tools for vectors and vector-borne pathogens: COST Action EurNegVec, Training School 6

Ferramentas de filogenética e genética populacional para o estudo de vetores e os seus patogénios: Ação COST EurNegVec, Training School 6

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Resumo

A Filogenética e a Genética Populacional proporcionam informação acerca de processos ecológicos e evolutivos importantes para as doenças transmitidas por vetores, através da análise de padrões espaciais e temporais de variação genética em vetores de artrópodes e dos seus agentes patogénicos.
O Centro de Saúde Global e Medicina Tropical (GHMT) / Instituto de Higiene e Medicina Tropical (IHMT) acolheu uma *Training School* internacional sobre "Ferramentas de filogenética e genética populacional para o estudo de vetores e os seus patogénios" (TS6), no quadro do Programa COST através da Ação *EurNegVec (European Network for Neglected Vectors and Vector-Borne Infections BMBS COST Action TD1303)*.
Os principais objetivos desta ação de formação foram apoiar os formandos a: 1) aprender os princípios básicos de estudos de filogenética e genética populacional; 2) compreender as implicações de tais estudos para a vigilância e controlo de doenças transmitidas por vetores; 3) treinar em programas específicos e exercícios práticos.
Neste artigo apresentamos uma sinopse desta *Training School* de uma semana, dos seus principais conteúdos e participantes.

Palavras Chave:
Ação COST, filogenética, genética populacional, *Training School*, doenças transmitidas por vetores.

Abstract

Phylogenetics and Population Genetics provide knowledge on ecological and evolutionary processes significant to vector-borne diseases, through the analysis of spatial and temporal patterns of genetic variation in arthropod vectors and their pathogens.
The Centre for Global Health and Tropical Medicine (GHTM) / Institute of Hygiene and Tropical Medicine (IHMT) hosted an international Training School on “Phylogenetic and population genetics tools for vectors and vector-borne pathogens” (TS6), within the COST Framework EurNegVec (the European Network for Neglected Vectors and Vector-Borne Infections BMBS COST Action TD1303).
The main aims of the Training School were to help the trainees to: 1) learn the basic principles of phylogenetics and population genetics studies; 2) understand the implications of such studies for the surveillance and control of vector-borne diseases; 3) to train on several dedicated software. In this paper we present a synopsis of this one-week Training School, of its main contents and participants.

Key Words:
COST Action, phylogenetics, population genetics, Training School, vector-borne diseases.

Context

COST framework

COST is the longest running European framework supporting transnational cooperation among researchers and scholars across Europe. It is a unique mean to jointly develop ideas and new initiatives across all fields of science and technology, through Pan-European networking of nationally funded research activities. Based on an European intergovernmental framework for cooperation in science and technology, COST has been contributing, since its creation in 1971, to closing the gap between science, policy makers and society throughout Europe and beyond. It anticipates and complements the activities of the EU Framework Programmes, constituting a "bridge" towards the scientific communities of COST Inclusiveness Target Countries. It also increases the mobility of researchers across Europe and fosters the establishment of scientific excellence [1].

COST aims at enabling breakthrough scientific developments leading to new concepts and products. It thereby contributes to strengthening Europe's research and innovation capacities.

In order to achieve its mission [2], COST endeavours to:

- Build capacity by connecting high-quality scientific communities in Europe and worldwide
- Provide networking opportunities for Early Stage Researchers (ESR)
- Increase research impact on policy makers, regulatory bodies and national decision makers as well as on the private sector.

COST Actions are bottom-up science and technology networks, open to researchers and stakeholders with a duration of four years. They are active through a range of networking tools, such as workshops, conferences, training schools, short-term scientific missions and dissemination activities.

Training Schools aim at widening, broadening and sharing knowledge relevant to the Action's objectives through the delivery of intensive training on a new and emerging subject [3].

EUR
NEG
VEC
European Network for Neglected Vectors and Vector-Borne Infections

EURNEGVEC Action

Arthropod vectors and vector-borne diseases are frequently zoonotic infections and although their most significant clinical effects are often on the human population, the main infection sources are dependent on vectors, animal reservoirs and environmental factors. Hence, their surveillance and control require efficient and appropriately standardised methods, integrated knowledge and awareness among researchers, academics and policy-makers along with well-trained young scientists [4].

Within the COST Framework, the European Network for Neglected Vectors and Vector-Borne Infections (EurNegVec) BMBS COST Action TD1303 was supported from 2014 till 2017.

EURNEGVEC aimed at promoting all of these values and apply them in the field of vectors (ticks, mosquitoes, sand flies, midges and fleas) and vector-borne pathogens (viruses, bacteria, protozoa and nematodes).

The main objective of the Action was to establish a powerful transboundary network of partner institutions across Europe that were involved in education and research related to arthropod-transmitted infectious diseases of man and animals, a network addressing the growing importance of vector-borne diseases at a time of Global Change, all integrated under the One Health concept, and reflecting the complexity and demands of current high-end research [5].

This Action was organized in five Working Groups (WG) [6]

WG1	The "One Health" concept in the ecology of vector-borne diseases
WG2	Barcoding, molecular diagnosis and next generation sequencing
WG3	Geospatial tools in vector research
WG4	Phylogenetics and phylogeography of vectors and vector-borne pathogens
WG5	Rare and emerging vector-borne pathogens

Three researchers from the IHMT were members of this Action: Ana Domingos (WG2), Carla Maia (WG1), and Patrícia Salgueiro (WG2 & WG4).

IHMT / GHTM

GHTM (Global Health and Tropical Medicine) is a R&D Centre that congregates IHMT Research. The GHTM mission is to produce knowledge on global health and tropical medicine, develop tools and strengthen health systems through excellence in research, training and systems implementation. Within this mission one of its specific aims is to reinforce local to global capacity to control vector borne diseases [7].

The Centre brings together researchers with a track record in Tropical Medicine and International/Global Health and aims at tackling neglected and emerging diseases under a multidisciplinary approach, covering aspects from basic biomedical research to public health policies.

Population genetics and phylogenetics help to understand

ecological and evolutionary processes (i.e., mutation, genetic drift, natural selection, and migration) important to vector-borne diseases through the analysis of spatial and temporal patterns of genetic variation in arthropod vectors and their pathogens.
Many GHTM researchers have skills and use regularly bioinformatics tools applied to the phylogenetics and population genetics studies of several vectors and vector-borne pathogens.
The Training School 6 on the "Phylogenetic and population genetics tools for vectors and vector-borne pathogens" was held at the Instituto de Higiene e Medicina Tropical (IHMT) in Lisbon, Portugal between 23rd -27th of January 2017.

Objectives

This Training School focused on the application of phylogenetics and population genetics tools in vector and vector-borne pathogens research. It was organized in theoretical and practical sessions in order to:

1. Understand the basic principles of phylogenetics and population genetics necessary to conceive and develop such studies.
2. Learn from examples of phylogeographic and population genetic studies on vectors and vector-borne pathogens.
3. Understand the implications of such studies for the surveillance of vector-borne disease and vector control.
4. Practice on several Population genetics and Phylogenetic analysis programs.

We have made use of the following freeware programs: Seaview, Jalview, Mega6, Beast, Tracer, FigTree, SplitsTree4, Structure, Arlequin, Genepop, Clumpak, Harvester, PhyML.
All learning materials were available for all the trainees through the IHMT's Moodle site (http://moodle.ihmt.unl.pt/) previously prepared by the Informatics team of the Institute, which also helped in setting up the class room and gave support to individual trainees with specific technical problems.

Team

Local organizers:
Patrícia Salgueiro, Celeste Figueiredo

Trainers (9):
Ana Abecasis-AA, Andrea Clemencia Pineda-ACP, Carla Maia- CM, João Pinto-JP, Marta Pingarilho-MP, Patrícia Salgueiro-PS, Ricardo Parreira-RP, Sofia Cortes-SC (IHMT/GHTM, Lisbon, Portugal)
Special invitation: Alejandro Cabezas-Cruz-ACC (Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, Faculty of Science, University of South Bohemia, Ceské Budejovice, Czech Republic)

Training School 6

Program available in the site [8]: http://www.eurnegvec.org/6ts.html.

Day 1 (22nd January): The trainees arrived in Lisbon in the afternoon and settled in.

Day 2 (23rd January): The training school was officially opened by Professor Lenea Campino (President of the Scientific Council of IHMT) at 15h. All the trainers and trainees introduced themselves. The organizer Patrícia Salgueiro made a short overview of the course. To close the day Alejandro Cabezas-Cruz gave a motivational Conference entitled: "What makes great scientists great? Stay Hungry, Stay Foolish".
During morning and afternoon sessions, the organization provided coffee-breaks to all participants. The lunches occurred in the canteen of the Institute.

Day 3 (24th January): The first session was divided in two lectures: 1) "Genetic structure of mosquito vectors: Impact on the epidemiology and control of malaria" by João Pinto; 2) "Molecular Epidemiology of Mosquito vectors: *Aedes sp.* Studies" by P. Salgueiro.
The second session, in the afternoon, continued with a major practical session on Population genetics data analysis involving: 1) Basic principles in population genetics, 2) Overview of the most common programs, 3) Practical exercises, by the same trainers as in the morning.

Day 4 (25th January): The morning session was initiated by Ana Abecasis with an overview on "Basic concepts in sequence alignment and phylogenetic analysis", followed by Ricardo Parreira who presented a lecture on "Molecular Epidemiology and Phylogenetic Analyses of Arboviruses Transmitted by Mosquitoes".
The afternoon session was spent on practical sessions: 1) Aligning sequences using Mega, 2) Construction and interpretation of phylogenetic trees: Mega, Phylip and PhyML, with several input files, with the support of AA, RP, MP, ACP.
Day 5 (26th January): The training school was opened by Carla Maia and Sofia Cortes with a lecture on "Molecular Epidemiology of Leishmanioses", followed by a lecture on "The evolution of tick-pathogen interactions" by Alejandro Cabezas-Cruz.

Training School 6, Group photo at IHMT. Lisbon, 23-27 January 2017

In the afternoon, A. Cabezas-Cruz continued with a major practical session involving phylogenetic analysis of bacteria in ticks, with the support of RP, MP, ACP. Short tutorial sessions were organized to answer the trainee's specific needs with the involved trainers.

In that evening, some trainers and most of the trainees had a social dinner together in a nearby restaurant with traditional Portuguese food.

Day 6 (27th January): During the last morning, the trainees were organized in different working groups assigned to different trainers according to the specific training needs of each trainee: 1) Phylogenetic data analysis, 2) Microsatellite data analysis, 3) Network analysis. All trainers were available for these tutorial sessions.

At the end of the session, trainees were invited to complete the evaluation form available on-line. Finally, the Training School 6 was officially closed by Professor Lenea Campino, the President of the Scientific Council of the IHMT.

Trainees

From 55 initial applications from 22 countries, we have selected 28 trainees from 20 countries (Albania, Bulgaria, Czech Republic, Estonia, Germany, Greece, Italy, Latvia, Lithuania, Moldova, Palestine, Portugal (8), Romania (2), Serbia, Spain, Sweden, Switzerland, Tunisia, Turkey) and 23 Academic Institutions (Al-Quds University, Aristotle Univ. Thessaloniki, Bavarian State Authority for Health and Food Safety, Daugavpils University, Ecole Nationale de Médecine Vétérinaire de Sidithabet, Tunis, Estonian University of Life Sciences, Fac.Med.Vet Lisboa, Facultad de Farmacia Universidad de Granada, Faculty of Veterinary Medicine, University of Lisbon, Hacettepe University, IHMT-Univ Nova Lisboa, Institute of Biodiversity and Ecosystem Research, Institute of Zoology, Academy of Sciences of Moldova, Institute of Public Health Tirana, National Veterinary Institute SVA, Swiss Tropical and Public Health Institute, Univ. Belgrade-Institute for Medical Research, Univ. Evora, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, University of Bari, Dept of Veterinary Medicine, University of Bristol – Life Sciences, University of Veterinary and Pharmaceutical Sciences Brno, Vytautas Magnus University).

The majority of the trainees were PhD students (13), or Post-Doc Researchers (12), 11 of which qualified as ESR. We had two MSc and one MSc students.

Evaluation

The evaluation form of the Training School and the results are available at the site [9]: https://goo.gl/SM1smz.

The training school was very well accepted by all the trainees and trainers from both a scientific and a social point of view. The majority of trainees considered all the courses to be very relevant, showed high satisfaction overall, and 96% would recommend it to others.

Therefore, we consider that the main objectives were completely achieved.

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