# Epicollect Field practical

## Introduction

Healthcare-associated infections (HCAIs) are becoming increasingly difficult to treat due to emerge and spread of antimicrobial resistance (AMR) leading to longer hospital stays, increased healthcare costs and worse prognosis. The World Health Organization (WHO) declared antibiotic resistance as one of the top ten global public health threats facing humanity. AMR is genetically encoded, mediated by acquisition of new genes, gene copy number, or mutations in regulatory and coding regions of existing chromosomal genes. Mobilizable gene-based resistance is of particular concern, as horizontal gene transfer via mobile genetic elements (MGEs) can mediate rapid spread of resistance across strains of the same bacterial population and across different bacterial organisms.

Carbapenem resistance is a major clinical concern. Carbapenems are a family of broad-spectrum beta-lactams used as last-line antibiotics, only used to treat bacteria that are already resistant to many other antibiotics. Over the last decades, resistance to carbapenems, most often caused by carbapenemase genes, has spread worldwide, with outbreaks of carbapenemase-producing bacteria reported in many hospitals globally. *Klebsiella spp*. and *Escherichia coli* are the two species most often associated with carbapenemase genes, although these genes can also be found in a variety of other carbapenemase-producing *Enterobacterales* (CPE). Whole genome sequencing (WGS) has been used successfully to elucidate hospital outbreaks, although most often targeting a single carbapenemase gene and/or bacterial species.

In this course, we will investigate the epidemiology of CPE bacteria in a single hospital where CPE cases were identified over 6 years of continuous surveillance of clinical diagnostic and screening (rectal swab or stool) samples from hospital inpatients.

We will read disk diffusion results to determine the susceptibility of these bacterial isolates to a range of different antibiotics. Next, we will use whole-genome sequence (WGS) data to determine bacterial species, type bacterial strains and establish the genetic relatedness of these strains, which will allow us to determine if CPE cases are caused by clonal outbreaks in this hospital or independently acquired cases. Finally, we will investigate the genetic determinants of phenotypic resistance, and for acquired AMR genes their genetic context and mode of transmission, using a combination of short- and long-read sequencing.

The dataset we will analyse was drawn from a prospective observational cohort study conducted at a single-large hospital in the United Kingdom (Roberts *et al.* 2024. https://doi.org/10.1099/mgen.0.001048). The place of origin and patient metadata was made-up for the purpose of this exercise.

We will collectively investigate a total of twenty-four CPE isolates identified in the same hospital, where each of you will be assigned a single case for detailed investigation. You will collect epidemiological information on your assigned CPE isolate using the Epicollect5 mobile phone application. Each of you will be assigned to one group, and each group will be given a different location. In later practicals this week, you will also

collect antibiotic susceptibility testing results (disk diffusion) and genotypic information on these isolates.

Epicollect is a free and easy-to-use mobile data-gathering platform that includes a website to create your own project and forms. Custom made forms can then be populated using the Epicollect mobile App by any user, as we will exemplify in this exercise, and includes tools to analyse and export your collected data.

**Collecting data with mobile phones**

Form groups of two and pick-up a mobile phone. Make sure the location (GPS) in your phone and WIFI are turned on. Connect to the WIFI network using the credentials provided.

Open the Epicollect5 app on your phone and select the project named ‘Thailand CPE outbreak’. If such a project is not displayed, click on ‘Add Project’ to search for it (Figure 1).

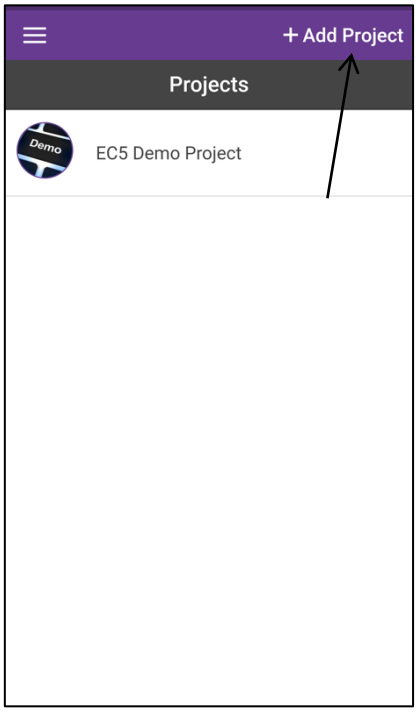


**Figure 1 Select project in Epicollect5**

Type in ‘Thailand CPE outbreak’ and click on the icon to add the project (Figure 2).


**Figure 2 Add project Thailand CPE outbreak**

Walk to the location assigned to your group. You will find one or more paper sheets with information on CPE cases (example shown in Figure 3).

## Epicollect5 Exercise Group 1

| **Case information** | |
|---|---|
| Barcode |   |
| Strain ID | cpe001 |
| Patient ID | P_010 |
| Gender* | Male |
| Age* (years) | 64 |
| Sample type | Clinical - bronchoalveolar lavage |
| Sampling date (day/month/year) | 06/07/2016 |
| Length of hospital stay (days) | 73 |

| **Laboratory and genomic information** | | |
|---|---|---|
| Bacterial species | | |
| Bacterial strain type (sequence type) | | |
| Plasmid types | | |
| **Antimicrobial susceptibility** | | |
| CPE mechanism | | |
| Antimicrobial | Phenotypic (R/I/S/NA) ** | Genotypic *** |
| Amikacin (AK) | | |
| Gentamicin (G) | | |
| Tobramycin (TOB) | | |
| Ciprofloxacin (CIP) | | |
| Trimethoprim-Sulfamethoxazole (SXT) | | |
| Ampicillin (AMP) | | |
| Cefuroxime (CFR) | | |
| Cefotaxime (CFT) | | |
| Meropenem (MPN) | | |
| Amoxycillin clavulanic acid (AMC) | | |
| Piperacillin tazobactam (PTZ) | | |

| Other sample information |
|---|
| |

NOTES:
* Demographic data of CPE cases (age and gender) made up for the purpose of this practical.
** Phenotypic antibiotic resistance as determined by disk diffusion, see previously completed sheet.
*** Genetic determinants (genes & mutations) of antibiotic resistance as determined from genome assemblies by bioinformatic tools like AMRFinder, ResFinder or Pathogenwatch.

**Figure 3 Printed sheet on one CPE case**

Click on ‘Add entry’ to enter the epidemiological information printed on your sheet (Figure 4).

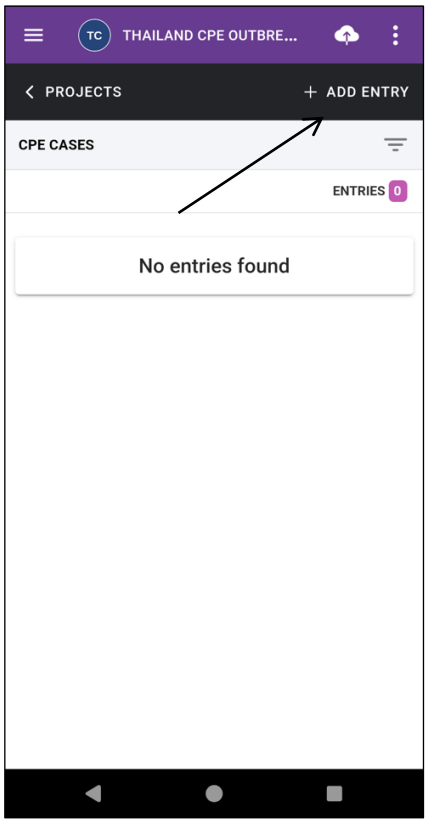


**Figure 4 Add a new entry in Epicollect5**

You will be directed to a form that you will need to fill in by copying the information on the printed sheet. Start by typing in the strain Id (Figure 5).

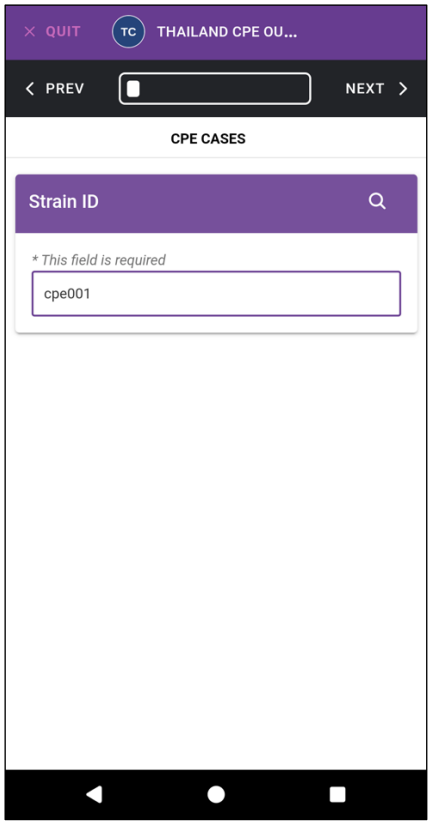


**Figure 5 Enter Strain Id in the Epicollect form**

Then enter the patient name the isolate came from (Figure 6).

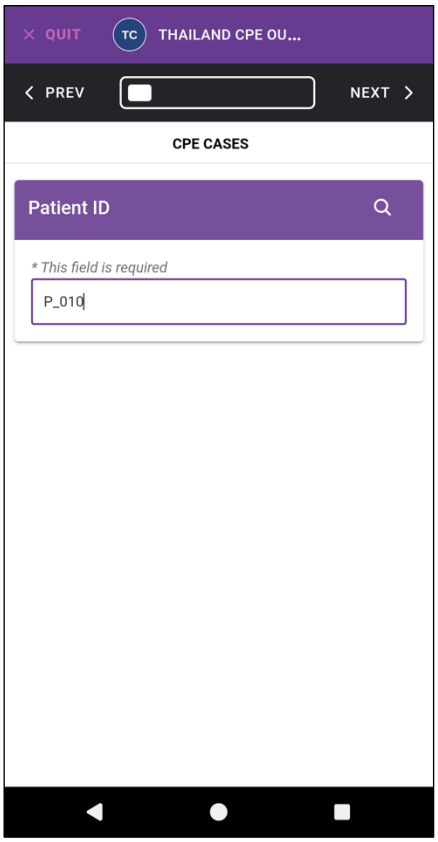


**Figure 6 Patient Name field in the Epicollect from**

Next, you will be asked to scan the barcode at the top of your printed sheet (Figure 7).


Figure 7 Scanning a barcode in an entry from

**Next, you will be asked to introduce the gender and age of your CPE case.**

You will also need to add the GPS coordinates where you found your CPE case by clicking on ‘Update location’ (Figure 8).

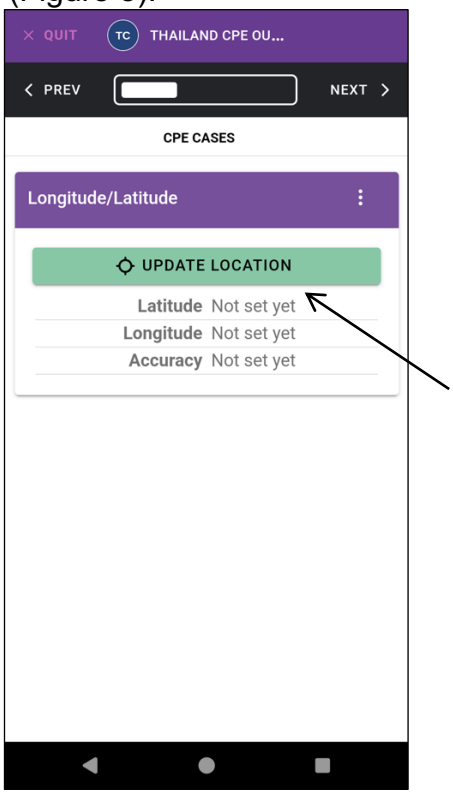


**Figure 8 Adding geolocation information in EpiCollect5**

You will be prompted to introduce the sample type of your CPE case (Figure 9 and 10).

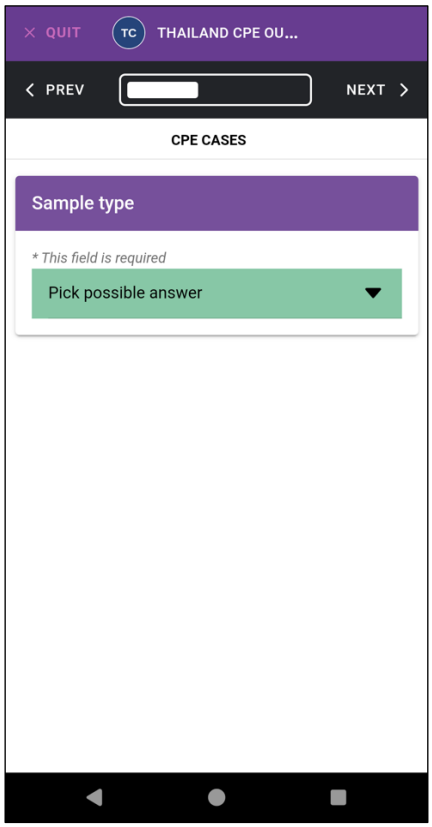


**Figure 9 Sample type of your CPE case**

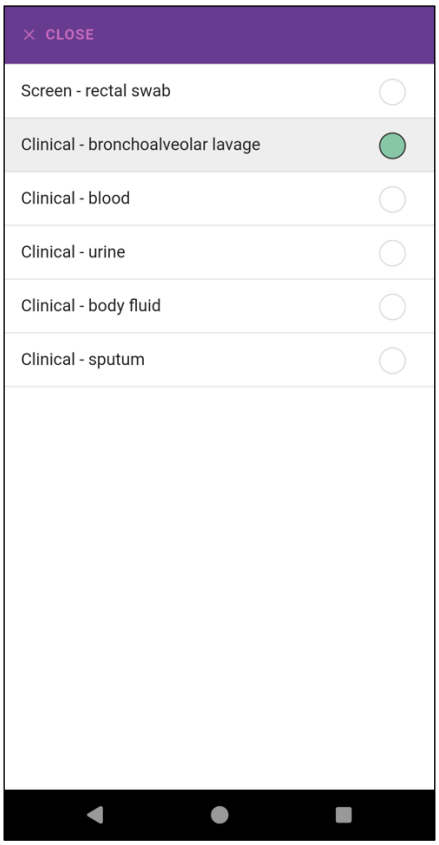


**Figure 10 Choosing the sample type of your CPE case**

Next, introduce the sampling date (Figure 11).

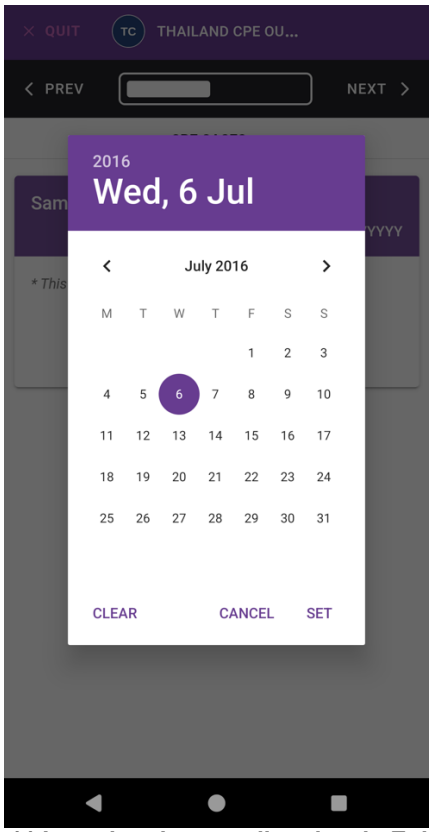


**Figure 11 Inputting the sampling data in Epicollect**

In the final steps you will be asked to select the bacterial species, sequence type, plasmid type, antibiotic susceptibility, and genetic determinants of AMR. We will obtain this information later on this course, select ‘Not Available’ in these fields for the moment.