Contact Information
If you have any questions about this report,
please email LOMWRU **info@tropmedres.ac**

LOMWRU

LOMWRU Annual Report 2021

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit

LOMWRU

ANNUAL REPORT 2021

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit

LOMWRU (Lao PDR)
lomwruinfo@tropmedres.ac

Designed by:
Suriyong Khamla-iad
Wannachat Chaichan

Edited and produced by: John Bleho

Table of Contents

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit

Cover photos © LOMWRU 2022.

© LOMWRU 2022.

The Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit

ກ່ຽວກັບໜ່ວຍງານຄົ້ນຄວ້າຂອງພວກເຮົາ

ໂຄງການຮ່ວມມືຄົ້ນຄວ້າດ້ານພະຍາດເຂດຮ້ອນລະຫວ່າງໂຮງໝໍມະໂຫສົດ - ມະຫາວິທະຍາໄລອ໋ອກຟອດ-ແວວຄຳຕູ໊ສ ຫຼື The Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU) ແມ່ນໜ່ວຍງານຄົ້ນຄວ້າທີ່ມີການຮ່ວມມືລະຫວ່າງມະຫາວິທະຍາໄລອ໋ອກຟອດ ແລະ ໂຮງໝໍມະໂຫສົດ, ນະຄອນຫຼວງວຽງຈັນ, ສປປ ລາວ ໂດຍໄດ້ຮັບທຶນຊ່ວຍເຫຼືອຫຼັກ ຈາກແວວຄຳຕູ໊ສ ປະເທດອັງກິດ. ພວກເຮົາຍັງແມ່ນສ່ວນໜຶ່ງຂອງເຄືອຂ່າຍໜ່ວຍງານຄົ້ນຄວ້າພະຍາດເຂດຮ້ອນ (MORU Tropical Health Network) ທີ່ມີສູນຄົ້ນຄ້ວາ ຕັ້ງຢູ່ ປະເທດໄທ, ກຳປູເຈຍ, ສປປ ລາວ, ພະມ້າ ແລະ ສາທາລະນະລັດ ປະຊາທິປະໄຕ ຄອງໂກ.

ປະຈຸບັນ ພວກເຮົາມີພະນັກງານທັງໝົດ 82 ຄົນ ຊຶ່ງລວມມີ ພະນັກງານທີ່ເຮັດວຽກປະຈຳຢູ່ນະຄອນຫຼວງວຽງຈັນ ແລະ ຕ່າງແຂວງ ທີ່ເປັນໜຶ່ງໃນວຽກງານການຮ່ວມມືຄົ້ນຄ້ວາ, ແລະ ໃນນັ້ນຍັງມີ ພະນັກງານພາກລັດຈາກພະແນກຈຸລິນຊີວິທະຍາ ຈຳນວນ 20 ຄົນ ໂດຍມີ ດຣ ມະນີວັນ ວົງສຸວັດ ເປັນຫົວໜ້າພະແນກ. ໜ່ວຍງານຄົ້ນຄວ້າ LOMWRU ມີ ຫ້ອງວິເຄາະທາງພັນທຸກຳ, ຫ້ອງວິເຄາະເຊໂຣໂລຊີ ແລະ ຫ້ອງວິເຄາະຄວາມປອດໄພລະດັບ 3 (BSL3) ສຳລັບປູກເຊື້ອ Rickettsial, *Mycobacterium* spp., *B. pseudomallei* ແລະ ເຊື້ອໄວຣັສ. ສຈ. ປອ. ດຣ ມາຍຟອງ ມາຍຊາຍ, ຮອງອະທິການບໍດີມະຫາວິທະຍາໄລ ວິທະຍາສາດສຸຂະພາບ ຊ່ວຍຊີ້ນຳວຽກງານຮ່ວມມືຄົ້ນຄວ້າກັບບັນດາ ແຂວງ ແລະ ວຽກງານຄົ້ນຄວ້າພາກສະໜາມ.

ໜ່ວຍງານຄົ້ນຄວ້າ LOMWRU ໄດ້ສະໜັບສະໜູນການບົ່ງມະຕິພະຍາດທີ່ເກີດຈາກເຊື້ອຈຸລະຊີບໃນ ສ.ປ.ປ ລາວ, ສະໜັບສະໜູນການເຝິກອົບຮົມ ບັນດານັກເຕັກນິກ ແລະ ນັກວິທະຍາສາດການແພດລາວ ແລະ ຍັງຈັດຕັ້ງປະຕິບັດການສຶກສາຄົ້ນຄວ້າໂດຍສະເພາະຂົງເຂດທີ່ກ່ຽວກັບພະຍາດຊຶມເຊື້ອ.

Who we are

The Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU) is a research collaboration between the University of Oxford and Mahosot Hospital in Vientiane, Lao PDR with core funding from the Wellcome Trust in the UK. We are part of the MORU Tropical Health Network which has research units in Thailand, Cambodia, Laos, Myanmar and Democratic Republic of Congo.

Currently there is a team of 82 research and support staff in the capital and the provinces working on projects as part of the collaboration, including 20 Lao Government employees led by Dr Manivanh Vongsouvath, Head of the Mahosot Microbiology Laboratory. In addition, LOMWRU has molecular and serology laboratories and a BSL3 laboratory for rickettsial, *Mycobacterium* spp., *Burkholderia pseudomallei* and viral culture. The Head of Field Research is Professor Mayfong Mayxay, who is Vice President of the University of Health Sciences in Vientiane. LOMWRU supports microbiological diagnosis in Laos, trains Lao medical technologists and scientists, and conducts research on a wide range of infectious diseases.

ຮູບພາບໜ່ວຍງານ LOMWRU ທີ່ຕຶກເກົ່າພະແນກຈຸລິນຊີວິທະຍາ ໂຮງໝໍມະໂຫສົດ, ນະຄອນຫຼວງວຽງຈັນ. © LOMWRU 2022.
Photographer: Micka Perier.

MESSAGE FROM THE DIRECTOR

ຄຳເຫັນຂອງທ່ານ **Professor Elizabeth Ashley**

ຄຳເຫັນຂອງຜູ້ອຳນວຍການ
ໃນປີ 2021, ການລະບາດຂອງພະຍາດ COVID-19 ແມ່ນຍັງໄດ້ເປັນຫົວຂໍ້ທີ່ພົ້ນເດັ່ນຢູ່ໃນຊີວິດປະຈຳວັນຂອງພວກເຮົາ. ປະເທດລາວກໍ່ໄດ້ຈັດຕັ້ງປະຕິບັດມາດຕະການຄວບຄຸມ ແລະ ປ້ອງກັນຫຼາຍຢ່າງ ເພື່ອຊະລໍການແຜ່ລະບາດຢ່າງເປັນວົງກວ້າງຢູ່ໃນຊຸມຊົນຂອງເຊື້ອ SARS-CoV-2 ແລະ ຫຼີກລ້ຽງບໍ່ໃຫ້ຄົນເຈັບຢູ່ໃນລະບົບສາທາລະນະສຸກລົ້ນ ເຊິ່ງເປັນການຊື້ເວລາຈົນກວ່າຈະມີວັກແຊັງປ້ອງກັນຢູ່ໃນປະເທດ.

ຢູ່ LOMWRU ພວກເຮົາກໍ່ມີຄວາມພາກພູມໃຈທີ່ໄດ້ປະກອບສ່ວນເຂົ້າໃນວຽກງານການກວດຫາເຊື້ອແຫ່ງຊາດ ໂດຍການຊ່ວຍໂຮງໝໍມະໂຫສົດໃນການບໍລິການດ້ານການບົ່ງມະຕິພະຍາດ COVID-19, ເຊິ່ງຕົວຢ່າງທີ່ໄດ້ຮັບແມ່ນສົ່ງມາຈາກສູນວິເຄາະ ແລະ ລະບາດວິທະຍາແຫ່ງຊາດທຸກວັນໃນປີ 2021 ໂດຍມີ ດຣ. ມະນີວັນ ວົງສຸວັດ ເປັນຜູ້ຄຸ້ມຄອງບໍລິຫານ. ນອກນັ້ນພວກເຮົາໄດ້ສືບຕໍ່ວຽກງານການຄົ້ນຄວ້າວິໄຈ ແຕ່ວຽກງານດັ່ງກ່າວກໍ່ໄດ້ຊະລໍຕົວເນື່ອງຈາກຄົນເຈັບບໍ່ເຂົ້າມາກວດຢູ່ໂຮງໝໍ ແລະ ການຈຳກັດການເດີນທາງເຮັດໃຫ້ການຈັດຕັ້ງປະຕິບັດໂຄງການໃໝ່ມີຄວາມຫຍຸ້ງຍາກ. ພະຍາດ COVID ຍັງມີຜົນກະທົບຕໍ່ການສຶກສາອົບຮົມນຳອີກໂດຍເຮັດໃຫ້ນັກວິທະຍາສາດໜຸ່ມນ້ອຍຜູ້ທີ່ໄດ້ຮັບທຶນບໍ່ສາມາດເດີນທາງໄປຮຽນຢູ່ຕ່າງປະເທດ.

ໃນບົດລາຍງານສະບັບນີ້ ພວກເຮົານຳສະເໜີວຽກງານບາງຢ່າງກ່ຽວກັບພະຍາດ COVID, ພ້ອມກັບຜົນການຄົ້ນຄວ້າວິໄຈທີ່ພົ້ນເດັ່ນໃນປີ 2021 ແລະ ການຝຶກອົບຮົມຕ່າງໆ.

ຮູບພາບລຽນຕາມເຂັມໂມງ ຈາກດ້ານເທິງຊ້າຍ: ທີມງານທ່ານໝໍ ແລະ ນັກເຕັກນິກດ້ານແລັບ ທີ່ກຳລັງເບິ່ງຜົນກວດຄົນເຈັບ, ນາງ Anne Pando ແລະ ນາງ ເກສອນ ປະດິດ ທີ່ເຮັດວຽກໃນຫ້ອງແລັບ BSL-3, ນາງ Leigh Jones ທີ່ນຳພາການເຝິກອົບຮົມດ້ານການຂຽນແບບຫຼັກວິທະຍາສາດ, ຮູບພາບຕຶກໃໝ່ຂອງພະແນກຊຶມເຊື້ອ ໂຮງໝໍມະໂຫສົດ, ແລະ ນາງ ມາລາວັນ ວົງສຸວັດ ແລະ ນາງ ລັດສະນີພອນ ບຸດທະສາວົງ ທີ່ເຮັດວຽກໃນຫ້ອງແລັບທາງດ້ານໄວຣັສ. © LOMWRU 2022.

ໃນປີ 2021 ຖືວ່າເປັນປີທີ່ສຳຄັນອີກປີສຳລັບໂຄງການ LOMWRU ເນື່ອງຈາກພວກເຮົາໄດ້ມີການຍ້າຍຫ້ອງການ ແລະ ຫ້ອງວິເຄາະເຂົ້າໃນໂຮງໝໍມະໂຫສົດຫຼັງໃໝ່ໃນເດືອນພະຈິກ ທີ່ໄດ້ຮັບການຊ່ວຍເຫຼືອໂດຍລັດຖະບານຈີນ ເຊິ່ງໂຄງການປຸກສ້າງໄລຍະທຳອິດ ແມ່ນສຳເລັດ ແລະ ໄລຍະທີສອງແມ່ນກຳລັງດຳເນີນການຢູ່.

ສ່ວນທີ່ເຫຼືອສຳລັບຂ້າພະເຈົ້າແມ່ນການກ່າວຄຳຂອບໃຈ ທ່ານ ປອ ດຣ ຊຸຊາດ ວົງພະຈັນ, ອຳນວຍການໂຮງໝໍມະໂຫສົດ, ແລະ ຮອງອຳນວຍການ ທ່ານນາງ ບົວວັນ ປະທຸມທອງ, ດຣ. ໄຊຊະນະ ສົມບັນດິດ, ດຣ. ບຸນໂຮມ ກັນທະວົງ ແລະ ດຣ.ໄຄສີ ລາຊະວົງ ແລະ ທຸກພະແນກທີ່ໃຫ້ການຮ່ວມມື ແລະ ຊ່ວຍເຫຼືອຢ່າງຕໍ່ເນື່ອງ. ພວກເຮົາຫວັງວ່າຈະໄດ້ພົບໝູ່ເພື່ອນ ແລະ ເພື່ອນຮ່ວມງານ ຢູ່ວຽງຈັນ ໃນອີກສອງສາມເດືອນຂ້າງໜ້າ ເມື່ອມີການຜ່ອນຜັນມາດຕະການປ້ອງກັນພະຍາດ COVID.

Professor Elizabeth A Ashley
ຜູ້ອຳນວຍການ LOMWRU

The LOMWRU team shown in front of the Old Microbiology Laboratory in Mahosot Hospital, Vientiane. © LOMWRU 2022. Photographer: Micka Perier.

MESSAGE FROM THE DIRECTOR

Message from Professor Elizabeth Ashley

In 2021, the COVID-19 pandemic was the dominant theme in all of our lives once again. Laos implemented a series of control measures to delay widespread community transmission of SARS-CoV-2 and avoided the healthcare system becoming overwhelmed, buying precious time until vaccines were available in the country.

In LOMWRU we were pleased to be able to contribute to the national testing programme by supporting Mahosot Hospital run the diagnostic service for COVID-19, receiving specimens from the National Centre for Laboratory Epidemiology on a daily basis in 2021, which was managed by Dr Manivanh Vongsouvath. We continued our research activities but these slowed down as patients stayed away from hospitals and travel restrictions made launching new studies more difficult. COVID also impacted on training with junior scientists unable to travel abroad to take up hard-earned scholarships.

In this report we present some of our COVID-related work, as well as some highlights from our 2021 research outputs and training programmes.

The year 2021 was momentous for LOMWRU for another reason as, in November, we moved from our laboratories and offices to our new home in the newly built Mahosot Hospital, donated to Laos by the Chinese government. Phase one of the building is complete and phase two is underway.

Shown, *clockwise from top left*: Ms Amphaivanh Suepsanith in the microbiology lab, the biosafety team preparing to fumigate the lab, Anne Pando and Kaisone Padith in BSL-3 lab, the new Infectious Diseases Building in Mahosot Hospital, Mrs Anisone Chanthongthip training in the molecular lab. © LOMWRU 2022.

It just remains for me to thank Dr Susath Vongphachanh, Director of Mahosot Hospital, Deputy Directors Mrs Bouavanh Pathoumthong, Dr Xaysana Sombandith, Dr Bounhome Kanthavong and Dr Khaysy Rassavong, and all other departments wholeheartedly for their continued collaboration and support. We hope to see friends and colleagues in Vientiane in the months ahead as COVID restrictions ease.

Best wishes,

Professor Elizabeth A Ashley
Director

ຮູບພາບ ດຣ Rebecca Inglis ຜູ້ຊ່ຽວຊານດ້ານເບິ່ງແຍງຄົນເຈັບໜັກ ແລະ ເປັນນັກສຶກສາປະລິນຍາເອກ ຈາກມະຫາວິທະຍາໄລ Oxford ທີ່ກຳລັງອົບຮົມປະຕິບັດດ້ານ ICU ພ້ອມດ້ວຍ ດຣ ຄຳໃສ ເດດລີຊາ ຫົວໜ້າພະແນກຟື້ນຟູໜ້າທີ່ການ. ໃນໄລຍະທຳອິດທີ່ພະຍາດ COVID-19 ແຜ່ລະບາດ, ດຣ Rebecca ໄດ້ຮັບລາງວັນ Institutional Translational Partnership Award ໃນການປັບຫຼັກສູດໃຫ້ເຂົ້າກັບການເບິ່ງແຍງກໍລະນີຄົນເຈັບໜັກທີ່ເປັນພະຍາດໂຄວິດ ເຊິ່ງເປັນຫຼັກສູດເຝິກອົບຮົມເພື່ອປັບປຸງການເບິ່ງແຍງຄົນເຈັບໜັກໃຫ້ດີຂຶ້ນ. ຫຼັກສູດດັ່ງກ່າວໄດ້ຖືກຮັບຮອງຈາກອົງການອະນາໄມໂລກ ແລະ ລັດຖະບານລາວ ແລະ ໄດ້ນຳໃຊ້ໃນພະແນກ ICU ທົ່ວປະເທດ ໄດ້ເຖິງ 21 ໜ່ວຍງານ ICU ທີ່ມີບຸກຄະລາກອນເຖິງ 128 ຄົນ ຈາກການອົບຮົມຈາກ ດຣ Rebecca ແລະ ທີມງານ. © LOMWRU 2022.

LOMWRU COVID-19 activities in 2021

ກິດຈະກຳ ທີ່ກ່ຽວກັບ ພະຍາດ COVID

ການບົ່ງມະຕິ

ຕັ້ງແຕ່ມີການລະບາດຂອງພະຍາດ COVID-19 ທາງໂຄງການ LOMWRU ກໍ່ໄດ້ຊ່ວຍໂຮງໝໍມະໂຫສົດໃນການຕັ້ງລະບົບ PCR ເພື່ອກວດຕົວຢ່າງທີ່ສົ່ງມາແຕ່ສູນວິເຄາະ ແລະ ລະບາດວິທະຍາແຫ່ງຊາດກວດ ທຸກວັນທັງວັນເສົາ ແລະ ວັນອາທິດ. ມາຮອດທ້າຍປີ 2021 ພວກເຮົາໄດ້ກວດໄປທັງໝົດ 40,850 ຕົວຢ່າງ. ວິທີການຫຼັກໆ ທີ່ພວກເຮົາໃຊ້ແມ່ນ SARS-CoV-2 E-gene probe based real-time RT-PCR. ເຕັກນິກ SARS-CoV-2 N1 (US CDC) qRT-PCR ແມ່ນໃຊ້ເພື່ອຢັ້ງຢືນຜົນກວດ ໃນກໍລະນີຜົນກວດ SARS-CoV-2 E-gene ເປັນ equivocal results. ພວກເຮົາໄດ້ຊື້ເຄື່ອງກວດ GeneXpert system ເພື່ອຮັບປະກັນວ່າພວກເຮົາຕອບສະໜອງຜົນກວດໃຫ້ແກ່ຄົນເຈັບທີ່ມານອນໂຮງໝໍມະໂຫສົດ ໄດ້ຢ່າງວ່ອງໄວ ແລະ ທັນການ.

ຮູບພາບ ນາງ ຈ່ອຍ ສີລິສຸກ (ດ້ານຂວາ) ແລະ ດຣ Tamalee Roberts ທີ່ກຳລັງໃຊ້ເຄື່ອງ GeneXpert ເທື່ອທຳອິດໃນເດືອນມັງກອນ, ທີ່ພະແນກຈຸລິນຊີວິທະຍາ ເພື່ອບົ່ງມະຕິພະຍາດ MDR-TB. ເຄື່ອງມື GeneXpert ນີ້ເຮັດໃຫ້ເພີ່ມປະສິດທິພາບການບົ່ງມະຕິພະຍາດວັນນະໂລກ ແລະ ຊ່ວຍໃຫ້ທີມງານສາມາດບໍລິການການບົ່ງມະຕິພະຍາດ COVID-19 ໃນໂຮງໝໍມະໂຫສົດຕະຫຼອດ 24ຊົ່ວໂມງ. © LOMWRU 2022.

ຮູບນາງຈ່ອຍ ສີລິສຸກ (ຂວາມື) ແລະ Dr Tamalee Roberts ທີ່ກຳລັງໃຊ້ເຄື່ອງ GeneXpert ຢູ່ໃນຫ້ອງວິເຄາະຈຸລິນຊີວິທະຍາ ເຊິ່ງເຄື່ອງ ຖືກນຳໃຊ້ທຳອິດໃນເດືອນມັງກອນ ໃນການບົ່ງມະຕິ ເຊື້ອວັນນະໂລກທີ່ຕ້ານຕໍ່ຢາຫຼາຍຊະນິດ (MDR-TB). ການມີເຄື່ອງ GeneXpert ຊ່ວຍໃຫ້ພວກເຮົາຫຼຸດໄລຍະເວລາໃນການບົ່ງມະຕິວັນນະໂລກ ແລະ ພວກເຮົາໃຫ້ການບໍລິການຕະຫຼອດ 24 ຊົ່ວໂມງ / 7 ວັນ ສຳລັບການບົ່ງມະຕິພະຍາດ COVID-19 ຢູ່ໂຮງໝໍມະໂຫສົດ.

ວຽກງານການຄົ້ນຄວ້າ ແລະ ການເຝົ້າລະວັງ

ພວກເຮົາໄດ້ເຮັດການສຶກສາທົດລອງ ໃນເດືອນມິຖຸນາ ປີ 2021 ເຊິ່ງຈຸດປະສົງແມ່ນການສຳຫຼວດຫາຄວາມສ່ຽງໃນການຕິດເຊື້ອຈາກການສຳພັດໃນຄົວເຮືອນ ຢູ່ລາວ ທີ່ມີຄົນເຈັບຖືກບົ່ງມະຕິພະຍາດ COVID-19 ແລະ ໄດ້ອອກກັບບ້ານຫຼັງຈາກປິ່ນປົວໄດ້ 14-17 ວັນ, ບໍ່ວ່າຜົນກວດດ້ວຍເຕັກນິກ PCR ຂອງພວກເຂົາຈະຍັງບວກ ຫຼື ບໍ່, ການຕັດສິນໃຈໃຫ້ອອກໂຮງໝໍແມ່ນບໍ່ໄດ້ອີງໃສ່ຜົນກວດ PCR ຕ້ອງລົບສອງຄັ້ງ ເຊິ່ງເປັນນະໂຍບາຍທີ່ຈັດຕັ້ງປະຕິບັດຢູ່ລາວຕັ້ງແຕ່ເລີ່ມມີການລະບາດຂອງພະຍາດ.

ໃນລະຫວ່າງວັນທີ 20 ພຶດສະພາ 2021 ແລະ 27 ສິງຫາ 2021 ພວກເຮົາໄດ້ເອົາຄົນເຈັບເຂົ້າໃນການສຶກສາ 55 ກໍລະນີ ແລະ 84 ກໍລະນີສຳພັດ ທີ່ຢູ່ໃນ 27 ຄົວເຮືອນ. ພວກເຮົາບໍ່ໄດ້ພົບເຫັນຫຼັກຖານການແຜ່ເຊື້ອ SARS-CoV-2 ໃຫ້ແກ່ຜູ້ສຳພັດກັບກໍລະນີທີ່ອອກໂຮງໝໍ ແລະ ຜົນກວດໂຄວິດຍັງບວກດ້ວຍເຕັກນິກ PCR ເຊິ່ງເປັນການສະໜັບສະໜູນນະໂຍບາຍການໃຫ້ອອກແບບໃໝ່.

ຮູບພາບ ນາງ ໂອ້ຍອານົງ ພອນມີໄຊ, ນັກເຕັກນິກດ້ານແລັບ ທີ່ກຳລັງເຮັດວຽກໃນຫ້ອງແລັບທາງດ້ານໄວຣັສ. © LOMWRU 2022.

ໂດຍການສະໜັບສະໜູນຂອງ NAMRU-2 ພວກເຮົາໄດ້ເຮັດການເຝົ້າລະວັງເຊື້ອໄວຣັສທີ່ກໍ່ໃຫ້ເກີດການຊຶມເຊື້ອລະບົບຫາຍໃຈ ຢູ່ ໂຮງໝໍແຂວງ 4 ແຫ່ງຢູ່ລາວ (ຫຼວງນ້ຳທາ, ຊຽງຂວາງ, ສະລາວັນ ແລະ ອັດຕະປື) ຢູ່ໃນຊ່ວງຂອງການລະບາດໂຄວິດ, ແລະ ໄດ້ສະໜອງຂໍ້ມູນໃຫ້ແກ່ the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC). ຄືດັ່ງທີ່ໄດ້ພົບເຫັນຢູ່ໃນປະເທດອື່ນ, ເຊື້ອໄວຣັສອື່ນໆທີ່ພົບເຫັນເລື້ອຍໆເຊັ່ນ ເຊື້ອ influenza ແລະ respiratory syncytial virus ແມ່ນກວດບໍ່ພົບໃນທາງປະຕິບັດໃນປີ 2021. Dr Audrey Dubot-Pérès, ຫົວໜ້າໜ່ວຍງານຈຸລະໂລກວິທະຍາ ຢູ່ LOMWRU ໄດ້ຮັບ Institutional Translational Partnership Award (Wellcome Trust) ແລະ ໄດ້ສຶກສາເບິ່ງວ່າການເຝົ້າລະວັງຢູ່ເຂດຫ່າງໄກສອກຫຼີກອາດເຮັດໄດ້ງ່າຍຂຶ້ນບໍ່ ເຊັ່ນ ການກວດນ້ຳລາຍຢູ່ໃນເຈ້ຍຊັບ ຫຼື ຕົວຢ່າງຕ້ອຍ ແລ້ວສົ່ງມາຫ້ອງວິເຄາະສູນກາງ ຢູ່ໃນອຸນຫະພູມຫ້ອງ ແທນທີ່ຈະເປັນການເກັບຕົວຢ່າງຜົ້ງດັງພາກສ່ວນເລິກ ທີ່ເປັນມາດຕະຖານ ທີ່ຕ້ອງເກັບໃນພູມປູກສິ່ງເຊື້ອ ແລະ ຂົນສົ່ງດ້ວຍຄວາມເຢັນ.

ໂດຍການຮ່ວມມືກັບ ດຣ. ຈັນທະລາ ສຸກສາຄອນ, ຫົວໜ້າສູນບໍລິຈາກເລືອດແຫ່ງຊາດ, ພວກເຮົາໄດ້ເຮັດການສຳຫຼວດຊອກຫາທາດກາຍຕ້ານ ໃນເລືອດຜູ້ບໍລິຈາກຢູ່ລາວ ເພື່ອໃຫ້ເຂົ້າໃຈດີຂຶ້ນກ່ຽວກັບວິວັດທະນາການຂອງການລະບາດພະຍາດໂຄວິດ 19 ຢູ່ລາວ.

ມາຮອດທ້າຍປີ 2021 ພວກເຮົາໄດ້ທຶນຈາກ the Wellcome Trust ເພື່ອດຳເນີນການກວດຫາສາຍພັນຂອງ SARS-CoV-2 ທີ່ໄຈ້ແຍກໄດ້ຢູ່ລາວ ດ້ວຍເຕັກນິກ nanopore sequencing ເພື່ອຊ່ວຍໃນການເຝົ້າລະວັງດ້ານພັນທຸກຳແຫ່ງຊາດ ແລະ ສາກົນ.

ການຝຶກອົບຮົມ

Dr Rebecca Inglis, ເຊິ່ງເປັນຊ່ຽວຊານດ້ານເບິ່ງແຍງຄົນເຈັບໜັກ ແລະ ກໍເປັນນັກສຶກສາປະລິນຍາເອກ (ມະຫາວິທະຍາໄລ Oxford) ມາຈາກລາຊະອານາຈັກອັງກິດ ທີ່ໂຄງການ LOMWRU ໃຫ້ການຮັບຕ້ອນ. ສ່ວນໜຶ່ງຂອງບົດປະລິນຍາເອກຂອງລາວ ລາວໄດ້ພັດທະນາ ແລະ ປະເມີນຫຼັກສູດການຝຶກອົບຮົມ ເພື່ອປັບປຸງການເບິ່ງແຍງຄົນເຈັບໜັກໃຫ້ດີຂຶ້ນ. ວິທີວິທະຍາແມ່ນໃຊ້ເຕັກນິກການປ່ຽນພຶດຕິກຳ ເຊິ່ງລາວໄດ້ສະແດງໃຫ້ເຫັນວ່າ ເຕັກນິກດັ່ງກ່າວສາມາດປັງປຸງການເບິ່ງແຍງຄົນເຈັບໜັກຢູ່ຫ້ອງຟື້ນຟູຊີບ 3 ແຫ່ງ ຢູ່ລາວ ບ່ອນທີ່ລາວເຮັດການສຶກສາ. ໃນຊ່ວງທຳອິດຂອງການລະບາດ Rebecca ໄດ້ຮັບທຶນ an Institutional Translational Partnership Award ເພື່ອປັບຫຼັກສຸດໃຫ້ເຂົ້າກັບການເບິ່ງກໍລະນີຄົນເຈັບໜັກທີ່ເປັນໂຄວິດ. ຫຼັກສູດປັບປຸງແມ່ນໄດ້ຮັບການຮັບຮອງໂດຍອົງການອະນາໄມໂລກ, ແລະ ລັດຖະບານລາວກໍ່ຮັບເອົາຫຼັກສູດ, ແລະ ດຣ. Rebecca ແລະ ທີມງານຄູຝຶກຂອງລາວກໍ່ໄດ້ໃຫ້ການຝຶກອົບຮົມພະນັກງານຢູ່ຫ້ອງຟື້ນຟູຊີບທຸກແຫ່ງຢູ່ລາວ, ເຊິ່ງໃນນັ້ນມີພະນັກງານຈຳນວນ 128 ທ່ານ ຢູ່ ຫ້ອງຟື້ນຟູຊີບ 21 ແຫ່ງໄດ້ຮັບການຝຶກອົບຮົມ.

Critical care specialty trainee and DPhil student (University of Oxford) Dr Rebecca Inglis giving ICU training with Dr Khamsay Detleuxay, Director of the Department of Healthcare & Rehabilitation. The training course Rebecca developed to improve the care of adults critically ill with COVID-19 was accredited by the WHO, taken up by the Lao government, and rolled out to every ICU in the country by Rebecca and her trainers. The intervention reached 128 staff in 21 ICUs. © LOMWRU 2022.

LOMWRU COVID-19 activities in 2021

Diagnostics

Since early in the COVID-19 pandemic LOMWRU supported Mahosot Hospital to set up and perform PCR testing on specimens distributed by the National Centre for Laboratory Epidemiology seven days a week. By the end of 2021 we had processed 40,850 swabs. The main method we used was SARS-CoV-2 E-gene probe based real-time RT-PCR. SARS-CoV-2 N1 (US CDC) qRT-PCR is performed for confirmation in case of SARS-CoV-2 E-gene equivocal results. We also purchased a GeneXpert system to ensure we could provide a round-the-clock testing service for patients in Mahosot Hospital.

Mrs Joy Silisouk (*right*) and Dr Tamalee Roberts are shown in Mahosot Microbiology Laboratory with the GeneXpert machine, used for the first time in January, with a diagnosis of MDR-TB. Having GeneXpert enables us to reduce delays in TB diagnosis and provide a 24/7 service for COVID-19 diagnosis in Mahosot Hospital. © LOMWRU 2022.

Research and surveillance

We launched a pilot study in June 2021, aiming to investigate the risk of infection to household contacts in Laos if patients diagnosed with COVID-19 were discharged from hospital after 14-17 days, regardless of whether they still had a positive PCR result, rather than basing the decision to discharge on two negative PCR test results which was the policy that had been implemented in Laos since the start of the pandemic.

From 20 May 2021-27 August 2021 we enrolled 55 cases and 84 contacts in 27 households in the study. We found no evidence of onward transmission of SARS-CoV-2 to contacts of cases discharged home with a positive PCR result supporting changes in the discharge policy.

Xao Vang, lab technician, shown scanning a GeneXpert cartridge in the microbiology laboratory. © LOMWRU 2022.

With support from NAMRU-2 we have been conducting respiratory virus surveillance in collaboration with four provincial hospitals in Laos (Luang Namtha, Xieng Khuang, Salavan and Attapeu) during the pandemic, and sharing data with the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC). As has been noted in other countries, other viruses that would typically be circulating, such as influenza and respiratory syncytial virus, practically disappeared in 2021. Dr Audrey Dubot-Pérès, Head of Virology in LOMWRU received an Institutional Translational Partnership Award (Wellcome Trust) and is examining whether surveillance in remote areas could be made simpler e.g. by testing saliva on filter paper or swabs transported at ambient temperature to a central laboratory, instead of the reference standard of a nasopharyngeal swab, stored in virus transport medium and transported cold.

In collaboration with Dr Chanthala Souksakhone and the National Blood Centre we have conducted a serosurvey of blood donors in Laos to gain a better understanding of the evolution of the pandemic in the country.

Towards the end of 2021 we were awarded funding from the Wellcome Trust to start nanopore sequencing of Lao SARS-CoV-2 isolates to support national and global genomic surveillance efforts.

Training

Dr Rebecca Inglis is a critical care specialty trainee and DPhil student (University of Oxford) from the UK hosted by LOMWRU. As part of her DPhil, she developed and evaluated a training course to improve the care of critically ill adults. The methodology employs behaviour change techniques that she was able to show led to a measurable improvement in patient care in the three intensive care units (ICUs) in Laos where it was piloted. At the start of the pandemic, Rebecca won an Institutional Translational Partnership Award to adapt the course for critically ill COVID patients. The revised course was accredited by the WHO, taken up by the Lao government, and rolled out to every ICU in the country by Rebecca and her trainers. The intervention reached 128 staff in 21 ICUs.

ຮູບພາບ ດຣ ວິລະດາ ຈັນສະມຸດ ແລະ ດຣ ດານ້ອຍ ຈອມມະນາມ ທີ່ກຳລັງເຮັດການສຳຫຼວດການນຳໃຊ້ຢາຕ້ານເຊື້ອໃນ 1 ໂຮງໝໍສູນກາງ ແລະ 5 ໂຮງໝໍແຂວງ ທຸກໆປີ. © LOMWRU 2022.

Research highlights in 2021

ຜົນການຄົ້ນຄວ້າທີ່ພົ້ນເດັ່ນໃນປີຜ່ານມາ

ໃນທີ່ນີ້ພວກເຮົາຍົກໃຫ້ເຫັນຜົນການໄດ້ຮັບຂອງບາງຄົ້ນຄວ້າຂອງ LOMWRU ແລະ ອົງການຈັດຕັ້ງຄູ່ຮ່ວມງານຕ່າງໆ ທີ່ຖືກຕີພິມໃນປີ 2021. ບັນຊີລາຍຊື່ ແລະ ບົດຄັດຫຍໍ້ແມ່ນສາມາດເບິ່ງໄດ້ຢູ່ໃນພາກການຕີພິມເຜີຍແຜ່ຂອງບົດລາຍງານນີ້.

ການຕ້ານຢາຕໍ່ຕ້ານເຊື້ອຈຸລະຊີບ

ການຕ້ານຢາຕໍ່ຕ້ານເຊື້ອຈຸລະຊີບຍັງສືບຕໍ່ເປັນຫົວຂໍ້ໃຫຍ່ໃນປີ 2021. ບົດທົບທວນຄືນເອກະສານ ທີ່ໄດ້ລວບລວມເອົາຂໍ້ມູນກ່ຽວກັບການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບ (AMR) ແລະ ການໃຊ້ຢາຕ້ານເຊື້ອຈຸລະຊີບ (AMU) ຈາກວາລະສານທີ່ຖືກຕີພິມ ແລະ ບົດລາຍງານ ຫລືຖານຂໍ້ມູນທີ່ບໍ່ຖືກຕີພິມ ໃນ ສປປ ລາວ ໂດຍການລວບລວມຂອງ ທ່ານ ດຣ ວິລະດາ ຈັນສະມຸດ ໄດ້ສຳເລັດໃນປີ 2021 ແລະ ຜົນຂອງການບົດທົບທວນຄືນເອກະສານນີ້ ໄດ້ຖືກຕີພິມຖືກຕີພິມ ໃນວາລະສານສາກົນ BMJ Global Health.

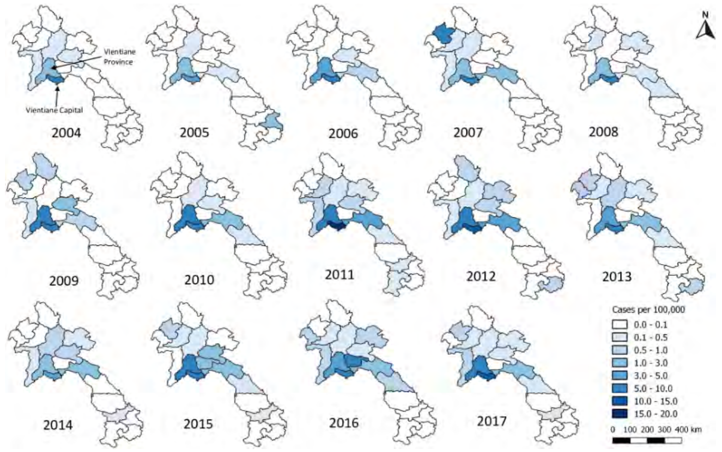
ຫນຶ່ງໃນຄວາມກັງວົນທີ່ສຳຄັນໃນ ສປປ ລາວ ແມ່ນການເພີ່ມຂຶ້ນຂອງ extra-spectrum beta lactamase (ESBL)-producing *Escherichia coli*. ໃນປີ 2021 ທີ່ຜ່ານມາ, ປະມານ 50% ຂອງການຕິດເຊື້ອໃນກະແສເລືອດທີ່ມີສາເຫດມາຈາກເຊື້ອ *E.coli* ທີ່ຖືກບົ່ງມະຕິຈາກຫ້ອງຈຸລິນຊີວິທະຍາ ໂຮງໝໍມະໂຫສົດ ແມ່ນ ESBL+, ຊຶ່ງຫມາຍຄວາມວ່າ ceftriaxone, ທີ່ເປັນທາງເລືອກຂອງການປິ່ນປົວແບບ empirical ສຳລັບຄົນເຈັບທີ່ມີພາວະ sepsis, ແມ່ນບໍ່ມີປະສິດທິພາບໃນການປິ່ນປົວໃນກໍລະນີນີ້. ປັດໄຈສຳຄັນທີ່ກ່ຽວຂ້ອງໃນການຂັບເຄື່ອນອັດຕາການຊຶມເຊື້ອທີ່ເກີດຂື້ນໃໝ່ທີ່ສູງໃນຊຸມຊົນແມ່ນຍັງບໍ່ຈະແຈ້ງ.

ພວກເຮົາໄດ້ຮ່ວມມືກັບຄູ່ຮ່ວມງານຈາກມະຫາວິທະຍາໄລ Helsinki ໃນປະເທດ Finland, Swiss Tropical and Public Health Institute, ແລະ ມະຫາວິທະຍາໄລ Birmingham ໃນ UK, ເພື່ອສຶກສາກ່ຽວກັບການຮັບເອົາເຊື້ອ ESBL ຂອງນັກທ່ອງທ່ຽວຕ່າງປະເທດທີ່ມາວຽງຈັນ. ນີ້ແມ່ນການສຶກສາໄປຂ້າງໜ້າ, ເກັບຕົວຢ່າງທຸກໆວັນ, ເຊິ່ງໄດ້ເລີ່ມຕົ້ນໃນປີ 2015. ນັກທ່ອງທ່ຽວຊາວເອີຣົບທັງໝົດ 20 ຄົນທີ່ມາ ສປປ ລາວ, ໄດ້ອາສາສະໝັກສະໜອງຕົວຢ່າງອາຈົມປະຈຳວັນ ແລະ ຕື່ມແບບສອບຖາມປະຈຳວັນເປັນເວລາ 22 ວັນ. ການປະກົດຕົວຂອງເຊື້ອຈຸລິນຊີກລາມລົບ ທີ່ຖື ESBL+ ຖືກໄຈ້ແຍກ ໂດຍຫ້ອງຈຸລິນຊີວິທະຍາ, ໂຮງໝໍມະໂຫສົດ ແລະ ໄດ້ຖືກຢືນຢັນຕໍ່ມາໂດຍການເຮັດ whole-genome sequencing ຢູ່ທີ່ມະຫາວິທະຍາໄລ Birmingham. ໃນຕອນທ້າຍຂອງການສຶກສານີ້ພົບວ່າ ອັດຕາທີ່ເຊື້ອຈຸລິນຊີກລາມລົບ ທີ່ຖື ESBL+ ແມ່ນ 70%, ແນວໃດກໍ່ຕາມ, ຜົນການເກັບຕົວຢ່າງປະຈຳວັນໄດ້ເປີດເຜີຍວ່າ ຜູ້ເຂົ້າຮ່ວມທັງຫມົດແມ່ນໄດ້ຮັບເຊື້ອຈຸລິນຊີກລາມລົບທີ່ຖື ESBL+ ນະຈຸດເວລາໃດໜຶ່ງທີ່ພວກເຮົາໄດ້ທຳການຕິດຕາມ. ໃນຈຳນວນທັງຫມົດ 83 unique strains ທີ່ຖືກໄຈ້ແຍກໄດ້, 4 (20%) ໄດ້ມີຫຼາຍ strains ຮ່ວມກັນ. ປະກົດການ ການຖືເຊື້ອຊົ່ວຄາວໄດ້ຖືກພົບເຫັນຫຼາຍຄັ້ງ.

ສປປ ລາວ, ກໍ່ຄືກັນກັບປະເທດອື່ນໆທີ່ມີລາຍໄດ້ປານກາງ

ການເພີ່ມທະວີຄວາມເຂັ້ມແຂງຂອງຫ້ອງທົດລອງໃນການເຝົ້າລະວັງແມ່ນກຳລັງຖືກຈັດຕັ້ງປະຕິບັດໃນທົ່ວປະເທດ. ທຶນຮອນສຳລັບວຽກງານນີ້ຈຳນວນຫຼວງຫຼາຍແມ່ນມາຈາກລັດຖະບານປະເທດອັງກິດໂດຍຜ່ານໂຄງການຊ່ວຍເຫຼືອ Fleming ໃນຮູບແບບ Fleming Fund country grant, ໂດຍຕັ້ງຊື່ຕາມທ່ານ Alexander Fleming ຜູ້ທີ່ຄົ້ນພົບ penicillin ໃນປີ 1928. ຄວາມຍືນຍົງຂອງການເຝົ້າລະວັງ AMR ແມ່ນເປັນເລື່ອງທີ່ໜ້າກັງວົນ. Tamalee Roberts ຈາກ LOMWRU ໄດ້ທຳການວິເຄາະຄ່າໃຊ້ຈ່າຍໃນການກວດຄົ້ນຫາ AMR, ເຊິ່ງຄາດຄະເນວ່າ, ຄ່າໃຊ້ຈ່າຍຕໍ່ຕົວຢ່າງແມ່ນເລີ່ມແຕ່ $22–31 (ສຳລັບການປະຕິບັດການໃນຫ້ອງທົດລອງ ທີ່ມີຕົວຢ່າງ 10,000 ຕົວຢ່າງ/ປີ) ຫຼື $11–12 (ສຳລັບການປະຕິບັດການໃນຫ້ອງທົດລອງ ທີ່ມີຕົວຢ່າງ 100,000 ຕົວຢ່າງ/ປີ) ໂດຍບໍ່ລວມຄ່າໃຊ້ຈ່າຍໃນການກໍ່ສ້າງຫ້ອງທົດລອງ. ຄ່າໃຊ້ຈ່າຍຕໍ່ເຊື້ອທີ່ໄຈ້ແຍກໄດ້ ແມ່ນເລີ່ມແຕ່ $215–304 (ສຳລັບ 10,000 ຕົວຢ່າງ) ແລະ $105–122 (ສຳລັບ 100,000 ຕົວຢ່າງ), ເຊິ່ງຫຼາຍກວ່າຄ່າໃຊ້ຈ່າຍສະເລ່ຍຕໍ່ຫົວຄົນໃນການດູແລສຸຂະພາບໃນ ສປປ ລາວ.

ຈຳພວກພະຍາດຕິດເຊື້ອຣິກແກັດເຊຍ (RICKETTSIAL INFECTIONS)



ຮູບພາບ ຈຳນວນປະຊາກອນທີ່ມີເຊື້ອພະຍາດ scrub typhus ຕໍ່ 100,000 ຄົນໃນແຕ່ລະແຂວງໃນ ສປປ ລາວ ແຕ່ປີ 2004 – 2017.

ຄວາມເຂົ້າໃຈກ່ຽວກັບກ່ຽວກັບຮູບແບບການແຜ່ລະບາດຂອງພະຍາດ scrub typhus & murine typhus ຢູ່ລາວ ຕາມລະດູການ ແມ່ນຍັງໜ້ອຍ. ນັກວິທະຍາສາດ ຂອງໂຄງການ LOMWRU ຮ່ວມມືກັບ Daniel Parker ຈາກມະຫາວິທະຍາໄລ California, Irvine ໄດ້ສຶກສາຜົນກະທົບຂອງສະພາບແວດລ້ອມ ແລະ ອາກາດ ຕໍ່ການແຜ່ລະບາດຂອງສອງພະຍາດດັ່ງກ່າວ. ຜົນການຄົ້ນຄວ້າໄດ້ຊີ້ໃຫ້ເຫັນວ່າ ອຸບັດການການເກີດພະຍາດ ແລະ ແຈກຢາຍທາງດ້ານສະຖານທີ່ຂອງສອງເຊື້ອນີ້ ອາດເພີ່ມຂຶ້ນ ເນື່ອງຈາກບັນຫາໂລກຮ້ອນ ແລະ ການເພີ່ມຂຶ້ນຂອງປະລິມານນ້ຳ. ການສຶກສາຍັງຊີ້ໃຫ້ເຫັນວ່າການຂະຫຍາຍຕົວເມືອງ, ອາດຂະຫຍາຍພື້ນທີ່ສ່ຽງທີ່ຈະຕິດພະຍາດ murine typhus. ອັດຕາການຕິດເຊື້ອ murine typhus ສູງໃນລະດູແລ້ງ, ໃນຂະນະທີ່ ກໍລະນີທີ່ຕິດເຊື້ອ scrub typhus ແມ່ນມີທ່າອ່ຽງສ່ວນຫຼາຍມາແຕ່ບ້ານທີ່ມີລະດັບປະລິມານໜ້ານ້ຳທີ່ສູງ ແລະ ມີພືດພັນຫຼາຍ.

ຄວາມເຂົ້າໃຈຂອງພວກເຮົາ ຍັງຈຳກັດຫຼາຍກ່ຽວກັບປັດໄຈຕ່າງໆທີ່ປະກອບກັນ ເຮັດໃຫ້ພື້ນທີ່ໃດໜຶ່ງເປັນອານາເຂດສ່ຽງສູງຕໍ່ການເກີດພະຍາດສະຄຣາບໄທຟັດ (scrub typhus), ຊຶ່ງເປັນສາເຫດສຳຄັນ ພາໃຫ້ເປັນພະຍາດ ທີ່ມີອາການໄຂ້ ເກີດຂຶ້ນຢູ່ໃນປະເທດລາວ ແລະ ບ່ອນອື່ນໆ ໃນແຖບອາຊີຕາເວັນອອກສ່ຽງໃຕ້. ດຣ ໄອໂວ ແອວລິອອດ (Dr Ivo Elliott) ໄດ້ດຳເນີນການສືບສວນ ກ່ຽວກັບຕົວໄຮອ່ອນ (ໄຮທີ່ລອກຄາບມາຈາກຕົວອ່ອນໆ) (chiggers) (ແມງພາຫະນຳເຊື້ອ *Orientia tsutsugamushi* ຊຶ່ງເປັນສາເຫດ ກໍ່ໃຫ້ເກີດພະຍາດສະກຣາບ ໄທຟັດ) ແລະ ສັດລ້ຽງລູກດ້ວຍນ້ຳນົມຂະໜາດນ້ອຍ ໂດຍການສຶກສາທາງນິເວດວິທະຍາ ເປັນເວລາ 18 ເດືອນ ໃນສະຖານທີ່ 3 ແຫ່ງ ທີ່ມີການແຜ່ເຊື້ອຂອງພະຍາດສະຄຣາບໄທຟັດ ໄປສູ່ຄົນຢ່າງຫຼວງຫຼາຍ ຢູ່ແຂວງຊຽງຣາຍ, ປະເທດໄທ. ເພິ່ນໄດ້ໃຊ້ ເຂົ້າສາລີເປັນເຫຍື່ອລໍ້ສັດ ໃສ່ໄວ້ໃນກົງດັກຈັບສັດ ແລະ ໄດ້ວາງກົງດັກເຫຼົ່ານັ້ນ ເປັນຍ່ານເປັນຍ່ານຫ່າງກັນ ຕາມພື້ນທີ່ ທີ່ກວດກາພະຍາດ ເພື່ອເປົ້າໝາຍຈັບ ສັດລ້ຽງລູກດ້ວຍນ້ຳນົມຂະໜາດນ້ອຍ ເອົາມາກວດກາເບິ່ງແມງໄຮອ່ອນ. ເພິ່ນນຳເອົາ ແພຈຸລັງຂອງສັດມາເປັນຕົວຢ່າງ ກວດຫາເຊື້ອ *Orientia tsutsugamushi* ດ້ວຍ PCR. ການພັນລະນາອັດຕາ ແລະ ການເຄື່ອນເໜັງຂອງ

ເຊື້ອ *Orientia tsutsugamushi* ໃນໄຣອ່ອນ ແລະ ໃນສັດນ້ອຍດັ່ງກ່າວ ທີ່ເປັນໄປຕາມເວລາ ແມ່ນຜົນຫຼັກໆທີ່ອອກມາຂອງການສຶກສານີ້. ອັດຕາການຕິດເຊື້ອໃນຄົນທີ່ສູງນັ້ນ ແມ່ນກ່ຽວພັນກັບ ຈຳນວນຕົວໄຣອ່ອນຫຼວງຫຼາຍທີ່ຕິດເຊື້ອ. ໃນພື້ນທີ່ໃດໆຂອງການສຶກສາຄັ້ງນີ້ ບໍ່ພົບວ່າ ມີແຫຼ່ງລະບາດເປັນຍ່ອມໆ (ບໍ່ກະຈາຍທົ່ວ) ທີ່ຄົງເດີມບໍ່ປ່ຽນແປງ.

ບົດລາຍງານປະຈຳປີ

ໜ່ວຍງານຄຸນນະພາບຢາ (MEDICINE QUALITY)

ໃນປີ 2021 ໜ່ວຍງານຄຸນນະພາບຢາໄດ້ເຜີຍແຜ່ບົດຕີພິມ “A multiphase evaluation of portable screening devices to assess medicines quality for national Medicines Regulatory Authorities.” ລົງໃນວາລະສານການຄົ້ນຄວ້າ ແລະ ວິໄຈ PLOS.

ປັດຈຸບັນ ໜ່ວຍງານຄຸ້ມຄອງຢາໃນບັນດາປະເທດລາຍໄດ້ຕ່ຳ ແລະ ລາຍໄດ້ປານກາງຫຼາຍປະເທດ ຍັງຄົງຂາດແຄນຊັບພະຍາກອນທີ່ສຳຄັນຢູ່. ເຄື່ອງມືແບບພົກພາທີ່ເປັນນະວັດຕະກຳອັນທັນສະໄໝ ສາມາດທີ່ຈະຊ່ວຍຍົກລະດັບປະສິດທິພາບໃນການເຮັດວຽກຂອງໜ່ວຍງານຄຸ້ມຄອງຢາ ໃນການຕິດຕາມຢາຫຼັງຈາກຈຳໜ່າຍສູ່ຕະຫຼາດແລ້ວ, ເພື່ອກວດຫາ ແລະ ກຳຈັດຢາທີ່ບໍ່ໄດ້ມາດຕະຖານ ຫຼື ຢາປອມກ່ອນທີ່ຈະໄປຮອດມືຂອງຄົນເຈັບ. ເຖິງແມ່ນວ່າເຄື່ອງມືເຫຼົ່ານີ້ໄດ້ສ້າງຄວາມຫວັງໃນການສ້າງຄວາມເຂັ້ມແຂງໃຫ້ຜູ້ກວດກາຢາໃນວຽກງານການກວດກາຄຸນນະພາບຢາທີ່ຢູ່ໃນລະບົບ, ແຕ່ໜ່ວຍງານຄຸ້ມຄອງກໍຍັງຂາດຄວາມຮູ້ກ່ຽວກັບປະສິດທິພາບ, ຂໍ້ຈຳກັດ ແລະ ຄວາມຄຸ້ມຄ່າຂອງເຄື່ອງມືເຫຼົ່ານັ້ນ. ການສຶກສານີ້ມີຈຸດປະສົງເພື່ອຊ່ວຍໃຫ້ເຮົາມີຄວາມເຂົ້າໃຈດີຂຶ້ນຕໍ່ກັບບັນຫາດັ່ງກ່າວ. ໜ່ວຍງານຄຸນນະພາບຢາໄດ້ຮ່ວມມືກັບໜ່ວຍງານພາກລັດຂອງ ສປປ ລາວ, ສະຖາບັນເຕັກໂນໂລຊີ Georgia (ສະຫະລັດອາເມລິກາ) ແລະ ໜ່ວຍງານ MORU ປະເທດໄທ ເພື່ອຈັດຕັ້ງປະຕິບັດການປະເມີນ ແລະ ສົມທຽບເຄື່ອງມືແບບພົກພາ. ຈຸດປະສົງແມ່ນເພື່ອສະໜອງຂໍ້ມູນຫຼັກຖານທີ່ຊ່ວຍໃຫ້ໜ່ວຍງານຄຸ້ມຄອງຢາຕັດສິນໃຈງ່າຍຂຶ້ນ ວ່າເຄື່ອງມືທັນສະໄໝເຫຼົ່ານີ້ແທດເໝາະກັບການກວດກາຢາໃນປະເທດພວກເຂົາຫຼືບໍ່ ແລະ ເຄື່ອງມືເຫຼົ່ານີ້ຄວນຖືກຕິດຕັ້ງຢູ່ໃສ ແລະ ແນວໃດ. ການສຶກສາດັ່ງກ່າວເປັນສ່ວນໜຶ່ງຂອງໂຄງການ Results for Malaria Elimination and Communicable Diseases Control (RECAP) ພາຍໃຕ້ກອງທຶນ Regional Malaria and Communicable Disease Trust Fund (RMTF) ຂອງທະນາຄານພັດທະນາອາຊີ (ADB). ວຽກງານນີ້ໄດ້ຖືກອະທິບາຍໄວ້ໃນຊຸດເອກະສານທັງໝົດ 5 ສະບັບ.

ເຄື່ອງມືແບບພົກພາຈຳນວນ 12 ເຄື່ອງໄດ້ຖືກຄັດເລືອກໂດຍອີງຕາມການທົບທວນຫຼັກຖານທາງວິທະຍາສາດທີ່ມີຢູ່. ນັບຕັ້ງແຕ່ຊຸດກວດບົ່ງມະຕິແບບໄວ ຂະໜາດນ້ອຍ, ໄປຈົນເຖິງເຄື່ອງ spectrometers ຂະໜາດນ້ອຍ ທີ່ສາມາດເຊື່ອມຕໍ່ກັບໂທລະສັບໄດ້, spectrometers ແບບຖື, ແລະ ເຄື່ອງມືຂະໜາດໃຫຍ່ ເຊັ່ນ Minilab ເຊິ່ງເປັນຊຸດທົດລອງໃນຫີບເດີນທາງ. ເຄື່ອງມືແຕ່ລະອັນໄດ້ຖືກປະເມີນໃນຫ້ອງທົດລອງ, ຢູ່ພາກສະໜາມ ພ້ອມທັງໄດ້ຮັບການປະເມີນຄວາມຄຸ້ມຄ່າອີກດ້ວຍ. ເຖິງວ່າ ການຄົ້ນພົບທີ່ສຳຄັນຂອງການສຶກສານີ້ ໄດ້ເພີ່ມຄວາມຮູ້ຄວາມເຂົ້າໃຈຂອງພວກເຮົາໃນການໃຊ້ການເຄື່ອງມືດັ່ງກ່າວ, ແຕ່ມັນກໍຍັງສະແດງໃຫ້ເຫັນວ່າ ໃນປັດຈຸບັນຍັງບໍ່ມີເຄື່ອງມືອຸປະກອນໃດທີ່ມີປະສິດທິພາບໃນການກວດກາຄຸນນະພາບຂອງຢາທັງໝົດໄດ້. ຈາກວຽກງານທີ່ກ່າວມານີ້ ໄດ້ສະຫຼຸບວ່າ ຍັງມີຂໍ້ຄົງຄ້າງທີ່ສຳຄັນໃນຫຼັກຖານວິທະຍາສາດຢູ່ ແລະ ເປັນອຸປະສັກທີ່ສຳຄັນສຳລັບໜ່ວຍງານຄຸ້ມຄອງທີ່ຕ້ອງການນຳໃຊ້ອຸປະກອນເຫຼົ່ານີ້ໃນລະບົບການເຝົ້າລະວັງຂອງພວກເຂົາ. ເຖິງຢ່າງໃດກໍຕາມ, ເມື່ອໃດທີ່ປະໂຫຍດ ແລະ ຂໍ້ຈຳກັດຂອງເຄື່ອງມືເຫຼົ່ານີ້ຖືກກຳນົດໃຫ້ໃຊ້ກັບຢາທີ່ຫຼາກຫຼາຍໄດ້ດີຂຶ້ນກວ່າເກົ່າ, ມັນຈະເປັນຄວາມຫວັງອັນສຳຄັນໃນການສ້າງຄວາມເຂັ້ມແຂງໃຫ້ໜ່ວຍງານກວດກາຢາທົ່ວໂລກ.

ການຮ່ວມມືໃນການຄົ້ນຄວ້າວິທະຍາສາດ

ໂຄງການຄົ້ນຄວ້າພະຍາດເຂດຮ້ອນລະຫວ່າງ ໂຮງໝໍມະໂຫສົດ-ແວວຄຳຕູ້ສ-ມະຫາວິທະຍາໄລອ໋ອກຟອດ ຫຼື LOMWRU ແມ່ນ ໜຶ່ງ ໃນ ຫ້າ ຂອງໜ່ວຍງານຄົ້ນຄວ້າວິທະຍາສາດ ທີ່ນອນຢູ່ໃນເຄືອຂ່າຍ MORU Tropical Health Network ຫຼື MORU, ຊີ້ນຳໂດຍ ທ່ານສາດສະດາຈານ Nick Day ປະຈຳທີ່ໜ່ວຍງານຄົ້ນຄ້ວາພະຍາດເຂດຮ້ອນ ມະຫິດົນ-ອ໋ອກຟອດ, ພາກວິຊາພະຍາດເຂດຮ້ອນ, ມະຫາວິທະຍາໄລມະຫິດົນ, ບາງກອກ, ປະເທດໄທ. ໜ່ວຍງານຄຸນນະພາບຢາຂອງພວກເຮົາແມ່ນ ເຊື່ອມໂຍງໂດຍກົງກັບ ຖານຂໍ້ມູນຂອງພະຍາດຊຶມເຊື້ອແບບສັງເກດການ ຫຼື the Infectious Disease Data Observatory (IDDO) ທີ່ອ໋ອກຟອດ ບ່ອນທີ່ທ່ານສາດສະດາຈານ Paul Newton ແລະ ທ່ານ ດຣ Céline Caillet ຊີ້ນຳກຸ່ມຄົ້ນຄວ້າຄຸນນະພາບຢາ. ໂຄງການຄົ້ນຄວ້າພະຍາດເຂດຮ້ອນລະຫວ່າງ ໂຮງໝໍມະໂຫສົດ-ແວວຄຳຕູ້ສ-ມະຫາວິທະຍາໄລອ໋ອກຟອດ ໄດ້ຮ່ວມມືກັບບັນດາຄູ່ຮ່ວມມືໃນໂຄງການຄົ້ນຄວ້າວິທະຍາສາດຕ່າງໆ ກັບເຄືອຂ່າຍຂອງ MORU ແລະ ໄດ້ຮັບການສະໜັບສະໜູນ ດ້ານວິທະຍາສາດ ແລະ ບໍລິຫານຈັດການຈາກໜ່ວຍງານທີ່ຢູ່ບາງກອກ, ປະເທດໄທ. ສອງໂຄງການຄົ້ນຄວ້າຮ່ວມກັນກັບ MORU ທີ່ພວກເຮົາໄດ້ປະຕິບັດ ໃນປີ 2021 ເຊິ່ງສຸມໃສ່ວຽກງານການຄົ້ນຄວ້າເພື່ອຍົກສູງຄຸນນະພາບການປິ່ນປົວຄົນເຈັບທີ່ມີໄຂ້. ໂຄງການຄົ້ນຄ້ວາ Spot Sepsis ແມ່ນການສຶກສາໃນຫຼາຍສູນການຄົ້ນຄວ້າເຊິ່ງໄດ້ຮັບທຶນສະໜັບສະໜູນຈາກ ແພດບໍ່ມີພົມແດນ (Médecins Sans Frontières) ແລະ Wellcome (ຜູ້ຮ່ວມການສຶກສາຫຼັກ ທ່ານ Sakib Burza ແລະ ທ່ານ Yoel Lubell), ເຊິ່ງມີຈຸດປະສົງເອົາຄົນເຈັບເດັກຈຳນວນ 4,900 ຄົນເຂົ້າຮ່ວມການສຶກສາ ແລະ ພັດທະນາສູດຄຳນວນເພື່ອຄາດຄະເນປັດໄຈສ່ຽງຄວາມຮຸນແຮງ, ສົມທົບກັບ ການວັດແທກ biomarkers ຂອງຄົນເຈັບ ແລະ ອາການຄລີນິກ ທີ່ຈຸດຄັດແຍກ, ສຳລັບເດັກທີ່ມີອາຍຸລະຫວ່າງ 1 ເດືອນ ຫາ 5 ປີ ທີ່ມີອາການໄຂ້ກະທັນຫັນ ໃນສະພາບທີ່ມີຄວາມຂາດເຂີນທາງດ້ານຊັບພະຍາກອນ. ສຳລັບໂຄງການຄົ້ນຄ້ວານີ້ ມີ ສອງສູນການຄົ້ນຄວ້າໃນລາວ (ໂຮງໝໍແຂວງ ສາລະວັນ ແລະ ສະຫວັນນະເຂດ) ໂດຍ ດຣ ໄຊຍະເພັດ ຣັດຕະນະວົງ ຮັບຜິດຊອບເປັນຜູ້ປະສານງານໂຄງການປະຈຳລາວ. ຄົນເຈັບ ສອງທ່ານທຳອິດທີ່ເຂົ້າຮ່ວມການສຶກສາ ແມ່ນ ໃນວັນພະຫັດ ທີ 10 ເດືອນກັນຍາ ປີ 2020 ແລະ ພວກເຮົາສິ້ນສຸດການເອົາຄົນເຈັບເຂົ້າຮ່ວມານສຶກສາໃນປີ 2021. ຜົນການຄົ້ນຄວ້າຂອງໂຄງການສຶກສານີ້ຈະສາມາດເຜີຍແຜ່ໄດ້ໃນທ້າຍປີ 2022.

ໂຄງການຄົ້ນຄວ້າທີ ສອງຮ່ວມກັບ MORU ແມ່ນ the Southeast Asia Community Trials Network (SEACTN), ໄດ້ຮັບທຶນສະໜັບສະໜູນຈາກ Wellcome Trust ແລະ ຊີ້ນຳໂດຍທ່ານສາດສະດາຈານ Yoel Lubell ທີ່ MORU, ບາງກອກ. ຈຸດປະສົງຂອງໂຄງການຄົ້ນຄວ້ານີ້ ແມ່ນ ເພື່ອສ້າງຄວາມຮູ້ຄວາມເຂົ້າໃຈກ່ຽວກັບລະບາດວິທະຍາຂອງໄຂ້ໃນເຂດຊົນນະບົດໃນຫ້າປະເທດ ທີ່ຢູ່ໃນຂົງເຂດອາຊີໃຕ້ ແລະ ອາຊີຕາເວັນອອກສຽງໃຕ້ໃຫ້ດີຂຶ້ນ ໂດຍ ພັດທະນາຂອບເຂດຂອງໜ້າວຽກ ສຳລັບເກັບກຳຂໍ້ມູນກ່ຽວກັບຄວາມຮຸນແຮງ ແລະ ຜົນກະທົບຂອງໄຂ້. ໂຄງການ LOMWRU ໄດ້ດຳເນີນແຜນວຽກ A ທີ່ແຂວງສະຫວັນນະເຂດ ໂດຍໄດ້ຮັບການຊີ້ນຳຈາກ ທ່ານ ດຣ ຕຽງຄຳ ປ້ອງວົງສາ (ຮອງຫົວໜ້າພະແນກສາທາລະນະສຸກແຂວງ).

ກອງປະຊຸມຄັ້ງປະຖົມມະເລີກຂອງໂຄງການຄົ້ນຄວ້າໄດ້ຖືກຈັດຂຶ້ນທີ່ເມືອງອາດສະພັງທອງ ກ່າວເປີດກອງປະຊຸມໂດຍທ່ານຮອງເຈົ້າເມືອງ ເມືອງອາດສະພັງທອງ ທ່ານ ສົມລິດ ເທບພະວົງ.

ການຮ່ວມມືລະຫວ່າງ ໂຄງການຄົ້ນຄວ້າພະຍາດເຂດຮ້ອນລະຫວ່າງ ໂຮງໝໍມະໂຫສົດ-ແວວຄຳຕູ້ສ-ມະຫາວິທະຍາໄລອ໋ອກຟອດ ແລະ ສະຖາບັນຄົ້ນຄ້ວາເພື່ອການພັດທະນາຝຣັ່ງ (the Institut de recherche pour le développement ຫຼື IRD) ແມ່ນ ຍ້ອນຫຼັງໄປໃນປີ 2006. ທີ່ທ່ານ ດຣ Audrey Dubot-Pérès ຫົວໜ້າໜ່ວຍງານ ຈຸລະໂລກວິທະຍາ ປະຈຳ LOMWRU ເຊິ່ງປະຈຸບັນ ປະຈຳການຢູ່ ໜ່ວຍງານຈຸລະໂລກ ທີ່ເກີດຂຶ້ນໃໝ່ (UVE), ທີ່ເມືອງ ມາກຊາຍ, ປະເທດຝຣັ່ງ. ນັບແຕ່ປີ 2011 ເປັນຕົ້ນມາ, ທ່ານ ດຣ Alain Pierret ແລະ ທ່ານ ດຣ Anne Pando ໄດ້ເລີ້ມຄືນການຄົ້ນຄວ້າ ເຊື້ອ *B. pseudomallei* ທີ່ຢູ່ໃນດິນ.

ໂຄງການຮ່ວມມືຂອງພວກເຮົາກັບ NAMRU-2 ເພື່ອເຝົ້າລະວັງພະຍາດ ຍັງໄດ້ສືບຕໍ່ຈົນເຖິງປີ 2021 ໂດຍມີຄູ່ຮ່ວມງານໃນໄລຍະຍາວ ທີ່ໂຮງໝໍແຂວງ ຊຽງຂວາງ, ຫຼວງນ້ຳທາ, ສາລະວັນ ແລະ ອັດຕະປື. ພວກເຮົາໄດ້ອະທິບາຍການເກີດຂຶ້ນໃໝ່ຂອງພະຍາດ COVID-19 ສາຍພັນ ເດລຕ້າ ແລະ ໂອໄມຄອນ ໃນຄົນເຈັບທີ່ເຂົ້າຮ່ວມໃນທຸກໆສູນການສຶກສາ ແລະ ແບ່ງປັນຂໍ້ມູນດັ່ງກ່າວກັບ ສະມາຄົມສາກົນ ການຕິດເຊື້ອລະບົບຫາຍໃຈກະທັນຫັນຮຸນແຮງ ແລະ ພະຍາດຊຶມເຊື້ອທີ່ເກີດຂຶ້ນໃໝ່ ຫຼື International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC).

ນັບແຕ່ປີ 2015 ເປັນຕົ້ນມາ, ໂຄງການ LOMWRU ໄດ້ຮ່ວມມືກັບ ສະຖາບັນການຄົ້ນຄ້ວາເດັກ ເມີດອສ, ເມວເບີນ, ປະເທດອົດສະຕາລີ ເພື່ອຄົ້ນຄວ້າເຖິງຜົນກະທົບຂອງການສັກຢາ PCV-13 vaccine ຢູ່ໃນລາວ, ຊີ້ນຳໂດຍທ່ານສາດສະດາຈານ Fiona Russell. ນອກນັ້ນຍັງໄດ້ສຶກສາປະສິດຕິພາບຂອງ PCV-13 vaccine ໃນການປ້ອງກັນເຊື້ອ pneumococcal ທີ່ມີສາຍພັນທີ່ຕ້ານຕໍ່ຢາຕ້ານເຊື້ອ ພວກເຮົາໄດ້ສຶກສາຄຸນລັກສະນະການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອ ແລະ ຄວາມຮຸນແຮງທີ່ຂຶ້ນໃໝ່ຈາກກຸ່ມ non-PCV types.

ໃນປີ 2021 ນີ້ ພວກເຮົາໄດ້ເລີ່ມການຮ່ວມມືໃໝ່ກັບ PATH ແລະ ດຳເນີນໂຄງການຄົ້ນຄວ້າກ່ຽວກັບຜົນກະທົບທາງດ້ານເສດຖະກິດ ໃນຄອບຄົວຂອງຄົນເຈັບທີ່ເປັນພະຍາດອັກເສບສະໝອງຍີ່ປຸ່ນ ໂດຍຄາດຄະເນຄ່າໃຊ້ຈ່າຍໃນໄລຍະເບື້ອງຕົ້ນ ແລະ ການຟື້ນຟູໃນໄລຍະຍາວ ແລະ ການປິ່ນປົວອາການເສດເຫຼືອໂດຍອີງຕາມຄວາມຮຸນແຮງ ໃນ ສປປ ລາວ

Dr Vilada Chansamouth and Dr Danoy Chommanam (*top left*) conduct point prevalence surveys of antimicrobial use at six central and provincial hospitals three times every year. © LOMWRU 2022.

Research highlights in 2021

Here we highlight a selection of research outputs of LOMWRU and partner organisations published in 2021. The complete list with abstracts is found in the Publications section of the report.

Antimicrobial resistance (AMR)

Antimicrobial resistance (AMR) continued to be a major theme in 2021. The review of all published and grey literature on AMR and antimicrobial use (AMU) from Laos led by Dr Vilada Chansamouth was finalized in 2021 and findings summarised in a publication in *BMJ Global Health*.

One of the major concerns in Laos is the increase in extended-spectrum beta lactamase (ESBL)-producing *Escherichia coli*. In 2021 around 50% of bloodstream infections caused by *E. coli* diagnosed in Mahosot Hospital Microbiology Laboratory were ESBL+, meaning ceftriaxone, a common empirical treatment choice for patients with sepsis, would be ineffective. The relative importance of different drivers for these high rates in infections acquired in the community is not clear.

We collaborated with partners from Finland's University of Helsinki, the Swiss Tropical and Public Health Institute, and the UK's University of Birmingham, to study ESBL acquisition in international travellers to Vientiane. In this prospective, daily, real-time sampling study, which started in 2015, 20 European visitors to Laos volunteered to provide daily stool samples and complete daily questionnaires for 22 days. Presence of any ESBL+ Gram negative bacteria identified by the Mahosot Hospital Microbiology Laboratory was confirmed subsequently by whole-genome sequencing at the University of Birmingham. While ESBL colonisation rates were 70% at the end of the study, the daily sampling revealed that all participants had acquired ESBL-producing Gram-negative bacteria at some point during the study. A total of 83 unique strains were identified, with some shared by up to four (20%) participants. Multiple transient colonisation events were identified.

Laos, like many other middle-income countries, is strengthening laboratory surveillance, with much of this work funded by the UK Government's Fleming Fund country grant scheme, named after Alexander Fleming who discovered penicillin in 1928. Sustainability of AMR surveillance is a concern. Tamalee Roberts of LOMWRU led a cost analysis of AMR detection which estimated that, excluding capital costs to set up the laboratory, the cost per **specimen** ranged from $22–31 (for laboratories processing 10,000 specimens/year) or $11–12 (for laboratories processing 100,000 specimens/year). Cost per **isolate** ranged from $215–304 (10,000 specimens) and $105–122 (100,000 specimens) - well above the average per capita spend on healthcare in Laos.

Chansamouth V, Mayxay M, Dance DA, et al. Antimicrobial use and resistance data in human and animal sectors in the Lao PDR: evidence to inform policy. *BMJ Glob Health*. 2021;6(12):e007009. doi: 10.1136/bmjgh-2021-007009

Dynamics of intestinal multidrug-resistant bacteria colonisation contracted by visitors to a high-endemic setting: a prospective, daily, real-time sampling study. Kantele A, Kuenzli E, Dunn SJ, et al. *Lancet Microbe*. 2021;2(4):e151-e158. doi: 10.1016/S2666-5247(20)30224-X

Antimicrobial resistance detection in Southeast Asian hospitals is critically important from both patient and societal perspectives, but what is its cost? Roberts T, Luangasanatip N, Ling CL, et al. *PLOS Glob Public Health*. 2021;1(10):e0000018. Published 2021 Oct 13. doi: 10.1371/journal.pgph.0000018

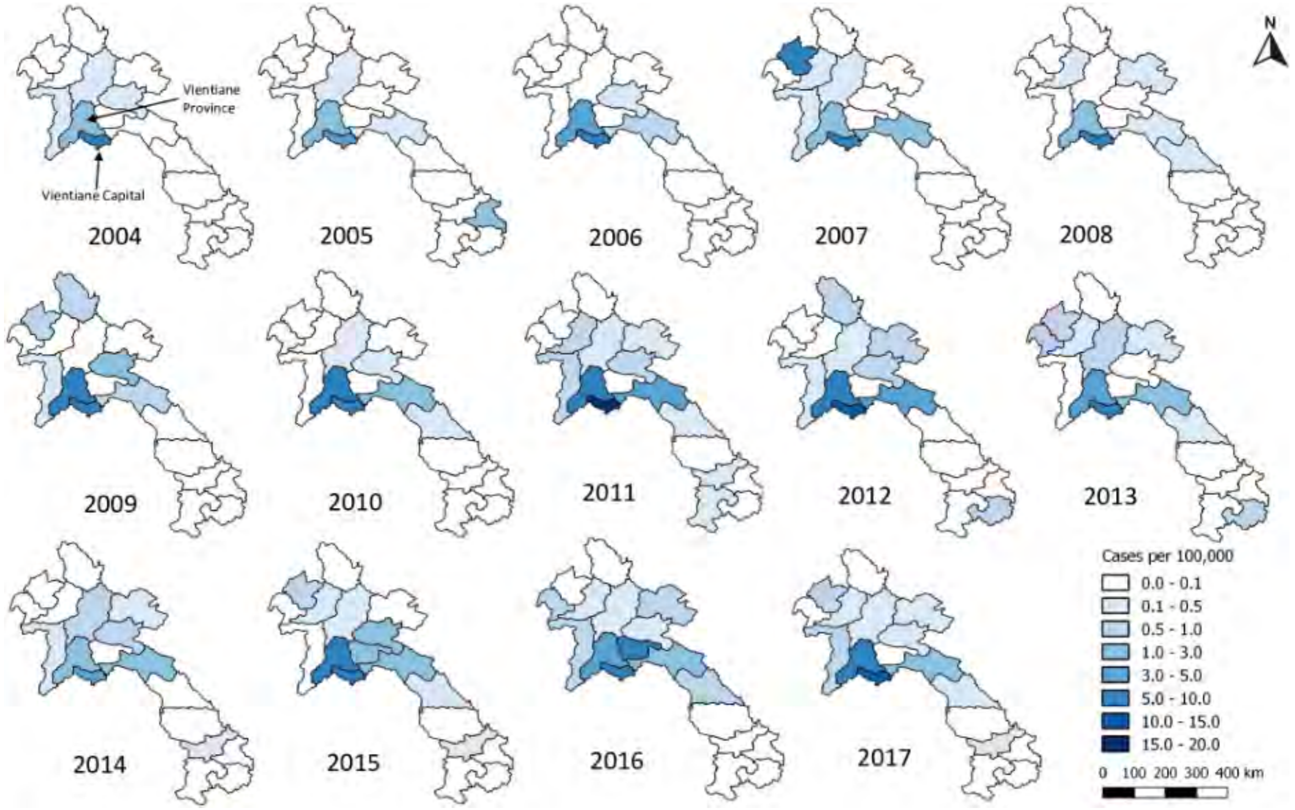
Rickettsial infections

Little is known about the temporal dynamics of scrub typhus and murine typhus in Laos. LOMWRU scientists, collaborating with Daniel Parker from the University of California, Irvine, studied the impacts of climate and the environment on these two diseases. With global heating and risks of attendant higher precipitation, the results suggest that the incidence and spatial distribution of both diseases may increase. The data suggest that as cities expand, high risk areas for murine typhus will also expand. While murine typhus peaked during the dry season, scrub typhus cases were were more likely to come from villages with higher levels of surface flooding and vegetation.

A spatio-temporal analysis of scrub typhus and murine typhus in Laos; implications from changing landscapes and climate. Roberts T, Parker DM, Bulterys PL, et al. *PLoS Negl Trop Dis*. 2021;15(8):e0009685. Published 2021 Aug 25. doi: 10.1371/journal.pntd.0009685

We have very limited understanding of the factors that determine an area to be at high risk for scrub typhus, an important cause of febrile illness in Laos and elsewhere in Southeast Asia. Dr Ivo Elliott investigated chiggers (the vector of *Orientia tsutsugamushi*, the causative agent of scrub typhus) and small mammals over an 18-month period in a detailed ecological study at three sites of high human scrub typhus transmission in Chiang Rai Province, Thailand. Traps baited with corn were placed at intervals across surveillance sites with the aim of trapping small mammals and examining them for chiggers. Animal tissue was screened *Orientia tsutsugamushi* by PCR. The principal output of this work was a description of the rates and dynamics of *O. tsutsugamushi* in chiggers and small mammals over time. High rates of human infection were associated with higher numbers of infected chiggers. There were no consistent discrete foci of infection identified at any of the study sites.

Orientia tsutsugamushi dynamics in vectors and hosts: ecology and risk factors for foci of scrub typhus transmission in northern Thailand. Elliott I, Thangnimitchok N, Chaisiri K, et al. *Parasit Vectors*. 2021;14(1):540. Published 2021 Oct 18. doi: 10.1186/s13071-021-05042-4



Patients with scrub typhus per 100,000 people per province in Laos from 2004 –2017.

Medicine Quality

In 2021, the Medicine Quality Research Group (MQRG) published a PLOS collection *A multiphase evaluation of portable screening devices to assess medicines quality for national Medicines Regulatory Authorities*.

Medicines Regulatory Authorities (MRAs) in many low- and middle-income countries are under-resourced. New innovative portable tools could help improve MRA efficiency in post-market surveillance of medicines, to better detect and remove substandard or falsified medicines before they reach patients. Although they hold promise for empowering medicine inspectors in screening medicine quality in supply systems, regulators lack independent information on their performance, limitations and cost-effectiveness. This study aimed to help fill this gap in our understanding. The Medicine Quality Research Group worked in collaboration with the Government of the Lao PDR, the Georgia Institute of Technology (USA) and MORU in Thailand to conduct an independent evaluation and comparison of portable devices. This aimed to provide evidence to facilitate MRAs' decisions about whether these new technologies are appropriate for screening of medicines in their countries and where and how they should be deployed. The study was part of the Results for Malaria Elimination and Communicable Diseases Control (RECAP) under the Regional Malaria and Communicable Disease Trust Fund (RMTF) at the Asian Development Bank. This work has been described in this series of five papers.

Twelve portable devices were chosen following a review of the available scientific evidence. These ranged from small single-use rapid diagnostic test kits, through to small spectrometers that can be connected to mobile phones, hand-held spectrometers, and larger devices such as the Minilab, a laboratory in suitcases. Each device was evaluated in the laboratory, the field and for cost-effectiveness. The study's key findings increase our knowledge of the use of these devices but show that it is currently unlikely that any one device would be able to effectively monitor the quality of all medicines. This work concluded that major gaps in the scientific evidence remain and are key barriers for regulators wishing to implement devices in their surveillance systems. However, these devices, when their advantages and limitations are better defined for diverse medicines hold great promise for empowering medicine inspectors globally.

Sounding out falsified medicines from genuine medicines using Broadband Acoustic Resonance Dissolution Spectroscopy (BARDS). Alfarsi A, Caillet C, Fawbert G, et al. *Sci Rep*. 2021;11(1):12643. Published 2021 Jun 16. doi: 10.1038/s41598-021-90323-2

Research collaborations

LOMWRU is one of the five research units of the MORU Tropical Health Network, directed by Professor Nick Day of the Mahidol Oxford Tropical Medicine Research Unit in the Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand. Our Medicine Quality team is linked to the Infectious Disease Data Observatory (IDDO) in Oxford where Professor Paul Newton and Dr Céline Caillet lead the Medicine Quality Research Group. LOMWRU collaborates on several MORU network research projects and receives strong scientific and administrative support from the Bangkok Unit. Two MORU projects we worked on in 2021 were concerned with improving the management of patients with febrile illness. The Spot Sepsis study is a multicentre study sponsored by Médecins Sans Frontières and Wellcome (Co-PIs Sakib Burza and Yoel Lubell), which aims to study 4,900 children and develop a risk prediction algorithm, combining measurements of host biomarkers and clinical features at the point-of-triage, for children aged between 1 month and 5 years with an acute febrile illness in resource-limited settings. There were two sites in Laos (Salavan and Savannakhet Provincial Hospitals) and the Lao country coordinator for the project was Dr Sayaphet Rattanavong. The first two Lao participants were recruited on Thursday 10th September, 2020 and we completed recruitment in 2021. Results should be available by the end of 2022.

The second MORU project is the Southeast Asia Community Trials Network (SEACTN), funded by the Wellcome Trust and led by Professor Yoel Lubell in MORU, Bangkok. The aim is to better understand the epidemiology of febrile illness in rural areas in five countries of South and Southeast Asia by developing a framework for the collection of information about the burden and impact of febrile illness. LOMWRU launched Work Package A of the project in Savannakhet province with Dr Tiengkham Pongvongsa (Deputy Director of the Provincial Health Office). Our first sensitization meetings in Atsaphanthong district was opened by the District Vice Governor Mr Samlit Thepphavong.

The collaboration between LOMWRU and the Institut de recherche pour le développement (IRD) dates back to 2006. Dr Audrey Dubot-Pérès is the Head of Virology at LOMWRU but now based in the Unité des Virus Emergents (UVE), Marseille, France. Since 2011, Dr Alain Pierret and Dr Anne Pando have been researching *B. pseudomallei* in the soil.

Our collaborative disease surveillance with NAMRU-2 continued throughout 2021 with our longstanding provincial hospital collaborators in Xieng Khuang, Luang Namtha, Salavan and Attapeu. We described the emergence of COVID-19 delta and omicron variants among patients attending all sites and shared data with the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC)

Since 2015 LOMWRU has collaborated with the Murdoch Children's Research Institute, Melbourne, Australia on studies led by Professor Fiona Russell looking at the impact of introducing PCV-13 vaccine in Laos. As well as determining theeffectiveness of PCV-13 against phenotypic AMR pneumococcal carriage we are characterising the antimicrobial resistance and virulence of emerging non-PCV types.

In 2021 we started a new collaboration with PATH and are working on a project to look at the economic impact of Japanese encephalitis on families by estimating the cost of initial and long-term rehabilitation and sequelae care by severity in Lao PDR.

Training highlights 2021

LOMWRU has an active PhD and Master's programme for Lao and international students.

Post-doctoral researchers

Dr Weerawat Phuklia, LOMWRU postdoctoral scientist and Wellcome Trust International Training Fellow is spending one year at Washington State University in the laboratory of Dr Anders Omsland whose group works on the pathogenesis of bacterial obligate intracellular parasites.

Following his successful PhD defence with the University of Amsterdam in 2020, **Dr Koukeo Phommasone**, Deputy Head of Mahosot Hospital Microbiology Laboratory, graduated in 2021. Due to COVID he was unable to travel to the Netherlands to collect his certificate in person. Dr Koukeo is now leading the implementation of a large multi-country project sponsored by MORU in Bangkok which is taking place in health centres in three districts of Savannakhet province, called the South and Southeast Asian Community-based Trials Network (SEACTN). SEACTN aims to strengthen primary health care for management of febrile illness at health centre level.

Doctoral students

The Nuffield Department of Medicine (NDM), University of Oxford, commended the work of **Dr Rebecca Inglis**, carried out as her DPhil research in Laos, and later as the COVID pandemic unfolded. For her DPhil, Rebecca developed and tested an intervention to improve the care of critically ill adults in Laos. The Essential Critical Care course uses interactive training methods to teach a context-adapted curriculum to nurses and doctors. Early in the pandemic, Rebecca won an Institutional Translational Partnership Award to adapt her DPhil intervention for critically ill COVID patients. The revised course was accredited by the WHO, taken up by the Lao government, and rolled out to every ICU in the country by Rebecca and her trainers. Rebecca developed two further COVID courses using the behaviour change blueprint pioneered in her DPhil. These courses were funded by Australia and the EU respectively as part of multi-million-dollar grants and have been delivered to all 17 provincial hospitals and 100 district hospitals in Laos.

Dr Vilada Chansamouth is in the final year of her DPhil with the University of Oxford as part of her Wellcome Trust International Training Fellowship. She is studying the implementation of national antimicrobial treatment guidelines, delivered in paper-based format and on a smartphone application on prescribing in a stepped-wedge cluster-randomised trial.

Master's students

We hosted one Master's student from the International Master's Course in Tropical Medicine and International Health at the Lao Tropical and Public Health Institute this year. **Dr Vannavong Siritana**'s project was on *Molecular techniques to identify potential bacterial pathogens in negative haemoculture fluid from febrile patients at Mahosot Hospital*. His supervisors were Dr Matt Robinson, Dr Andrew Simpson and Professor Mayfong Mayxay.

Dr Vilayouth Phimolsarnnousith was in London, UK studying for a Master's in Medical Microbiology at the London School of Hygiene & Tropical Medicine as part of his Wellcome International Master's Fellowship. Dr Vilayouth is shown having tea with Prof Paul Newton in Oxford.

Mr Vanheuang Phommadeechack, LOMWRU molecular bacteriology junior scientist is in Bangkok studying for a Master's in Tropical Medicine at Mahidol University. He was awarded the Sylvia Meek scholarship for Entomology. The scholarship was set up in 2016 in memory of Dr Sylvia Meek, a highly respected scientist and well known for her contributions to the fight against infectious diseases, and malaria in particular. The scholarship supports students from across the world to study entomology at universities in Nigeria, South Africa and Thailand. Vanheuang was the only student to be awarded the scholarship this year at Mahidol.

Other training

In 2021, nine Lao government microbiology laboratory technicians travelled to Chiang Mai University for a six month a bespoke intensive microbiology course. The course was created by the Faculty of Associated Medical Sciences following a request by LOMWRU and course fees were covered by the UK Fleming Fund as one activity of the Laos country grant.

Lao government laboratory technicians in front of Chiang Mai University, Thailand. LOMWRU worked with the Faculty of Medical Sciences in Chiang Mai University to develop a six-month intensive course in microbiology for nine Lao government laboratory technicians in 2021. © LOMWRU 2022.

In addition, the Microbiology Laboratory in Mahosot Hospital hosted several laboratory technicians from provincial hospitals for training in microbiology. Matt Robinson, Mr Vanheuang Phommadeechack and Mrs Joy Silisouk also travelled to Luang Namtha, Xieng Khuang and Salavan provinces to conduct biosafety training, which was part of our Fleming Fund Lao country grant phase 2 activities.

LOMWRU publications in 2021

In 2021 LOMWRU published 69 articles or letters in peer-reviewed journals and had four conference abstracts accepted. Abstracts are reproduced below with articles grouped by theme.

Microbiology including antimicrobial resistance (AMR)

Antimicrobial use and resistance data in human and animal sectors in the Lao PDR: evidence to inform policy. Chansamouth V, Mayxay M, Dance DA, Roberts T, Phetsouvanh R, Vannachone B, Vongsouvath M, Davong V, Inthavong P, Khounsy S, Keohavong B, Keoluangkhot V, Choumlivong K, Day NP, Turner P, Ashley EA, van Doorn HR, Newton PN. *BMJ Glob Health*. 2021 Nov;6(12):e007009. doi: 10.1136/bmjgh-2021-007009. PMID: 34853032; PMCID: PMC8638151.

This review of AMR in Lao PDR shows that current resistance levels are low for some GLASS pathogens, offering the country an opportunity to act quickly to implement strategies and interventions to roll out new guidelines with enhanced one-health antibiotic stewardship, reduce antibiotic use without prescriptions, enhance surveillance and improve AMR understanding.

OBJECTIVES:	To review the scientific evidence base on antimicrobial use (AMU) and antimicrobial resistance (AMR) in human and animal sectors in the Lao PDR (Laos).
METHODS:	We reviewed all publications from July 1994 (the first article describing AMR in Laos) to December 2020. Electronic searches were conducted using Google Scholar and PubMed with specific terms relating to AMR and AMU in Lao, French and English languages.
FINDINGS:	We screened 1,357 peer-reviewed and grey reports by title and abstract and then full articles/reports. Of 80 included, 66 (83%) related to human health, nine (11%) to animal health, four (5%) to both animal and human health and one (1%) to the environment. Sixty-two (78%) were on AMR and 18 (22%) on AMU. Extended spectrum beta lactamase-producing *Escherichia coli* was the greatest concern identified; the proportion of isolates increased fivefold from 2004 to 2016 (2/28 (7%) to 27/78 (35%)) from blood cultures submitted to the Microbiology Laboratory, Mahosot Hospital, Vientiane. Carbapenem resistant *Escherichia coli* was first identified in 2015. Methicillin-resistant *Staphylococcus aureus* (MRSA) was uncommon, with 15 cases of MRSA from blood cultures between its first identification in 2017 and December 2020. AMR patterns of global antimicrobial resistance surveillance system (GLASS) target pathogens from livestock were less well documented. There were few data on AMU in human health and none on AMU in livestock. The first hospital AMU survey in Laos showed that 70% (1,386/1,981) of in-patients in five hospitals from 2017 to 2018 received antimicrobial(s). Antibiotic self-medication was common.
CONCLUSION:	AMR in Laos is occurring at relatively low proportions for some GLASS pathogens, giving the country a window of opportunity to act quickly to implement strategies to protect the population from a worsening situation. Urgent interventions to roll out new guidelines with enhanced one-health antibiotic stewardship, reduce antibiotic use without prescriptions, enhance surveillance and improve understanding of AMU and AMR are needed.

Evolutionary histories and antimicrobial resistance in *Shigella flexneri* and *Shigella sonnei* in Southeast Asia. Chung The H, Bodhidatta L, Pham DT, Mason CJ, Ha Thanh T, Voong Vinh P, Turner P, Hem S, Dance DAB, Newton PN, Phetsouvanh R, Davong V, Thwaites GE, Thomson NR, Baker S, Rabaa MA. *Commun Biol*. 2021 Mar 19;4(1):353. doi: 10.1038/s42003-021-01905-9. PMID: 33742111; PMCID: PMC7979695

Conventional disease surveillance for shigellosis in developing country settings relies on serotyping and low-resolution molecular typing, which fails to contextualise the evolutionary history of the genus. Here, we interrogated a collection of 1,804 *Shigella* whole genome sequences from organisms isolated in four continental Southeast Asian countries (Thailand, Vietnam, Laos, and Cambodia) over three decades to characterise the evolution of both *S. flexneri* and *S. sonnei*. We show that *S. sonnei* and each major *S. flexneri* serotype are comprised of genetically diverse populations, the majority of which were likely introduced into Southeast Asia in the 1970s-1990s. Intranational and regional dissemination allowed widespread propagation of both species across the region. Our data indicate that the epidemiology of *S. sonnei* and the major *S. flexneri* serotypes were characterised by frequent clonal replacement events, coinciding with changing susceptibility patterns against contemporaneous antimicrobials. We conclude that adaptation to antimicrobial pressure was pivotal to the recent evolutionary trajectory of *Shigella* in Southeast Asia.

Dance DAB, Wuthiekanun V, Baird RW, Norton R, Limmathurotsakul D, Currie BJ. **Interpreting *Burkholderia pseudomallei* disc diffusion susceptibility test results by the EUCAST method.** *Clin Microbiol Infect*. 2021 Jun;27(6):827-829. doi: 10.1016/j.cmi.2021.02.017. Epub 2021 Feb 23. PMID: 33636339.

Dance DAB, Batty EM. **Harnessing genomics in the battle against antimicrobial resistance and neglected tropical diseases.** *EBioMedicine*. 2021 Jan;63:103178. doi: 10.1016/j.ebiom.2020.103178. Epub 2020 Dec 16. PMID: 33340997; PMCID: PMC7750543.

Commentary to an article in this issue of EBioMedicine on a new tool called ARDaP for detecting AMR in next generation sequencing (NGS) data for B. pseudomallei.

ISARIC Clinical Characterisation Group. The value of open-source clinical science in pandemic response: lessons from ISARIC. *Lancet Infect Dis*. 2021 Dec;21(12):1623-1624. doi: 10.1016/S1473-3099(21)00565-X. Epub 2021 Oct 4. Erratum in: *Lancet Infect Dis*. 2021 Dec;21(12):e363. PMID: 34619109; PMCID: PMC8489876.

Evolution of Multidrug Resistance in *Plasmodium falciparum*: a Longitudinal Study of Genetic Resistance Markers in the Greater Mekong Subregion. Imwong M, Suwannasin K, Srisutham S, Vongpromek R, Promnarate C, Saejeng A, Phyo AP, Proux S, Pongvongsa T, Chea N, Miotto O, Tripura R, Nguyen Hoang C, Dysoley L, Ho Dang Trung N, Peto TJ, Callery JJ, van der Pluijm RW, Amaratunga C, Mukaka M, von Seidlein L, Mayxay M, Thuy-Nhien NT, Newton PN, Day NPJ, Ashley EA, Nosten FH, Smithuis FM, Dhorda M, White NJ, Dondorp AM. *Antimicrob Agents Chemother*. 2021 Nov 17;65(12):e0112121. doi: 10.1128/AAC.01121-21. Epub 2021 Sep 13. PMID: 34516247; PMCID: PMC8597770.

Data from this study on markers of P. falciparum resistance to artemisinins, piperaquine and mefloquine in samples from Southeast Asia between 2007 and 2019 suggest that mefloquine and piperaquine resistance mechanisms may be counterbalancing, supporting the development of ASMQ plus piperaquine as a triple artemisinin combination therapy.

Increasing drug resistance in *Plasmodium falciparum* to artemisinins and their ACT partner drugs jeopardises effective antimalarial treatment. Resistance is worst in the Greater Mekong Subregion. Monitoring genetic markers of resistance can help to guide antimalarial therapy. Markers of resistance to artemisinins (PfKelch mutations), mefloquine (amplification of *P. falciparum* multidrug resistance-1, PfMDR1), and piperaquine (PfPlasmepsin2/3 amplification and specific P. falciparum chloroquine resistance transporter, PfCRT, mutations) were assessed in 6,722 *P. falciparum* samples from Vietnam, Lao PDR, Cambodia, Thailand, Myanmar between 2007 and 2019. Against a high background prevalence of PfKelch mutations, PfMDR1 and PfPlasmepsin2/3 amplification closely followed regional drug pressures over time. PfPlasmepsin2/3 amplification preceded piperaquine-resistance associated PfCRT mutations in Cambodia, and reached a peak prevalence of 23/28 (82%) in 2015. This declined to 57/156 (38%) after changing first-line treatment away from dihydroartemisinin-piperaquine to artesunate-mefloquine (ASMQ) between 2014 and 2017. PfMDR1 amplification increased from 0/293 (0%) between 2012 and 2017 to 12/156 (8%) in 2019. Amplification of PfMDR1 and PfPlasmepsin2/3 in the same parasites was extremely rare (4/6,722; 0.06%) and dispersed over time. Mechanisms conferring mefloquine and piperaquine resistance may be counterbalancing. This supports the development of ASMQ plus piperaquine as a triple artemisinin combination therapy.

Dynamics of intestinal multidrug-resistant bacteria colonisation contracted by visitors to a high-endemic setting: a prospective, daily, real-time sampling study. Kantele A, Kuenzli E, Dunn SJ, Dance DAB, Newton PN, Davong V, Mero S, Pakkanen SH, Neumayr A, Hatz C, Snaith A, Kallonen T, Corander J, McNally A. *Lancet Microbe*. 2021 Apr;2(4):e151-e158. doi: 10.1016/S2666-5247(20)30224-X. PMID: 33821248; PMCID: PMC8009952.

This prospective, daily, real-time study of 20 European visitors to Lao PDR is the first to characterise the dynamics of multidrug-resistant Gram-negative bacterial colonisation during travel. Multiple transient colonisation events indicated that travellers are exposed to a greater burden of multidrug-resistant bacteria than previously thought, underscoring a need for preventing travellers' diarrhoea and limit antibiotic use.

BACKGROUND:	Antimicrobial resistance is highly prevalent in low-income and middle-income countries. International travel contributes substantially to the global spread of intestinal multidrug-resistant Gram-negative bacteria. Hundreds of millions of annual visitors to low-income and middle-income countries are all exposed to intestinal multidrug-resistant Gram-negative bacteria resulting in 30-70% of them being colonised at their return. The colonisation process in high-exposure environments is poorly documented because data have only been derived from before travel and after travel sampling. We characterised colonisation dynamics by exploring daily stool samples while visiting a low-income and middle-income countries.
METHODS:	In this prospective, daily, real-time sampling study 20 European visitors to Laos volunteered to provide daily stool samples and completed daily questionnaires for 22 days. Samples were initially assessed at Mahosot Hospital, Vientiane, Laos, for acquisition of extended-spectrum β-lactamase-producing (ESBL) Gram-negative bacteria followed by whole-genome sequencing of isolates at MicrobesNG, University of Birmingham, Birmingham, UK. The primary outcome of the study was to obtain data on the dynamics of intestinal multidrug-resistant bacteria acquisition.
FINDINGS:	Between Sept 18 and Sept 20, 2015, 23 volunteers were recruited, of whom 20 (87%) European volunteers were included in the final study population. Although colonisation rates were 70% at the end of the study, daily sampling revealed that all participants had acquired ESBL-producing Gram-negative bacteria at some point during the study period; the colonisation status varied day by day. Whole-genome sequencing analysis ascribed the transient pattern of colonisation to sequential acquisition of new strains, resulting in a loss of detectable colonisation by the initial multidrug-resistant Gram-negative strains. 19 (95%) participants acquired two to seven strains. Of the 83 unique strains identified (53 *Escherichia coli*, 10 *Klebsiella* spp, and 20 other ESBL-producing Gram-negative bacteria), some were shared by as many as four (20%) participants.
INTERPRETATION:	To our knowledge, this is the first study to characterise in real-time the dynamics of acquiring multidrug-resistant Gram-negative bacterial colonisation during travel. Our data show multiple transient colonisation events indicative of constant microbial competition and suggest that travellers are exposed to a greater burden of multidrug-resistant bacteria than previously thought. The data emphasise the need for preventing travellers' diarrhoea and limiting antibiotic use, addressing the two major factors predisposing colonisation.
FUNDING:	The Finnish Governmental Subsidy for Health Science Research; The Scandinavian Society for Antimicrobial Chemotherapy; the Sigrid Jusélius Foundation; Biotechnology and Biological Sciences Research Council; Wellcome Trust; Medical Research Council; The Royal Society; Joint Programming Initiative on Antimicrobial Resistance; and European Research Council.

Surveillance strategies using routine microbiology for antimicrobial resistance in low- and middle-income countries. Lim C, Ashley EA, Hamers RL, Turner P, Kesteman T, Akech S, Corso A, Mayxay M, Okeke IN, Limmathurotsakul D, van Doorn HR. *Clin Microbiol Infect*. 2021 Oct;27(10):1391-1399. doi: 10.1016/j.cmi.2021.05.037. Epub 2021 Jun 7. PMID: 34111583.

This review of strategies for AMR surveillance using routine microbiology results in LMICs suggests that innovative strategies that can be easily implemented and sustained with minimal costs will be useful for improving AMR data availability and quality.

BACKGROUND:	Routine microbiology results are a valuable source of antimicrobial resistance (AMR) surveillance data in low- and middle-income countries (LMICs) as well as in high-income countries. Different approaches and strategies are used to generate AMR surveillance data.
OBJECTIVES:	We aimed to review strategies for AMR surveillance using routine microbiology results in LMICs and to highlight areas that need support to generate high quality AMR data.
SOURCES:	We searched papers that used routine microbiology to describe the epidemiology of AMR and drug resistant infections in LMICs in PubMed. We also included papers that, from our perspective, were critical in highlighting the biases and challenges or employed specific strategies to overcome these in reporting AMR surveillance in LMICs.
CONTENT:	Topics covered included strategies of identifying AMR cases (including case-finding based on isolates from routine diagnostic specimens and case-based surveillance of clinical syndromes), of collecting data (including cohort, point-prevalence survey, and case-control), of sampling AMR cases (including lot quality assurance surveys), and of processing and analysing data for AMR surveillance in LMICs.

IMPLICATIONS	The various AMR surveillance strategies warrant a thorough understanding of their limitations and potential biases to ensure maximum utilization and interpretation of local routine microbiology data across time and space. For instance, surveillance using case-finding based on results from clinical diagnostic specimens is relatively easy to implement and sustain in LMIC settings but the estimates of incidence and proportion of AMR is at risk of biases due to underuse of microbiology. Case-based surveillance of clinical syndrome generates informative statistics that can be translated to clinical practices but needs financial and technical support, and locally-tailored trainings to sustain. Innovative AMR surveillance strategies that can be easily implemented and sustained with minimal costs will be useful for improving AMR data availability and quality in LMICs.

Antimicrobial-Resistant *Escherichia coli* Strains and Their Plasmids in People, Poultry, and Chicken Meat in Laos. Moser AI, Kuenzli E, Campos-Madueno EI, Büdel T, Rattanavong S, Vongsouvath M, Hatz C, Endimiani A. *Front Microbiol*. 2021 Jul 26;12:708182. doi: 10.3389/fmicb.2021.708182. PMID: 34381435; PMCID: PMC8350485.

This whole-genome sequencing (WGS)-based study of extended-spectrum cephalosporin- (ESC-) and colistin-resistant Escherichia coli strains (CST-R-Ec) isolates in Lao PDR showed a high prevalence of AMR-Ec in the local population, poultry, and chicken meat.

Antimicrobial resistant (AMR) Enterobacterales are widely distributed among the healthy population of the Indochinese peninsula, including Laos. However, the local reservoir of these pathogens is currently not known and possible sources such as agricultural settings and food have rarely been analysed. In this work, we investigated the extended-spectrum cephalosporin- (ESC-) and colistin-resistant *Escherichia coli* strains (CST-R-Ec) isolated from the gut of local people, faeces of poultry, and from chicken meat (60 samples in each group) in Laos. Whole-genome sequencing (WGS) analysis based on both short- and long-read sequencing approaches were implemented. The following prevalence of ESC-R-Ec and CST-R-Ec were recorded, respectively: local people (70 and 15%), poultry (20 and 23.3%), and chicken meat (21.7 and 13.3%). Core-genome analysis, coupled with sequence type (ST)/core-genome ST (cgST) definitions, indicated that no common AMR-Ec clones were spreading among the different settings. ESC-R-Ec mostly possessed bla (CTX-M-15) and bla (CTX-M-55) associated to ISEcp1 or IS26. The majority of CST-R-Ec carried mcr-1 on IncX4, IncI2, IncP1, and IncHI1 plasmids similar or identical to those described worldwide; strains with chromosomal mcr-1 or possessing plasmid-mediated mcr-3 were also found. These results indicate a high prevalence of AMR-Ec in the local population, poultry, and chicken meat. While we did not observe the same clones among the three settings, most of the bla (CTX-Ms) and mcr-1/-3 were associated with mobile-genetic elements, indicating that horizontal gene transfer may play an important role in the dissemination of AMR-Ec in Laos. More studies should be planned to better understand the extent and dynamics of this phenomenon.

Antimicrobial resistance detection in Southeast Asian hospitals is critically important from both patient and societal perspectives, but what is its cost? Roberts T, Luangasanatip N, Ling CL, Hopkins J, Jaksuwan R, Lubell Y, Vongsouvath M, van Doorn HR, Ashley EA, Turner P. *PLOS Glob Public Health*. 2021 Oct 13;1(10):e0000018. doi: 10.1371/journal.pgph.0000018. PMID: 34746931; PMCID: PMC7611947.

This study estimated the financial cost of setting up and running a microbiology laboratory for organism identification and antimicrobial susceptibility testing. These costs may be prohibitive in many LMIC settings without donor support, highlighting the need for developing cheaper and cost-effective equipment and reagents for AMR surveillance in LMICs.

Antimicrobial resistance (AMR) is a major threat to global health. Improving laboratory capacity for AMR detection is critically important for patient health outcomes and population level surveillance. We aimed to estimate the financial cost of setting up and running a microbiology laboratory for organism identification and antimicrobial susceptibility testing as part of an AMR surveillance programme. Financial costs for setting up and running a microbiology laboratory were estimated using a top-down approach based on resource and cost data obtained from three clinical laboratories in the Mahidol Oxford Tropical Medicine Research Unit network. Costs were calculated for twelve scenarios, considering three levels of automation, with equipment sourced from either of the two leading manufacturers, and at low and high specimen throughput. To inform the costs of detection of AMR in existing labs, the unit cost per specimen and per isolate were also calculated using a micro-costing approach. Establishing a laboratory with the capacity to process 10,000 specimens per year ranged from $254,000 to $660,000 while the cost for a laboratory processing 100,000 specimens ranged from $394,000 to $887,000. Excluding capital costs to set up the laboratory, the cost per specimen ranged from $22-31 (10,000 specimens) and $11-12 (100,000 specimens). The cost per isolate ranged from $215-304 (10,000 specimens) and $105-122 (100,000 specimens). This study provides a conservative estimate of the costs for setting up and running a microbiology laboratory for AMR surveillance from a healthcare provider perspective. In the absence of donor support, these costs may be prohibitive in many low- and middle- income country (LMIC) settings. With the increased focus on AMR detection and surveillance, the high laboratory costs highlight the need for more focus on developing cheaper and cost-effective equipment and reagents so that laboratories in LMICs have the potential to improve laboratory capacity and participate in AMR surveillance.

High burden of infections caused by ESBL-producing MDR *Escherichia coli* in paediatric patients, Yangon, Myanmar. San T, Moe I, Ashley EA, San N. *JAC Antimicrob Resist*. 2021 Feb 14;3(1):dlab011. doi: 10.1093/jacamr/dlab011. PMID: 33615221; PMCID: PMC7882151.

This study reported a high frequency of ESBL-producing and MDR E. coli in children attending Yangon Children's Hospital in Myanmar, where access to effective second-line antimicrobials is limited.

BACKGROUND:	There is mounting evidence of a high burden of antimicrobial-resistant infections in children in low- and middle-income countries (LMICs).
OBJECTIVES:	To detect the frequency of ESBL-producing Escherichia coli in clinical specimens from paediatric patients attending Yangon Children's Hospital in Myanmar.
METHODS:	All children attending Yangon Children's Hospital who had clinical specimens submitted to the hospital diagnostic microbiology laboratory from June 2019 to December 2019 were included in the study. Specimens were processed routinely using standard methods with BD Phoenix used for pathogen identification and susceptibility testing. Presence of ESBLs was determined using the cephalosporin/clavulanate combination disc method with confirmation by PCR.
RESULTS:	From 3462 specimens submitted to the Microbiology Laboratory, a total of 123 E. coli were isolated. Among them, 100 isolates were phenotypically ESBL producers, 94 (76.4%) of which were confirmed by PCR [82/94 (87%) CTX-M, 72/94 (77%) TEM, 1/94 (1%) SHV]. Most of the ESBL-producing E. coli were isolated from urine samples (52.1%, 49/94) and the majority were from the surgical unit (61.7%, 58/94). Only 34/94 (36%) isolates were susceptible to meropenem.
CONCLUSIONS:	This study confirms a high proportion of infections caused by ESBL-producing and MDR E. coli in children hospitalized in Yangon, where access to effective second-line antimicrobials is limited.

Epidemiology of Extended-Spectrum Beta-Lactamase and Carbapenemase-Producing Enterobacterales in the Greater Mekong Subregion: A Systematic-Review and Meta-Analysis of Risk Factors Associated With Extended-Spectrum Beta-Lactamase and Carbapenemase Isolation. Singh SR, Teo AKJ, Prem K, Ong RT, Ashley EA, van Doorn HR, Limmathurotsakul D, Turner P, Hsu LY. *Front Microbiol*. 2021 Nov 26;12:695027. doi: 10.3389/fmicb.2021.695027. PMID: 34899618; PMCID: PMC8661499.

BACKGROUND:	Despite the rapid spread of extended-spectrum beta-lactamase (ESBL) producing-Enterobacterales (ESBL-E) and carbapenemase-producing Enterobacterales (CPE), little is known about the extent of their prevalence in the Greater Mekong Subregion (GMS). In this systematic review, we aimed to determine the epidemiology of ESBL-E and CPE in clinically significant Enterobacterales: *Escherichia coli* and *Klebsiella pneumoniae* from the GMS (comprising of Cambodia, Laos, Myanmar, Thailand, Vietnam and Yunnan province and Guangxi Zhuang region of China).
METHODS:	Following a list of search terms adapted to subject headings, we systematically searched databases: Medline, EMBASE, Scopus and Web of Science for articles published on and before October 20th, 2020. The search string consisted of the bacterial names, methods involved in detecting drug-resistance phenotype and genotype, GMS countries, and ESBL and carbapenemase detection as the outcomes. Meta-analyses of the association between the isolation of ESBL from human clinical and non-clinical specimens were performed using the "METAN" function in STATA 14.
RESULTS:	One hundred and thirty-nine studies were included from a total of 1,513 identified studies. Despite the heterogeneity in study methods, analysing the prevalence proportions on log-linear model scale for ESBL-producing *E. coli* showed a trend that increased by 13.2% (95%CI: 6.1-20.2) in clinical blood specimens, 8.1% (95%CI: 1.7-14.4) in all clinical specimens and 17.7% (95%CI: 4.9-30.4) increase in carriage specimens. Under the log-linear model assumption, no significant trend over time was found for ESBL-producing *K. pneumoniae* and ESBL-E specimens. CPE was reported in clinical studies and carriage studies post 2010, however a trend could not be determined because of the small dataset. Twelve studies were included in the meta-analysis of risk factors associated with isolation of ESBL. Recent antibiotic exposure was the most studied variable and showed a significant positive association with ESBL-E isolation (pooled OR: 2.9, 95%CI: 2.3-3.8) followed by chronic kidney disease (pooled OR: 4.7, 95%CI: 1.8-11.9), and other co-morbidities (pooled OR: 1.6, 95%CI: 1.2-2.9).
CONCLUSIONS:	Data from GMS is heterogeneous with significant data-gaps, especially in community settings from Laos, Myanmar, Cambodia and Yunnan and Guangxi provinces of China. Collaborative work standardizing the methodology of studies will aid in better monitoring, surveillance and evaluation of interventions across the GMS.

Knowledge, Attitudes, Perception and Reported Practices of Healthcare Providers on Antibiotic Use and Resistance in Pregnancy, Childbirth and Children under Two in Lao PDR: A Mixed Methods Study. Sychareun V, Sihavong A, Machowska A, Onthongdee X, Chaleunvong K, Keohavong B, Eriksen J, Hanson C, Vongsouvath M, Marrone G, Brauner A, Mayxay M, Kounnavong S, Lundborg CS. *Antibiotics (Basel)*. 2021 Nov 27;10(12):1462. doi: 10.3390/antibiotics10121462. PMID: 34943674; PMCID: PMC8698782.

BACKGROUND:	Overuse and misuse of antibiotics contribute unnecessarily to antibiotic resistance (ABR), and are thereby global health threats. Inappropriate prescriptions of antibiotics during pregnancy, delivery and early childhood are widespread across the world. This study aimed to assess knowledge, attitudes, and reported practices of healthcare providers (HCPs) and to explore their perceptions regarding antibiotic use and ABR related to pregnancy, childbirth, and children under two in Lao PDR.
METHODS:	This is a mixed methods study with data collection in 2019 via structured interviews among 217 HCPs (medical doctors/assistant doctors, midwives/nurses, pharmacists/assistant pharmacists and drug sellers), who prescribed/dispensed antibiotics in one rural and one urban district in Vientiane province and individual qualitative interviews with 30 HCPs and stakeholders.
RESULTS:	Of the HCPs, 36% had below average knowledge regarding antibiotic use and ABR, and 67% reported prescribing antibiotics for uncomplicated vaginal delivery. Half of the HCPs did not believe that their prescribing contributed to ABR, and only 9% had participated in antibiotic education.
CONCLUSIONS:	A substantial number of HCPs had suboptimal knowledge and prescribed antibiotics unnecessarily, thereby contributing to ABR. Continuous education and regular supervision of HCPs is recommended to improve the use of antibiotics related to pregnancy, childbirth, and young children.

Laboratory informatics capacity for effective antimicrobial resistance surveillance in resource-limited settings. Turner P, Rupali P, Opintan JA, Jaoko W, Feasey NA, Peacock SJ, Ashley EA. *Lancet Infect Dis*. 2021 Jun;21(6):e170-e174. doi: 10.1016/S1473-3099(20)30835-5. Epub 2021 Apr 15. PMID: 33865461.

Antimicrobial resistance (AMR) is a major threat to human health globally. Surveillance is a key activity to determine AMR burden, impacts, and trends and to monitor effects of interventions. Surveillance systems require efficient capture and onward sharing of high-quality laboratory data. Substantial investment is being made to improve laboratory capacity, particularly in low-income and middle-income countries (LMICs) with high disease burdens. However, building capacity for effective laboratory data management remains an under-resourced area, which, unless addressed, will limit progress towards comprehensive AMR surveillance in LMICs. The lack of a fit-for-purpose and open-source laboratory information management system software is of particular concern. In this Personal View, we summarise the technical requirements for microbiology laboratory data management, provide a snapshot of laboratory data management in LMIC laboratories, and describe the key steps required to improve the situation. Without action to improve information technology infrastructure and data management systems in microbiology laboratories, the ongoing efforts to develop capacity for AMR surveillance in LMICs might not realise their full potential.

Antimicrobial resistance in commensal opportunistic pathogens isolated from non-sterile sites can be an effective proxy for surveillance in bloodstream infections. Vihta KD, Gordon NC, Stoesser N, Quan TP, Tyrrell CSB, Vongsouvath M, Ashley EA, Chansamouth V, Turner P, Ling CL, Eyre DW, White NJ, Crook D, Peto TEA, Walker AS. *Sci Rep*. 2021 Dec 3;11(1):23359. doi: 10.1038/s41598-021-02755-5. PMID: 34862445; PMCID: PMC8642463.

Antimicrobial resistance (AMR) surveillance in bloodstream infections (BSIs) is challenging in low/middle-income countries (LMICs) given limited laboratory capacity. Other specimens are easier to collect and process and are more likely to be culture-positive. In 8102 *E. coli* BSIs, 322,087 *E. coli* urinary tract infections, 6952 S. aureus BSIs and 112,074 S. *aureus* non-sterile site cultures from Oxfordshire (1998-2018), and other (55,296 isolates) rarer commensal opportunistic pathogens, antibiotic resistance trends over time in blood were strongly associated with those in other specimens (maximum cross-correlation per drug 0.51-0.99). Resistance prevalence was congruent across drug-years for each species (276/312 (88%) species-drug-years with prevalence within ± 10% between blood/other isolates). Results were similar across multiple countries in high/middle/low income-settings in the independent ATLAS dataset (103,559 isolates, 2004-2017) and three further LMIC hospitals/programmes (6154 isolates, 2008-2019). AMR in commensal opportunistic pathogens cultured from BSIs is strongly associated with AMR in commensal opportunistic pathogens cultured from non-sterile sites over calendar time, suggesting the latter could be used as an effective proxy for AMR surveillance in BSIs.

A call to action: time to recognise melioidosis as a neglected tropical disease. Savelkoel J, Dance DAB, Currie BJ, Limmathurotsakul D, Wiersinga WJ. *Lancet Infect Dis*. 2022 Jun;22(6):e176-e182. doi: 10.1016/S1473-3099(21)00394-7. Epub 2021 Dec 23. PMID: 34953519.

Melioidosis is a tropical infection caused by the soil bacterium *Burkholderia pseudomallei*. Despite the substantial impact of this often-overlooked pathogen on both the health-care systems and economies of numerous low-income and middle-income countries around the world, melioidosis is not officially classified as a neglected tropical disease (NTD) by WHO. Melioidosis causes a higher estimated disease burden and mortality than many other recognised NTDs, with deaths primarily occurring among rural poor populations in low-income and middle-income countries. Fortunately, the impact of melioidosis in a region can be reduced once awareness is established of its known or suspected endemicity. In this Personal View, we provide evidence in support of official recognition of melioidosis as an NTD. We urge member states to request that WHO revisit their NTD list and appeal to government and philanthropic organisations to establish programmes in endemic countries to control melioidosis in order to reduce its global health burden.

Geographical distribution of *Burkholderia pseudomallei* in soil in Myanmar. Swe MMM, Win MM, Cohen J, Phyo AP, Lin HN, Soe K, Amorncha P, Wah TT, Win KKN, Ling C, Parker DM, Dance DAB, Ashley EA, Smithuis F. *PLoS Negl Trop Dis*. 2021 May 24;15(5):e0009372. doi: 10.1371/journal.pntd.0009372. PMID: 34029325; PMCID: PMC8143414.

This nationwide soil study confirmed a widespread distribution of B. pseudomallei in Myanmar, suggesting further clinical studies to obtain a better picture of the burden of melioidosis in the country.

BACKGROUND:	*Burkholderia pseudomallei* is a Gram-negative bacterium found in soil and water in many tropical countries. It causes melioidosis, a potentially fatal infection first described in 1911 in Myanmar. Melioidosis is a common cause of sepsis and death in South and South-east Asia, but it is rarely diagnosed in Myanmar. We conducted a nationwide soil study to identify areas where *B. pseudomallei* is present.
METHODOLOGY/ PRINCIPAL FINDINGS:	We collected soil samples from 387 locations in all 15 states and regions of Myanmar between September 2017 and June 2019. At each site, three samples were taken at each of three different depths (30, 60 and 90 cm) and were cultured for *B. pseudomallei* separately, along with a pooled sample from each site (i.e. 10 cultures per site). We used a negative binomial regression model to assess associations between isolation of *B. pseudomallei* and environmental factors (season, soil depth, soil type, land use and climate zones). *B. pseudomallei* was isolated in 7 of 15 states and regions. Of the 387 sites, 31 (8%) had one or more positive samples and of the 3,870 samples cultured, 103 (2.7%) tested positive for *B. pseudomallei*. *B. pseudomallei* was isolated more frequently during the monsoon season [RR-2.28 (95% CI: 0.70-7.38)] and less in the hot dry season [RR-0.70 (95% CI: 0.19-2.56)] compared to the cool dry season, and in the tropical monsoon climate zone [RR-2.26; 95% CI (0.21-6.21)] compared to the tropical dry winter climate zone. However, these associations were not statistically significant. *B. pseudomallei* was detected at all three depths and from various soil types (clay, silt and sand). Isolation was higher in agricultural land (2.2%), pasture land (8.5%) and disused land (5.8%) than in residential land (0.4%), but these differences were also not significant.
CONCLUSION/ SIGNIFICANCE:	This study confirms a widespread distribution of *B. pseudomallei* in Myanmar. Clinical studies should follow to obtain a better picture of the burden of melioidosis in Myanmar.

A multi-country study using MALDI-TOF mass spectrometry for rapid identification of *Burkholderia pseudomallei*. Watthanaworawit W, Roberts T, Hopkins J, Gassiep I, Norton R, Robinson MT, Silisouk J, Sar P, Sao S, Amornchai P, Limmathurotsakul D, Wuthiekanun V, Nosten F, Simpson AJH, Turner P, Ling CL. *BMC Microbiol*. 2021 Jul 16;21(1):213. doi: 10.1186/s12866-021-02276-1. PMID: 34266382; PMCID: PMC8283998.

BACKGROUND:	*Burkholderia pseudomallei* is the bacterial causative agent of melioidosis, a difficult disease to diagnose clinically with high mortality if not appropriately treated. Definitive diagnosis requires isolation and identification of the organism. With the increased adoption of MALDI-TOF MS for the identification of bacteria, we established a method for rapid identification of *B. pseudomallei* using the Vitek MS, a system that does not currently have *B. pseudomallei* in its in-vitro diagnostic database.
RESULTS:	A routine direct spotting method was employed to create spectra and SuperSpectra. An initial *B. pseudomallei* SuperSpectrum was created at Shoklo Malaria Research Unit (SMRU) from 17 reference isolates (46 spectra). When tested, this initial SMRU SuperSpectrum was able to identify 98.2% (54/55) of Asian isolates, but just 46.7% (35/75) of Australian isolates. Using spectra (430) from different reference and clinical isolates, two additional SMRU SuperSpectra were created. Using the combination of all SMRU SuperSpectra with seven existing SuperSpectra from Townsville, Australia 119 (46.7%) Asian isolates and 31 (46.7%) Australian isolates were correctly identified. In addition, no misidentifications were obtained when using these 11 SuperSpectra when tested with 34 isolates of other bacteria including the closely related species *Burkholderia thailandensis* and *Burkholderia cepacia*.
CONCLUSIONS:	This study has established a method for identification of *B. pseudomallei* using Vitek MS, and highlights the impact of geographical differences between strains for identification using this technique.

Enhanced melioidosis surveillance in patients attending four tertiary hospitals in Yangon, Myanmar. Win MM, Win KKN, Wah TT, Aye SN, Htwe TT, Zin KN, Aung MT, Aung WW, Ashley EA, Smithuis F, Rigas V, Currie BJ, Mayo M, Webb JR, Ling CL, Htun ZT, Dance DAB. *Epidemiol Infect*. 2021 Jun 22;149:1-23. doi: 10.1017/S095026882100128X. PMID: 34158136; PMCID: PMC8276317.

To investigate the current epidemiology of melioidosis in Yangon, Myanmar, between June 2017 and May 2019 we conducted enhanced surveillance for melioidosis in four tertiary hospitals in Yangon, where the disease was first discovered in 1911. Oxidase-positive Gram-negative rods were obtained from the microbiology laboratories and further analysed at the Department of Medical Research. Analysis included culture on Ashdown agar, the three disc sensitivity test (gentamicin, colistin and co-amoxiclav), latex agglutination, API 20 NE, antibiotic susceptibility testing, and a subset underwent molecular confirmation with a *Burkholderia pseudomallei* specific assay. Twenty one of 364 isolates (5.7%) were confirmed as *B. pseudomallei* and were mostly susceptible to the antibiotics used in standard therapy for melioidosis. Ten patients were from Yangon Region, nine were from Ayeyarwaddy region, and one each was from Kayin and Rakhine States. A history of soil contact was given by seven patients, five had diabetes mellitus and one had renal insufficiency. The patients presented with septicaemia (12 cases), pneumonia (three cases), urinary tract infection (two cases) and wound infection (four cases). Eighteen patients survived to hospital discharge. This study highlights the likelihood that melioidosis may be far more common, but underdiagnosed, in more rural parts of Myanmar as in other countries in SE Asia.

Evaluation of the Panbio *Leptospira* IgM ELISA among Outpatients Attending Primary Care in Southeast Asia. Dhawan S, Althaus T, Lubell Y, Suwancharoen D, Blacksell SD. *Am J Trop Med Hyg*. 2021 Mar 15;104(5):1777-1781. doi: 10.4269/ajtmh.20-0818. PMID: 33724923; PMCID: PMC8103482.

This study evaluated the Panbio Leptospira ELISA IgM in febrile patients in Southeast Asia to show that the utility of the Leptospira IgM ELISA for both serodiagnosis and seroprevalence is limited in this setting.

Despite estimates suggesting *Leptospira* spp. is endemic in Southeast Asia, evidence remains limited. Diagnostic accuracy evaluations based on *Leptospira* ELISA mainly rely on hospitalized and severe patients; therefore, studies measuring the pathogen burden may be inaccurate in the community. We evaluated the Panbio *Leptospira* ELISA IgM among 656 febrile outpatients attending primary care in Chiangrai, Thailand, and Hlaing Tha Yar, Yangon, Myanmar. ELISA demonstrated limited diagnostic accuracy for the detection of acute leptospiral infection using the manufacturer recommended cutoff, with a sensitivity of 71.4% and specificity of 36.4%, and an area under the receiver operator characteristic curve value of 0.65 (95% CI: 0.41-0.89), compared with our reference test, the PCR assay. ELISA also performed poorly as a screening tool for detecting recent exposure to *Leptospira* spp. compared with the "gold-standard" microscopic agglutination test, with a specificity of 42.7%. We conclude that the utility of the *Leptospira* IgM ELISA for both serodiagnosis and seroprevalence is limited in our setting.

***Orientia tsutsugamushi* dynamics in vectors and hosts: ecology and risk factors for foci of scrub typhus transmission in northern Thailand.** Elliott I, Thangnimitchok N, Chaisiri K, Wangrangsimakul T, Jaiboon P, Day NPJ, Paris DH, Newton PN, Morand S. *Parasit Vectors*. 2021 Oct 18;14(1):540. doi: 10.1186/s13071-021-05042-4. PMID: 34663445; PMCID: PMC8524837.

BACKGROUND:	Scrub typhus is an important neglected vector-borne zoonotic disease across the Asia-Pacific region, with an expanding known distribution. The disease ecology is poorly understood, despite the large global burden of disease. The key determinants of high-risk areas of transmission to humans are unknown.
METHODS:	Small mammals and chiggers were collected over an 18-month period at three sites of differing ecological profiles with high scrub typhus transmission in Chiang Rai Province, northern Thailand. Field samples were identified and tested for *Orientia tsutsugamushi* by real-time PCR. The rates and dynamics of infection were recorded, and positive and negative individuals were mapped over time at the scale of single villages. Ecological analyses were performed to describe the species richness, community structure and interactions between infected and uninfected species and habitats. Generalised linear modelling (GLM) was applied to examine these interactions.
RESULTS:	The site with the highest rates of human infection was associated with the highest number of infected chigger pools (41%), individual chiggers (16%), proportion of the known vector species *Leptotrombidium deliense* (71%) and chigger index (151). Chigger species diversity was lowest (Shannon diversity index H': 1.77) and rodent density appeared to be high. There were no consistent discrete foci of infection identified at any of the study sites. The small mammals *Rattus tanezumi* and *Bandicota indica* and the chiggers *L. deliense* and *Walchia kritochaeta* emerged as central nodes in the network analysis. In the GLM, the end of the dry season, and to a lesser extent the end of the wet season, was associated with *O. tsutsugamushi*-infected small mammals and chiggers. A clear positive association was seen between *O. tsutsugamushi*-positive chigger pools and the combination of *O. tsutsugamushi*-positive chigger pools and *O. tsutsugamushi*-positive small mammals with lowland habitats.
CONCLUSIONS:	These findings begin to reveal some of the factors that may determine high-risk foci of scrub typhus at a fine local scale. Understanding these factors may allow practical public health interventions to reduce disease risk. Further studies are needed in areas with diverse ecology.

Targeted capture and sequencing of *Orientia tsutsugamushi* genomes from chiggers and humans. Elliott I, Thangnimitchok N, de Cesare M, Linsuwanon P, Paris DH, Day NPJ, Newton PN, Bowden R, Batty EM. *Infect Genet Evol*. 2021 Jul;91:104818. doi: 10.1016/j.meegid.2021.104818. Epub 2021 Mar 23. PMID: 33771726; PMCID: PMC8164161.

Scrub typhus is a febrile disease caused by *Orientia tsutsugamushi*, transmitted by larval stage *Trombiculid mites* (chiggers), whose primary hosts are small mammals. The phylogenomics of *O. tsutsugamushi* in chiggers, small mammals and humans remains poorly understood. To combat the limitations imposed by the low relative quantities of pathogen DNA in typical *O. tsutsugamushi* clinical and ecological samples, along with the technical, safety and cost limitations of cell culture, a novel probe-based target enrichment sequencing protocol was developed. The method was designed to capture variation among conserved genes and facilitate phylogenomic analysis at the scale of population samples. A whole-genome amplification step was incorporated to enhance the efficiency of sequencing by reducing duplication rates. This resulted in on-target capture rates of up to 93% for a diverse set of human, chigger, and rodent samples, with the greatest success rate in samples with real-time PCR C(t) values below 35. Analysis of the best-performing samples revealed phylogeographic clustering at local, provincial and international scales. Applying the methodology to a comprehensive set of samples could yield a more complete understanding of the ecology, genomic evolution and population structure of *O. tsutsugamushi* and other similarly challenging organisms, with potential benefits in the development of diagnostic tests and vaccines.

Genetic diversity of *Leptospira* isolates in Lao PDR and genome analysis of an outbreak strain. Grillová L, Robinson MT, Chanthongthip A, Vincent AT, Nieves C, Oppelt J, Mariet JF, Lorioux C, Vongsouvath M, Mayxay M, Phonemeexay O, Rattanavong S, Phommasone K, Douangnouvong A, Šmajs D, Veyrier FJ, Newton PN, Picardeau M. *PLOS Negl Trop Dis*. 2021 Dec 28;15(12):e0010076. doi: 10.1371/journal.pntd.0010076. PMID: 34962921; PMCID: PMC8746763.

Whole genomic sequencing and analysis of Leptospira isolates performed in this study revealed a high genetic diversity, with the most prevalent genotype (CG272) being a highly clonal group, associated with deaths and with a large outbreak in both Lao PDR and Thailand.

BACKGROUND:	Although Southeast Asia is one of the most leptospirosis afflicted regions, little is known about the diversity and molecular epidemiology of the causative agents of this widespread and emerging zoonotic disease.

METHODOLOGY/ PRINCIPAL FINDINGS:	We used whole genome sequencing to examine genetic variation in 75 *Leptospira* strains isolated from patients in the Lao PDR (Laos) between 2006 and 2017. Eleven serogroups from 4 *Leptospira* species and 43 cgMLST-defined clonal groups (CGs) were identified. The most prevalent CG was CG272 (n = 18, 26.8%), composed of L. interrogans serogroup Autumnalis isolates. This genotype was recovered throughout the 12-year period and was associated with deaths, and with a large outbreak in neighbouring Thailand. Genome analysis reveals that the CG272 strains form a highly clonal group of strains that have, for yet unknown reasons, recently spread in Laos and Thailand. Additionally, accessory genes clearly discriminate CG272 strains from the other *Leptospira* strains.
CONCLUSION/ SIGNIFICANCE:	The present study reveals a high diversity of *Leptospira* genotypes in Laos, thus extending our current knowledge of the pan- and core-genomes of these life-threatening pathogens. Our results demonstrate that the CG272 strains belong to a unique clonal group, which probably evolved through clonal expansion following niche adaptation. Additional epidemiological studies are required to better evaluate the spread of this genotype in Southeast Asia. To further investigate the key factors driving the virulence and spread of these pathogens, more intense genomic surveillance is needed, combining detailed clinical and epidemiological data.

A spatio-temporal analysis of scrub typhus and murine typhus in Laos; implications from changing landscapes and climate. Roberts T, Parker DM, Bulterys PL, Rattanavong S, Elliott I, Phommasone K, Mayxay M, Chansamouth V, Robinson MT, Blacksell SD, Newton PN. *PLoS Negl Trop Dis*. 2021 Aug 25;15(8):e0009685. doi: 10.1371/journal.pntd.0009685. PMID: 34432800; PMCID: PMC8386877.

This study of scrub typhus (ST) and murine typhus (MT) in Laos with 2003-2017 samples showed that MT was positively and ST negatively associated with residence in Vientiane Capital. ST was highly seasonal peaking in the wet season whilst MT peaked in the dry season.

BACKGROUND:	Scrub typhus (ST) and murine typhus (MT) are common but poorly understood causes of fever in Laos. We examined the spatial and temporal distribution of ST and MT, with the intent of informing interventions to prevent and control both diseases.
METHODOLOGY/ PRINCIPAL FINDINGS:	This study included samples submitted from 2003 to 2017 to Mahosot Hospital, Vientiane, for ST and MT investigation. Serum samples were tested using IgM rapid diagnostic tests. Patient demographic data along with meteorological and environmental data from Laos were analysed. Approximately 17% of patients were positive for either ST (1,337/8,150 patients tested) or MT (1,283/7,552 patients tested). While both diseases occurred in inhabitants from Vientiane Capital, from the univariable analysis MT was positively and ST negatively associated with residence in Vientiane Capital. ST was highly seasonal, with cases two times more likely to occur during the wet season months of July-September compared to the dry season whilst MT peaked in the dry season. Multivariable regression analysis linked ST incidence to fluctuations in relative humidity whereas MT was linked to variation in temperature. Patients with ST infection were more likely to come from villages with higher levels of surface flooding and vegetation in the 16 days leading up to diagnosis.
CONCLUSION:	The data suggest that as cities expand, high risk areas for MT will also expand. With global heating and risks of attendant higher precipitation, these data suggest that the incidence and spatial distribution of both MT and ST will increase.

Rickettsial infections: A blind spot in our view of neglected tropical diseases. Salje J, Weitzel T, Newton PN, Varghese GM, Day N. *PLOS Negl Trop Dis*. 2021 May 13;15(5):e0009353. doi: 10.1371/journal.pntd.0009353. PMID: 33983936; PMCID: PMC8118261.

Rickettsial diseases are a group of vector-borne bacterial infections that cause acute febrile illness with potentially severe or fatal complications. These vector-borne diseases are prevalent in tropical and subtropical regions worldwide and disproportionately affect poorer communities but are scientifically underrecognized. Despite this, they are not included in the World Health Organization's list of neglected tropical diseases nor were they mentioned in Peter Hotez's recent reflections on "What constitutes a neglected tropical disease?" in PLOS Neglected Tropical Diseases [1]. Here we present the case that rickettsial infections, as an overlooked cause of morbidity, mortality, and economic losses in marginalized populations, should be recognized as neglected tropical diseases. We describe how this oversight is the result of a number of factors and how it negatively impacts patient outcomes. We then propose measures to address the neglect of rickettsial infections in both scientific research and public health interventions.

Systematic review of the scrub typhus treatment landscape: Assessing the feasibility of an individual participant-level data (IPD) platform. Saraswati K, Maguire BJ, McLean ARD, Singh-Phulgenda S, Ngu RC, Newton PN, Day NPJ, Guérin PJ. *PLoS Negl Trop Dis*. 2021 Oct 14;15(10):e0009858. doi: 10.1371/journal.pntd.0009858. PMID: 34648517; PMCID: PMC8547739.

This systematic literature review shows that scrub typhus knowledge gaps could be addressed by establishing an individual participant-level data (IPD) platform to facilitate pooling and harmonisation of currently scattered data and enable in-depth investigation of priority research questions to inform clinical practice and improve health outcomes.

BACKGROUND:	Scrub typhus is an acute febrile illness caused by intracellular bacteria from the genus *Orientia*. It is estimated that one billion people are at risk, with one million cases annually mainly affecting rural areas in Asia-Oceania. Relative to its burden, scrub typhus is understudied, and treatment recommendations vary with poor evidence base. These knowledge gaps could be addressed by establishing an individual participant-level data (IPD) platform, which would enable pooled, more detailed and statistically powered analyses to be conducted. This study aims to assess the characteristics of scrub typhus treatment studies and explore the feasibility and potential value of developing a scrub typhus IPD platform to address unanswered research questions.
METHODOLOGY/ PRINCIPAL FINDINGS:	We conducted a systematic literature review looking for prospective scrub typhus clinical treatment studies published from 1998 to 2020. Six electronic databases (Ovid Embase, Ovid Medline, Ovid Global Health, Cochrane Library, Scopus, Global Index Medicus), ClinicalTrials.gov, and WHO ICTRP were searched. We extracted data on study design, treatment tested, patient characteristics, diagnostic methods, geographical location, outcome measures, and statistical methodology. Among 3,100 articles screened, 127 were included in the analysis. 12,079 participants from 12 countries were enrolled in the identified studies. ELISA, PCR, and eschar presence were the most commonly used diagnostic methods. Doxycycline, azithromycin, and chloramphenicol were the most commonly administered antibiotics. Mortality, complications, adverse events, and clinical response were assessed in most studies. There was substantial heterogeneity in the diagnostic methods used, treatment administered (including dosing and duration), and outcome assessed across studies. There were few interventional studies and limited data collected on specific groups such as children and pregnant women.

CONCLUSION:	There were a limited number of interventional trials, highlighting that scrub typhus remains a neglected disease. The heterogeneous nature of the available data reflects the absence of consensus in treatment and research methodologies and poses a significant barrier to aggregating information across available published data without access to the underlying IPD. There is likely to be a substantial amount of data available to address knowledge gaps. Therefore, there is value for an IPD platform that will facilitate pooling and harmonisation of currently scattered data and enable in-depth investigation of priority research questions that can, ultimately, inform clinical practice and improve health outcomes for scrub typhus patients.

The Development of an Abattoir-Based Surveillance System in Lao PDR for the Detection of Zoonoses in Large Ruminants: Q Fever and Brucellosis Seroepidemiology as a Pilot Study. Siengsanan-Lamont J, Douangngeun B, Theppangna W, Khounsy S, Phommachanh P, Selleck PW, Matsumoto N, Gleeson LJ, Blacksell SD. *Animals (Basel)*. 2021 Mar 8;11(3):742. doi: 10.3390/ani11030742. PMID: 33800515; PMCID: PMC8001590.

Although animal health surveillance programmes are useful for gaining information to help improve global health and food security, these programmes can be challenging to establish in developing economies with a low-resource base. This study focused on establishing a national surveillance system initiated by the Lao PDR government using a passive surveillance system of abattoir samples as a pilot model, and to gain information on contagious zoonoses, particularly Q fever and brucellosis, in the large ruminant population. A total of 683 cattle and buffalo samples were collected from six selected provinces of Lao PDR between March-December 2019. Out of 271 samples tested, six samples (2.2%, 95% confidence interval (CI) of 1.0, 4.8) were positive in the Q fever antibody ELISA test. Only one sample (out of 683; 0.2%, 95% CI 0.0, 0.8) tested positive to the Brucella antibody ELISA test. Seroprevalence of these important zoonoses in Lao PDR were relatively low in cattle and buffaloes; however, extensive animal movement within the country was identified which could increase risks of spreading transboundary diseases. The study highlights the importance of ongoing animal health surveillance and the need to find cost-effective approaches for its long-term sustainability.

Whole-Genome Assemblies of 16 *Burkholderia pseudomallei* Isolates from Rivers in Laos. Liechti N, Zimmermann RE, Zopfi J, Robinson MT, Pierret A, Ribolzi O, Rattanavong S, Davong V, Newton PN, Wittwer M, Dance DAB. *Microbiol Resour Announc*. 2021 Jan 28;10(4):e01226-20. doi: 10.1128/MRA.01226-20. PMID: 33509986; PMCID: PMC7844071.

We report 16 *Burkholderia pseudomallei* genomes, including 5 new multilocus sequence types, isolated from rivers in Laos. The environmental bacterium *B. pseudomallei* causes melioidosis, a serious infectious disease in tropical and subtropical regions. The isolates are geographically clustered in one clade from around Vientiane, Laos, and one clade from further south.

Impact of delays to incubation and storage temperature on blood culture results: a multi-centre study. Ling CL, Roberts T, Soeng S, Cusack TP, Dance DAB, Lee SJ, Reed TAN, Hinfonthong P, Sihalath S, Sengduangphachanh A, Watthanaworawit W, Wangrangsimakul T, Newton PN, Nosten FH, Turner P, Ashley EA. *BMC Infect Dis*. 2021 Feb 12;21(1):173. doi: 10.1186/s12879-021-05872-8. PMID: 33579205; PMCID: PMC7881545.

This study addressed a knowledge gap on transportation and storing of blood cultures in Southeast Asian countries showing that incubation with minimal delay maximizes pathogen recovery and timely result reporting. Suggested strategies to minimize impact of unavoidable delays include transportation at a temperature ≤ 25 °C and blind sub-cultures prior to incubation.

BACKGROUND:	Blood cultures are one of the most important tests performed by microbiology laboratories. Many hospitals, particularly in low and middle-income countries, lack either microbiology services or staff to provide 24 h services resulting in delays to blood culture incubation. There is insufficient guidance on how to transport/store blood cultures if delays before incubation are unavoidable, particularly if ambient temperatures are high. This study set out to address this knowledge gap.
METHODS:	In three South East Asian countries, four different blood culture systems (two manual and two automated) were used to test blood cultures spiked with five common bacterial pathogens. Prior to incubation the spiked blood culture bottles were stored at different temperatures (25 °C, in a cool-box at ambient temperature, or at 40 °C) for different lengths of time (0 h, 6 h, 12 h or 24 h). The impacts of these different storage conditions on positive blood culture yield and on time to positivity were examined.
RESULTS:	There was no significant loss in yield when blood cultures were stored < 24 h at 25 °C, however, storage for 24 h at 40 °C decreased yields and longer storage times increased times to detection.
CONCLUSIONS:	Blood cultures should be incubated with minimal delay to maximize pathogen recovery and timely result reporting; however, this study provides some reassurance that unavoidable delays can be managed to minimize negative impacts. If delays to incubation ≥ 12 h are unavoidable, transportation at a temperature not exceeding 25 °C, and blind sub-cultures prior to incubation should be considered.

Effects of hydrological regime and land use on in-stream *Escherichia coli* concentration in the Mekong basin, Lao PDR. Nakhle P, Ribolzi O, Boithias L, Rattanavong S, Auda Y, Sayavong S, Zimmermann R, Soulileuth B, Pando A, Thammahacksa C, Rochelle-Newall EJ, Santini W, Martinez JM, Gratiot N, Pierret A. *Sci Rep*. 2021 Feb 10;11(1):3460. doi: 10.1038/s41598-021-82891-0. PMID: 33568764; PMCID: PMC7876097.

This study of Escherichia coli as faecal indicator bacteria (FIB) demonstrated faecal contamination at most catchment sites across Lao PDR, with a seasonality characterized by higher E. coli concentrations during the rainy season mostly in mountainous northern Lao PDR and in Vientiane province.

In the basin of the Mekong, over 70 million people rely on unimproved surface water for their domestic requirements. Surface water is often contaminated with faecal matter and yet little information exists on the underlying mechanisms of faecal contamination in tropical conditions at large watershed scales. Our objectives were to (1) investigate the seasonality of faecal contamination using *Escherichia* coli as faecal indicator bacteria (FIB), and (2) establish links between the faecal contamination in stream water and its controlling factors (hydrology and land use). We present the results of (1) a sampling campaign at the outlet of 19 catchments across Lao PDR, in both the dry and the rainy seasons of 2016, and (2) a 10-day interval monitoring conducted in 2017 and 2018 at three point locations of three rivers (Nam Ou, Nam Suang, and Mekong) in northern Lao PDR. Our results show the presence of faecal contamination at most of the sampled sites, with a seasonality characterized by higher and extreme *E. coli* concentrations occurring during the rainy season. The highest *E. coli* concentrations, strongly correlated with total suspended sediment concentrations, were measured in catchments dominated by unstocked forest areas, especially in mountainous northern Lao PDR and in Vientiane province.

Molecular Detection of Pathogens in Negative Blood Cultures in the Lao People's Democratic Republic. Ter SK, Rattanavong S, Roberts T, Sengduangphachanh A, Sihalath S, Panapruksachat S, Vongsouvath M, Newton PN, Simpson AJH, Robinson MT. *Am J Trop Med Hyg*. 2021 Mar 1;104(4):1582-1585. doi: 10.4269/ajtmh.20-1348. PMID: 33646978; PMCID: PMC8045604.

Bloodstream infections cause substantial morbidity and mortality. However, despite clinical suspicion of such infections, blood cultures are often negative. We investigated blood cultures that were negative after 5 days of incubation for the presence of bacterial pathogens using specific (*Rickettsia* spp. and Leptospira spp.) and a broad-range 16S rRNA PCR. From 190 samples, 53 (27.9%) were positive for bacterial DNA. There was also a high background incidence of dengue (90/112 patient serum positive, 80.4%). Twelve samples (6.3%) were positive for *Rickettsia* spp., including two *Rickettsia typhi*. The 16S rRNA PCR gave 41 positives; *Escherichia coli* and *Klebsiella pneumoniae* were identified in 11 and eight samples, respectively, and one *Leptospira* species was detected. Molecular investigation of negative blood cultures can identify potential pathogens that will otherwise be missed by routine culture. Patient management would have been influenced in all 53 patients for whom a bacterial organism was identified, and 2.3-6.1% of patients would likely have had an altered final outcome. These findings warrant further study, particularly to determine the cost-benefit for routine use, ways of implementation, and timing of PCR for organisms such as *Rickettsia* and *Leptospira*, which are important pathogens in rural Asia.

Indirect effects of 13-valent pneumococcal conjugate vaccine on pneumococcal carriage in children hospitalised with acute respiratory infection despite heterogeneous vaccine coverage: an observational study in Lao People's Democratic Republic. Chan J, Lai JYR, Nguyen CD, Vilivong K, Dunne EM, Dubot-Pérès A, Fox K, Hinds J, Moore KA, Nation ML, Pell CL, Xeuatvongsa A, Vongsouvath M, Newton PN, Mulholland K, Satzke C, Dance DAB, Russell FM; PneuCAPTIVE Lao PDR Research Group. *BMJ Glob Health*. 2021 Jun;6(6):e005187. doi: 10.1136/bmjgh-2021-005187. PMID: 34108146; PMCID: PMC8191607.

This study showed a marked coverage heterogeneity of PCV13 against VT pneumococcal nasopharyngeal carriage among hospitalised children in Lao PDR, however individual vaccination with PCV13 was effective against vaccine type carriage.

INTRODUCTION:	Empiric data on indirect (herd) effects of pneumococcal conjugate vaccines (PCVs) in settings with low or heterogeneous PCV coverage are limited. The indirect effects of PCV, which benefits both vaccinated and non-vaccinated individuals, are mediated by reductions in vaccine-type (VT) carriage (a prerequisite for disease). The aim of this study among hospitalised children in Lao People's Democratic Republic (Lao PDR) is to determine the effectiveness of a 13-valent PCV (PCV13) against VT pneumococcal nasopharyngeal carriage (direct effects) and the association between village-level PCV13 coverage and VT carriage (indirect effects).
METHODS:	Pneumococcal nasopharyngeal carriage surveillance commenced in December 2013, shortly after PCV13 introduction (October 2013). We recruited and swabbed children aged 2-59 months admitted to hospital with acute respiratory infection. Pneumococci were detected using *lytA* quantitative real-time PCR and serotyped using microarray. PCV13 status and village-level PCV13 coverage were determined using written immunisation records. Associations between both PCV13 status and village-level PCV13 coverage and VT carriage were calculated using generalised estimating equations, controlling for potential confounders.
RESULTS:	We enrolled 1423 participants and determined PCV13 coverage for 368 villages (269 863 children aged under 5 years). By 2017, median village-level vaccine coverage reached 37.5%, however, the IQR indicated wide variation among villages (24.1-56.4). Both receipt of PCV13 and the level of PCV13 coverage were independently associated with a reduced odds of VT carriage: adjusted PCV13 effectiveness was 38.1% (95% CI 4.1% to 60.0%; p=0.032); and for each per cent increase in PCV13 coverage, the estimated odds of VT carriage decreased by 1.1% (95% CI 0.0% to 2.2%; p=0.056). After adjustment, VT carriage decreased from 20.0% to 12.8% as PCV13 coverage increased from zero to 60% among under 5.
CONCLUSIONS:	Despite marked heterogeneity in PCV13 coverage, we found evidence of indirect effects in Lao PDR. Individual vaccination with PCV13 was effective against VT carriage.

Evaluation strategies for measuring pneumococcal conjugate vaccine impact in low-resource settings. von Mollendorf C, Lim R, Choummanivong M, Sychareun V, Vilivong K, Lai JYR, Chan J, Dunne EM, Phommachanh S, Moore KA, Ortika BD, Gray A, Weaver R, Mayxay M, Phetsouvanh R, Datta SS, Fox K, Newton PN, Mulholland KE, Nguyen CD, Dance DAB, Satzke C, Russell FM. *Expert Rev Vaccines*. 2021 Aug 19:1-9. doi: 10.1080/14760584.2021.1965474. PMID: 34378467.

OBJECTIVES:	Pneumococcal conjugate vaccines (PCVs) are effective in reducing pneumococcal disease. We measured 13-valent PCV (PCV13) effect on different pneumococcal outcomes using diverse studies in Lao People's Democratic Republic.
METHODS:	Studies included: pre-PCV13 population-based record review of hospitalized childhood pneumonia cases; acute respiratory infection (ARI) study post-PCV13 to demonstrate effectiveness (VE) against hypoxic pneumonia; invasive pneumococcal disease (IPD) surveillance in all ages (2004-2018); carriage studies in children hospitalized with ARI (2013-2019); community carriage surveys pre- and post-PCV13.
CONCLUSIONS:	Despite limited baseline data, we found evidence of PCV13 impact on disease and carriage. Our approach could be used in similar settings to augment existing WHO PCV evaluation guidelines.

Ambulatory induction phase treatment of cryptococcal meningitis in HIV integrated primary care clinics, Yangon, Myanmar. Warrell CE, Macrae C, McLean ARD, Wilkins E, Ashley EA, Smithuis F, Tun NN. *BMC Infect Dis*. 2021 Apr 21;21(1):375. doi: 10.1186/s12879-021-06049-z. PMID: 33882845; PMCID: PMC8059000.

BACKGROUND:	Cryptococcal meningitis (CM) is a common HIV-associated opportunistic-infection worldwide. Existing literature focusses on hospital-based outcomes of induction treatment. This paper reviews outpatient management in integrated primary care clinics in Yangon.
METHODS:	This retrospective case note review analyses a Myanmar HIV-positive patient cohort managed using ambulatory induction-phase treatment with intravenous amphotericin-B-deoxycholate (0.7-1.0 mg/kg) and oral fluconazole (800 mg orally/day).

RESULTS:	Seventy-six patients were diagnosed between 2010 and 2017. The median age of patients diagnosed was 35 years, 63% were male and 33 (45%) were on concurrent treatment for tuberculosis. The median CD4 count was 60 at the time of diagnosis. Amphotericin-B-deoxycholate infusions precipitated 56 episodes of toxicity, namely hypokalaemia, nephrotoxicity, anaemia, febrile reactions, phlebitis, observed in 44 patients (58%). One-year survival (86%) was higher than existing hospital-based treatment studies.
CONCLUSION:	Ambulation of patients in this cohort saved 1029 hospital bed days and had better survival outcomes when compared to hospital-based studies in other resource constrained settings.

Virology

The Impact of Preparedness in Defying COVID-19 Pandemic Expectations in the Lower Mekong Region: A Case Study. Corwin A, Plipat T, Phetsouvanh R, Mayxay M, Xangsayarath P, Quynh Mai LT, Oum S, Kuddus MA. *Am J Trop Med Hyg*. 2021 Jan 28;104(4):1519-1525. doi: 10.4269/ajtmh.20-1499. PMID: 33534744; PMCID: PMC8045646.

Dire COVID-19 expectations in the Lower Mekong Region (LMR) can be understood as Cambodia, the Lao PDR, Myanmar, Thailand, and Vietnam have stared down a succession of emerging infectious disease (EID) threats from neighbouring China. Predictions that the LMR would be overwhelmed by a coming COVID-19 tsunami were felt well before the spread of the COVID-19 pandemic had been declared. And yet, the LMR, excepting Myanmar, has proved surprisingly resilient in keeping COVID-19 contained to mostly sporadic cases. Cumulative case rates (per one million population) for the LMR, including or excluding Myanmar, from January 1 to October 31 2020, are 1,184 and 237, respectively. More telling are the cumulative rates of COVID-19-attributable deaths for the same period of time, 28 per million with and six without Myanmar. Graphics demonstrate a flattening of pandemic curves in the LMR, minus Myanmar, after managing temporally and spatially isolated spikes in case counts, with negligible follow-on community spread. The comparable success of the LMR in averting pandemic disaster can likely be attributed to years of preparedness investments, triggered by avian influenza A (H5N1). Capacity building initiatives applied to COVID-19 containment included virological (influenza-driven) surveillance, laboratory diagnostics, field epidemiology training, and vaccine preparation. The notable achievement of the LMR in averting COVID-19 disaster through to October 31, 2020 can likely be credited to these preparedness measures.

Preprints in times of COVID19: the time is ripe for agreeing on terminology and good practices. Ravinetto R, Caillet C, Zaman MH, Singh JA, Guerin PJ, Ahmad A, Durán CE, Jesani A, Palmero A, Merson L, Horby PW, Bottieau E, Hoffmann T, Newton PN. *BMC Med Ethics*. 2021 Jul 28;22(1):106. doi: 10.1186/s12910-021-00667-7. PMID: 34320970; PMCID: PMC8320096.

Over recent years, the research community has been increasingly using preprint servers to share manuscripts that are not yet peer-reviewed. Even if it enables quick dissemination of research findings, this practice raises several challenges in publication ethics and integrity. In particular, preprints have become an important source of information for stakeholders interested in COVID-19 research developments, including traditional media, social media, and policy makers. Despite caveats about their nature, many users can still confuse pre-prints with peer-reviewed manuscripts. If unconfirmed but already widely shared first-draft results later prove wrong or misinterpreted, it can be very difficult to "unlearn" what we thought was true. Complexity further increases if unconfirmed findings have been used to inform guidelines. To help achieve a balance between early access to research findings and its negative consequences, we formulated five recommendations:

(a) consensus should be sought on a term clearer than 'pre-print', such as 'Unrefereed manuscript', "Manuscript awaiting peer review" or ''Non-reviewed manuscript"; (b) Caveats about unrefereed manuscripts should be prominent on their first page, and each page should include a red watermark stating 'Caution-Not Peer Reviewed'; (c) pre-print authors should certify that their manuscript will be submitted to a peer-review journal, and should regularly update the manuscript status; (d) high level consultations should be convened, to formulate clear principles and policies for the publication and dissemination of non-peer reviewed research results; (e) in the longer term, an international initiative to certify servers that comply with good practices could be envisaged.

Awake Proning as an Adjunctive Therapy for Refractory Hypoxemia in Non-Intubated Patients with COVID-19 Acute Respiratory Failure: Guidance from an International Group of Healthcare Workers. Stilma W, Åkerman E, Artigas A, Bentley A, Bos LD, Bosman TJC, de Bruin H, Brummaier T, Buiteman-Kruizinga LA, Carcò F, Chesney G, Chu C, Dark P, Dondorp AM, Gijsbers HJH, Gilder ME, Grieco DL, Inglis R, Laffey JG, Landoni G, Lu W, Maduro LMN, McGready R, McNicholas B, de Mendoza D, Morales-Quinteros L, Nosten F, Papali A, Paternoster G, Paulus F, Pisani L, Prud'homme E, Ricard JD, Roca O, Sartini C, Scaravilli V, Schultz MJ, Sivakorn C, Spronk PE, Sztajnbok J, Trigui Y, Vollman KM, van der Woude MCE. *Am J Trop Med Hyg*. 2021 Mar 11;104(5):1676-1686. doi: 10.4269/ajtmh.20-1445. PMID: 33705348; PMCID: PMC8103477.

Based on advice from international healthcare professionals from high- and low- and middle-income countries (LMICs) with known expertise in awake proning, we provide pragmatic recommendations with indications and contraindications for the use of awake proning in LMICs.

Non-intubated patients with acute respiratory failure due to COVID-19 could benefit from awake proning. Awake proning is an attractive intervention in settings with limited resources, as it comes with no additional costs. However, awake proning remains poorly used probably because of unfamiliarity and uncertainties regarding potential benefits and practical application. To summarize evidence for benefit and to develop a set of pragmatic recommendations for awake proning in patients with COVID-19 pneumonia, focusing on settings where resources are limited, international healthcare professionals from high- and low- and middle-income countries (LMICs) with known expertise in awake proning were invited to contribute expert advice. A growing number of observational studies describe the effects of awake proning in patients with COVID-19 pneumonia in whom hypoxemia is refractory to simple measures of supplementary oxygen. Awake proning improves oxygenation in most patients, usually within minutes, and reduces dyspnea and work of breathing. The effects are maintained for up to 1 hour after turning back to supine, and mostly disappear after 6-12 hours. In available studies, awake proning was not associated with a reduction in the rate of intubation for invasive ventilation. Awake proning comes with little complications if properly implemented and monitored. Pragmatic recommendations including indications and contraindications were formulated and adjusted for resource-limited settings. Awake proning, an adjunctive treatment for hypoxemia refractory to supplemental oxygen, seems safe in non-intubated patients with COVID-19 acute respiratory failure. We provide pragmatic recommendations including indications and contraindications for the use of awake proning in LMICs.

Low seroprevalence of COVID-19 in Lao PDR, late 2020. Virachith S, Pommelet V, Calvez E, Khounvisith V, Sayasone S, Kounnavong S, Maxay M, Xangsayarath P, Temmam S, Eloit M, Escriou N, Rose T, Vongphayloth K, Hübschen JM, Lacoste V, Somlor S, Phonekeo D, Brey PT, Black AP. *Lancet Reg Health West Pac*. 2021 Aug;13:100197. doi: 10.1016/j.lanwpc.2021.100197. Epub 2021 Jul 14. PMID: 34278365; PMCID: PMC8277598.

This SARS-CoV-2 seroprevalence study found no evidence for significant SARS-CoV-2 circulation in Lao PDR before September 2020, probably due to early decisive measures taken by the government, social behavior, and low population density.

BACKGROUND:	In 2020 Lao PDR had low reported COVID-19 cases but it was unclear whether this masked silent transmission. A seroprevalence study was done August - September 2020 to determine SARS-CoV-2 exposure.
METHODS:	Participants were from the general community (n=2433) or healthcare workers (n=666) in five provinces and bat/wildlife contacts (n=74) were from Vientiane province. ELISAs detected anti- SARS-CoV-2 Nucleoprotein (N; n=3173 tested) and Spike (S; n=1417 tested) antibodies. Double-positive samples were checked by IgM/IgG rapid tests. Controls were confirmed COVID-19 cases (n=15) and pre-COVID-19 samples (n=265). Seroprevalence for the general community was weighted to account for complex survey sample design, age and sex.
FINDINGS:	In pre-COVID-19 samples, 5·3%, [95% CI=3·1-8·7%] were anti-N antibody single-positive and 1·1% [0·3-3·5%] were anti-S antibody single positive. None were double positive. Anti-N and anti-S antibodies were detected in 5·2% [4·2-6·5%] and 2·1% [1·1-3·9%] of the general community, 2·0% [1·1-3·3%] and 1·4% [0·5-3·7%] of healthcare workers and 20·3% [12·6-31·0%] and 6·8% [2·8-15·3%] of bat/wildlife contacts. 0·1% [0·02-0·3%] were double positive for anti-N and anti-S antibodies (rapid test negative).
INTERPRETATION:	We find no evidence for significant SARS-CoV-2 circulation in Lao PDR before September 2020. This likely results from early decisive measures taken by the government, social behavior, and low population density. High anti-N / low anti-S seroprevalence in bat/wildlife contacts may indicate exposure to cross-reactive animal coronaviruses with threat of emerging novel viruses.
FUNDING:	Agence Française de Développement. Additional; Institut Pasteur du Laos, Institut Pasteur, Paris and Luxembourg Ministry of Foreign and European Affairs ("PaReCIDS II").

Correction: Doum, D., et al. Dengue Seroprevalence and Seroconversion in Urban and Rural Populations in Northeastern Thailand and Southern Laos. Doum D, Overgaard HJ, Mayxay M, Suttiprapa S, Saichua P, Ekalaksananan T, Tongchai P, Rahman MS, Haque U, Phommachanh S, Pongvongsa T, Rocklöv J, Paul R, Pientong C. *Int. J. Environ. Res. Public Health* 2020, 17, 9134. *Int J Environ Res Public Health*. 2021 Feb 4;18(4):1439. doi: 10.3390/ijerph18041439. Erratum for: Int J Environ Res Public Health. 2020 Dec 07;17(23): PMID: 33557444; PMCID: PMC7913739.

Dengue diagnostic test use to identify *Aedes*-borne disease hotspots. Dubot-Pérès A, Vongsouvath M, Phimolsarnnousith V, Ashley EA, Newton PN. *Lancet Planet Health*. 2021 Aug;5(8):e503. doi: 10.1016/S2542-5196(21)00174-1. PMID: 34390665.

Letter.

Development and Comparison of Dengue Vulnerability Indices Using GIS-Based Multi-Criteria Decision Analysis in Lao PDR and Thailand. Zafar S, Shipin O, Paul RE, Rocklöv J, Haque U, Rahman MS, Mayxay M, Pientong C, Aromseree S, Poolphol P, Pongvongsa T, Vannavong N, Overgaard HJ. *Int J Environ Res Public Health*. 2021 Sep 6;18(17):9421. doi: 10.3390/ijerph18179421. PMID: 34502007; PMCID: PMC8430616.

Dengue is a continuous health burden in Laos and Thailand. We assessed and mapped dengue vulnerability in selected provinces of Laos and Thailand using multi-criteria decision approaches. An ecohealth framework was used to develop dengue vulnerability indices (DVIs) that explain links between population, social and physical environments, and health to identify exposure, susceptibility, and adaptive capacity indicators. Three DVIs were constructed using two objective approaches, Shannon's Entropy (SE) and the Water-Associated Disease Index (WADI), and one subjective approach, the Best-Worst Method (BWM). Each DVI was validated by correlating the index score with dengue incidence for each spatial unit (district and subdistrict) over time. A Pearson's correlation coefficient (r) larger than 0.5 and a p-value less than 0.05 implied a good spatial and temporal performance. Spatially, DVI (WADI) was significantly correlated on average in 19% (4-40%) of districts in Laos (mean r = 0.5) and 27% (15-53%) of subdistricts in Thailand (mean r = 0.85). The DVI (SE) was validated in 22% (12-40%) of districts in Laos and in 13% (3-38%) of subdistricts in Thailand. The DVI (BWM) was only developed for Laos because of lack of data in Thailand and was significantly associated with dengue incidence on average in 14% (0-28%) of Lao districts. The DVI (WADI) indicated high vulnerability in urban centres and in areas with plantations and forests. In 2019, high DVI (WADI) values were observed in sparsely populated areas due to elevated exposure, possibly from changes in climate and land cover, including urbanization, plantations, and dam construction. Of the three indices, DVI (WADI) was the most suitable vulnerability index for the study area. The DVI (WADI) can also be applied to other water-associated diseases, such as Zika and chikungunya, to highlight priority areas for further investigation and as a tool for prevention and interventions.

The impact of African swine fever virus on smallholder village pig production: An outbreak investigation in Lao PDR. Matsumoto N, Siengsanan-Lamont J, Halasa T, Young JR, Ward MP, Douangngeun B, Theppangna W, Khounsy S, Toribio JLML, Bush RD, Blacksell SD. *Transbound Emerg Dis*. 2021 Sep;68(5):2897-2908. doi: 10.1111/tbed.14193. Epub 2021 Jul 7. PMID: 34146447.

An outbreak of African swine fever virus (ASFV), which causes a deadly disease of pigs, was investigated in Lao PDR villages affected in 2019, revealing that ASFV will require increased local government resources, knowledge of informal trader activity and wild boar monitoring alongside education and support to address intra-village risk factors such as free-ranging, incorrect waste disposal and swill feeding.

African swine fever virus (ASFV) causes a deadly disease of pigs which spread through southeast Asia in 2019. We investigated one of the first outbreaks of ASFV in Lao People's Democratic Republic amongst smallholder villages of Thapangtong District, Savannakhet Province. In this study, two ASFV affected villages were compared to two unaffected villages. Evidence of ASFV-like clinical signs appeared in pig herds as early as May 2019, with median epidemic days on 1 and 18 June in the two villages, respectively. Using participatory epidemiology mapping techniques, we found statistically significant spatial clustering in both outbreaks ($p < 0.001$). Villagers reported known risk factors for ASFV transmission - such as free-ranging management systems and wild boar access - in all four villages. The villagers reported increased pig trader activity from Vietnam before the outbreaks; however, the survey did not determine a single outbreak source. The outbreak caused substantial household financial losses with an average of nine pigs lost to the disease, and Monte Carlo analysis estimated this to be USD 215 per household. ASFV poses a significant threat to food and financial security in smallholder communities such as Thapangtong, where 40.6% of the district's population are affected by poverty. This study shows ASFV management in the region will require increased local government resources, knowledge of informal trader activity and wild boar monitoring alongside education and support to address intra-village risk factors such as free-ranging, incorrect waste disposal and swill feeding.

Seroepidemiology of Foot and Mouth Disease using passive surveillance techniques in selected provinces of Lao PDR. Siengsanan-Lamont J, Douangngeun B, Theppangna W, Khounsy S, Phommachanh P, Kamolsiripichaiporn S, Udon R, Seeyo KB, Selleck PW, Matsumoto N, Gleeson LJ, Blacksell SD. *Trop Anim Health Prod*. 2021 May 2;53(2):303. doi: 10.1007/s11250-021-02734-y. PMID: 33934210; PMCID: PMC8088427.

Foot and Mouth Disease (FMD) is a high-impact, contagious transboundary animal disease that is endemic in Southeast Asia. Abattoir samples were routinely collected in six selected provinces between March and December 2019. A total of 1280 samples of abattoir animals were tested for FMD Non-Structural Protein (NSP) antibodies to indicate natural infections. Overall, 22.8% were seropositive for FMD NSP antibodies while seroprevalence of cattle (n = 469), buffalo (n = 214), and pigs (n = 597) were 44.6%, 35.0%, and 1.3%, respectively. The highest seroprevalence destination province was Xiengkhouang (35.3% of 272 samples), followed by Savannakhet (27.0% of 244 samples). Risk factors for evidence of natural infection identified by a multivariate logistic regression model included age groups (p-value = 0.02) and origin provinces (p-value = 2.8 × 10(-5)) of the animals. There were significant differences of FMD NSP seroprevalence between age groups and origin provinces of the animals. The odds ratio of a seropositive result in the less than 1 year old group was 2.5 (95% CI; 1.4, 4.4) when compared to the 3-4 years old group, while the odds ratios for animals that originated from Khammouane and Xiengkhouang provinces were 4.5 (95% CI; 1.1, 18.7) and 2.4 (95% CI; 1.4, 4.1), respectively, when compared to Champasak province. Serotype-specific antibody ELISA for 44 NSP antibody-positive samples revealed evidence of FMD serotypes O and A virus circulation in some provinces. Despite the passive abattoir survey providing useful information on FMD virus previous exposure and geographic locations of the animals, timely information on FMD virus circulation and distribution is also crucial to an effective control program. Alternative approaches to increase the cost-effectiveness of the surveillance network are also discussed.

Malaria

An open dataset of *Plasmodium falciparum* genome variation in 7,000 worldwide samples. MalariaGEN, Ahouidi A, Ali M, Almagro-Garcia J, Amambua-Ngwa A, Amaratunga C, Amato R, Amenga-Etego L, Andagalu B, Anderson TJC, Andrianaranjaka V, Apinjoh T, Ariani C, Ashley EA, Auburn S, Awandare GA, Ba H, Baraka V, Barry AE, Bejon P, Bertin GI, Boni MF, Borrmann S, Bousema T, Branch O, Bull PC, Busby GBJ, Chookajorn T, Chotivanich K, Claessens A, Conway D, Craig A, D'Alessandro U, Dama S, Day NP, Denis B, Diakite M, Djimdé A, Dolecek C, Dondorp AM, Drakeley C, Drury E, Duffy P, Echeverry DF, Egwang TG, Erko B, Fairhurst RM, Faiz A, Fanello CA, Fukuda MM, Gamboa D, Ghansah A, Golassa L, Goncalves S, Hamilton WL, Harrison GLA, Hart L, Henrichs C, Hien TT, Hill CA, Hodgson A, Hubbart C, Imwong M, Ishengoma DS, Jackson SA, Jacob CG, Jeffery B, Jeffreys AE, Johnson KJ, Jyothi D, Kamaliddin C, Kamau E, Kekre M, Kluczynski K, Kochakarn T, Konaté A, Kwiatkowski DP, Kyaw MP, Lim P, Lon C, Loua KM, Maïga-Ascofaré O, Malangone C, Manske M, Marfurt J, Marsh K, Mayxay M, Miles A, Miotto O, Mobegi V, Mokuolu OA, Montgomery J, Mueller I, Newton PN, Nguyen T, Nguyen TN, Noedl H, Nosten F, Noviyanti R, Nzila A, Ochola-Oyier LI, Ocholla H, Oduro A, Omedo I, Onyamboko MA, Ouedraogo JB, Oyebola K, Pearson RD, Peshu N, Phyo AP, Plowe CV, Price RN, Pukrittayakamee S, Randrianarivelojosia M, Rayner JC, Ringwald P, Rockett KA, Rowlands K, Ruiz L, Saunders D, Shayo A, Siba P, Simpson VJ, Stalker J, Su XZ, Sutherland C, Takala-Harrison S, Tavul L, Thathy V, Tshefu A, Verra F, Vinetz J, Wellems TE, Wendler J, White NJ, Wright I, Yavo W, Ye H. *Wellcome Open Res*. 2021 Jul 13;6:42. doi: 10.12688/wellcomeopenres.16168.2. PMID: 33824913; PMCID: PMC8008441.

This paper reports curated genome variation data on 7,000 Plasmodium falciparum samples from MalariaGEN partner studies in 28 malaria-endemic countries.

MalariaGEN is a data-sharing network that enables groups around the world to work together on the genomic epidemiology of malaria. Here we describe a new release of curated genome variation data on 7,000 *Plasmodium falciparum* samples from MalariaGEN partner studies in 28 malaria-endemic countries. High-quality genotype calls on 3 million single nucleotide polymorphisms (SNPs) and short indels were produced using a standardised analysis pipeline. Copy number variants associated with drug resistance and structural variants that cause failure of rapid diagnostic tests were also analysed. Almost all samples showed genetic evidence of resistance to at least one antimalarial drug, and some samples from Southeast Asia carried markers of resistance to six commonly-used drugs. Genes expressed during the mosquito stage of the parasite life-cycle are prominent among loci that show strong geographic differentiation. By continuing to enlarge this open data resource we aim to facilitate research into the evolutionary processes affecting malaria control and to accelerate development of the surveillance toolkit required for malaria elimination.

A Comparison of Surface and Total Deltamethrin Levels of Insecticide-Treated Nets and Estimation of the Effective Insecticidal Lifetime. Green M, Mayxay M, Pongvongsa T, Phompida S, Swamidoss I, Smith S, Irish S, Newton P. *Am J Trop Med Hyg*. 2021 Nov 15;106(1):334-337. doi: 10.4269/ajtmh.21-0144. PMID: 34781252; PMCID: PMC8733494.

The ability to anticipate the useful lifetime of an insecticide-treated mosquito net (ITN) would provide a proactive approach for planning net distribution programs. Therefore, we used an exponential decay model of deltamethrin depletion to predict the effective insecticidal lifetime of PermaNet® 2.0 nets used in the Lao PDR. Residual deltamethrin was measured using two nondestructive analytical field methods; X-ray fluorescence (total levels) and a colorimetric field test (surface levels) at 12 and 24 months postdistribution. The model assumes that the 12-month depletion rate can be used to predict future levels. The median total and surface deltamethrin levels for the Lao nets at 12 months were 31.2 and 0.0743 mg/m2, respectively. By defining a failed net as having total deltamethrin levels of less than 15 mg/m2 or a surface level less than 0.0028 mg/m2, it was predicted that 50% of the group of nets will fail at about 27 months after distribution.

Genetic surveillance in the Greater Mekong subregion and South Asia to support malaria control and elimination. Jacob CG, Thuy-Nhien N, Mayxay M, Maude RJ, Quang HH, Hongvanthong B, Vanisaveth V, Ngo Duc T, Rekol H, van der Pluijm R, von Seidlein L, Fairhurst R, Nosten F, Hossain MA, Park N, Goodwin S, Ringwald P, Chindavongsa K, Newton P, Ashley E, Phalivong S, Maude R, Leang R, Huch C, Dong LT, Nguyen KT, Nhat TM, Hien TT, Nguyen H, Zdrojewski N, Canavati S, Sayeed AA, Uddin D, Buckee C, Fanello CI, Onyamboko M, Peto T, Tripura R, Amaratunga C, Myint Thu A, Delmas G, Landier J, Parker DM, Chau NH, Lek D, Suon S, Callery J, Jittamala P, Hanboonkunupakarn B, Pukrittayakamee S, Phyo AP, Smithuis F, Lin K, Thant M, Hlaing TM, Satpathi P, Satpathi S, Behera PK, Tripura A, Baidya S, Valecha N, Anvikar AR, Ul Islam A, Faiz A, Kunasol C, Drury E, Kekre M, Ali M, Love K, Rajatileka S, Jeffreys AE, Rowlands K, Hubbart CS, Dhorda M, Vongpromek R, Kotanan N, Wongnak P, Almagro Garcia J, Pearson RD, Ariani CV, Chookajorn T, Malangone C, Nguyen T, Stalker J, Jeffery B, Keatley J, Johnson KJ, Muddyman D, Chan XHS, Sillitoe J, Amato R, Simpson V, Gonçalves S, Rockett K, Day NP, Dondorp AM, Kwiatkowski DP, Miotto O. *Elife*. 2021 Aug 10;10:e62997. doi: 10.7554/eLife.62997. PMID: 34372970; PMCID: PMC8354633.

The new GenRe-Mekong platform for genetic surveillance of malaria in the Greater Mekong Subregion provides detailed knowledge about local level drug resistance, facilitates regional data sharing and monitoring of resistant strains spreading to help decision-making by NMCPs.

BACKGROUND:	National Malaria Control Programmes (NMCPs) currently make limited use of parasite genetic data. We have developed GenRe-Mekong, a platform for genetic surveillance of malaria in the Greater Mekong Subregion (GMS) that enables NMCPs to implement large-scale surveillance projects by integrating simple sample collection procedures in routine public health procedures.
METHODS:	Samples from symptomatic patients are processed by SpotMalaria, a high-throughput system that produces a comprehensive set of genotypes comprising several drug resistance markers, species markers and a genomic barcode. GenRe-Mekong delivers Genetic Report Cards, a compendium of genotypes and phenotype predictions used to map prevalence of resistance to multiple drugs.

RESULTS:	GenRe-Mekong has worked with NMCPs and research projects in eight countries, processing 9623 samples from clinical cases. Monitoring resistance markers has been valuable for tracking the rapid spread of parasites resistant to the dihydroartemisinin-piperaquine combination therapy. In Vietnam and Laos, GenRe-Mekong data have provided novel knowledge about the spread of these resistant strains into previously unaffected provinces, informing decision-making by NMCPs.
CONCLUSIONS:	GenRe-Mekong provides detailed knowledge about drug resistance at a local level, and facilitates data sharing at a regional level, enabling cross-border resistance monitoring and providing the public health community with valuable insights. The project provides a rich open data resource to benefit the entire malaria community.
FUNDING:	The GenRe-Mekong project is funded by the Bill and Melinda Gates Foundation (OPP11188166, OPP1204268). Genotyping and sequencing were funded by the Wellcome Trust (098051, 206194, 203141, 090770, 204911, 106698/B/14/Z) and Medical Research Council (G0600718). A proportion of samples were collected with the support of the UK Department for International Development (201900, M006212), and Intramural Research Program of the National Institute of Allergy and Infectious Diseases.

Clustering of malaria in households in the Greater Mekong Subregion: operational implications for reactive case detection. Mukaka M, Peerawaranun P, Parker DM, Kajeechiwa L, Nosten FH, Nguyen TN, Hien TT, Tripura R, Peto TJ, Phommasone K, Mayxay M, Newton PN, Imwong M, Day NPJ, Dondorp AM, White NJ, von Seidlein L. *Malar J*. 2021 Aug 26;20(1):351. doi: 10.1186/s12936-021-03879-9. PMID: 34446009; PMCID: PMC8393740.

Malaria reactive case detection (the testing and, if positive, treatment of close contacts of index case) was evaluated in the Greater Mekong subregion, with results suggesting that it has a negligible impact on the malaria burden but implies substantial costs in terms of human and financial resources.

BACKGROUND:	Malaria reactive case detection is the testing and, if positive, treatment of close contacts of index cases. It is included in national malaria control programmes of countries in the Greater Mekong Subregion to accelerate malaria elimination. Yet the value of reactive case detection in the control and elimination of malaria remains controversial because of the low yield, limited evidence for impact, and high demands on resources.
METHODS:	Data from the epidemiological assessments of large mass drug administration (MDA) studies in Myanmar, Vietnam, Cambodia and Laos were analysed to explore malaria infection clustering in households. The proportion of malaria positive cases among contacts screened in a hypothetical reactive case detection programme was then determined. The parasite density thresholds for rapid diagnostic test (RDT) detection was assumed to be > 50/µL (50,000/mL), for dried-blood-spot (DBS) based PCR > 5/µL (5000/mL), and for ultrasensitive PCR (uPCR) with a validated limit of detection at 0.0022/µL (22/mL).
RESULTS:	At baseline, before MDA, 1223 *Plasmodium* infections were detected uPCR in 693 households. There was clustering of *Plasmodium* infections. In 637 households with asymptomatic infections 44% (278/637) had more than one member with *Plasmodium* infections. In the 132 households with symptomatic infections, 65% (86/132) had more than one member with *Plasmodium* infections. At baseline 4% of households had more than one *Plasmodium falciparum* infection, but three months after MDA no household had more than one *P. falciparum* infected member. Reactive case detection using DBS PCR would have detected ten additional cases in six households, and an RDT screen would have detected five additional cases in three households among the 169 households with at least one RDT positive case. This translates to 19 and 9 additional cases identified per 1000 people screened, respectively. Overall, assuming all febrile RDT positive patients would seek treatment and provoke reactive case detection using RDTs, then 1047 of 1052 (99.5%) *Plasmodium* infections in these communities would have remained undetected.
CONCLUSIONS:	Reactive case detection in the Greater Mekong subregion is predicted to have a negligible impact on the malaria burden, but it has substantial costs in terms of human and financial resources.

Development of weight and age-based dosing of daily primaquine for radical cure of vivax malaria. Taylor WR, Hoglund RM, Peerawaranun P, Nguyen TN, Hien TT, Tarantola A, von Seidlein L, Tripura R, Peto TJ, Dondorp AM, Landier J, H Nosten F, Smithuis F, Phommasone K, Mayxay M, Kheang ST, Say C, Neeraj K, Rithea L, Dysoley L, Kheng S, Muth S, Roca-Feltrer A, Debackere M, Fairhurst RM, Song N, Buchy P, Menard D, White NJ, Tarning J, Mukaka M. *Malar J*. 2021 Sep 9;20(1):366. doi: 10.1186/s12936-021-03886-w. PMID: 34503519; PMCID: PMC8427859.

This study proposes 14-day weight-based (5 dosing bands) and age-based (4 dosing bands) primaquine regimens against high-frequency relapsing tropical P. vivax; the weight-based is the preferred regimen, as it showed less dose variability compared to the age-based regimen. Pharmacokinetic data in small children are urgently needed.

BACKGROUND:	Malaria reactive case detection is the testing and, if positive, treatment of close contacts of index cases. It is included in national malaria control programmes of countries in the Greater Mekong Subregion to accelerate malaria elimination. Yet the value of reactive case detection in the control and elimination of malaria remains controversial because of the low yield, limited evidence for impact, and high demands on resources.
METHODS:	The recommended adult target dose of 0.5 mg/kg/day (30 mg in a 60 kg patient) is highly efficacious against tropical *P. vivax* and was assumed to produce optimal drug exposure. Primaquine doses were calculated using allometric scaling to derive a weight-based primaquine regimen over a weight range from 5 to 100 kg. Growth curves were constructed from an anthropometric database of 53,467 individuals from the Greater Mekong Subregion (GMS) to define weight-for-age relationships. The median age associated with each weight was used to derive an age-based dosing regimen from the weight-based regimen.

RESULTS:	The proposed weight-based regimen has 5 dosing bands: (i) 5-7 kg, 5 mg, resulting in 0.71-1.0 mg/kg/day; (ii) 8-16 kg, 7.5 mg, 0.47-0.94 mg/kg/day; (iii) 17-40 kg, 15 mg, 0.38-0.88 mg/kg/day; (iv) 41-80 kg, 30 mg, 0.37-0.73 mg/kg/day; and (v) 81-100 kg, 45 mg, 0.45-0.56 mg/kg/day. The corresponding age-based regimen had 4 dosing bands: 6-11 months, 5 mg, 0.43-1.0 mg/kg/day; (ii) 1-5 years, 7.5 mg, 0.35-1.25 mg/kg/day; (iii) 6-14 years, 15 mg, 0.30-1.36 mg/kg/day; and (iv) ≥ 15 years, 30 mg, 0.35-1.07 mg/kg/day.
CONCLUSIONS:	The proposed weight-based regimen showed less variability around the primaquine dose within each dosing band compared to the age-based regimen and is preferred. Increased dose accuracy could be achieved by additional dosing bands for both regimens. The age-based regimen might not be applicable to regions outside the GMS, which must be based on local anthropometric data. Pharmacokinetic data in small children are needed urgently to inform the proposed regimens.

Non-malaria febrile illness

Prediction of disease severity in young children presenting with acute febrile illness in resource-limited settings: a protocol for a prospective observational study. Chandna A, Aderie EM, Ahmad R, Arguni E, Ashley EA, Cope T, Dat VQ, Day NPJ, Dondorp AM, Illanes V, De Jesus J, Jimenez C, Kain K, Suy K, Koshiaris C, Lasry E, Mayxay M, Mondal D, Perera R, Pongvongsa T, Rattanavong S, Rekart M, Richard-Greenblatt M, Shomik M, Souvannasing P, Tallo V, Turner C, Turner P, Waithira N, Watson JA, Yosia M, Burza S, Lubell Y. *BMJ Open*. 2021 Jan 25;11(1):e045826. doi: 10.1136/bmjopen-2020-045826. PMID: 33495264; PMCID: PMC7839891.

This proposed prospective observational study aims to develop a prognostic clinical prediction tool to assist community healthcare providers identify febrile children who might benefit from referral or admission for facility-based medical care.

INTRODUCTION:	In rural and difficult-to-access settings, early and accurate recognition of febrile children at risk of progressing to serious illness could contribute to improved patient outcomes and better resource allocation. This study aims to develop a prognostic clinical prediction tool to assist community health-care providers identify febrile children who might benefit from referral or admission for facility-based medical care.
METHODS AND ANALYSIS:	This prospective observational study will recruit at least 4900 paediatric inpatients and outpatients under the age of 5 years presenting with an acute febrile illness to seven hospitals in six countries across Asia. A venous blood sample and nasopharyngeal swab is collected from each participant and detailed clinical data recorded at presentation, and each day for the first 48 hours of admission for inpatients. Multianalyte assays are performed at reference laboratories to measure a panel of host biomarkers, as well as targeted aetiological investigations for common bacterial and viral pathogens. Clinical outcome is ascertained on day 2 and day 28. Presenting syndromes, clinical outcomes and aetiology of acute febrile illness will be described and compared across sites. Following the latest guidance in prediction model building, a prognostic clinical prediction model, combining simple clinical features and measurements of host biomarkers, will be derived and geographically externally validated. The performance of the model will be evaluated in specific presenting clinical syndromes and fever aetiologies.

ETHICS AND DISSEMINATION:	The study has received approval from all relevant international, national and institutional ethics committees. Written informed consent is provided by the caretaker of all participants. Results will be shared with local and national stakeholders, and disseminated via peer-reviewed open-access journals and scientific meetings. TRIAL REGISTRATION NUMBER: NCT04285021.

Anticipating the future: prognostic tools as a complementary strategy to improve care for patients with febrile illnesses in resource-limited settings. Chandna A, Osborn J, Bassat Q, Bell D, Burza S, D'Acremont V, Fernandez-Carballo BL, Kain KC, Mayxay M, Wiens M, Dittrich S. *BMJ Glob Health*. 2021 Jul;6(7):e006057. doi: 10.1136/bmjgh-2021-006057. PMID: 34330761; PMCID: PMC8327814.

In low-income and middle-income countries, most patients with febrile illnesses present to peripheral levels of the health system where diagnostic capacity is very limited. In these contexts, accurate risk stratification can be particularly impactful, helping to guide allocation of scarce resources to ensure timely and tailored care. However, reporting of prognostic research is often imprecise and few prognostic tests or algorithms are translated into clinical practice. Here, we review the often-conflated concepts of prognosis and diagnosis, with a focus on patients with febrile illnesses. Drawing on a recent global stakeholder consultation, we apply these concepts to propose three use-cases for prognostic tools in the management of febrile illnesses in resource-limited settings: (1) guiding referrals from the community to higher-level care; (2) informing resource allocation for patients admitted to hospital and (3) identifying patients who may benefit from closer follow-up post-hospital discharge. We explore the practical implications for new technologies and reflect on the challenges and knowledge gaps that must be addressed before this approach could be incorporated into routine care settings. Our intention is that these use-cases, alongside other recent initiatives, will help to promote a harmonised yet contextualised approach for prognostic research in febrile illness. We argue that this is especially important given the heterogeneous settings in which care is often provided for patients with febrile illnesses living in low-income and middle-income countries.

Defining the burden of febrile illness in rural South and Southeast Asia: an open letter to announce the launch of the Rural Febrile Illness project. Chandna A, Chew R, Shwe Nwe Htun N, Peto TJ, Zhang M, Liverani M, Brummaier T, Phommasone K, Perrone C, Pyae Phyo A, Sattabongkot J, Roobsoong W, Nguitragool W, Sen A, Ibna Zaman S, Sandar Zaw A, Batty E, Waithira N, Abdad MY, Blacksell SD, Bodhidatta L, Callery JJ, Fagnark W, Huangsuranun W, Islam S, Lertcharoenchoke S, Lohavittayavikant S, Mukaka M, Moul V, Kumer Neogi A, Nedsuwan S, Pongvongsa T, Ponsap P, Richard-Greenblatt M, Schilling WHK, Thaipadungpanit J, Tripura R, Dondorp AM, Mayxay M, White NJ, Nosten F, Smithuis F, Ashley EA, Maude RJ, Day NPJ, Lubell Y. *Wellcome Open Res*. 2022 Mar 10;6:64. doi: 10.12688/wellcomeopenres.16393.2. PMID: 34017924; PMCID: PMC8080974.

This Open Letter announces the start of the new multi-country, multi-site Rural Febrile Illness (RFI) project to be implemented as part of the South and Southeast Asian Community-based Trials Network (SEACTN) research programme to define the epidemiological baseline of febrile illness and the role of VHWs in five remote and underserved areas of Asia where malaria endemicity is declining and access to health services is limited.

In rural areas of South and Southeast Asia malaria is declining but febrile illnesses still account for substantial morbidity and mortality. Village health workers (VHWs) are often the first point of contact with the formal health system, and for patients with febrile illnesses they can provide early diagnosis and treatment of malaria. However, for the majority of febrile patients, VHWs lack the training, support and resources to provide further care. Consequently, treatable bacterial illnesses are missed, antibiotics are overused and poorly targeted, and patient attendance wanes along with declining malaria. This Open Letter announces the start of a new initiative, the Rural Febrile Illness (RFI) project, the first in a series of projects to be implemented as part of the South and Southeast Asian Community-based Trials Network (SEACTN) research programme. This multi-country, multi-site project will begin in Bangladesh, Cambodia, Lao PDR, and Myanmar and will define the epidemiological baseline of febrile illness in five remote and underserved areas of Asia where malaria endemicity is declining and access to health services is limited. The RFI project aims to determine the incidence, causes and outcomes of febrile illness; understand the opportunities, barriers and appetite for adjustment of the role of VHWs to include management of non-malarial febrile illnesses; and establish a network of community healthcare providers and facilities capable of implementing interventions designed to triage, diagnose and treat patients presenting with febrile illnesses within these communities in the future.

Inter-prescriber variability in the decision to prescribe antibiotics to febrile patients attending primary care in Myanmar. Swe MMM, Ashley EA, Althaus T, Lubell Y, Smithuis F, Mclean ARD. *JAC Antimicrob Resist*. 2021 Jan 19;3(1):dlaa118. doi: 10.1093/jacamr/dlaa118. PMID: 33506197; PMCID: PMC7814214.

This study quantified prescriber variability in antibiotic prescription to patients with acute fever in primary care clinics in Myanmar; results showed there was substantial inter-prescriber variation, to be considered when designing trials and stewardship programmes aiming to reduce inappropriate antibiotic prescribing.

BACKGROUND:	Most antibiotic prescribing occurs in primary care. Even within the same health facility, there may be differences between prescribers in their tendency to prescribe antibiotics, which may be masked by summary data. We aimed to quantify prescriber variability in antibiotic prescription to patients with acute fever in primary care clinics in Myanmar.
METHODS:	We conducted a secondary analysis of prescribing data from 1090 patient consultations with 40 prescribing doctors from a trial investigating the effect of point-of-care C-reactive protein (CRP) tests on antibiotic prescription for acute fever. We used multilevel logistic regression models to assess inter-prescriber variability in the decision to prescribe antibiotics.
RESULTS:	The median odds ratio (MOR) in the unadjusted model was 1.82 (95% CI: 1.47-2.56) indicating that when two prescribers from this population are randomly selected then in half of these pairs the odds of prescription will be greater than 1.82-fold higher in one prescriber than the other. The estimated variability from this sample of prescribers corresponds to a population of prescribers where the top 25% of prescribers will prescribe antibiotics to over 41% of patients while the bottom 25% will prescribe antibiotics to less than 23% of patients. Inter-prescriber variation in antibiotic prescribing remained after adjustment for patient characteristics and CRP information ($P < 0.001$).
CONCLUSIONS:	Despite sharing the same management guidelines, there was substantial inter-prescriber variation in antibiotic prescription to patients with acute fever. This variation should be considered when designing trials and stewardship programmes aiming to reduce inappropriate antibiotic prescribing.

Medicine Quality

Sounding out falsified medicines from genuine medicines using Broadband Acoustic Resonance Dissolution Spectroscopy (BARDS). Alfarsi A, Caillet C, Fawbert G, Lawrence S, Krüse J, McSweeney S, O'Mahony M, Dondorp A, Newton PN, Fitzpatrick D. *Sci Rep*. 2021 Jun 16;11(1):12643. doi: 10.1038/s41598-021-90323-2. PMID: 34135361; PMCID: PMC8209214.

Lao PDR has played a leading role in medicine quality research globally. This paper assessed BARDS (Broadband Acoustic Resonance Dissolution Spectroscopy) as a method to quickly determine whether medicine products in the form of tablets and capsules were falsified or genuine, demonstrating its usefulness to screen the quality of medicines.

The trade in falsified medicine has increased significantly and it is estimated that global falsified sales have reached $100 billion in 2020. The EU Falsified Medicines Directive states that falsified medicines do not only reach patients through illegal routes but also via the legal supply chain. Falsified medicines can contain harmful ingredients. They can also contain too little or too much active ingredient or no active ingredient at all. BARDS (Broadband Acoustic Resonance Dissolution Spectroscopy) harnesses an acoustic phenomenon associated with the dissolution of a sample (tablet or powder). The resulting acoustic spectrum is unique and intrinsic to the sample and can be used as an identifier or signature profile. BARDS was evaluated in this study to determine whether a product is falsified or genuine in a rapid manner and at lower cost than many existing technologies. A range of genuine and falsified medicines, including falsified antimalarial tablets from south-east Asia, were tested, and compared to their counterpart genuine products. Significant differences between genuine and falsified doses were found in their acoustic signatures as they disintegrate and dissolve. Principal component analysis was employed to differentiate between the genuine and falsified medicines. This demonstrates that the tablets and capsules included here have intrinsic acoustic signatures which could be used to screen the quality of medicines.

Evaluation of portable devices for medicine quality screening: Lessons learnt, recommendations for implementation, and future priorities. Caillet C, Vickers S, Vidhamaly V, Boutsamay K, Boupha P, Zambrzycki S, Luangasanatip N, Lubell Y, Fernández FM, Newton PN. *PLoS Med*. 2021 Sep 30;18(9):e1003747. doi: 10.1371/journal.pmed.1003747. PMID: 34591861; PMCID: PMC8483386.

Céline Caillet and co-authors discuss a Collection on use and legitimacy for the evaluation of medicine quality.

A comparative field evaluation of six medicine quality screening devices in Laos. Caillet C, Vickers S, Zambrzycki S, Fernández FM, Vidhamaly V, Boutsamay K, Boupha P, Peerawaranun P, Mukaka M, Newton PN. *PLoS Negl Trop Dis*. 2021 Sep 30;15(9):e0009674. doi: 10.1371/journal.pntd.0009674. PMID: 34591852; PMCID: PMC8483322.

Lao PDR has continued to play a leading role in medicine quality research globally. This Laotian pilot study, which tested six devices' utility and usability in detecting substandard and falsified medicines, cautions that overconfidence in devices may cause harm by reducing inspectors' investment in visual inspection and provides insight into devices' advantages and limitations.

BACKGROUND:	Medicine quality screening devices hold great promise for post-market surveillance (PMS). However, there is little independent evidence on their field utility and usability to inform policy decisions. This pilot study in the Lao PDR tested six devices' utility and usability in detecting substandard and falsified (SF) medicines.

METHODOLOGY/ PRINCIPAL FINDINGS:	Observational time and motion studies of the inspections by 16 Lao medicine inspectors of 1) the stock of an Evaluation Pharmacy (EP), constructed to resemble a Lao pharmacy, and 2) a sample set of medicines (SSM); were conducted without and with six devices: four handheld spectrometers (two near infrared: MicroPHAZIR RX, NIR-S-G1 & two Raman: Progeny, Truscan RM); one portable mid-infrared spectrometer (4500a), and single-use paper analytical devices (PAD). User experiences were documented by interviews and focus group discussions. Significantly more samples were wrongly categorised as pass/fail with the PAD compared to the other devices in EP inspections ($p<0.05$). The numbers of samples wrongly classified in EP inspections were significantly lower than in initial visual inspections without devices for 3/6 devices (NIR-S-G1, MicroPHAZIR RX, 4500a). The NIR-S-G1 had the fastest testing time per sample (median 93.5 sec, $p<0.001$). The time spent on EP visual inspection was significantly shorter when using a device than for inspections without devices, except with the 4500a, risking missing visual clues of samples being SF. The main user errors were the selection of wrong spectrometer reference libraries and wrong user interpretation of PAD results. Limitations included repeated inspections of the EP by the same inspectors with different devices and the small sample size of SF medicines.
CONCLUSIONS/ SIGNIFICANCE:	This pilot study suggests policy makers wishing to implement portable screening devices in PMS should be aware that overconfidence in devices may cause harm by reducing inspectors' investment in visual inspection. It also provides insight into the advantages/limitations of diverse screening devices in the hands of end-users.

Multiphase evaluation of portable medicines quality screening devices. Caillet C, Vickers S, Zambrzycki S, Luangasanatip N, Vidhamaly V, Boutsamay K, Boupha P, Lubell Y, Fernández FM, Newton PN. *PLoS Negl Trop Dis*. 2021 Sep 30;15(9):e0009287. doi: 10.1371/journal.pntd.0009287. PMID: 34591864; PMCID: PMC8483331.

An introduction to a multiphase, collaborative multicountry study in the PLOS Collection, "A multiphase evaluation of portable screening devices to assess medicines quality for national Medicines Regulatory Authorities," conducted between 2016 and 2018 as part of the Results for Malaria Elimination and Communicable Diseases Control (RECAP) under the Regional Malaria and Communicable Disease Trust Fund (RMTF) at the Asian Development Bank. (see Research Highlights)

The quality of medical products for cardiovascular diseases: a gap in global cardiac care. Do NT, Bellingham K, Newton PN, Caillet C. *BMJ Glob Health*. 2021 Sep;6(9):e006523. doi: 10.1136/bmjgh-2021-006523. PMID: 34521627; PMCID: PMC8442059.

This literature of substandard and falsified (SF) cardiovascular medicines/devices suggest that SF cardiovascular products are likely to be a serious public health problem that has received limited attention and highlight the need for more research.

OBJECTIVE:	Good quality cardiovascular medicines and devices are crucial in the prevention and management of the ever-growing threats of cardiovascular diseases (CVDs) globally. Yet our current understanding of the extent and impact of substandard and falsified (SF) cardiovascular medical products is poor. Our objective was to review the available literature on SF cardiovascular medicines/devices, with a focus on prevalence studies to discuss their impacts on public health.

METHODS:	Searches were conducted in Embase, PubMed, Web of Science, Google Scholar, Google and websites with interest in medicines/devices quality up to 31 August 2020. Articles in English and French identified in these searches were screened for eligibility. The Medicine Quality Assessment Reporting Guidelines was used to assess the quality of prevalence surveys, and we report according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses statement.
RESULTS:	A total of 279 articles were included, which were subcategorised into prevalence surveys (n=28), equivalence studies (n=118), stability studies (n=5), routine quality control analyses (n=15), bioavailability studies (n=2), recalls/ seizures/case reports (n=77), general discussions (n=24) and reviews (n=10). A failure frequency (defined as the proportion of samples that failed at least one quality test described in the report) of 525 (15.4%) was observed for the 3414 samples tested for quality in the 27 prevalence surveys with sufficient information for inclusion in our quantitative analysis. Nineteen surveys (70.4%) used convenience outlet sampling. The majority (88.8%, 3032/3414) of samples included in prevalence surveys were collected from low-income and middle-income countries. The most common defects were out-of-specification active ingredient(s) content, impurity/contaminant content and impaired dissolution. We found 26 incidents describing SF cardiovascular devices with 181 related deaths but no prevalence surveys.
CONCLUSIONS:	The data suggest that SF cardiovascular products are likely to be a serious public health problem that has received limited attention. We do not suggest that 15.4% of cardiovascular medicines are SF, and our findings highlight the need for more research with robust methodology to provide more accurate prevalence estimates in order to inform policy and implement measures to ensure the quality of cardiovascular medicines and devices within the supply chain. Ensuring that CVD medical products are of good quality would help ensure effectiveness and that the benefits of therapy are realised in the prevention and treatment of CVDs.

Implementation of field detection devices for antimalarial quality screening in Lao PDR-A cost-effectiveness analysis. Luangasanatip N, Khonputsa P, Caillet C, Vickers S, Zambrzycki S, Fernández FM, Newton PN, Lubell Y. *PLoS Negl Trop Dis*. 2021 Sep 30;15(9):e0009539. doi: 10.1371/journal.pntd.0009539. PMID: 34591842; PMCID: PMC8483304.

This study evaluated cost effectiveness of introducing medicine quality screening devices in post-market surveillance in pharmacies in Lao PDR focusing on their outcome in detecting SF ACTs, which was shown to be likely cost-effective in the Laos context.

Substandard and falsified (SF) antimalarials have devastating consequences including increased morbidity, mortality and economic losses. Portable medicine quality screening devices are increasingly available, but whether their use for the detection of SF antimalarials is cost-effective is not known. We evaluated the cost-effectiveness of introducing such devices in post-market surveillance in pharmacies in Laos, conservatively focusing on their outcome in detecting SF artemisinin-based combination therapies (ACTs). We simulated the deployment of six portable screening devices: two handheld near-infrared [MicroPHAZIR RX, NIR-S-G1], two handheld Raman [Progeny, TruScan RM]; one portable mid-infrared [4500a FTIR] spectrometers, and single-use disposable paper analytical devices [PADs]. We considered two scenarios with high and low levels of SF ACTs. Different sampling strategies in which medicine inspectors would test 1, 2, or 3 sample(s) of each brand of ACT were evaluated. Costs of inspection including device procurement, inspector time, reagents, reference testing, and replacement with genuine ACTs were estimated.

Outcomes were measured as disability adjusted life years (DALYs) and incremental cost-effectiveness ratios were estimated for each device compared with a baseline of visual inspections alone. In the scenario with high levels of SF ACTs, all devices were cost-effective with a 1-sample strategy. In the scenario of low levels of SF ACTs, only four devices (MicroPHAZIR RX, 4500a FTIR, NIR-S-G1, and PADs) were cost-effective with a 1-sample strategy. In the multi-way comparative analysis, in both scenarios the NIR-S-G1 testing 2 samples was the most cost-effective option. Routine inspection of ACT quality using portable screening devices is likely to be cost-effective in the Laos context. This work should encourage policy-makers or regulators to further investigate investment in portable screening devices to detect SF medicines and reduce their associated undesired health and economic burdens.

Laboratory evaluation of twelve portable devices for medicine quality screening. Zambrzycki SC, Caillet C, Vickers S, Bouza M, Donndelinger DV, Geben LC, Bernier MC, Newton PN, Fernández FM. *PLoS Negl Trop Dis*. 2021 Sep 30;15(9):e0009360. doi: 10.1371/journal.pntd.0009360. PMID: 34591844; PMCID: PMC8483346.

Evaluation of twelve devices to detect falsified medicines (wrong or none of the active pharmaceutical ingredient (API)) is reported in this paper demonstrating high accuracy, but API quantitation for formulations equivalent to substandard medicines proved more difficult.

BACKGROUND:	Post-market surveillance is a key regulatory function to prevent substandard and falsified (SF) medicines from being consumed by patients. Field deployable technologies offer the potential for rapid objective screening for SF medicines.
METHODOLOGY AND FINDINGS:	We evaluated twelve devices: three near infrared spectrometers (MicroPHAZIR RX, NIR-S-G1, Neospectra 2.5), two Raman spectrometers (Progeny, TruScan RM), one mid-infrared spectrometer (4500a), one disposable colorimetric assay (Paper Analytical Devices, PAD), one disposable immunoassay (Rapid Diagnostic Test, RDT), one portable liquid chromatograph (C-Vue), one microfluidic system (PharmaChk), one mass spectrometer (QDa), and one thin layer chromatography kit (GPHF-Minilab). Each device was tested with a series of field collected medicines (FCM) along with simulated medicines (SIM) formulated in a laboratory. The FCM and SIM ranged from samples with good quality active pharmaceutical ingredient (API) concentrations, reduced concentrations of API (80% and 50% of the API), no API, and the wrong API. All the devices had high sensitivities (91.5 to 100.0%) detecting medicines with no API or the wrong API. However, the sensitivities of each device towards samples with 50% and 80% API varied greatly, from 0% to 100%. The infrared and Raman spectrometers had variable sensitivities for detecting samples with 50% and 80% API (from 5.6% to 50.0%). The devices with the ability to quantitate API (C-Vue, PharmaChk, QDa) had sensitivities ranging from 91.7% to 100% to detect all poor quality samples. The specificity was lower for the quantitative C-Vue, PharmaChk, & QDa (50.0% to 91.7%) than for all the other devices in this study (95.5% to 100%).
CONCLUSIONS:	The twelve devices evaluated could detect medicines with the wrong or none of the APIs, consistent with falsified medicines, with high accuracy. However, API quantitation to detect formulations similar to those commonly found in substandards proved more difficult, requiring further technological innovation.

Other

Maternal health literacy on mother and child health care: A community cluster survey in two southern provinces in Laos. Phommachanh S, Essink DR, Wright PE, Broerse JEW, Mayxay M. *PLoS One*. 2021 Mar 29;16(3):e0244181. doi: 10.1371/journal.pone.0244181. PMID: 33780460; PMCID: PMC8007003.

RATIONALE:	Increased maternal health literacy (MHL) has contributed considerably to maternal and child health outcomes in many countries. Malnutrition, and low coverage of child vaccination and breastfeeding are major health concerns in Laos, but there is little insight into mothers' literacy on these issues. The aim of this study was to identify the level of MHL of Lao mothers and to explore factors influencing it, in order to provide evidence that can inform policies and planning of health services.
METHODS:	A cross-sectional survey was conducted using a questionnaire on health literacy (ability to access, understand, appraise and apply health-related information) in relation to care during pregnancy, childbirth, and the postpartum period. We interviewed 384 mothers with children aged under five years; 197 from urban and 187 from rural areas. Descriptive and inferential statistics were applied to analyse the data.
RESULTS:	Overall, MHL of Lao mothers was very low in both urban and rural areas; 80% of mothers had either inadequate or problematic MHL, while only 17.4% had sufficient and 3.5% excellent MHL. The MHL scores were significantly higher in urban than in rural areas. One third of mothers found it very difficult to access, understand, appraise and apply information on mother and child (MCH). Health personnel were the main source of MCH information for the mothers. Years of schooling, own income, health status, and number of ANC visits significantly predicted a higher level of MHL (R square = 0.250; adjusted R square = 0.240, P = <0.001).
CONCLUSIONS:	MHL of Lao mothers was inadequate in both urban and rural areas. Socio-demographics and key practices of the mothers were significantly associated with a better level of MHL. Health education on MHL to mothers in both urban and rural areas needs attention, and could best be done by improving the quality of health providers' provision of information.

The 20-minute whole blood clotting test (20WBCT) for snakebite coagulopathy-A systematic review and meta-analysis of diagnostic test accuracy. Lamb T, Abouyannis M, de Oliveira SS, Shenoy K R, Geevar T, Zachariah A, Sharma SK, Bhatt N, Mukaka M, Harriss E, Lalloo DG, Ashley EA, Monteiro WM, Smithuis F, Eddleston M. *PLoS Negl Trop Dis*. 2021 Aug 10;15(8):e0009657. doi: HYPERLINK "https://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0009657" 10.1371/journal.pntd.0009657. PMID: 34375338; PMCID: PMC8405032.

This systematic review and meta-analysis showed that, in the absence of laboratory clotting assays, a 20-minute whole blood clotting test (20WBCT) used to detect coagulopathy following snakebite remains a highly specific and fairly sensitive bedside test, but cautions clinicians to be aware of the importance of operator training, standardized equipment and lower sensitivity in detecting mild coagulopathy and resolution of coagulopathy following antivenom.

BACKGROUND:	The 20-minute whole blood clotting test (20WBCT) has been used to detect coagulopathy following snakebite for almost 50 years. A systematic review and meta-analysis of the 20WBCT was conducted to evaluate the accuracy of the 20WBCT to detect coagulopathy, indicative of systemic envenoming.
METHODS AND FINDINGS:	Databases were searched from inception up to 09/12/2020 to identify studies that compared the 20WBCT and INR/fibrinogen on five or more subjects. Data was extracted from full-text articles by two reviewers using a predetermined form. Authors of 29 studies that lacked sufficient details in the manuscript were contacted and included if data meeting the inclusion criteria were provided. Included studies were evaluated for bias using a tailored QUADAS-2 checklist. The study protocol was prospectively registered on PROSPERO database (CRD42020168953). The searches identified 3,599 studies, 15 met the inclusion criteria and 12 were included in the meta-analysis. Data was reported from 6 countries and included a total of 2,270 patients. The aggregate weighted sensitivity of the 20WBCT at detecting INR >1.4 was 0.84 (CI 0.61 to 0.94), the specificity was 0.91 (0.76 to 0.97) and the SROC AUC was 0.94 (CI 0.91 to 0.96). The aggregate weighted sensitivity of the 20WBCT at detecting fibrinogen <100 mg/dL was 0.72 (CI 0.58 to 0.83), the specificity was 0.94 (CI 0.88 to 0.98) and the SROC AUC was 0.93 (0.91 to 0.95). Both analyses that used INR and fibrinogen as the reference test displayed considerable heterogeneity.
CONCLUSIONS:	In the absence of laboratory clotting assays, the 20WBCT remains a highly specific and fairly sensitive bedside test at detecting coagulopathy following snakebite. However, clinicians should be aware of the importance of operator training, standardized equipment and the lower sensitivity of the 20WBCT at detecting mild coagulopathy and resolution of coagulopathy following antivenom.

The prevalence and clinical features associated of hypothyroidism among Thai systemic sclerosis patients. Paolee Y, Foocharoen C, Charoensri S, Mayxay M, Mahakkanukrauh A, Suwannaroj S, Nanagara R. *Sci Rep*. 2021 Jul 21;11(1):14902. doi: HYPERLINK "https://www.nature.com/articles/s41598-021-94371-6" 10.1038/s41598-021-94371-6. PMID: 34290330; PMCID: PMC8295267.

Thyroid disease, particularly hypothyroidism, has been reported in systemic sclerosis (SSc). Some clinical features of SSc can also present in hypothyroidism. Our aims were to determine the prevalence of, and describe clinical features associated with hypothyroidism in SSc patients. We conducted a historical cohort study of adult SSc patients who underwent screening thyroid function tests at the Scleroderma Clinic, Khon Kaen University, Thailand, between 2009 and 2018. The patients who had any thyroid disorders before the onset of SSc and were diagnosed as an overlap syndrome were excluded. A total of 200 SSc were included according to sample size calculation, among whom the female to male ratio was 2:1. The majority of cases (137; 69.5%) were diffuse cutaneous SSc subset. The mean age was 55.8 ± 10.7 years and the median duration of disease was 4.9 (IQR 1.6-9.9) years. Of the total, 9 had primary hypothyroidism (prevalence 4.5%; 95%CI 2.1-8.4) and 22 had subclinical hypothyroidism (prevalence 11%; 95%CI 7.0-16.2). Of the latter 22, 71% had dcSSc. Logistic regression analysis indicated that unexplained anemia was significantly associated with either subclinical hypothyroid or hypothyroidism (OR 2.74; 95% CI 1.17-6.47), whereas Raynaud's phenomenon had a negative association (OR 0.28; 95% CI 0.11-0.66). Neither severity of skin tightness nor internal organ involvement were associated with hypothyroidism among SSc patients. Clinical-subclinical hypothyroidism is uncommon among SSc patients, it is frequently associated with anemia, and less *so* Raynaud's phenomenon. Clinical-subclinical hypothyroidism should thus be considered in cases of unexplained anemia in SSc patients.

A landscape analysis of health technology assessment capacity in the Association of South-East Asian Nations region. Sharma M, Teerawattananon Y, Dabak SV, Isaranuwatchai W, Pearce F, Pilasant S, Sabirin J, Mayxay M, Guerrero M, Phuong NK, Sastroasmoro S, Htoo TS. *Health Res Policy Syst*. 2021 Feb 11;19(1):19. doi: HYPERLINK "https://health-policy-systems.biomedcentral.com/articles/10.1186/s12961-020-00647-0" 10.1186/s12961-020-00647-0. PMID: 33573676; PMCID: PMC7879649.

This mixed survey questionnaire study evaluated the status and capacity of health technology assessment (HTA) in ASEAN countries, revealing a need for efforts to mitigate the gaps between HTA demand and supply while ensuring adequate participation from stakeholders towards fair and transparent decisions on resource allocation.

BACKGROUND:	Progress towards achieving Universal Health Coverage and institutionalizing healthcare priority setting through health technology assessment (HTA) in the Association of South-East Asian Nations (ASEAN) region varies considerably across countries because of differences in healthcare expenditure, political support, access to health information and technology infrastructure. To explore the status and capacity of HTA in the region, the ASEAN Secretariat requested for member countries to be surveyed to identify existing gaps and to propose solutions to help countries develop and streamline their priority-setting processes for improved healthcare decision-making.
METHODS:	A mixed survey questionnaire with open- and closed-ended questions relating to HTA governance, HTA infrastructure, supply and demand of HTA and global HTA networking opportunities in each country was administered electronically to representatives of HTA nodal agencies of all ASEAN members. In-person meetings or email correspondence were used to clarify or validate any unclear responses. Results were collated and presented quantitatively.
RESULTS:	Responses from eight out of ten member countries were analysed. The results illustrate that countries in the ASEAN region are at different stages of HTA institutionalization. While Malaysia, Singapore and Thailand have well-established processes and methods for priority setting through HTA, other countries, such as Cambodia, Indonesia, Lao PDR, Myanmar, the Philippines and Vietnam, have begun to develop HTA systems in their countries by establishing nodal agencies or conducting ad-hoc activities.
DISCUSSION AND CONCLUSION:	The study provides a general overview of the HTA landscape in ASEAN countries. Systematic efforts to mitigate the gaps between the demand and supply of HTA in each country are required while ensuring adequate participation from stakeholders so that decisions for resource allocation are made in a fair, legitimate and transparent manner and are relevant to each local context.

Observational study of adult respiratory infections in primary care clinics in Myanmar: understanding the burden of melioidosis, tuberculosis and other infections not covered by empirical treatment regimes. Warrell CE, Phyo AP, Win MM, McLean ARD, Watthanaworawit W, Swe MMM, Soe K, Lin HN, Aung YY, Ko CK, Waing CZ, Linn KS, Aung YPW, Aung NM, Tun NN, Dance DAB, Smithuis FM, Ashley EA. *Trans R Soc Trop Med Hyg*. 2021 Aug 2;115(8):914-921. doi: HYPERLINK "https://academic.oup.com/trstmh/article/115/8/914/6157741?login=false" 10.1093/trstmh/trab024. PMID: 33681986; PMCID: PMC8326957.

BACKGROUND:	Lower respiratory infections constitute a major disease burden worldwide. Treatment is usually empiric and targeted towards typical bacterial pathogens. Understanding the prevalence of pathogens not covered by empirical treatment is important to improve diagnostic and treatment algorithms.

METHODS: A prospective observational study in peri-urban communities of Yangon, Myanmar was conducted between July 2018 and April 2019. Sputum specimens of 299 adults presenting with fever and productive cough were tested for *Mycobacterium tuberculosis* (microscopy and GeneXpert MTB/RIF [*Mycobacterium tuberculosis*/resistance to rifampicin]) and *Burkholderia pseudomallei* (Active Melioidosis Detect Lateral Flow Assay and culture). Nasopharyngeal swabs underwent respiratory virus (influenza A, B, respiratory syncytial virus) polymerase chain reaction testing.

RESULTS: Among 299 patients, 32% (95% confidence interval [CI] 26 to 37) were diagnosed with tuberculosis (TB), including 9 rifampicin-resistant cases. TB patients presented with a longer duration of fever (median 14 d) and productive cough (median 30 d) than non-TB patients (median fever duration 6 d, cough 7 d). One case of melioidosis pneumonia was detected by rapid test and confirmed by culture. Respiratory viruses were detected in 16% (95% CI 12 to 21) of patients.

CONCLUSIONS: TB was very common in this population, suggesting that microscopy and GeneXpert MTB/RIF on all sputum samples should be routinely included in diagnostic algorithms for fever and cough. Melioidosis was uncommon in this population.

Cluster of Angiostrongyliasis Cases Following Consumption of Raw Monitor Lizard in the Lao People's Democratic Republic and Review of the Literature. Yang L, Darasavath C, Chang K, Vilay V, Sengduangphachanh A, Adsamouth A, Vongsouvath M, Keolouangkhot V, Robinson MT. *Trop Med Infect Dis*. 2021 Jun 22;6(3):107. doi: HYPERLINK "https://www.mdpi.com/2414-6366/6/3/107" 10.3390/tropicalmed6030107. PMID: 34206193; PMCID: PMC8293387.

Angiostrongyliasis in humans causes a range of symptoms from mild headache and myalgia to neurological complications, coma and death. Infection is caused by the consumption of raw or undercooked intermediate or paratenic hosts infected with *Angiostrongylus cantonensis* or via contaminated vegetables or water. We describe a cluster of cases involved in the shared meal of wild raw monitor lizard in the Lao PDR. Seven males, aged 22-36 years, reported headaches, abdominal pain, arthralgia, myalgia, nausea/vomiting, diarrhoea, neurological effects and loss of appetite. Five were admitted to hospital. The final diagnosis was made by clinical presentation and case history, and positive A. *cantonensis* PCR for two cases. All hospitalized patients recovered fully following supportive treatment. The remaining two individuals sought local home remedies and made a full recovery. Whilst most published reports concern infections via consumption of molluscs, few detailed reports exist on infections that result from the consumption of reptiles and there exists little awareness in Lao PDR. This case cluster, which originates from a single meal, highlights the potential public health risk of the consumption of raw and wild-caught meat in Lao PDR and the Southeast Asia region. Without specific diagnostics, clinical history and the consideration of recent food consumption are important when evaluating patients.

Conference and meeting presentations

70th Annual (Virtual) Meeting of the American Society of Tropical Medicine & Hygiene (ASTMH)
Causes of Acute Respiratory Infection among Hospitalized Patients in Northern Laos – A Case-Control Study (Poster presentation)

Koukeo Phommasone, Xaipasong Xaiyaphet, Jose A. Garcia-Rivera*, Robert D. Hontz*, Viengmone Pathavongsa, Patsalin Keomoukda, Malavanh Vongsouvath, Mayfong Mayxay, Manivanh Vongsouvath, Paul N Newton, Elizabeth A Ashley, Audrey Dubot-Pérès

* U.S. Naval Medical Research Unit TWO (NAMRU-2), Singapore and Phnom Penh, Cambodia.

ABSTRACT

BACKGROUND: With the advent of highly sensitive real-time PCR, a diversity of pathogens are identified from the nasopharyngeal swabs of patients with acute respiratory infections (ARIs). However, the detection of micro-organisms in the upper respiratory tract does not necessarily mean that they were the cause. We conducted a matched case-control study, nested in a large fever aetiology project, to facilitate determination of the aetiology of ARI in hospitalised patients in northern Laos.

METHODS: Consenting febrile patients of any age admitted to Xiengkhuang Provincial Hospital were included in the case-control study if they had an ARI presentation (≥ one of: cough, rhinorrhoea, nasal congestion, sore throat, difficulty breathing or abnormal chest auscultation). One control for each included case, matched by sex, age and village of residence, was recruited within 2 weeks of patient enrolment if they did not have fever and ARI presentation. Nasopharyngeal swabs were collected from participants and tested for 33 pathogens by probe-based multiplex real-time (RT-)PCR (FastTrack Diagnostics Respiratory pathogen 33 kit). Attributable fraction of illness for a given microorganism was calculated by comparing results between patients and controls (=100 *[OR-1]/OR).

RESULTS: Between 24 June 2019 and 24 June 2020, 205 ARI patients and 205 matching controls were recruited. After excluding 8 pairs due to age mismatch, 197 pairs remained in the analysis. Males were predominant with sex ratio 109:88 and children <5 years old accounted for 56% of participants. At least one potential pathogen was detected in 172 (87%) patients and 175 (89%) controls. 17.8% of all ARI cases were attributable to influenza B, 17.2% to influenza A, 7.5% to human metapneumovirus, and 6.5% to respiratory syncytial virus (RSV).

CONCLUSIONS: Determining aetiology of ARI remains challenging. Among hospitalised Lao ARI patients presenting at a provincial hospital in northern Laos, most were attributed to a viral cause, particularly influenza A, influenza B, human metapneumovirus, or RSV.

Predicting mortality in febrile adult patients: a prospective validation of the MEWS, qSOFA and UVA scores in four health care settings in Africa and South-East Asia (oral presentation)

Oliver Baerenbold, Quique Bassat, John Bradley, Justina M. Bramugy, Mabvuto Chimenya, John A. Crump, Edward Green, Kevin Kain, Sham Lal, Manophab Luangraj, David C. W. Mabey, Ioana D. Olaru, Molly Sibanda, Shunmay Yeung, Christopher C. Moore, Heidi Hopkins

Identifying patients with the highest risk of mortality from easily measurable variables can improve prioritization and thus resource allocation of potentially life-saving interventions. The modified early warning score (MEWS), the quick Sequential (Sepsis-Related) Organ Failure Assessment (qSOFA), and the Universal Vital Assessment (UVA) score were developed as risk-stratification tools but need external validation in new patient groups and settings. We included in the analysis in- and outpatients aged ≥16 years presenting with fever at four sites in Laos, Malawi, Mozambique, and Zimbabwe as part of a prospective study of infectious causes of fever (Febrile Illness Evaluation in a Broad Range of Endemicities - FIEBRE). We determined mortality at a follow-up visit after at least 26 days. We evaluated predictive capacity based on the area under the receiver operating curve (AUC), as well as sensitivity at a cut-off which gives 90% specificity. We enrolled 4,023 patients; 1,715 (43%) inpatients, 2,336 (58%) female, median (IQR) age 33 (24 – 45) years, and 782 (19%) HIV-infected. Of the total, 1,182 (29%) were in Laos, 807 (20%) in Malawi, 998 (25%) in Mozambique, and 1036 (26%) in Zimbabwe. Complete outcome information was available for

3,432 (85%); 210 (6.1%) died, including 187 (13.2%) inpatients and 23 (1.1%) outpatients. The UVA had an AUC of 0.77 (95% CI 0.74 – 0.81), outperforming both MEWS with AUC 0.65 (95% CI 0.61 – 0.69) and qSOFA with AUC 0.68 (95% CI 0.65 – 0.72). The relative performance of the scores remained the same on sensitivity analysis assuming patients with missing outcome data either all lived, or all died. The observed AUC of UVA was higher than MEWS and qSOFA in each site, varying from 0.88 (95% CI 0.79 – 0.99) in Malawi to 0.75 (95% CI 0.69 – 0.81) in Laos. At a set specificity of 90%, UVA sensitivity (95% CI) was 46.5% (39.9% – 53.0%) compared to 18.6% (10.9% - 27.5%) for qSOFA, and 22.9% (17.5% - 28.8%) for MEWS. Our findings suggest that of the scores assessed, UVA best predicts mortality in febrile adults across a range of health care settings in Africa and south-east Asia, and may be well-suited for clinical use in similar contexts.

The main pathogens causing febrile illness and implications for fever management in Laos; results from the FIEBRE study. (Poster presentation)

Manophab Luangraj, Vilayouth Phimonsarnnousith, Khamfong Kanlaya, Somvai Singhasaiyaseng, Vilada Chansamouth, Audrey Dubot-Pérès, Andrew Simpson, Manivanh Vongsouvath, Viengmon Davong, Sham Lal, Chrissy Roberts, Heidi Hopkins, David Mabey, Paul N Newton, Elizabeth A Ashley, Mayfong Mayxay.

Dr Manivanh Vongsouvath (2nd *from left*), Head of the Mahosot Microbiology Laboratory, pictured with three former directors of Mahosot Hospital at a basci to mark the opening of the new hospital, from *left*: Dr Phisith Phoudsavath, Dr Chanpheng Tamavong and Dr Bounthaphany Bounxouei. © LOMWRU 2022.

Management of febrile illness in Laos typically relies on clinical assessment and empiric treatment, as laboratory confirmation is often not available, except for malaria and dengue rapid tests.
The standard empiric treatment of inpatients with sepsis or febrile illness in Laos is parenteral ceftriaxone. Vientiane Provincial Hospital in northern Laos was one site of the multicentre FIEBRE (Febrile Illness in a Broad Range of Endemicities) study which performed a comprehensive evaluation of the causes of febrile illness in inpatients and outpatients of all ages. We aimed to describe the leading pathogens diagnosed from FIEBRE patients recruited in Laos. Between October 2018 and October 2020, 1972 patients were enrolled. Laboratory testing included blood culture, malaria microscopy, molecular or serological testing for Histoplasma-antigen, PCR and serology for dengue, Zika, chikungunya, and JEV, PCR for respiratory pathogens, plus *Leptospira* and rickettsial serology (results awaited). Among 1972 patients, 135 (6.8%) had positive blood cultures. Of these, 17 (12.6%) grew *Burkholderia pseudomallei*, 8 (5.9%) *Escherichia coli* (4 ESBL positive), 7 (5.2%) *Staphylococcus aureus* (2 MRSA), 3 (2.2%) *Klebsiella pneumoniae*, 2 (1.5%) *Talaromyces marneffei*, and 2 (1.5%) *Streptococcus pneumoniae*. None of our patients tested positive for malaria. From the first batch of testing, 5/382 (1.3%) samples were positive for Histoplasma-Ag. From 605 samples, 24 (3.9%) were positive for dengue. Of 669 pharyngeal samples, 218 (32.6%) tested positive for respiratory viruses. 1207 (61.4%) patients received antibiotics, of which 799 (66.2%) were cephalosporins. Our results reveal the leading infectious causes of febrile illness in rural Vientiane. Results to date show viruses accounted for most diagnoses, particularly respiratory viruses and dengue. Despite this, antimicrobial prescribing rates were high, while the diagnostic yield from blood cultures was low. We demonstrated melioidosis and ESBL-producing Enterobacterales are prevalent in this part of Laos, with important implications for empiric prescribing in severely ill patients with sepsis.

2021 International Conference on Typhoid & Other Invasive Salmonelloses, 6-8 Dec 2021.
The reality of diagnosing typhoid in settings with limited laboratory capacity - particularly during a pandemic. A case study from Lao PDR (no abstract). Tamalee Roberts- oral presentation.

Other activities in 2021

Public Engagement

LOMWRU has continued its programme of community, public and policy engagement activities when COVID restrictions permitted.

World Antibiotic Awareness Week 2021

To mark World Antimicrobial Awareness Week (WAAW) 2021 there were a number of events around Lao PDR. WAAW is celebrated from 18-24 November every year, and the 2021 theme, Spread Awareness, Stop Resistance, calls on One Health stakeholders, policymakers, health care providers, and the general public to be Antimicrobial Resistance (AMR) Awareness champions.

With support from Prof Li Yang Hsu and his team in the National University of Singapore, and Micro Lab/LOMWRU colleagues, Dr Vilada Chansamouth produced a video which was posted on the DCDC website and Centre of Information and Education Health Facebook Page. She also launched a photography competition as part of her WAAW engagement activities at Mahosot Hospital, with the winners shown above.

LAO Medical Journal

LOMWRU continues to support publication of the Lao Medical Journal. The latest issue was published in April 2021.

Reduce, Reuse, Recycle

LOMWRU has continued with its recycling campaign with 342kg of cans, glass, paper and plastic recycled in 2021. All staff need to be congratulated for their continual support for recycling in the unit.

Recognition and awards

Professor Mayfong Mayxay received a Hitachi Global Foundation Asia Innovation Award. This program, launched in 2020, recognises individuals and groups that undeniably served public interests through their outstanding achievements in research and development (R&D) in the fields of science and technology. A total of 12 recipients received awards.

ASTMH (American Society of Tropical Medicine & Hygiene)

ASTMH Distinguished International Fellow formally recognizes up to eight individuals who have made eminent contributions to a particular aspect of tropical medicine or hygiene. Professor Paul Newton received this well-deserved recognition which was announced during the ASTMH 2021 annual meeting.

Farewells in 2021

Dr Andrew Simpson, Senior Clinical Microbiologist, left LOMWRU after 2 and half years to return to the UK. Dr Susath Vongphachanh, Director of Mahosot Hospital, presented him with a certificate in recognition of his support to Mahosot Hospital and we would all like to extend our sincere thanks to him for all his contributions to LOMWRU and other organisations in Laos and wish him the best of luck in his new job. © LOMWRU 2022.

THANK YOU TO OUR FUNDERS!

Project funders in 2021

We would like to thank all of our funders for their very generous support of projects in 2021

wellcome

BILL & MELINDA GATES foundation

UKaid from the British people

BIOMÉRIEUX

NAVAL MEDICAL RESEARCH CENTER U.S. NAVY

FIND Diagnosis for all

Aix Marseille université

IRD

Inserm

EFS ÉTABLISSEMENT FRANÇAIS DU SANG

IRBA

AP HM

MÉDITERRANÉE INFECTION

Contact Information

For permissions or inquiries about LOMWRU,
kindly contact us at LOMWRUinfo@tropmedres.ac.