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

LOMWRU Annual Report 2024

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit

LOMWRU.

LOMWRU (Lao PDR)
lomwruinfo@tropmedres.ac

Annual Report 2024

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit

Designed by
Suriyong Khamla-iad
Wannachat Chaichan

Edited and produced by John Bleho

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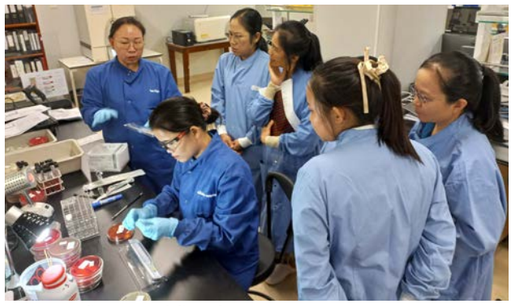
Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU)



ກ່ຽວກັບໜ່ວຍງານຄົ້ນຄວ້າຂອງພວກເຮົາ

ໂຄງການຮ່ວມມືຄົ້ນຄວ້າດ້ານພະຍາດເຂດຮ້ອນລະຫວ່າງໂຮງໝໍມະໂຫສົດ - ມະຫາວິທະຍາໄລອ໋ອກຟອດ-ແອວຄຳຕັ໊ສ ຫຼື The Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU) ແມ່ນໜ່ວຍງານທີ່ມີ ການຮ່ວມມືລະຫວ່າງມະຫາວິທະຍາໄລອ໋ອກຟອດ ແລະ ໂຮງໝໍມະໂຫສົດ, ນະຄອນຫຼວງວຽງຈັນ, ສປປ ລາວ ໂດຍ ໄດ້ຮັບທຶນຊ່ວຍເຫຼືອຫຼັກ ຈາກແອວຄຳຕັ໊ສ ປະເທດອັງກິດ. ພວກເຮົາຍັງແມ່ນສ່ວນໜຶ່ງຂອງສູນງານຊາດຂອງ MORU Major International Programme (MIP) ທີ່ມີ 8 ສູນຄົ້ນຄວ້າຫຼັກຕັ້ງຢູ່ ປະເທດໄທ, ກຳປູເຈຍ, ສປປ ລາວ, ມຽນມາ ແລະ ສາທາລະນະລັດ ປະຊາທິປະໄຕ ຄອງໂກ. ການຮ່ວມມືລະຫວ່າງ ໂຄງການຄົ້ນຄວ້າພະຍາດເຂດຮ້ອນລະຫວ່າງ ໂຮງໝໍມະໂຫສົດ-ແອວຄຳຕັ໊ສ-ມະຫາວິທະຍາໄລ ອ໋ອກຟອດ ແລະ ສະຖາບັນຄົ້ນຄວ້າເພື່ອການພັດທະນາຝຣັ່ງ Institut de Recherche pour le Développement ຫຼື IRD) ແມ່ນ ເລີ່ມມາຕັ້ງແຕ່ປີ 2009. ປະຈຸບັນ ພວກເຮົາມີພະນັກງານທັງໝົດ 65 ຄົນ ຊຶ່ງລວມມີ ພະນັກງານທີ່ເຮັດວຽກປະຈຳຢູ່ນະຄອນຫຼວງວຽງຈັນ ແລະ ຕ່າງແຂວງ ທີ່ເປັນໜຶ່ງໃນວຽກງານການຮ່ວມມືຄົ້ນຄວ້າ, ແລະ ພະນັກງານພາກລັດຈາກພະແນກຈຸລິນຊີ ວິທະຍາ ຈຳນວນ 24 ຄົນ ໂດຍມີ ດຣ ມະນີ ວັນ ວົງສຸວັດ ຫົວໜ້າພະແນກຈຸລິນຊີວິທະຍາ ແລະ ຮອງໜ່ວຍງານໄວຣັດວິທະຍາ. ໜ່ວຍງານຄົ້ນຄວ້າ LOMWRU ມີ ຫ້ອງວິເຄາະ ທາງພັນທຸກຳ, ຫ້ອງວິເຄາະເຊໂຣໂລຊີ ແລະ ຫ້ອງວິເຄາະຄວາມປອດໄພລະດັບ 3 (BSL3) ສຳລັບປຸກເຊື້ອ *Rickettsial, Mycobacterium* spp., *B. pseudomallei* ແລະ ເຊື້ອໄວຣັສ. ສຈ. ປອ. ດຣ ມາຍຟອງ ມາຍຊາຍ, ອະທິການບໍດີ ມະຫາວິທະຍາໄລ ວິທະຍາສາດ ສຸຂະພາບ ຊ່ວຍຊີ້ນຳວຽກງານຮ່ວມມືຄົ້ນຄວ້າ ກັບບັນດາແຂວງ ແລະ ວຽກ ງານຄົ້ນຄວ້າພາກສະໜາມ. ໜ່ວຍງານຄົ້ນຄວ້າ LOMWRU ໄດ້ສະໜັບສະໜູນການບົ່ງມະຕິພະຍາດທີ່ເກີດຈາກເຊື້ອຈຸລະຊີບໃນ ສ.ປ.ປ ລາວ, ສະໜັບສະໜູນການຝຶກອົບຮົມ ບັນດານັກເຕັກນິກ ແລະ ນັກວິທະຍາສາດການແພດລາວ ແລະ ຍັງຈັດຕັ້ງປະຕິບັດການສຶກສາຄົ້ນຄວ້າ ໂດຍສະເພາະຂົງເຂດທີ່ກ່ຽວກັບພະຍາດຊຶມເຊື້ອ.

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 Major International Programme (MIP), which has eight permanent research units in Thailand, Cambodia, Laos, Myanmar and the Democratic Republic of Congo (DRC). The Virology department has been partially supported by the Unité des Virus Émergents (UVE), Marseille, France, funded by the Institut de Recherche pour le Développement (IRD), since 2006. Currently, a team of 65 research and support staff in the capital and the provinces work on projects as part of the collaboration, alongside 24 Lao Government employees led by Dr Manivanh Vongsouvath, Director of the Mahosot Microbiology Laboratory and Deputy Head of Virology. 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 Prof Mayfong Mayxay, who is 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.

Mahosot Hospital Inauguration Ceremony attended by Lao PDR Prime Minister HE Sonexay Siphandone and HE Li Qiang, Prime Minister of the People's Republic of China.

ພິທີເປີດນຳໃຊ້ຕຶກໂຮງໝໍມະໂຫສົດ ໂດຍໄດ້ຮັບກຽດເຂົ້າຮ່ວມຈາກທ່ານນາຍົກລັດຖະມົນຕີລາວ ທ່ານ ສອນໄຊ ສີພັນດອນ ແລະ ທ່ານນາຍົກລັດຖະມົນຕີຈີນ ທ່ານ Li Qiang

ຄຳເຫັນຂອງ ທ່ານ Prof Elizabeth Ashley

ໃນປີ 2024 ສປປ ລາວ ໄດ້ຮັບກຽດເປັນເຈົ້າພາບກອງປະຊຸມສຸດຍອດອາຊຽນ ພາຍໃຕ້ຄຳຂວັນ "ເພີ່ມທະວີການເຊື່ອມຈອດ ແລະ ຄວາມເຂັ້ມແຂງອາຊຽນ". ທ່ານລັດຖະມົນຕີການຕ່າງປະເທດແຫ່ງສະຫະລາຊະອານາຈັກອັງກິດ ທ່ານ David Lammy ໄດ້ເຂົ້າຮ່ວມກອງປະຊຸມລັດຖະມົນຕີການຕ່າງປະເທດອາຊຽນ ແລະ ໄດ້ມີໂອກາດມາຢ້ຽມຢາມ LOMWRU ພ້ອມດ້ວຍທ່ານເອກອັກຄະລາຊະທູດອັງກິດປະຈຳ ສປປ ລາວ ທ່ານ Melanie Barlow ເພື່ອຮັບຟັງຂໍ້ມູນໂຄງການຂອງກອງທຶນ UK Fleming Fund ທີ່ສົ່ງເສີມການເຝົ້າລະວັງ ການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບພາຍໃນປະເທດ. ໃນປີ 2024 LOMWRU ແລະ ໂຮງໝໍມະໂຫສົດ ໄດ້ສືບຕໍ່ເຮັດວຽກຮ່ວມກັບໂຮງໝໍແຂວງທັງ 5 ແຂວງຄື: ແຂວງສາລະວັນ, ແຂວງສະຫວັນນະເຂດ, ແຂວງວຽງຈັນ, ແຂວງຊຽງຂວາງ ແລະ ແຂວງຫຼວງນ້ຳທາ, ປະຈຸບັນບັນດາໂຮງໝໍແຂວງດັ່ງກ່າວ ສາມາດກວດວິເຄາະຕົວຢ່າງທາງດ້ານຈຸລິນຊີວິທະຍາໄດ້ເອງ ເຊິ່ງສະແດງໃຫ້ເຫັນຄວາມສຳເລັດຂອງໂຄງການນີ້ໃນໄລຍະເລີ່ມຕົ້ນ. ປີທີ່ຜ່ານມາ ຢູ່ນະຄອນຫຼວງວຽງຈັນເປັນອີກໜຶ່ງປີທີ່ມີຄວາມສຳຄັນຫຼາຍຕໍ່ອົງກອນພວກເຮົາ ເມື່ອໂຮງໝໍມະໂຫສົດໄດ້ສຳເລັດການກໍ່ສ້າງອາຄານໃໝ່ໄລຍະທີ 2 ແລະ ໄດ້ຈັດພິທີເປີດນຳໃຊ້ຕຶກໃໝ່ໃນວັນທີ 12 ຕຸລາ, ໂດຍມີທ່ານນາຍົກລັດຖະມົນຕີລາວ ທ່ານ ສອນໄຊ ສີພັນດອນ ແລະ ທ່ານນາຍົກລັດຖະມົນຕີຈີນ ທ່ານ Li Qiang ໄດ້ໃຫ້ກຽດເຂົ້າຮ່ວມພິທີ.

ສຳລັບ LOMWRU ໃນປີ 2024 ກໍເປັນປີທີ່ແຫ່ງຄວາມສຳເລັດທີ່ດີອີກປີໜຶ່ງທີ່ພວກເຮົາມີບັນດິດຈົບການສຶກສາລະດັບປະລິນຍາເອກ 2 ຄົນ, ນັກສຶກສາປະລິນຍາໂທ 9 ຄົນ ແລະ ບົດຕີພິມການຄົ້ນຄວ້າວິທະຍາສາດ ຈຳນວນ 46 ບົດ. ພວກເຮົາຫວັງວ່າຈະປະສົບຜົນສຳເລັດຍິ່ງຂຶ້ນໄປອີກໃນປີ 2025 ເຊິ່ງຈະເປັນປີທີ່ພວກເຮົາຈະສະເຫຼີມສະຫຼອງຄົບຮອບ 25 ປີ. ຕະຫຼອດໄລຍະເສັ້ນທາງທີ່ຜ່ານມາຈົນເຖິງປະຈຸບັນນີ້ ຈະເປັນເວລາສຳຄັນທີ່ພວກເຮົາຈະເບິ່ງຍ້ອນກັບໄປ ແລະ ທົບທວນຜົນສຳເລັດທີ່ຜ່ານມາຕັ້ງແຕ່ປີ 2000, ແລະ ພິຈາລະນາເພີ່ມຕື່ມວ່າພວກເຮົາຈະສາມາດເພີ່ມຜູນໝາກຜົນຕໍ່ໄປໃນອະນາຄົດໄດ້ຕື່ມຄືແນວໃດຈາກການເຮັດສຶກສາຄົ້ນຄວ້າ ເພື່ອສົ່ງເສີມສຸຂະພາບຂອງຄົນລາວໃຫ້ດີຍິ່ງຂຶ້ນ.

ສຸດທ້າຍນີ້ ຂ້າພະເຈົ້າຂໍກ່າວຄຳຂອບໃຈແກ່ທ່ານ ປອ ດຣ ຊຸຊາດ ວົງພະຈັນ, ຜູ້ອຳນວຍການໂຮງໝໍມະໂຫສົດ ແລະ ຄະນະອຳນວຍການ ທ່ານນາງ ບົວວັນ ປະທຸມທອງ, ດຣ ໄຊຊະນະ ສົມບັນດິດ, ດຣ ບຸນໂຮມ ກັນທະວົງ ແລະ ດຣ ໄຄສີ ລາຊະວົງ ພ້ອມທັງພາກສ່ວນອື່ນໆໃນໂຮງໝໍມະໂຫສົດທີ່ໄດ້ສືບຕໍ່ໃຫ້ການຮ່ວມມື ແລະ ການສະໜັບສະໜູນທີ່ດີແກ່ພວກເຮົາ.

ດ້ວຍຄວາມນັບຖື ແລະ ຮັກແພງ,

Professor Elizabeth A Ashley
ຜູ້ອຳນວຍການ LOMWRU

UK Foreign Secretary the Rt Hon Mr David Lammy (*centre*) and British Ambassador to Lao PDR HE Melanie Barlow (*2nd left*) visited LOMWRU to learn more about the Fleming Fund country grant to strengthen antimicrobial resistance surveillance. Photo: Gov't of UK.

ທ່ານລັດຖະມົນຕີການຕ່າງປະເທດແຫ່ງສະຫະລາຊະອານາຈັກອັງກິດ ທ່ານ David Lammy ແລະ ທ່ານເອກອັກຄະລາຊະທູດອັງກິດປະຈຳ ສປປ ລາວ ທ່ານ Melanie Barlow ໄດ້ມາຢ້ຽມຢາມ LOMWRU ເພື່ອຮັບຟັງຂໍ້ມູນໂຄງການຂອງກອງທຶນ UK Fleming Fund ທີ່ສົ່ງເສີມການເຝົ້າລະວັງ ການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບ. ຮູບພາບໂດຍ: UK gov official

Message from the Director Professor Elizabeth Ashley

In 2024 Laos chaired the Association of Southeast Asian Nations (ASEAN) with the theme of *Enhancing Connectivity and Resilience*. The UK Foreign Secretary, the Rt Hon David Lammy, attended the ASEAN Foreign Ministers meeting and took the time to drop into LOMWRU with HE Melanie Barlow, the British Ambassador to Laos, to hear more about the UK Fleming Fund initiative to strengthen antimicrobial resistance (AMR) surveillance in the country. LOMWRU and Mahosot Hospital continued to work with our partners in five provincial hospitals in Laos in 2024 (Salavan, Savannakhet, Vientiane, Xieng Khouang and Luang Namtha) who are now processing their own microbiology samples, an indicator of the success of this initiative.

Here in Vientiane, it was another momentous year for our host organisation, Mahosot Hospital, when the second phase of hospital building was completed. On 12 Oct 2024, Lao PDR Prime Minister HE Sonexay Siphandone and HE Li Qiang, Prime Minister of the People's Republic of China, attended a ceremony to inaugurate the new building.

LOMWRU had a productive year in 2024, with two new PhD graduates, nine MSc graduates and 46 scientific publications. We hope to top this in 2025 when we will celebrate our Silver (25 year) Anniversary. This milestone will be a time to pause and reflect on what we have achieved since 2000, and also to consider how we can further increase our impact in the future with more research to improve the health of people in Laos and beyond.

Last but not least, I would like to extend my thanks to Dr Susath Vongphachanh, Director of Mahosot Hospital, and Deputy Directors Mrs Bouavanh Pathoumthong, Dr Xaysana Sombandith, Dr Bounhome Kanthavong and Dr Khaysy Rassavong, and to all other Mahosot Hospital colleagues for their continued collaboration and support.

Best wishes,

Professor Elizabeth A Ashley
Director

Mr Sao Vang, Microbiology laboratory technician, teaching technicians from the Fleming sites in Laos. © LOMWRU. Photographer: Tamalee Roberts.

ທ້າວ ຊ້າວ ວ່າງ, ນັກວິເຄາະເຕັກນິກ ພະແນກຈຸລິນຊີວິທະຍາ ໂຮງໝໍມະໂຫສົດ ໄດ້ໃຫ້ການເຝິກອົບຮົມແກ່ນັກວິເຄາະເຕັກນິກຂອງໂຮງໝໍແຂວງສະຫວັນນະເຂດ, ຫຼວງນໍ້າທາ, ສາລະວັນ ແລະ ຊຽງຂວາງ ເຊິ່ງເປັນພາກສ່ວນໜຶ່ງຂອງ Fleming fund ເພື່ອສົ່ງເສີມການເຝົ້າລະວັງການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບ (AMR). © LOMWRU. ຮູບພາບໂດຍ: Tamalee Roberts

ຜົນການຄົ້ນຄວ້າທີ່ພົ້ນເດັ່ນໃນປີ 2024

ການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບ (AMR) ແລະ ການນຳໃຊ້ຢາຕ້ານເຊື້ອຈຸລະຊີບ (AMU)

ຄູ່ມືການໃຫ້ຢາຕ້ານເຊື້ອຈຸລະຊີບແຫ່ງຊາດໄດ້ຖືກຮັບຮອງເອົາໃນປີ 2021 ແລະ ເຜີຍແຜ່ທົ່ວປະເທດໃນປີ 2023 ໂດຍກົມປິ່ນປົວ ແລະ ຟື້ນຟູໜ້າທີ່ການ, ກະຊວງສາທາລະນະສຸກ. ໃນລະຫວ່າງນັ້ນ, ຊ່ວງເດືອນ ທັນວາ ປີ 2022, ອົງການອະນາໄມໂລກໄດ້ເຜີຍແຜ່ປຶ້ມຄູ່ມືການນຳໃຊ້ຢາຕ້ານເຊື້ອ ຫຼື AWaRe (Access, Watch, Reserve) antibiotic book ເຊິ່ງເປັນຄູ່ມືແນະນຳການປິ່ນປົວພະຍາດຊຶມເຊື້ອທີ່ຖືກພົບເຫັນເລື້ອຍໆ ໃນຄົນເຈັບທີ່ເປັນເດັກນ້ອຍ ແລະ ຜູ້ໃຫຍ່ຫຼາຍກວ່າ 30 ພະຍາດ. ແຕ່ຫາກວ່າ, ການເຂົ້າເຖິງຄູ່ມືການໃຫ້ຢາຕ້ານເຊື້ອ ກໍບໍ່ສາມາດຮັບປະກັນວ່າ ຄຳແນະນຳຈາກຄູ່ມືດັ່ງກ່າວໄດ້ຖືກນຳເອົາມາຈັດຕັ້ງປະຕິບັດຕາມ. ດຣ ວິລະດາ ຈັນສະມຸດ ໄດ້ເຮັດການຄົ້ນຄວ້າ ທີ່ເປັນສ່ວນໜຶ່ງຂອງການສຶກສາໃນລະດັບຊັ້ນປະລິນຍາເອກ ເພື່ອທຳຄວາມເຂົ້າໃຈກ່ຽວກັບການໃຫ້ຢາຕ້ານເຊື້ອຈຸລິນຊີແກ່ຄົນເຈັບຂອງທ່ານໝໍລາວ ແລະ ປັດໄຈທີ່ມີຜົນຕໍ່ການນຳໃຊ້ຄູ່ມືການໃຫ້ຢາຕ້ານເຊື້ອ. ຜົນການສຶກສາໄດ້ສະແດງໃຫ້ຮູ້ວ່າ ສ່ວນໃຫຍ່ແລ້ວແພດໝໍ ອີງໃສ່ດຸນພິນິດ ແລະ ຊັບພະຍາກອນທີ່ມີໃນໂຮງໝໍຂອງຕົນ ເຊັ່ນ: ຢາຕ້ານເຊື້ອທີ່ມີຢູ່ ແລະ ຄວາມສາມາດໃນການກວດວິເຄາະຢູ່ໂຮງໝໍຕົນເປັນຕົ້ນ ເພື່ອພິຈາລະນາວ່າຈະໃຫ້ຢາຕ້ານເຊື້ອແກ່ຄົນເຈັບ ຫຼື ບໍ່. ສິ່ງທ້າທາຍຫຼັກໆຕໍ່ການໃຫ້ຢາຕ້ານເຊື້ອຢ່າງເໝາະສົມທີ່ຖືກກ່າວເຖິງເລື້ອຍໆນັ້ນ ແມ່ນຂໍ້ຈຳກັດໃນການເຂົ້າເຖິງຢາຕ້ານເຊື້ອບາງຊະນິດ ແລະ ຄວາມລ່າຊ້າຂອງຜົນກວດວິເຄາະທາງຈຸລິນຊີ. ແພດໝໍຫຼາຍທ່ານໃຫ້ຄວາມເຫັນວ່າບໍ່ຄ່ອຍໄດ້ນຳໃຊ້ຄູ່ມືການໃຫ້ຢາຕ້ານເຊື້ອ ເນື່ອງຈາກວ່າພວກເຂົາຈື່ຄຳແນະນຳທີ່ມີໃນຄູ່ມືໄດ້ແລ້ວ, ແລະ ຈຸດປະສົງການໃຊ້ປຶ້ມຄູ່ມືສ່ວນໃຫຍ່ ແມ່ນເພື່ອກວດເບິ່ງປະລິມານຂອງການໃຫ້ຢາ ແລະ ໄລຍະເວລາຂອງການປິ່ນປົວ.

ດຣ ວິລະດາ ຍັງໄດ້ທົບທວນການນຳໃຊ້ຄູ່ມືຢາຕ້ານເຊື້ອ AWaRe ຂອງອົງການອະນາໄມໂລກ ໂດຍອີງໃສ່ສະພາບເງື່ອນໄຂຕ່າງໆທີ່ມີໃນ ສປປ ລາວ ຫຼື ຢູ່ປະເທດທີ່ມີຊັບພະຍາກອນໜ້ອຍຄ້າຍຄືກັນ. ບົດລາຍງານໄດ້ສະແດງໃຫ້ເຫັນວ່າຄຳແນະນຳຈາກຄູ່ມື AWaRe ໃນການໃຫ້ຢາຕ້ານເຊື້ອນັ້ນ ອາດບໍ່ແທດເໝາະກັບທຸກໆສະພາບການລະບາດວິທະຍາຂອງພະຍາດຊຶມເຊື້ອ ແລະ ຮູບແບບການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຂອງເຊື້ອພະຍາດຢູ່ໃນ ສປປ ລາວ. ນອກນັ້ນ, ບົດທົບທວນຍັງຍົກໃຫ້ເຫັນເຖິງຂໍ້ທ້າທາຍຢູ່ພາຍໃນ ສປປ ລາວ ໃນການເຂົ້າເຖິງຢາຕ້ານເຊື້ອທີ່ຈຳເປັນ ແລະ ຢາຕ້ານເຊື້ອທີ່ຈຳເປັນໃນການຮັກສາຊີວິດຂອງຄົນເຈັບ. ປຶ້ມຄູ່ມື AWaRe ດັ່ງກ່າວນັ້ນໄດ້ກະຕຸ້ນໃຫ້ບັນດາປະເທດທີ່ກຳລັງພັດທະນາ ເຊັ່ນ ສປປ ລາວ ພິຈາລະນາໃນການຈັດຕັ້ງປະຕິບັດແນວທາງການບົ່ງມະຕິທາງເລືອກແບບໃໝ່ໆ ແລະ ເພີ່ມຂະຫຍາຍລາຍການຢາທີ່ຈຳເປັນພື້ນຖານ ເພື່ອໃຫ້ຄອບຄຸມເອົາຢາຕ້ານເຊື້ອຈຸລະຊີບທີ່ສຳຄັນອື່ນໆ.

Understanding hospital antimicrobial prescribing decisions and determinants of uptake of new local antimicrobial prescribing guidelines in Laos. Chansamouth V, Douangnouvong A, Thammavongsa P, Sombandith X, Keomany S, Rattana S, Newton PN, Day NP, Turner P, Mayxay M, van Doorn HR, Ashley EA. Wellcome *Open Res*. 2024 Sep 12;9:183. doi: 10.12688/wellcomeopenres.20884.2. PMID: 39301442; PMCID: PMC11411237.

Implementing the WHO AWaRe antibiotic book guidance in lower-resource settings: the case of the Lao PDR. Chansamouth V, Inlorkham P, Keohavong B, Bellingham K, van Doorn HR, Mayxay M, Newton PN, Turner P, Day NPJ, Ashley EA. *JAC Antimicrob Resist*. 2024 Jan 22;6(1):dlae004. doi: 10.1093/jacamr/dlae004. PMID: 38259905; PMCID: PMC10801825.

ໃນປີ 2023, ພວກເຮົາກໍໄດ້ສືບຕໍ່ສຶກສາກ່ຽວກັບການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບຢູ່ໃນປະເທດລາວ ໂດຍອີງໃສ່ແນວຄວາມຄິດສຸຂະພາບໜຶ່ງດຽວ. ດຣ ວິໄລພອນ ພົມສີສະຫວັດ, ນັກວິຊາການຄົ້ນຄວ້າສັດຕະວະແພດ, ຜູ້ທີ່ໄດ້ຮັບທຶນຈາກເຄືອຂ່າຍມະຫາວິທະຍາໄລສຸຂະພາບໜຶ່ງດຽວຂອງອາຊີຕາເວັນອອກສ່ຽງໃຕ້ ເຮັດການສຶກສາກ່ຽວກັບເຊື້ອ *Escherichia coli (E. coli)* ທີ່ຕ້ານຕໍ່ຢາຕ້ານເຊື້ອ colistin ຢູ່ໃນໝູ ແລະ ຄົນ. ໂດຍການສຶກສາແບບປະສົມປະສານນີ້ ໄດ້ສຶກສາຕົວຢ່າງໄຈ້ແຍກຈາກຕົວຢ່າງເລືອດຂອງຄົນເຈັບ 620 ຕົວຢ່າງ ແລະ ຕົວຢ່າງຕ້ອຍທະວານໝູ 895 ຕົວຢ່າງ, ສາມາດກວດພົບເຊື້ອ *E. coli* ທີ່ຕ້ານຕໍ່ຢາຕ້ານເຊື້ອ colistin ຈາກຕົວຢ່າງຂອງຄົນ 2.4% ແລະ ຈາກຕົວຢ່າງຂອງໝູ 65.0%. ຜົນການກວດທາງພັນທຸກຳ ເຫັນວ່າຢີນຕ້ານຕໍ່ຢາຕ້ານເຊື້ອ colistin ສ່ວນໃຫຍ່ແມ່ນຢີນ *mcr-1* (57.8%) ຮອງລົງມາແມ່ນຢີນ *mcr-3* (20.23%) ແລະ ອີກ 22.24% ແມ່ນມີຢີນ *mcr-1* ແລະ *mcr-3* ຢູ່ນຳກັນ. ຜົນການສຶກສາ ສະແດງໃຫ້ເຫັນວ່າມີການນຳໃຊ້ຢາຕ້ານເຊື້ອ colistin ຫຼາຍຢູ່ໃນຂະແໜງການລ້ຽງສັດ ແລະ ພົບຄວາມສ່ຽງດ້ານສາທາລະນະສຸກ ເຊິ່ງໄດ້ຍົກໃຫ້ເຫັນເຖິງຄວາມຈຳເປັນຂອງການນຳໃຊ້ນິຕິກຳ ແລະ ການກຳກັບການນຳໃຊ້ຢາຕ້ານເຊື້ອຢ່າງສົມເຫດສົມຜົນໃຫ້ເຂັ້ມງວດຍິ່ງຂຶ້ນ.

ຫຼາຍໆທ່ານຈະຄຸ້ນເຄີຍກັບເຊື້ອຈຸລິນຊີແກມລົບທີ່ຜະລິດ ESBL (extended spectrum beta-lactamase) ທີ່ເປັນສາເຫດເຮັດໃຫ້ເກີດການຕ້ານຕໍ່ຢາ ceftriaxone ຂອງເຊື້ອ *E. coli* ແລະ ເຊື້ອກຸ່ມ *Klebsiella* spp. ທີ່ຜະລິດເອນໄຊ AmpC β-lactamases ເຊິ່ງນີ້ກໍເປັນອີກສາເຫດໜຶ່ງເຮັດໃຫ້ເຊື້ອຈຸລະຊີບຕ້ານຕໍ່ຢາຕ້ານເຊື້ອ cephalosporin ລຸ້ນທີ 3. ການສຶກສາຮ່ວມກັນລະຫວ່າງ LOMWRU ແລະ ໜ່ວຍງານເອື້ອຍນ້ອງພວກເຮົາຢູ່ທີ່ປະເທດກຳປູເຈຍ ແລະ ໄທ ສະແດງໃຫ້ເຫັນວ່າ AmpC β-lactamase ເປັນສາເຫດສຳຄັນທີ່ເຮັດໃຫ້ຄົນເຈັບທີ່ອາໄສຢູ່ໃນພາກພື້ນອາຊີຕາເວັນອອກສ່ຽງໃຕ້ມີອາການຊຶມເຊື້ອ ແຕ່ອາດຈະກວດບໍ່ພົບ ເນື່ອງຈາກຄວາມຈຳກັດໃນການເຂົ້າເຖິງການກວດ ເຊິ່ງໄດ້ສົ່ງຜົນຕໍ່ການຮັກສາຄົນເຈັບບໍ່ໄດ້ຮັບຜົນດີທີ່ສຸດ.

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ວຽກງານການຮ່ວມມືກັບບັນດາຫ້ອງວິເຄາະຄູ່ຮ່ວມງານຂອງໂຮງໝໍແຂວງຫຼາຍແຫ່ງໃນປະເທດລາວ ໃນການສະໜັບສະໜູນຍົກສູງຄວາມສາມາດການກວດວິເຄາະທາງຈຸລິນຊີໃຫ້ມີຄຸນະພາບສູງ ທີ່ເປັນສ່ວນໜຶ່ງພາຍໃຕ້ທຶນຊ່ວຍເຫຼືອຂອງກອງທຶນ Fleming Fund ແລະ ການສຶກສາກ່ອນໜ້ານີ້ຂອງພວກເຮົາທີ່ສະແດງໃຫ້ເຫັນເຖິງຄ່າໃຊ້ຈ່າຍຂອງການກວດວິເຄາະທາງຈຸລິນຊີທີ່ສູງນັ້ນ ໄດ້ຍົກໃຫ້ເຫັນເຖິງຂໍ້ທ້າທາຍຂອງການຄໍ້າຈູນວຽກງານເຝົ້າລະວັງການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບ ໂດຍປາສະຈາກທຶນຮອນຊ່ວຍເຫຼືອຈາກພາຍນອກ ໂດຍສະເພາະແມ່ນຢູ່ປະເທດທີ່ກຳລັງພັດທະນາ. ເພື່ອເພີ່ມ

ຄວາມຕະໜັກຮູ້ກ່ຽວກັບບັນຫາດັ່ງກ່າວ ພວກເຮົາໄດ້ເຮັດການວິເຄາະທາງເສດຖະສາດເພື່ອປະເມີນຄ່າໃຊ້ຈ່າຍທີ່ມີມາຕໍ່ເນື່ອງຂອງລະບົບເຝົ້າລະວັງການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຈຸລະຊີບທີ່ເປັນມາດຕະຖານແຫ່ງຊາດ. ຜົນການວິເຄາະ ຄາດຄະເນວ່າ ບັນດາປະເທດທີ່ກຳລັງພັດທະນານັ້ນ ມີ 28 ປະເທດຈະມີຄ່າໃຊ້ຈ່າຍຫຼາຍກວ່າ 5% ຂອງລາຍຈ່າຍທົ່ວໄປຂອງລັດຖະບານຕໍ່ວຽກງານສາທາລະນະສຸກ (GGHE-D) ແລະ ມີຫຼາຍກວ່າ 2% ຂອງ GGHE-D ທັງໝົດ 46 ປະເທດ. ເພື່ອໃຫ້ເຫັນພາບຊັດເຈນຂຶ້ນ, ປະເທດທີ່ໄດ້ຮັບການສະໜັບສະໜູນຈາກ Gavi ໄດ້ໃຊ້ຈ່າຍ 3.3% ແລະ ເປັນ 2.4% ຂອງລາຍຈ່າຍທັງໝົດຂອງລັດຖະບານຕໍ່ວຽກງານສາທາລະນະສຸກ ໃນການເສີມສ້າງພູມຄຸ້ມກັນ ສົກປີ 2021. ພວກເຮົາສະຫຼຸບໄດ້ວ່າວຽກງານເຝົ້າລະວັງການຕ້ານຕໍ່ຢາຕ້ານເຊື້ອຢູ່ປະເທດກຳລັງພັດທະນານັ້ນບໍ່ສາມາດຍືນຍົງໄດ້ຖ້າຫາກປາສະຈາກກົນໄກການເງິນໄລຍະຍາວຂອງສາກົນ.

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ການບິ່ງມະຕີ

ພວກເຮົາມີຄວາມກະຕືລືລົ້ນສະເໝີໃນການປະເມີນເຄື່ອງມື ຫຼື ວິທີການກວດວິເຄາະແບບໃໝ່ ທີ່ງ່າຍໃນການນຳໃຊ້ຢູ່ເຂດຫ່າງໄກສອກຫຼີກ ແລະ ສອດຄ່ອງກັບຮູບແບບການລະບາດວິທະຍາຂອງພະຍາດຊຶມເຊື້ອຢູ່ປະເທດເຂດຮ້ອນ.

ພະຍາດເຂດຮ້ອນ ໂດຍສະເພາະແມ່ນພະຍາດຊຶມເຊື້ອອື່ນໆ ທີ່ບໍ່ແມ່ນໄຂ້ຍຸງມາລາເຣຍ, ທີ່ເປັນສາເຫດຂອງການເຈັບປ່ວຍ ແລະ ເສຍຊີວິດຢ່າງຫຼວງຫຼາຍຢູ່ໃນຂົງເຂດອາຊີ-ປາຊີຟິກ. ການບິ່ງມະຕິພະຍາດເຫຼົ່ານີ້ແມ່ນມີຄວາມທ້າທາຍຫຼາຍ ເນື່ອງຈາກອາການທາງຄລີນິກສ່ວນໃຫຍ່ແມ່ນຄ້າຍຄືກັນ. ການກວດຢູ່ຫ້ອງວິເຄາະທີ່ເປັນຮູບແບບດັ້ງເດີມເພື່ອຈຳແນກພະຍາດເຂດຮ້ອນເຫຼົ່ານັ້ນຈຳເປັນຕ້ອງມີພື້ນຖານໂຄງລ່າງຫຼາຍຢ່າງ ແລະ ຕ້ອງມີບຸກຄະລາກອນທີ່ມີປະສົບການ ເຊິ່ງມັນຈຳກັດການເຂົ້າເຖິງການບິ່ງມະຕິທີ່ຖືກຕ້ອງ ຢູ່ພື້ນທີ່ທີ່ມີການລະບາດຂອງເຊື້ອພະຍາດ ທີ່ຂາດຊັບພະຍາກອນ. ການນຳໃຊ້ເຄື່ອງກວດຫາເຊື້ອພະຍາດແບບໄວ (RDTs) ເປັນທາງອອກທີ່ສາມາດຫາຊື້ໄດ້ເພື່ອໃຊ້ໃນການຄຸ້ມຄອງພະຍາດ ແລະ ການເບິ່ງແຍງຄົນເຈັບ. ເຖິງແມ່ນວ່າຈະມີ RDT ສຳຫຼັບກວດຫາເຊື້ອພະຍາດຊະນິດອື່ນໆນອກຈາກໄຂ້ມາລາເຣຍແລ້ວກໍຕາມ ແຕ່ຍັງມີບັນຫາທາງດ້ານການເງິນ ແລະ ການເຂົ້າເຖິງເຄື່ອງກວດ ເພື່ອທີ່ຈະສ້າງການກວດແບບແຍກກວດຫາແຕ່ລະເຊື້ອນັ້ນ ຢູ່ຂົງເຂດທີ່ມີຂໍ້ຈຳກັດທາງດ້ານຊັບພະຍາກອນ. ເພື່ອຈັດການກັບສິ່ງທ້າທາຍເຫຼົ່ານີ້, ເຄື່ອງກວດທີ່ສາມາດກວດຫາເຊື້ອພະຍາດເຂດຮ້ອນຫຼາຍຊະນິດພ້ອມກັນໄດ້ໃນຄັ້ງດຽວອາດເປັນທາງອອກ. ການສຶກສານີ້ພວກເຮົາໄດ້ເຮັດການປະເມີນຄວາມຖືກຕ້ອງຊັດເຈນຂອງການກວດຫາເຊື້ອພະຍາດດ້ວຍແຜ່ນກວດ multiplex lateral flow immunoassay (DPP Fever Panel II Assay Asia, Chembio, Inc.) ທີ່ງ່າຍໃນການກວດ ເຊິ່ງສາມາດກວດຫາທາດພາຍຕ້ານ IgM ແລະ/ຫຼື Antigens ສະເພາະ ຂອງເຊື້ອພະຍາດ 7 ຊະນິດເຊັ່ນ: Scrub typhus, Murine typhus, Leptospirosis, Melioidosis, Dengue fever, Chikungunya, ແລະ Zika virus. ເຄື່ອງກວດວິເຄາະດັ່ງກ່າວໃຫ້ຜົນທຽບເທົ່າກັບຜົນກວດຈາກເຄື່ອງກວດທີ່ມີຂາຍທົ່ວໄປ ແລະ ຜົນກວດຈາກເຄື່ອງກວດມາດຕະຖານຈຳນວນໜຶ່ງ. ນອກນັ້ນ, ກໍຍັງໃຫ້ຜົນເທົ່າທຽມກັນລະຫວ່າງຕົວຢ່າງເລືອດລອມ ແລະ ຕົວຢ່າງເຊຣັ່ມ. ຖ້າຫາກນຳໃຊ້ແຜ່ນກວດເປັນເຄື່ອງໃຊ້ດຽວເພື່ອບິ່ງມະຕິອາການໄຂ້ກະທັນຫັນ ຈຳເປັນຕ້ອງໄດ້ປັບປ່ຽນຄ່າ cut-offs ໃຫ້ເໝາະສົມຕາມຈຸດປະສົງ ແລະ ຄວາມໄວໃນກວດພົບເຊື້ອ (sensitivity) ແລະ ຄວາມສະເພາະເຈາະຈົງ (specificity) ຕາມທີ່ຕ້ອງການ. ມີຄວາມຈຳເປັນທີ່ຈະສຶກສາກ່ຽວກັບການກຳນົດຄ່າ cut-offs ຢູ່ໃນພື້ນທີ່ລະບາດອື່ນ, ເພື່ອເພີ່ມອັດຕາການບິ່ງມະຕິພະຍາດຊຶມເຊື້ອເຂດຮ້ອນໃນຂົງເຂດທີ່ມີຊັບພະຍາກອນຈຳກັດ.

ໃນໄລຍະເລີ່ມຕົ້ນຂອງການລະບາດພະຍາດໂຄວິດ 19, ກ່ອນທີ່ຈະມີເຄື່ອງກວດຊອກຫາເຊື້ອພະຍາດແບບວ່ອງໄວ (RDT) ນັ້ນ, ເຕັກນິກການບິ່ງມະຕິທີ່ເປັນມາດຕະຖານ ແມ່ນການກວດທາງດ້ານພັນທຸກຳ (Real-time PCR) ເຊິ່ງຈຳເປັນຕ້ອງປະຕິບັດຢູ່ຫ້ອງວິເຄາະທີ່ມີຄວາມພ້ອມທາງດ້ານເຄື່ອງມື ແລະ ການຂົນສົ່ງຕົວຢ່າງທີ່ເກັບໃສ່ພູມປູກສະເພາະສຳລັບການນຳສົ່ງຕົວຢ່າງ (VTM) ທີ່ຕ້ອງຮັກສາໃນອຸນຫະພູມເຢັນ. ເຊິ່ງວິທີການດັ່ງກ່າວເປັນຂໍ້ຫຍຸ້ງຍາກທີ່ຈະປະຕິບັດຢູ່ເຂດຫ່າງໄກສອກຫຼີກ ເນື່ອງຈາກລະບົບຂົນສົ່ງຍັງບໍ່ສະດວກເທົ່າທີ່ຄວນ. ພາຍໃຕ້ການຊີ້ນຳຂອງທ່ານນາງ ດຣ Audrey Dubot-Pérès, ພວກເຮົາໄດ້ເຮັດການສຶກສາຢູ່ໂຮງໝໍແຂວງສາມແຫ່ງໃນປະເທດລາວ ເພື່ອສົມທຽບການກວດຫາເຊື້ອພະຍາດ SARS-CoV-2 ຈາກຕົວຢ່າງສົດ ແລະ ຕົວຢ່າງທີ່ເກັບດ້ວຍແຜ່ນຊັບແຫ້ງ (neat and dried spot sample) ແລ້ວສົ່ງມາກວດຢູ່ຫ້ອງວິເຄາະຈຸລິນຊີຂອງໂຮງໝໍມະໂຫສົດ ພາຍໃຕ້ອຸນຫະພູມປົກກະຕິ ແລະ ຈາກຕົວຢ່າງທີ່ເກັບ ແລະ ນຳສົ່ງດ້ວຍວິທີມາດຕະຖານ.

ໃນຈຳນວນຜູ້ເຂົ້າຮ່ວມການສຶກສາ 479 ຄົນ, ສາມາດກວດພົບເຊື້ອພະຍາດໂຄວິດ 19 ຈາກຕົວຢ່າງທີ່ເກັບດ້ວຍ VTM ຈຳນວນ 288 ຕົວຢ່າງ (60.1%). ອັດຕາການກວດພົບເຊື້ອທີ່ສອດຄ່ອງກັນສູງສຸດແມ່ນ ຕົວຢ່າງທີ່ເກັບດ້ວຍໄມ້ຕ້ອຍຜ້ຶງດັ່ງແຫ້ງ 84.8% (95% CI, 80.2% - 88.8%) ແລະ ຕົວຢ່າງນ້ຳລາຍ 89.2% (95% CI, 85.1% - 92.6%) ເມື່ອທຽບກັບການເກັບດ້ວຍ VTM ແລະ ພົບວ່າຕົວຢ່າງນ້ຳລາຍທີ່ເກັບໃສ່ແຜ່ນຊັບແຫ້ງນັ້ນເສຍຄວາມໄວ (sensitivity) ໃນການກວດພົບເຊື້ອ ແລະ ວິທີນີ້ອາດສາມາດນຳໄປປັບໃຊ້ເພື່ອກວດຫາເຊື້ອພະຍາດຊຶມເຊື້ອທາງລະບົບຫາຍໃຈອື່ນໄດ້ ເຊັ່ນ: ເຊື້ອໄຂ້ຫວັດໃຫຍ່.

Diagnostic accuracy of DPP Fever Panel II Asia tests for tropical fever diagnosis. Dhawan S, Dittrich S, Arafah S, Ongarello S, Mace A, Panapruksachat S, Boutthasavong L, Adsamouth A, Thongpaseuth S, Davong V, Vongsouvath M, Ashley EA, Robinson MT, Blacksell SD. *PLoS Negl Trop Dis*. 2024 Apr 10;18(4):e0012077. doi: 10.1371/journal.pntd.0012077. PMID: 38598549; PMCID: PMC11034646.

Dry Swabs and Dried Saliva as Alternative Samples for SARS-CoV-2 Detection in Remote Areas in Lao PDR. Sibounheuang B, Boutthasavong L, Chommanam D, Phommasone K, Panapruksachat S, Praphasiri V, Bouttavong S, Sisavath H, Christy NCV, Letizia AG, Mayxay M, Vongsouvath M, Ashley EA, Dubot-Pérès A. *Open Forum Infect Dis*. 2024 Jul 23;11(8):ofae433. doi: 10.1093/ofid/ofae433. PMID: 39145142; PMCID: PMC11322834.

Dr Koukeo Phommasone takes visiting collaborators from NAMRU-IP on a tour of the laboratory. From left: Dr Anousone Douangnouvong, Dr Koukeo Phommasone, and NAMRU-IP's LCDR Irina Etobayeva, LCDR Dawn Weir and Captain Andrew Letizia. © LOMWRU.

ດຣ ກຸແກ້ວ ພົມມະສອນ ໄດ້ນຳພາແຂກທີ່ເປັນຄູ່ຮ່ວມງານຈາກ NAMRU-IP ຢ້ຽມຢາມຫ້ອງວິເຄາະ (ພາບຈາກຊ້າຍຫາຂວາ: ດຣ ອານຸສອນ ດວງນຸວົງ, ດຣ ກຸແກ້ວ ພົມມະສອນ, LCDR Irina Etobayeva, LCDR Dawn Weir, Captain Andrew Letizia) © LOMWRU.

Research highlights in 2024

Here we highlight a selection of research outputs of LOMWRU and partner organisations published in 2024. The complete list with abstracts is found in the LOMWRU Publications in 2024 section of the report.

Antimicrobial resistance (AMR) and antimicrobial use (AMU)

The Lao national antimicrobial prescribing guidelines were issued in 2021 and rolled out across the country by the Department of Healthcare and Rehabilitation (DHR), Ministry of Health (MoH) in 2023. Meanwhile, in December 2022, the WHO published the AWaRe (Access, Watch, Reserve) antibiotic book with treatment guidance for

more than 30 common clinical infections in children and adults. Distributing guidelines does not guaran¬tee they will be followed. Dr Vilada Chansamouth conducted a qualitative study as part of her DPhil to understand how Lao clinicians prescribed antibiotics and the factors influencing their guideline uptake. The study revealed that most clinicians relied on their clinical judgment and hospital re¬sources, such as available antibiotics and laboratory diagnostic capacities in their hospitals. Key challenges to appropriate prescribing included limited access to certain antibiotics and delay in mi¬crobiology result turnaround times. Many clinicians reported infrequent use of the newly released antimicrobial prescribing guidelines because they could recall the treatment recommendations in the guidelines and the main purpose of their use was to check the dose and duration of the treatment.

Dr Vilada also assessed the WHO AWaRe book from the perspective of implementing it in Laos or similar low-resource settings. The report highlighted that not all recommendations in the AWaRe book align with epidemiology of infectious disease and patterns of antimicrobial susceptibility in Laos. It also emphasized the challenge of limited access to essential and life-saving antibiotics in the country. The AWaRe book encourages lower-middle income settings like Laos to consider alter¬native diagnostic approaches and expand the national essential medicines list to include additional antimicrobials.

Understanding hospital antimicrobial prescribing decisions and determinants of uptake of new local antimicrobial prescribing guidelines in Laos. Chansamouth V, Douangnouvong A, Thammavongsa P, Sombandith X, Keomany S, Rattana S, Newton PN, Day NP, Turner P, Mayxay M, van Doorn HR, Ashley EA. *Wellcome Open Res*. 2024 Sep 12;9:183. doi: 10.12688/wellcomeopenres.20884.2. PMID: 39301442; PMCID: PMC11411237.

Implementing the WHO AWaRe antibiotic book guidance in lower-resource settings: the case of the Lao PDR. Chansamouth V, Inlorkham P, Keohavong B, Bellingham K, van Doorn HR, Mayxay M, Newton PN, Turner P, Day NPJ, Ashley EA. *JAC Antimicrob Resist*. 2024 Jan 22;6(1):dlae004. doi: 10.1093/jacamr/dlae004. PMID: 38259905; PMCID: PMC10801825.

We continued to study AMR in Laos in 2024, taking a One Health approach. Our SEAOHUN (Southeast Asia One Health University Network) Fellow, research veterinarian Dr Vilaiphone Phomsisavath, reported on colistin resistance in *Escherichia coli* in pigs (carriage) and humans (invasive isolates). This cross-sectional study investigated 620 human blood culture isolates and 895 pig rectal swabs. Results revealed that 2.4% of human isolates and 65.0% of *E.coli* from pig samples were colistin-resistant. Molecular analysis showed that the detected colistin resistance genes of isolates were predominantly *mcr-1* (57.8%), followed by *mcr-3* (20.23%), with 22.24% of isolates co-harbouring both *mcr-1* and *mcr-3*. These findings highlight the extensive use of colistin in the animal sector and its public health risks, emphasizing the need for enforceable legislation and strengthened antimicrobial stewardship.

Many people are now familiar with ESBL (extended spectrum beta-lactamase)-producing Gram negative bacteria, causing ceftriaxone resistance in *E.coli* and *Klebsiella* spp. AmpC β-lactamases are another neglected cause of third-generation cephalosporin resistance in these organisms. This collaborative study between LOMWRU and our sister units in Cambodia and Thailand showed that AmpC β-lactamases are an important cause of infection in Southeast Asia that may be going undetected due to lack of access to testing, resulting in sub-optimal treatment for patients.

Investigation of *Escherichia coli* isolates from pigs and humans for colistin resistance in Lao PDR-a cross-sectional study. Phomsisavath V, Roberts T, Seupsanith A, Robinson MT, Nammanininh P, Chanthavong S, Chansamouth V, Vongsouvath M, Theppangna W, Christensen P, Blacksell SD, Mayxay M, Ashley EA. *One Health*. 2024 Apr 30;18:100745. doi: 10.1016/j.onehlt.2024.100745. PMID: 38725959; PMCID: PMC11079391.

AmpC β-lactamases detected in Southeast Asian *Escherichia coli* and *Klebsiella pneumoniae*. Roberts T, Ling CL, Watthanaworawit W, Cheav C, Sengduangphachanh A, Silisouk J, Hopkins J, Phommasone K, Batty EM, Turner P, Ashley EA. *JAC Antimicrob* Resist. 2024 Nov 28;6(6):dlae195. doi: 10.1093/jacamr/dlae195. PMID: 39610980; PMCID: PMC11604056.

LOMWRU works with our partner laboratories in provincial hospitals in Laos to support them to deliver high quality microbiological diagnosis on-site as part of the Fleming Fund country grant. Our previous study showing the high costs of diagnostic microbiology has highlighted the challenges to sustaining AMR surveillance without external funding support, especially in low-income countries (LICs) and lower middle-income countries (LMICs). To raise awareness around this issue we conducted an economic analysis to estimate the continued costs of a standard national AMR surveillance system. From our analysis, the costs are predicted to account for >5% of the total domestic general government health expenditure (GGHE-D) for 28 LMICs and more than 2% of GGHE-D for 46 LMICs. To put this into perspective, Gavi-supported countries spent 3.3% and 2.4% of total government health expenditure on immunization in 2021. We conclude that AMR surveillance is not sustainable in most LMICs without a long-term global financing mechanism.

Sustainable antimicrobial resistance surveillance: time for a global funding mechanism. Painter C, Limmathurotsakul D, Roberts T, van Doorn HR, Mayxay M, Lubell Y, Day NPJ, Turner P, Ashley EA. *Lancet Infect Dis*. 2024 Dec 17:S1473-3099(24)00649-2. doi: 10.1016/S1473-3099(24)00649-2. Epub ahead of print. PMID: 39706207.

Diagnostics

We are always keen to evaluate new diagnostic tools or methods that are simple to use in remote areas and aligned with the epidemiology of infectious diseases in tropical countries.

Tropical fevers, specifically those caused by non-malarial infectious agents, contribute to consider-able morbidity and mortality in the Asia-Pacific region. Diagnosis of these pathogens is challenging since the clinical signs are often indistinguishable. Conventional laboratory tests to differentiate between tropical diseases require substantial infrastructure and experienced staff, limiting access to accurate tests in low-resource endemic regions. Rapid diagnostic tools (RDTs) offer an affordable solution for disease management and patient care. Although RDTs are also available for detecting non-malarial pathogens, there are financial and accessibility issues in establishing multiple sepa¬rate tests in resource-constrained regions. To overcome these challenges, a multi-detection diag¬nostic platform with the capacity to diagnose a diverse range of tropical fevers would be a solution. This study evaluated the accuracy of an easier-to-use multiplex lateral flow immunoassay test (DPP Fever Panel II Assay Asia, Chembio, Inc.) that can detect IgM antibodies and/or specific antigens of seven common tropical diseases (Scrub typhus, Murine typhus, Leptospirosis, Melioidosis, Dengue fever, Chikungunya, and Zika virus). The test offers comparable diagnostic accuracy to commercial¬ly available tests and to some reference tests. The test also performs at equivalent accuracy with both blood and serum samples. If the fever panel were used as a stand-alone test for acute febrile illness diagnosis, cut-offs would need to be adjusted depending on the use of the test, and the desired sensitivity and specificity. There is a need to investigate the use of these cut-offs in other endemic regions, which could improve the rate of tropical fever diagnosis in low-resource settings.

During the early stages of the COVID-19 pandemic, before RDTs became available, the gold standard diagnostic test was real-time reverse transcription-polymerase chain reaction (PCR), which requires laboratory facilities and cold chain for transportation of samples in viral transport medium (VTM). This is difficult to implement in remote areas with weak transportation links. Led by Dr Audrey Dubot-Pérès, we conducted a study at three provincial hospitals in Laos to compare the detection of SARS-CoV-2 from neat and dried spot samples transported to our laboratory in Mahosot Hospital at ambient temperature to the gold standard method.

Among 479 enrolled participants, VTM samples tested positive for 288 (60.1%). High positive percent agreements were observed for dry swab (84.8%; 95% CI, 80.2%-88.8%) and saliva (89.2%; 95% CI, 85.1%-92.6%) as compared with VTM. There was a loss of sensitivity when saliva was dried on filter paper. This method could be generalisable to diagnosis of other respiratory infections eg influenza.

Diagnostic accuracy of DPP Fever Panel II Asia tests for tropical fever diagnosis. Dhawan S, Dittrich S, Arafah S, Ongarello S, Mace A, Panapruksachat S, Boutthasavong L, Adsamouth A, Thongpaseuth S, Davong V, Vongsouvath M, Ashley EA, Robinson MT, Blacksell SD. *PLoS Negl Trop Dis*. 2024 Apr 10;18(4):e0012077. doi: 10.1371/journal.pntd.0012077. PMID: 38598549; PMCID: PMC11034646.

Dry swabs and dried saliva as alternative samples for SARS-CoV-2 detection in remote areas in Lao PDR. Sibounheuang B, Boutthasavong L, Chommanam D, Phommasone K, Panapruksachat S, Praphasiri V, Bouttavong S, Sisavath H, Christy NCV, Letizia AG, Mayxay M, Vongsouvath M, Ashley EA, Dubot-Pérès A. *Open Forum Infect Dis*. 2024 Jul 23;11(8):ofae433. doi: 10.1093/ofid/ofae433. PMID: 39145142; PMCID: PMC11322834.

Dr Danoy Chommanam observing Dr Podjanee Jittamala enrolling a patient into the AD-ASTRA study in Bangkok. © MORU/LOMWRU.

ดร ดาน้อย ได้สังเกตเบิ่ง ดร Podjanee Jittamala ที่กำลังเอิาถิมเจับเข้ำภานสึกสา AD ASTRA ที่บางกอก. © MORU/LOMWRU.

Participants in Statistical analysis using R software, a short course conducted by MORU CTSG November 2024 at LOMWRU. © MORU. Photographer: Mavuto Mukaka.

ผะนักงานเข้ำธ่วมภานเฝิกอิบธึมวิเถาะข้ำมูนโดยใช้ โปูแกูม R ในเดือนผะจิก 2024 ที่ LOMWRU, สอนโดย MORU CTSG. ธุบผาบโดย: Mavuto Mukaka.

Training highlights in 2024

Postgraduate training

Here we present all of our postgraduate students who graduated or were studying for DPhil, PhD or Master's degrees in 2024, along with other training highlights.

Doctoral students

Two doctoral students graduated in 2024. Many congratulations to **Dr Vilada Chansamouth** who passed her DPhil viva on 19 Dec 2024 at the University of Oxford. Dr Vilada's thesis, *Evaluating the impact of a Lao language mobile phone antimicrobial use guideline application on antimicrobial prescribing in the Lao PDR*, was supervised by Elizabeth Ashley, Paul Newton, Mayfong Mayxay, Paul Turner, Rogier van Doorn and Nick Day.

Congratulations also go to **Dr Patricia Tabernero** who passed her PhD viva on 10 October 2024. Her thesis, *Understanding the prevalence and burden of poor quality antibiotics and anti-tuberculosis medicines*, at the University of Alcalá, Madrid, was supervised by Albert Figueras and Paul Newton. Patricia (*2nd left*) was examined by, *from left*, Prof Bruno González Zorn, Dr Harparkash Kaur, and Prof Francisco José Abajo. Based in LOMWRU from 2011 to 2014, Patricia was the first coordinator for what became MORU's Medicine Quality Research Group (MQRG).

Research Pharmacist **Khonsavath Bellingham** continues to study for her PhD through The Open University UK. Konnie aims to provide evidence that economic analysis is a necessary and achievable criteria that should be included in the antimicrobial selection process for the National Essential Medicines Listing of Lao PDR.

Master's students

Several LOMWRU students and alumni graduated with a Master's degree in 2024.

Manilung Nalongsack, LOMWRU Research Pharmacist, was awarded a prestigious Chevening Scholarship by the UK government and graduated with a Master's in Health Policy, Planning and Financing from the London School of Hygiene & Tropical Medicine (LSHTM) and the London School of Economics (LSE).

Vanheuang Phommadeechack, LOMWRU Rickettsia laboratory technician and BSL3 Manager, completed his MSc in Tropical Medicine at Mahidol University, Thailand. Vanheuang was awarded the Dr Sylvia Meek Scholarship for Entomology, the only awardee in Thailand for the 2022-2024 intake, which supports a new generation of public health specialists in Africa and Asia. Vanheuang's thesis, *The Accumulation of Vector-Borne Zoonosis in Companion Animals and Their Owners in Lao PDR*, looked at rickettsial pathogens infecting companion animals and their owners in Vientiane. Ectoparasites were identified using established morphological techniques, which were compared to molecular and MALDI-TOF methods of identification. *Rickettsia* spp. (including *R. asembonensis* and *R. felis*) were detected in 47.37% of fleas collected from dogs and cats, 3.52% of ticks collected from 142 dogs and 50% of lice collected from 2 dogs. Anaplasmataceae (including *Ehrlichia canis* and *Anaplasma platys*) were detected in 94.74% of fleas collected from dogs and cats, and 22.54% of ticks collected from dogs. Vanheuang also looked at the sero-positivity of both the pets and the owners, and found that 12% of cats and 1.32% of pet owners were positive for IgG against spotted fever group *Rickettsia*. The work described the risk exposure to vector-borne zoonotic disease to better understand the risk of transmission of infectious zoonotic diseases.

Dr Laddaphone Bounvilay and **Dr Inthaphavanh Kitignavong** graduated with an MSc in Public Health at the University of Auckland. **Dr Souksopha Banmanivong** and **Dr Thadsana Sayasone** graduated from the Lao Tropical and Public Health Institute and completed their projects with LOMWRU, *on Hepatitis E Virus Seroprevalence in Blood Donations from 17 Provincial Blood Centers, Lao PDR (Dr Souksopha),* and *Understanding the landscape of common sexually transmitted infections among people aged 15 years old and above at Vientiane Youth Center and National Dermatology Center: a cross-sectional study* (Dr Thadsana).

We supervised two students from the MSc in Tropical Medicine and International Health from the London School of Hygiene and Tropical Medicine (LSHTM). **Dr Sana Hasan**, a trainee anaesthetist, analysed data from the Mahosot Hospital Critical Care Registry, and **Dr Meghna Anil**, a trainee in Infectious Diseases, undertook a dengue sequencing project.

Dr Phillip Chigiya, physician and international student (Zimbabwe) from the University of Oxford MSc in International Health and Tropical Medicine, completed a project on the use of primaquine for radical cure for *P. vivax* malaria.

Ms Amphone Sengduangphachanh, Senior Mahosot Microbiology Laboratory technician, continues to study for an MSc in Clinical Microbiology and Laboratory Management, a hybrid course organized by Siriraj Hospital in Bangkok.

Funded by a scholarship from the Institute of Tropical Medicine (Antwerp) and the Belgian Development Cooperation, research veterinarian **Dr Vilaiphone Phomsisavath** is in the second year of her MSc course in Global One Health: diseases at the human-animal interface. This is a part-time course over two years, which includes periods of study in Belgium and South Africa.

There are more MScs to come, since two of our junior researchers, Dr Vannavong Siratana and Dr Mayulee Thalongsengchanh, were awarded Manaaki scholarships by the New Zealand government in 2024 to study for an MSc in Public Health, conditional on achieving the requisite English score. They enrolled in Vientiane College in January 2025.

Other training

Kaisone Padith, LOMWRU laboratory technician, was awarded a SEAMEO scholarship to attend the Diploma in Medical Microbiology course at the Institute for Medical Research, Kuala Lumpur, Malaysia.

Postdoctoral Scientist **Dr Weerawat Phuklia** (*back row, left of poster*) was one of 15 researchers selected to join the Wellcome-funded MORU-OUCRU Discovery Research Academy (MODRA) in 2024. The scheme targets postdoctoral researchers from Southeast Asia, with places awarded after an open competition. MODRA aims to nurture the next generation of scientific leaders in low- and middle-income countries of South Asia.

In 2024 **Mrs. Latsaniphone Boutthasavong** completed the first of three courses in the Certificate Program in Laboratory Leadership and Management (CPLLM). This program, a collaboration program between the University of Washington's Departments of Laboratory Medicine & Pathology and Global Health, delivers high-quality online learning for health professionals. It aims to enhance the leadership and management skills of laboratory staff in supervisory roles, empowering them to drive meaningful improvements in laboratory testing quality and operations.

Special mention to **Dr Noidavanh Kienthaouthone**, Infectious Diseases physician at Xieng Khouang Provincial Hospital, who received a scholarship to study for the Diploma in Tropical Medicine and Hygiene in London from September to December 2024.

LOMWRU interns

Dr Somxay Dadivong joined the Molecular bacteriology team for a three-month internship, under the Southeast Asia One Health University Network (SEAOHUN) Regional Internship Programme. The internship program provides opportunities for undergraduate students or recent bachelor's degree graduates in SEAOHUN member countries to gain hands-on experience working on One Health issues at renowned host organizations. Somxay, a medical student graduated from Lao University of Medical Sciences, worked on the WIViREIDS project, looking at pathogens found in wild animal markets.

Dr Nicola Bonadiman, an Italian infectious diseases doctor, spent a one month internship at LOMWRU, familiarizing himself with melioidosis and other diseases specific to Southeast Asia.

UK Fleming Fund Lao country grant

The Fleming Fund continued for its 5th year in Laos with LOMWRU and the Mahosot Hospital Microbiology Laboratory continuing to support activities in collaboration with Fondation Mérieux and the National Centre for Laboratory and Epidemiology (NCLE). The Fleming Fund is a UK Aid programme that aims to support the strengthening of national AMR surveillance systems and laboratories, and improve public awareness of AMR and global data use. LOMWRU/Mahosot Hospital support five provincial hospital laboratory sites within Laos (Xieng Khouang, Salavan, Luang Namtha, Savannakhet and Vientiane Province) with NCLE/Fondation Mérieux supporting another five.

In 2024 there was a focus on producing quality data and improving laboratory quality management systems (LQMS). The year kicked off with LQMS site assessments at the five laboratory sites in April. Also in April, two infectious diseases clinicians from each of the hospitals came to Mahosot Hospital for a Clinical Kick-Off meeting with diagnostic and antimicrobial stewardship training and the identification of Clinical Champions who can lead a clinical audit project within their sites. 2024 saw three rounds of laboratory training at Mahosot Hospital for provincial site staff focusing on LQMS and laboratory techniques. There were two rounds of onsite training at the provincial laboratories focusing on implementing LQMS, and one round of onsite clinical training by LOMWRU and Mahosot Hospital staff at the provincial sites with a focus on diagnostic stewardship and monitoring of the clinical audit projects. In December, one laboratory staff from each of the provincial laboratories travelled to Khon Kaen in Thailand to attend an intensive 2-day workshop on LQMS with a focus on internal audits. The staff were also able to visit an ISO accredited laboratory, which inspired the staff to improve their laboratory practices. This year also saw the introduction of monthly online meetings for both the site clinical and laboratory teams where clinical audit projects and LQMS implementation were monitored.

Following on from the success of the group workshop in 2023, another workshop was held in July 2024 which included staff from the five provincial hospitals (hospital directors, infectious diseases doctors, and laboratory staff), and representatives from Fondation Mérieux, NCLE and WHO. The workshop included updates on Fleming Fund activities for 2024, presentation of the clinical audit projects, laboratory assessment results, diagnostic stewardship, AMR dashboard progress, and the plan for antimicrobial prescription point-prevalence surveys (PPS) at the sites. In total, there were 14 laboratory staff and approximately 120 clinical staff trained in 2024 under Fleming Fund activities.

Whole-genome sequencing

Since the COVID-19 pandemic, LOMWRU lab technicians have attended a number of genome sequencing and bioinformatics courses. Most recently, Dr Siribun Panapruksacha, Ms Manila Souksavanh, and Mr Vanheuang Phommadeechack attended the ACORN integrated AMR program, at KEMRI in Kilifi, Kenya, 15-20 September 2024. The training focused on lab activities to prepare samples for whole genome sequencing and data analysis.

Media for One Health

In September 2024, Prof Mayfong Mayxay, Dr Matt Robinson, Dr Vilaiphone Phomsisavath, and Dr Koukeo Phommasone joined as trainers for the Media for One Health training course for Lao journalists on One Health issues. Organized by Canal France International (CFI) French Media Development Agency, the course aimed to provide local journalists with an understanding of One Health concepts and how to report on them, and how health research is carried out in Laos. The journalists also visited the Microbiology Laboratory at Mahosot Hospital and LOMWRU to understand what goes on behind the scenes. Attending the course were some notable Lao journalists, including Ms Phannga Southiphong (Lao National Television) and Mr Bounheng Southichak (Lao Youth Radio), pictured above with the LOMWRU Molecular Team. Other organizations represented included Lao National Radio, KPL Lao News Agency and Vientiane Mai Newspaper.

Pi Mai Lao 2024.
Photographer: Elizabeth Ashley.
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ธูบพาบโดย: Elizabeth Ashley.

LOMWRU publications in 2024

In 2024 LOMWRU published 46 articles, book chapters or letters in peer-reviewed journals and gave 12 presentations at scientific conferences. Abstracts are reproduced below with articles grouped by theme.

Microbiology including antimicrobial resistance (AMR)

WHO global research priorities for antimicrobial resistance in human health. Bertagnolio S, Dobreva Z, Centner CM, Olaru ID, Donà D, Burzo S, Huttner BD, Chaillon A, Gebreselassie N, Wi T, Hasso-Agopsowicz M, Allegranzi B, Sati H, Ivanovska V, Kothari KU, Balkhy HH, Cassini A, Hamers RL, Weezenbeek KV; WHO Research Agenda for AMR in Human Health Collaborators. WHO global research priorities for antimicrobial resistance in human health. *Lancet Microbe*. 2024 **5**(11): 100902. DOI: 10.1016/S2666-5247(24)00134-4. PMID: 39146948. PMCID: PMC11543637.

A thorough, structured process coordinated by the WHO, involving experts from 69 countries, produced 40 research priorities regarding AMR. The focus is on work deliverable by 2030 to harmonise with the Sustainable Development Goals (SDGs) and low-resource settings. The wide-ranging priorities encompass prevention, diagnosis, treatment, epidemiology, policy and awareness.

The WHO research agenda for AMR in human health has identified 40 research priorities to be addressed by the year 2030. These priorities focus on bacterial and fungal pathogens of crucial importance in addressing AMR, including drug-resistant pathogens causing tuberculosis. These research priorities encompass the entire people-centred journey, covering prevention, diagnosis, and treatment of antimicrobial-resistant infections, and addressing the overarching knowledge gaps in AMR epidemiology, burden and drivers, policies and regulations, and awareness and education. The research priorities were identified through a multistage process, starting with a comprehensive scoping review of knowledge gaps, with expert inputs gathered through a survey and open call. The priority setting involved a rigorous modified Child Health and Nutrition Research Initiative approach, ensuring global representation and applicability of the findings. The ultimate goal of this research agenda is to encourage research and investment in the generation of evidence to better understand AMR dynamics and facilitate policy translation for reducing the burden and consequences of AMR.

Implementing the WHO AWaRe antibiotic book guidance in lower-resource settings: the case of the Lao PDR. Chansamouth V, Inlorkham P, Keohavong B, Bellingham K, van Doorn HR, Mayxay M, Newton PN, Turner P, Day NPJ, Ashley EA. Implementing the WHO AWaRe antibiotic book guidance in lower-resource settings: the case of the Lao PDR. *JAC Antimicrob Resist*. 2024 **6**(1):dlae004. DOI: 10.1093/jacamr/dlae004. PMID: 38259905. PMCID: PMC10801825.

This publication describes how implementation of the WHO AWaRe antibiotic book is problematic in many settings because geography-specific diseases and resistance patterns are overlooked, and local access to antibiotics may not match recommendations. For example, melioidosis and rickettsial disease are common causes of sepsis in Laos but do not feature in the AWaRe book; likewise, none of the 'reserve' group antibiotics are available in Laos.

In 2022, WHO released the WHO AWaRe (Access, Watch, Reserve) antibiotic book to promote the rational use of antibiotics. Here, we review the AWaRe antibiotic book from the perspective of implementation in low-resource settings, using the Lao PDR (Laos) as a case study. Not all recommendations in the AWaRe antibiotic book match the epidemiology of infectious diseases and antimicrobial susceptibility patterns in Laos and other LMICs, for eg melioidosis, rickettsial disease and leptospirosis are common causes of sepsis and febrile illness in Laos but do not feature in the AWaRe book. Conversely, some infectious diseases like *Clostridioides difficile*-associated diarrhoea are in the AWaRe antibiotic book but rarely considered in Laos with no diagnostic tests available. Only 29/39 antibiotics in the AWaRe book are available in Laos, with no Reserve group antimicrobials available. The AWaRe book stimulates countries such as Laos to consider alternative diagnoses and include additional antimicrobials in the national essential medicines list (NEML). However, it should be updated to include regionally important pathogens currently not included. Comprehensive antibiotic use guidelines alone might not assure appropriate use or control overuse of antibiotics. Access to antibiotics is challenging in low-resource settings in terms of unavailability in the country (low demand or small market size), patchy access, especially for those living in remote areas, and unaffordability. All these systemic factors can contribute to inappropriate use of antibiotics. Improved access to antibiotics, strengthening diagnostic capacity, and promoting antibiotic stewardship should be combined.

Understanding hospital antimicrobial prescribing decisions and determinants of uptake of new local antimicrobial prescribing guidelines in Laos. Chansamouth V, Douangnouvong A, Thammavongsa P, Sombandith X, Keomany S, Rattana S, Newton PN, Day NP, Turner P, Mayxay M, van Doorn HR, Ashley EA. *Wellcome Open Res*. 2024 **9**:183. DOI: 10.12688/wellcomeopenres.20884.2. PMID: 39301442. PMCID: PMC11411237.

Thematic analysis of in-depth interviews demonstrates that antibiotic use is strongly influenced by clinical judgement and assessment of patients, access to antibiotics and laboratory results, habit, and recommendations from seniors. Increased compliance with antibiotic guidelines (which have been available since 2021) requires endorsement from senior medical leaders, education on guidelines and antibiotic use, and reliable access to recommended antibiotics.

- **BACKGROUND**

Antimicrobial use in Laos is among the highest in Southeast Asia. The first Lao comprehensive antimicrobial prescribing guidelines have been available since 2021. This study explored the determinants of antibiotic prescribing decisions and how the new prescribing guidelines were being used.

- **METHODS**

In August 2022, in-depth interviews were conducted with 16 Lao prescribers from two hospitals. Participants were questioned about their prescribing behaviours, attitudes to guidelines, how they learned about the guidelines and factors influencing their uptake. The interviews were audio-recorded, transcribed, and translated into English. Thematic analysis of the transcripts was conducted.

- **RESULTS**

Lao prescribers considered multiple factors before deciding to prescribe antibiotics to their patients. The most common factor was based on the clinical judgement of the prescribers. Lack of certain antibiotics and turnaround times of laboratory results were the main challenges to prescribing antibiotics appropriately. The majority of participants were satisfied with the guidelines, regarding them as comprehensive, simple and convenient. However, most participants admitted that they did not access the guidelines very often. The main reason was that they could remember the treatment recommendations because they treat similar diseases on a daily basis. Improving antibiotic knowledge was the most common recommendation to improve appropriate use of

antibiotics. Raising awareness of the guidelines and promoting their use should also be considered. In addition, heads of wards and policy and implementation leaders should support, monitor and give feedback on their use to encourage all prescribers to follow the guidelines.

▪ CONCLUSION

Several factors contribute to enhancing appropriate antibiotic prescription. Key factors for improving antibiotic prescription include enhancing prescribers' clinical knowledge, ensuring access to essential antibiotics, and updating guidelines regularly. Health leaders must get involved to promote their use.

Antibiotic prescribing practices and antibiotic use quality indicators in Luang Prabang, Lao PDR: a point prevalence survey in a tertiary care hospital. Elias C, Ha NT, Sengvilaipaserth O, Phaychith A, Chansamouth V, Phongsavath V, Keohavong B, Detleuxay K, Maniphonh P, Soukhaseum T, Vanhems P, Babin FX. *BMC Infect Dis*. 2024 **24**(1): 818. DOI: 10.1186/s12879-024-09614-4. PMID: 39138400. PMCID: PMC11321149.

Point prevalence of antibiotic use was assessed using WHO methodology at Luang Prabang hospital. Overall, 58.8% of patients were receiving antibiotics – with the highest rates on the surgical ward (93%). Only 14.9% of prescriptions were fully compliant with national guidelines. Reasons for high levels of non-guideline-based prescribing are multi-factorial, and these data highlight areas for active stewardship interventions.

▪ CONTEXT

The increase and global dissemination of antibiotic resistance limit the use of antibiotics to prevent and treat infections. Implementing antibiotic stewardship programs guided by local data on prescription profiles is a useful strategy to reduce the burden of antibiotic resistance. The aim was to determine the prevalence of antibiotic use and guideline compliance at Luang Prabang provincial hospital, Lao PDR.

▪ METHODS

A point prevalence survey of antibiotics was conducted among hospitalized patients admitted to Luang Prabang hospital (204 beds) in Lao PDR on 25 May 2023. All patients presenting at 8:00 AM were eligible. Sociodemographic data, indications for antibiotic use, and antibiotic prescriptions were collected from medical records using a paper-based questionnaire and entered into an electronic platform following WHO methodology. The prevalence of antibiotic use was determined.

▪ RESULTS

Out of the 102 patients included, 60 (58.8%) were undergoing antibiotic treatment, of which 33 (55.0%) received combination therapy, and 7 (10.5%) had two indications for antibiotic use. The highest prevalence was in the surgical ward (14/15, 93%) followed by general paediatrics (18/27, 67%). Out of the 100 antibiotic prescriptions, 47 (47%) were for community-acquired infections, 26 (26%) for surgical prophylaxis, 13 (13%) for hospital-acquired infections and 5 (5%) for medical prophylaxis. Twenty (20%) antibiotics were prescribed for obstetrics and gynaecology prophylaxis, 17 (17%) for intra-abdominal infections, and 10 (10.0%) for pneumonia treatment and bone and joint infections. The main antibiotics prescribed were ceftriaxone 36 (34.6%), metronidazole 18 (17.3%), ampicillin 8 (7.7%), and gentamicin 8 (7.7%). Only 2 (3%) samples were sent to the laboratory, one of which showed a positive culture for *Escherichia coli* Extended Spectrum β-Lactamase. According to the WHO Access Watch and Reserve classification, 55 (52.9%) molecules belonged to the Access category, 47 (49.1%) to the Watch category, and none to the Reserve category. Only 14.9% of antibiotic prescriptions were fully compliant with current guidelines.

▪ CONCLUSION

This study indicated a significant prevalence of antibiotic use and very low compliance with guidelines at Luang Prabang provincial hospital, Lao PDR. This highlights an urgent need for comprehensive strategies at all levels to optimize antibiotic use in hospitals, emphasizing diagnostic improvements, and continued research to address the factors driving this excessive antibiotic usage and improve adherence to guidelines.

Global burden of bacterial antimicrobial resistance 1990-2021: a systematic analysis with forecasts to 2050. GBD 2021 Antimicrobial Resistance Collaborators. *Lancet*. 2024 **404**(10459): 1199-1226. DOI: 10.1016/s0140-6736(24)01867-1. PMID: 39299261.

This extensive study charts the trends in antimicrobial resistance (AMR), with attributable and associated mortality, over 30 years. Age-specific mortality, country-by-country analysis, and pathogen-specific data are presented. A trend to fewer deaths between 1990 and 2021 has reversed dramatically, and 1.91 million attributable deaths annually are predicted in 2050. The potential impact of interventions such as developing novel antibiotics is discussed.

▪ BACKGROUND

AMR poses an important global health challenge in the 21st century. A previous study has quantified the global and regional burden of AMR for 2019, followed with additional publications that provided more detailed estimates for several WHO regions by country. To date, there have been no studies that produce comprehensive estimates of AMR burden across locations that encompass historical trends and future forecasts.

▪ METHODS

We estimated all-age and age-specific deaths and disability-adjusted life-years (DALYs) attributable to and associated with bacterial AMR for 22 pathogens, 84 pathogen-drug combinations, and 11 infectious syndromes in 204 countries and territories from 1990 to 2021. We collected and used multiple cause of death data, hospital discharge data, microbiology data, literature studies, single drug resistance profiles, pharmaceutical sales, antibiotic use surveys, mortality surveillance, linkage data, outpatient and inpatient insurance claims data, and previously published data, covering 520 million individual records or isolates and 19,513 study-location-years. We used statistical modelling to produce estimates of AMR burden for all locations, including those with no data. Our approach leverages the estimation of five broad component quantities: the number of deaths involving sepsis; the proportion of infectious deaths attributable to a given infectious syndrome; the proportion of infectious syndrome deaths attributable to a given pathogen; the percentage of a given pathogen resistant to an antibiotic of interest; and the excess risk of death or duration of an infection associated with this resistance. Using these components, we estimated disease burden attributable to and associated with AMR, which we define based on two counterfactuals: respectively, an alternative scenario in which all drug-resistant infections are replaced by drug-susceptible infections, and an alternative scenario in which all drug-resistant infections were replaced by no infection. Additionally, we produced global and regional forecasts of AMR burden until 2050 for three scenarios: a reference scenario that is a probabilistic forecast of the most likely future; a Gram-negative drug scenario that assumes future drug development that targets Gram-negative pathogens; and a better care scenario that assumes future improvements in health-care quality and access to appropriate antimicrobials. We present final estimates aggregated to the global, super-regional, and regional level.

▪ FINDINGS

In 2021, we estimated 4.71 million (95% UI 4·23-5·19) deaths were associated with bacterial AMR, including 1.14 million (1.00-1.28) deaths attributable to bacterial AMR. Trends in AMR mortality

over the past 31 years varied substantially by age and location. From 1990 to 2021, deaths from AMR decreased by more than 50% among children younger than 5 years yet increased by over 80% for adults 70 years and older. AMR mortality decreased for children younger than 5 years in all super-regions, whereas AMR mortality in people 5 years and older increased in all super-regions. For both deaths associated with and deaths attributable to AMR, methicillin-resistant *Staphylococcus aureus* increased the most globally (from 261,000 associated deaths [95% UI 150,000-372,000] and 57,200 attributable deaths [34,100-80,300] in 1990, to 550,000 associated deaths [500,000-600,000] and 130,000 attributable deaths [113,000-146,000] in 2021). Among Gram-negative bacteria, resistance to carbapenems increased more than any other antibiotic class, rising from 619,000 associated deaths (405,000-834,000) in 1990, to 1.03 million associated deaths (909,000-1.16 million) in 2021, and from 127,000 attributable deaths (82,100-171,000) in 1990, to 216,000 (168,000-264,000) attributable deaths in 2021. There was a notable decrease in non-COVID-related infectious disease in 2020 and 2021. Our forecasts show that an estimated 1.91 million (1.56-2.26) deaths attributable to AMR and 8.22 million (6.85-9.65) deaths associated with AMR could occur globally in 2050. Super-regions with the highest all-age AMR mortality rate in 2050 are forecasted to be South Asia and Latin America and the Caribbean. Increases in deaths attributable to AMR will be largest among those 70 years and older (65.9% [61.2-69.8] of all-age deaths attributable to AMR in 2050). In stark contrast to the strong increase in number of deaths due to AMR of 69.6% (51.5-89.2) from 2022 to 2050, the number of DALYs showed a much smaller increase of 9.4% (-6.9 to 29.0) to 46.5 million (37.7 to 57.3) in 2050. Under the better care scenario, across all age groups, 92.0 million deaths (82.8-102.0) could be cumulatively averted between 2025 and 2050, through better care of severe infections and improved access to antibiotics, and under the Gram-negative drug scenario, 11.1 million AMR deaths (9.08-13.2) could be averted through the development of a Gram-negative drug pipeline to prevent AMR deaths.

▪ INTERPRETATION

This study presents the first comprehensive assessment of the global burden of AMR from 1990 to 2021, with results forecasted until 2050. Evaluating changing trends in AMR mortality across time and location is necessary to understand how this important global health threat is developing and prepares us to make informed decisions regarding interventions. Our findings show the importance of infection prevention, as shown by the reduction of AMR deaths in those younger than 5 years. Simultaneously, our results underscore the concerning trend of AMR burden among those older than 70 years, alongside a rapidly ageing global community. The opposing trends in the burden of AMR deaths between younger and older individuals explains the moderate future increase in global number of DALYs versus number of deaths. Given the high variability of AMR burden by location and age, it is important that interventions combine infection prevention, vaccination, minimisation of inappropriate antibiotic use in farming and humans, and research into new antibiotics to mitigate the number of AMR deaths that are forecasted for 2050.

Estimating the subnational prevalence of antimicrobial resistant *Salmonella enterica* serovars Typhi and Paratyphi A infections in 75 endemic countries, 1990-2019: a modelling study. GRAM Typhoid Collaborators. *Lancet Glob Health*. 2024 **12**(3): e406-e418. DOI: 10.1016/s2214-109x(23)00585-5. PMID: 38365414. PMCID: PMC10882211.

This is the most extensive assimilation of phenotypic antimicrobial resistance (AMR) data for Salmonella enterica *serovars Typhi and Paratyphi A. Temporal trends between 1990 and 2019 are described. These findings are discussed in the context of sanitation and vaccination programmes, antimicrobial use and stewardship, and the on-going acquisition of accurate and timely data.*

▪ BACKGROUND

Enteric fever, a systemic infection caused by *Salmonella enterica* serovars Typhi and Paratyphi A, remains a major cause of morbidity and mortality in low-income and middle-income countries.

Enteric fever is preventable through the provision of clean water and adequate sanitation and can be successfully treated with antibiotics. However, high levels of AMR compromise the effectiveness of treatment. We provide estimates of the prevalence of AMR *S* Typhi and *S* Paratyphi A in 75 endemic countries, including 30 locations without data.

▪ METHODS

We used a Bayesian spatiotemporal modelling framework to estimate the percentage of multidrug resistance (MDR), fluoroquinolone non-susceptibility (FQNS), and third-generation cephalosporin resistance in *S* Typhi and *S* Paratyphi A infections for 1,403 administrative level one districts in 75 endemic countries from 1990 to 2019. We incorporated data from a comprehensive systematic review, public health surveillance networks, and large multicountry studies on enteric fever. Estimates of the prevalence of AMR and the number of AMR infections (based on enteric fever incidence estimates by the Global Burden of Diseases study) were produced at the country, super-region, and total endemic area level for each year of the study.

▪ FINDINGS

We collated data from 601 sources, comprising 184,225 isolates of *S* Typhi and *S* Paratyphi A, covering 45 countries over 30 years. We identified a decline of MDR *S* Typhi in South Asia and Southeast Asia, whereas in sub-Saharan Africa the overall prevalence increased from 6.0% (95% uncertainty interval 4.3-8.0) in 1990 to 72.7% (67.7-77.3) in 2019. Starting from low levels in 1990, the prevalence of FQNS *S* Typhi increased rapidly, reaching 95.2% (91.4-97.7) in South Asia in 2019. This corresponded to 2.5 million (1.5-3.8) MDR *S* Typhi infections and 7.4 million (4.7-11.3) FQNS *S* Typhi infections in endemic countries in 2019. The prevalence of third-generation cephalosporin-resistant *S* Typhi remained low across the whole endemic area over the study period, except for Pakistan where prevalence of third-generation cephalosporin resistance in *S* Typhi reached 61.0% (58.0-63.8) in 2019. For *S* Paratyphi A, we estimated low prevalence of MDR and third-generation cephalosporin resistance in all endemic countries, but a drastic increase of FQNS, which reached 95.0% (93.7-96.1; 3.5 million [2.2-5.6] infections) in 2019.

▪ INTERPRETATION

This study provides a comprehensive and detailed analysis of the prevalence of MDR, FQNS, and third-generation cephalosporin resistance in *S* Typhi and *S* Paratyphi A infections in endemic countries, spanning the last 30 years. Our analysis highlights the increasing levels of AMR in this preventable infection and serves as a resource to guide urgently needed public health interventions, such as improvements in water, sanitation and hygiene, and typhoid fever vaccination campaigns.

Antimicrobial susceptibility profiles of invasive bacterial infections among children from low- and middle-income countries in the Western Pacific Region (WPRO) – a systematic review and meta-analysis. Moore N, Ashley EA, Dickson BFR, Douangnouvong A, Panyaviseth P, Turner P, Williams PCM. *Lancet Regional Health - Western Pacific*. 2024 **51**: 101177. DOI: 10.1016/j.lanwpc.2024.101177. PMID: 39282136. PMCID: PMC11402324.

This article describes the relative lack of antimicrobial resistance (AMR) data from WHO Western Pacific LMICs. Data reveal significant resistance rates of common pathogens to WHO-recommended empiric antibiotics. Such worrying findings may explain the extensive use of "watch" antibiotics, and poor clinical outcomes in this population.

▪ BACKGROUND

AMR increasingly impacts paediatric mortality, particularly in resource-constrained settings. We aimed to evaluate the susceptibility profiles of bacteria causing infections in children from the Western Pacific region.

▪ METHODS

We conducted a systematic review and meta-analysis of bacteria responsible for common infections in children. We included studies published from January 2011 to December 2023

(PROSPERO CRD42021248722). Pooled susceptibilities were evaluated against empiric antibiotics recommended to treat common clinical syndromes.

▪ FINDINGS

Fifty-one papers met inclusion criteria, incorporating 18,330 bacterial isolates. Of available published data, only six countries from the region were represented. *Escherichia coli* revealed a pooled susceptibility to ampicillin of 17% (95% CI 12–23%, n = 3292), gentamicin 63% (95% CI 59–67%, n = 3956), and third-generation cephalosporins 59% (95% CI 49–69%, n = 3585). Susceptibility of *Klebsiella* spp. to gentamicin was 71% (95% CI 61–80%, n = 2323), third-generation cephalosporins 35% (95% CI 22–49%, n = 2076), and carbapenems 89% (95% CI 78–97%, n = 2080). Pooled susceptibility of *Staphylococcus aureus* to flucloxacillin was 72% (95% CI 58–83%, n = 1666), and susceptibility of *Streptococcus pneumoniae* meningitis isolates to ampicillin was 26% (95% CI 11–44%, n = 375), and 63% (95% CI 40–84%, n = 246) to third-generation cephalosporins.

▪ INTERPRETATION

The burden of AMR among bacteria responsible for common infections in children across the Western Pacific region is significant, and the currently recommended WHO antibiotics to treat these infections may be inefficacious. Strategies to improve the availability of high-quality data to understand the burden of AMR in the region are necessary.

Sustainable antimicrobial resistance surveillance: time for a global funding mechanism. Painter C, Limmathurotsakul D, Roberts T, van Doorn HR, Mayxay M, Lubell Y, Day NPJ, Turner P, Ashley EA. *Lancet Infect Dis*. 2024 S1473-3099(24)00649-2. DOI: 10.1016/s1473-3099(24)00649-2. PMID: 39706207.

The epidemiology and burden of antimicrobial resistance (AMR) is an overarching topic of the WHO Global Action Plan on AMR. For 46/136 LMICs, baseline surveillance would cost 2% of the national healthcare expenditure, rising to over 5% of healthcare expenditure for a further 28 countries. Adequate surveillance activities require urgent long-term global financing initiatives.

AMR is predicted to outstrip malaria, HIV, and tuberculosis combined as the leading infectious cause of death by 2050. Strengthening the knowledge and evidence base for AMR with surveillance and research is one of the five main objectives of the WHO Global Action Plan on AMR. While recent efforts to strengthen diagnosis and surveillance have been encouraging, these are unlikely to be sustainable without continued funding support in most low-resource settings. We estimated the continued costs of a standard national AMR surveillance system in LMICs. For 46 LMICs, the costs would account for more than 2% of their total domestic general government health expenditure (GGHE-D), and for 28 of these countries, the costs are more than 5% of their total GGHE-D. This high cost is not sustainable without a long-term global financing mechanism.

Investigation of *Escherichia coli* isolates from pigs and humans for colistin resistance in Lao PDR - a cross-sectional study. Phomsisavath V, Roberts T, Seupsanith A, Robinson MT, Nammanininh P, Chanthavong S, Chansamouth V, Vongsouvath M, Theppangna W, Christensen P, Blacksell SD, Mayxay M, Ashley EA. *One Health*. 2024 **18**:100745. DOI: 10.1016/j.onehlt.2024.100745. PMID: 38725959. PMCID: PMC11079391.

Colistin-resistant E. coli *was seen in 65% of rectal swabs from pigs and 2.4% of* E. coli *isolates from human blood cultures.* mcr-1 *and* mcr-3 *genes were detected, although* mcr-1 *was predominant; a significant minority of isolates harboured both genes.* mcr-2 *was not detected in any isolates. These data suggest widespread use of colistin in pig husbandry as a source of resistance in invasive human infections.*

▪ BACKGROUND

In Laos, colistin is not currently registered for use in humans. This One Health study aimed to estimate the prevalence of meat-producing pigs carrying colistin-resistant *Escherichia coli*, and investigate if *E. coli* causing invasive human infections were colistin-resistant.

▪ METHODS

Between September 2022 and March 2023, rectal swabs were collected from 895 pigs from abattoirs in 9/17 Lao provinces. Pig rectal swabs and stored *E. coli* isolates from human blood cultures, submitted to Mahosot Hospital Microbiology Laboratory between 2005 and 2022, were screened for colistin resistance on selective chromogenic agar with organism identification confirmed using MALDI-TOF MS. Suspected colistin-resistant isolates underwent colistin susceptibility testing by broth microdilution following European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines. Isolates with MIC values of ≥2 µg/ml were tested for plasmid-mediated colistin resistance genes (*mcr-1*, *mcr-2*, and *mcr-3*) by multiplex SYBR Green PCR.

▪ RESULTS

A total of 15/620 (2.41%) invasive human *E. coli* isolates were phenotypically colistin-resistant by broth microdilution (MIC values 4 to 8 µg/ml). The earliest isolate was from 2015 in a patient from Phongsaly province in Northern Laos. A total of 582/895 (65.02%) pig rectal swab samples contained colistin-resistant *E. coli*. The detected colistin resistance genes were predominantly *mcr-1* (57.8%, 346/598), followed by *mcr-3* (20.23%,121/598), and 22.24% (133/598) were found to co-harbour *mcr-1* and *mcr-3*. Among the 15 human isolates with colistin MIC values of ≥4 µg/ml, 12/15 were *mcr-1*.

▪ CONCLUSION

We found that colistin resistant *E. coli* is causing invasive infection in humans in Laos despite the fact it is not available for human use. Use in animals seems to be widespread, confirmed by high carriage rates of colistin-resistant *E. coli* in pigs. It is probable that food-producing animals are the source of colistin-resistant *E. coli* bloodstream infection in Laos, although these have been infrequent to date. This is a serious public health concern in the region that needs to be addressed by appropriate enforceable legislation.

AmpC β-lactamases detected in Southeast Asian *Escherichia coli* and *Klebsiella pneumoniae*. Roberts T, Ling CL, Watthanaworawit W, Cheav C, Sengduangphachanh A, Silisouk J, Hopkins J, Phommasone K, Batty EM, Turner P, Ashley EA. *JAC Antimicrob Resist*. 2024 **6**(6): dlae195. DOI: 10.1093/jacamr/dlae195. PMID: 39610980. PMCID: PMC11604056.

37% of E. coli *and* K. pneumoniae *isolates from 3 countries in Southeast Asia that were resistant to ceftriaxone, ceftazidime or cefpodoxime but negative for ESBL production were found to harbour AmpC beta-lactamases. Whole genome sequencing revealed diverse sequence types and chromosomal and plasmid-encoded beta-lactamase genes. These data mandate systematic screening for AmpC production with cefoxitin.*

▪ OBJECTIVES

AmpC β-lactamases are neglected compared with ESBL as a cause of third-generation cephalosporin (3GC) resistance in Enterobacterales in LMICs and the burden is unknown. The aim of this study was to investigate the presence of AmpC β-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* in clinical specimens from three clinical research laboratories in Southeast Asia.

▪ METHODS

Stored clinical isolates of *E. coli* and *K. pneumoniae* resistant to ceftriaxone or ceftazidime or cefpodoxime and ESBL confirmation test negative were screened using MASTDISCS AmpC, ESBL and Carbapenemase Detection Set-D72C. Short-read WGS was performed to identify *ampC* genes.

▪ RESULTS

Of 126 isolates collected between 2010 and 2020, 31 (24.6%) and 16 (12.7%) were phenotypically AmpC and inducible AmpC positive by MASTDISCS testing, respectively. All inducible AmpC isolates were ceftriaxone susceptible and 97.7% of AmpC/inducible AmpC isolates tested against cefoxitin were resistant. Through WGS, 17 and eight different STs were detected for the AmpC/inducible AmpC *E. coli* and *K. pneumoniae* isolates, respectively. Twelve different β-lactamase resistance genes were detected, with $bla_{(CMY-2)}$ most commonly in AmpC-positive isolates (20/31; 64.5%; 15 chromosomal, five plasmid). All inducible AmpC-positive isolates had the $bla_{(DHA-1)}$ gene (seven chromosomal, nine plasmid).

▪ CONCLUSION

Though uncommon, AmpC and inducible AmpC β-lactamases in *E. coli* and *K. pneumoniae* are an important cause of infection in Southeast Asia. With current testing methods, these infections may be going undetected, resulting in patients receiving suboptimal treatment.

Melioidosis

Identification of *Burkholderia cepacia* strains that express a *Burkholderia pseudomallei*-like capsular polysaccharide. Burtnick MN, Dance DAB, Vongsouvath M, Newton PN, Dittrich S, Sendouangphachanh A, Woods K, Davong V, Kenna DTD, Saiprom N, Sengyee S, Hantrakun V, Wuthiekanun V, Limmathurotsakul D, Chantratita N, Brett PJ. *Microbiol Spectr*. 2024 **12**(3): e0332123. DOI: 10.1128/spectrum.03321-23. PMID: 38299821. PMCID: PMC10913486.

This report describes 3 B. cepacia *and 2* B. thailandensis *isolates that contain the biosynthetic genes for, and express, 6-deoxyheptan – a capsular polysaccharide that is a highly conserved virulence factor and component of the* Burkholderia pseudomallei *outer membrane. These rare non-*pseudomallei *strains give false-positive results in latex agglutination and lateral flow tests designed to rapidly and accurately detect BPS.*

Burkholderia pseudomallei and *Burkholderia cepacia* are Gram-negative, soil-dwelling bacteria that are found in a wide variety of environmental niches. While *B. pseudomallei* is the causative agent of melioidosis in humans and animals, members of the *B. cepacia* complex typically only cause disease in immunocompromised hosts. In this study, we report the identification of *B. cepacia* strains isolated from either patients or soil in Laos and Thailand that express a *B. pseudomallei*-like 6-deoxyheptan capsular polysaccharide (CPS). These *B. cepacia* strains were initially identified based on their positive reactivity in a latex agglutination assay that uses the CPS-specific monoclonal antibody (mAb) 4B11. Mass spectrometry and *recA* sequencing confirmed the identity of these isolates as *B. cepacia* (formerly genomovar I). Total carbohydrates extracted from *B. cepacia* cell pellets reacted with *B. pseudomallei* CPS-specific mAbs MCA147, 3C5, and 4C4, but did not react with the *B. pseudomallei* lipopolysaccharide-specific mAb Pp-PS-W. Whole genome sequencing of the *B. cepacia* isolates revealed the presence of genes demonstrating significant homology to those comprising the *B. pseudomallei* CPS biosynthetic gene cluster. Collectively, our results provide compelling evidence that *B. cepacia* strains expressing the same CPS as *B. pseudomallei* co-exist in the environment alongside *B. pseudomallei*. Since CPS is a target that is often used for presumptive identification of *B. pseudomallei*, it is possible that the occurrence of these unique *B. cepacia* strains may complicate the diagnosis of melioidosis.

▪ IMPORTANCE

B. pseudomallei, the etiologic agent of melioidosis, is an important cause of morbidity and mortality in tropical and subtropical regions worldwide. The 6-deoxyheptan capsular polysaccharide (CPS) expressed by this bacterial pathogen is a promising target antigen that is useful for rapidly diagnosing melioidosis. Using assays incorporating CPS-specific monoclonal antibodies, we identified both clinical and environmental isolates of *B. cepacia* that express the same CPS antigen as *B. pseudomallei*. Because of this, it is important that staff working in melioidosis-endemic areas are aware that these strains co-exist in the same niches as *B. pseudomallei* and do not solely rely on CPS-based assays such as latex-agglutination, AMD Plus Rapid Tests, or immunofluorescence tests for the definitive identification of isolates.

Use of comparative genomics to resolve an unusual case of aminoglycoside susceptibility in the melioidosis pathogen *Burkholderia pseudomallei* in Bangladesh. Kaestli M, Farook S, Jilani MSA, Anwar S, Siddiqui TA, Mayo M, Podin Y, Webb JR, Dance DAB, Currie BJ. *Am J Trop Med Hyg*. 2024 **111**(5): 1056-1059. DOI: 10.4269/ajtmh.24-0144. PMID: 39226893.

An unusual gentamicin-susceptible Burkholderia pseudomallei *isolate was grown from a patient's elbow in Bangladesh. Whole genome sequencing demonstrated that it was closely related to sequence type ST881 – usually found in Malaysian Borneo, where the patient had lived. A non-synonymous mutation in the efflux pump* amrB *was identified. A mutation in* piuA*, which confers resistance to cefiderocol, was also identified.*

Melioidosis is an emerging tropical infectious disease with a rising global burden caused by the environmental bacterium *Burkholderia pseudomallei*. It is endemic in Southeast and South Asia, including Bangladesh. A rare aminoglycoside-susceptible *B. pseudomallei* isolate (Y2019) has recently been reported from a melioidosis patient in Dhaka, Bangladesh. To understand the geographical origins of Y2019, we subjected it and 10 other isolates from Bangladesh to whole-genome sequencing. In a phylogenetic tree with a global set of *B. pseudomallei* genomes, most Bangladeshi genomes clustered tightly within the Asian clade. In contrast, Y2019 was closely related to ST881 isolates from Sarawak, Malaysian Borneo, a gentamicin-sensitive sequence type, suggesting infection in Borneo. Y2019 also contained the same gentamicin sensitivity conferring nonsynonymous mutation in the drug efflux pump encoding the *amrB* gene. In the absence of a full travel history, whole-genome sequencing and bioinformatics tools have revealed the likely origin of this rare isolate.

Alfred Whitmore and the discovery of melioidosis. Savelkoel J, Dance DAB. *Emerg Infect Dis*. 2024 **30**(4): 752-756. DOI: 10.3201/eid3004.230693.

This article and the accompanying video provide a fascinating glimpse into the life of Alfred Whitmore – a British doctor who discovered Burkholderia pseudomallei *in Yangon, over 100 years ago. In remembering its discoverer, it is a sombre reminder to the world not to forget the disease again.*

We review the discovery of the tropical infectious disease melioidosis by Alfred Whitmore, a pathologist from England, and his assistant from India, C.S. Krishnaswami. We discuss how the subsequent disappearance of melioidosis from the medical literature of Burma holds parallels with the current neglect and under recognition of the disease. We urge global and national public health authorities to add melioidosis to existing neglected tropical diseases surveillance systems.

Melioidosis in patients with COVID-19 exposed to contaminated tap water, Thailand, 2021. Tantirat P, Chantarawichian Y, Taweewigyakarn P, Kripattanapong S, Jitpeera C, Doungngern P, Phiancharoen C, Tangwangvivat R, Hinjoy S, Sujariyakul A, Amornchai P, Wongsuvan G, Hantakun V, Wuthiekanun V, Thaipadungpanit J, Thomson NR, Dance DAB, Chewapreecha C, Batty EM, Limmathurotsakul D. Melioidosis in Patients with COVID-19 Exposed to Contaminated Tap Water, Thailand, 2021. *Emerg Infect Dis.* 2024 **30**(4): 791-794. DOI: 10.3201/eid3004.231476. PMID: 38526300. PMCID: PMC10977828.

An outbreak of melioidosis occurred in a field hospital set up to receive COVID-19 patients in Saraburi Province, Thailand. Environmental sampling identified B. pseudomallei *in both soil and non-potable tap water, and whole genome sequencing confirmed the tap water as the source. Repair of the chlorination system for the water brought the outbreak to a close.*

In September 2021, a total of 25 patients diagnosed with COVID-19 developed acute melioidosis after (median 7 days) admission to a COVID-19 field hospital in Thailand. Eight non-potable tap water samples and 6 soil samples were culture-positive for *B. pseudomallei*. Genomic analysis suggested contaminated tap water as the likely cause of illness.

Point mutation P174L of the *penA* gene endowing ceftazidime resistance to *Burkholderia pseudomallei* in China. Tian S, Wu X, Liu L, Li A, Li X, Pei H, Wang Y, Dance DAB, Chen H, Xia Q. *Drug Resist Updat*. 2024 **76**: 101121. DOI: 10.1016/j.drup.2024.101121. PMID: 39018660.

Whole-genome sequencing of a ceftazidime-resistant isolate of Burkholderia pseudomallei *identified a single point mutation in the* penA *gene, encoding a beta-lactamase. Deletion of this novel allele restored the susceptible phenotype. Exposure to ceftazidime is postulated to induce expression of* penA *and select for strains harbouring this mutation.*

In a clinical isolate of *B. pseudomallei* from Hainan, the association between the emergence of ceftazidime resistance and a novel PenA P174L allele was identified for the first time, providing an understanding of one mechanism by which ceftazidime resistance arises in *B. pseudomallei*.

Case Report: Soft tissue infection with *Burkholderia thailandensis* capsular variant: case report from the Lao PDR. Vannachone S, Luangraj M, Dance D, Chantratita N, Saiprom N, Seng R, Tandhavanant S, Rattanavong S, Simpson A, Roberts T. *Wellcome Open Res*. 2024 **9**: 421. DOI: 10.12688/wellcomeopenres.22706.1. PMID: 39246519. PMCID: PMC11377925.

This is the first report of Burkholderia thailandensis *from a clinical isolate (a foot abscess following a puncture injury) in Laos. The isolate is a capsular variant and expresses the same 200 kDa exo-polysaccharide as* B. pseudomallei*. Consequently, the latex-agglutination test for* B. pseudomallei *was positive, and final species identification required species-specific PCR and whole-genome sequencing.*

▪ BACKGROUND

B. thailandensis is an environmental bacteria closely related to *B. pseudomallei* that rarely causes infection in humans. Some environmental isolates have been shown to express a capsular polysaccharide known as *B. thailandensis* capsular variant (BTCV), but human infection has not previously been reported. Although *B. thailandenisis* has been identified in environmental samples in Laos before, there have not been any human cases reported.

▪ CASE

A 44-year-old man presented to a district hospital in Laos with a short history of fever and pain in his left foot. Physical examination identified a deep soft-tissue abscess in his left foot and an elevated white blood count. A deep pus sample was taken and melioidosis was suspected from preliminary laboratory tests. The patient was initially started on cloxacillin, ceftriaxone and metronidazole, and was then changed to ceftazidime treatment following local melioidosis treatment guidelines.

▪ LABORATORY METHODS

A deep pus sample was sent to Mahosot Hospital Microbiology Laboratory where a mixed infection was identified including *Burkholderia* sp. Conventional identification tests and API 20NE were inconclusive, and the *B. pseudomallei*-specific latex agglutination was positive. The isolate then underwent a *Burkholderia* species specific PCR which identified the isolate as *B. thailandensis*. The isolate was sent for sequencing on the Illumina NovaSeq 6000 system and multi-locus sequence typing analysis identified the isolate had the same sequence type (ST696) as *B. thailandensis* E555, a strain which expresses a *B. pseudomallei*-like capsular polysaccharide.

▪ CONCLUSION

This is the first report of human infection with *B. thailandensis* in Laos, and the first report of any human infection with the *B. thailandensis* capsular variant. Due to the potential for laboratory tests to incorrectly identify this bacteria, staff in endemic areas for *B. thailandensis* and *B. pseudomallei* should be aware and ensure that appropriate confirmatory methods are used to differentiate between the species.

***Burkholderia pseudomallei* bacteria in ornamental fish tanks, Vientiane, Laos, 2023.** Venkatesan T, Siritana V, Silisouk J, Roberts T, Robinson M, Dance DAB. *Emerg Infect Dis*. 2024 **30**(3): 599-600. DOI: 10.3201/eid3003.231674. PMID: 38407187. PMCID: PMC10902523.

Ornamental fish tanks have recently been identified as a source of infection with B. pseudomallei*. 111 domestic and commercial tanks were sampled in Vientiane, Laos. 1 tank was positive for BPS by PCR, but negative by enrichment culture. This demonstrates that BPS is present in fish tanks in Laos at low levels.*

In 2019, a melioidosis case in Maryland, USA was shown to have been acquired from an ornamental fish tank contaminated with *B. pseudomallei* bacteria, likely derived from Southeast Asia. We investigated the presence of *B. pseudomallei* in ornamental fish tanks in the endemic area of Vientiane, Laos.

Dr Koukeo Phommasone, Deputy Head of the Mahosot Microbiology Laboratory, at the World Melioidosis Congress in Darwin, Australia. Photographer: David Dance. © LOMWRU.

ດຣ ກຸເກ້ວ ພົມມະສອນ, ຮອງພະແນກຈຸລິນຊີວິທະຍາ ໂຮງໝໍມະໂຫສົດ ໃນງານ World Melioidosis Congress ໄດ້ຈັດຂຶ້ນທີ່ Darwin, Australia. ຮູບພາບໂດຍ: David Dance. © LOMWRU.

Malaria

Malaria epidemiology, surveillance and response for elimination in Lao PDR. Rotejanaprasert C, Malaphone V, Mayxay M, Chindavongsa K, Banouvong V, Khamlome B, Vilay P, Vanisavaeth V, Maude RJ. *Infect Dis Poverty*. 2024 **13**(1): 35. DOI: 10.1186/s40249-024-01202-7. PMID: 38783374. PMCID: PMC11112833.

Laos has a comprehensive and responsive suite of interventions for malaria control, working at local through to national levels. These are approaches and their rationale are described in detail,

along with useful historical and geo-political context. Malaria cases have fallen from 46,202 in 2012 to 6,409 in 2019, and the country continues making progress to towards malaria elimination by 2030.

BACKGROUND

Lao PDR has made significant progress in malaria control. The National Strategic Plans outline ambitious targets, aiming for the elimination of *Plasmodium falciparum* and *P. vivax* malaria from all northern provinces by 2025 and national elimination by 2030. This article presents an overview of malaria epidemiology, surveillance, and response systems in Lao PDR, emphasizing experiences and achievements in transmission reduction.

METHODS

Data on surveillance, monitoring and evaluation systems, human resources, infrastructure, and community malaria knowledge during 2010-2020 were systematically gathered from the national program and relevant documents. The collected information was synthesized, and discussions on challenges and future prospects were provided.

RESULTS

Malaria control and elimination activities in Lao PDR were implemented at various levels, with a focus on health facility catchment areas. There has been significant progress in reducing malaria transmission throughout the country. Targeted interventions, such as case management, vector control, and community engagement, using stratification of control interventions by catchment areas have contributed to the decline in malaria cases. In elimination areas, active surveillance strategies, including case and foci investigation, are implemented to identify and stop transmission. The surveillance system has facilitated timely detection and response to malaria cases, enabling these targeted interventions in higher-risk areas.

CONCLUSION

The malaria surveillance and response system in Lao PDR has played a crucial role in reducing transmission and advancing the country towards elimination. Challenges such as importation, drug resistance, and sustaining support require ongoing efforts. Further strengthening surveillance, improving access to services, and addressing transmission determinants are key areas of focus to achieve malaria elimination and enhance population health in Lao PDR.

Spatiotemporal patterns and association with climate for malaria elimination in Lao PDR: a hierarchical modelling analysis with two-step Bayesian model selection. Rotejanaprasert C, Malaphone V, Mayxay M, Chindavongsa K, Banouvong V, Khamlome B, Vilay P, Vanisavaeth V, Maude RJ. *Malar J*. 2024 **23**(1): 231. DOI: 10.1186/s12936-024-05064-0. PMID: 39098946. PMCID: PMC11298089.

Bayesian spatiotemporal modelling of malaria incidence over a decade as a function of province and key climatic variables demonstrated that rainfall and humidity are key factors in determining malaria transmission. This will allow targeted healthcare resource allocation in predicted high-transmission periods, as Laos progresses towards malaria elimination.

BACKGROUND

The government of Lao PDR has increased efforts to control malaria transmission in order to reach its national elimination goal by 2030. Weather can influence malaria transmission dynamics and should be considered when assessing the impact of elimination interventions but this relationship has not been well characterized in Lao PDR. This study examined the space-time association between climate variables and *P. falciparum* and *P. vivax* malaria incidence from 2010 to 2022.

METHODS

Spatiotemporal Bayesian modelling was used to investigate the monthly relationship, and model selection criteria were used to evaluate the performance of the models and weather variable specifications. As the malaria control and elimination situation was spatially and temporally dynamic during the study period, the association was examined annually at the provincial level.

RESULTS

Malaria incidence decreased from 2010 to 2022 and was concentrated in the southern regions for both *P. falciparum* and *P. vivax*. Rainfall and maximum humidity were identified as most strongly associated with malaria during the study period. Rainfall was associated with *P. falciparum* incidence in the north and central regions during 2010-2011, and with *P. vivax* incidence in the north and central regions during 2012-2015. Maximum humidity was persistently associated with *P. falciparum* and *P. vivax* incidence in the south.

CONCLUSION

Malaria remains prevalent in Lao PDR, particularly in the south, and the relationship with weather varies between regions but was strongest for rainfall and maximum humidity for both species. During peak periods with suitable weather conditions, vector control activities and raising public health awareness on the proper usage of intervention measures, such as indoor residual spraying and personal protection, should be prioritized.

Molecular markers of artemisinin resistance during falciparum malaria elimination in Eastern Myanmar. Thu AM, Phyo AP, Pateekhum C, Rae JD, Landier J, Parker DM, Delmas G, Watthanaworawit W, McLean ARD, Arya A, Reyes A, Li X, Miotto O, Soe K, Ashley EA, Dondorp A, White NJ, Day NP, Anderson TJC, Imwong M, Nosten F, Smithuis F. *Malar J*. 2024 **23**(1): 138. DOI: 10.1186/s12936-024-04955-6. PMID: 38720269. PMCID: PMC11078751.

The use of artemisinin combination therapy (ACT) in mass drug administration (MDA) campaigns could potentially accelerate the spread of artemisinin resistance. However, over the 6 years of an MDA campaign (2013-2019) in Eastern Myanmar, >5000 Plasmodium falciparum *isolates were characterised. Mutations in the kelch-13 gene, which determines artemisinin-resistance, remained stable or fell, while falciparum malaria was nearly eliminated.*

BACKGROUND

Artemisinin resistance in *P. falciparum* threatens global malaria elimination efforts. To contain and then eliminate artemisinin resistance in eastern Myanmar a network of community-based malaria posts was instituted and MDA with dihydroartemisinin-piperaquine (three rounds at monthly intervals) was conducted. The prevalence of artemisinin resistance during the elimination campaign (2013-2019) was characterized.

METHODS

Throughout the six-year campaign *P. falciparum* positive blood samples from symptomatic patients and from cross-sectional surveys were genotyped for mutations in kelch-13-a molecular marker of artemisinin resistance.

RESULTS

The program resulted in near elimination of falciparum malaria. Of 5,162 *P. falciparum* positive blood samples genotyped, 3,281 (63.6%) had K13 mutations. The prevalence of K13 mutations was 73.9% in 2013 and 64.4% in 2019. Overall, there was a small but significant decline in the proportion of K13 mutants ($p < 0.001$). In the MDA villages there was no significant change in the K13 proportions before and after MDA. The distribution of different K13 mutations changed substantially; F446I and P441L mutations increased in both MDA and non-MDA villages, while most other K13 mutations decreased. The proportion of C580Y mutations fell from 9.2% (43/467)

before MDA to 2.3% (19/813) after MDA ($p < 0.001$). Similar changes occurred in the 487 villages where MDA was not conducted.

▪ CONCLUSION

The malaria elimination program in Kayin state, eastern Myanmar, led to a substantial reduction in falciparum malaria. Despite the intense use of ACTs, both in treatment and MDA, this did not select for artemisinin resistance.

Does acute malnutrition in young children increase the risk of treatment failure following artemisinin-based combination therapy? A WWARN individual patient data meta-analysis. WWARN ACT Malaria and Malnutrition Study Group. *Lancet Glob Health*. 2024 **12**(4): e631-e640. DOI: 10.1016/s2214-109x(24)00003-2. PMID: 38485430. PMCID: 10951956.

Acute malnutrition in children under 5 with uncomplicated malaria is associated with delayed parasite clearance, and increased recrudescence and re-infection rates. This was true for all artemisinin-combination therapies (ACTs). Over 11% of children included in the studies were acutely malnourished, emphasizing the need to determine optimal treatment regimens for this growing group.

▪ BACKGROUND

The geographical, demographic, and socioeconomic distributions of malaria and malnutrition largely overlap. It remains unknown whether malnutrition affects the efficacy of WHO-recommended ACTs. A previous systematic review was inconclusive as data were sparse and heterogeneous, indicating that other methodological approaches, such as individual patient data meta-analysis, should be considered. The objective of this study was to conduct such a meta-analysis to assess the effect of malnutrition (wasting and stunting) on treatment outcomes in children younger than 5 years treated with an ACT for uncomplicated falciparum malaria.

▪ METHODS

We conducted a meta-analysis of individual patient data from studies identified through a systematic review of literature published between 1980 and 2018 in PubMed, Global Health, and Cochrane Libraries (PROSPERO CRD42017056934) and inspection of the WorldWide Antimalarial Resistance Network (WWARN) repository for ACT efficacy studies, including children younger than 5 years with uncomplicated falciparum malaria. The association of either acute (wasting) or chronic (stunting) malnutrition with day 42 PCR-adjusted risk of recrudescence (ie, return of the same infection) or reinfection after therapy was investigated using Cox regression, and with day 2 parasite positivity using logistic regression.

▪ FINDINGS

Data were included from all 36 studies targeted, 31 from Africa. Of 11,301 eligible children in 75 study sites, 11.5% were wasted (weight-for-height Z score [WHZ] <-2), and 31.8% were stunted (height-for-age Z score [HAZ] <-2). Decrease in WHZ was associated with increased risk of day 2 positivity (adjusted odds ratio 1.12, 95% CI 1.05-1.18 per unit; p=0·0002), treatment failure (adjusted hazard ratio [AHR] 1.14, 95% CI 1.02-1.26, p=0·016), and reinfection after therapy (AHR 1.09, 1.04-1.13, p=0·0003). Children with milder wasting (WHZ -2 to -1) also had a higher risk of recrudescence (AHR 1.85, 1.29-2.65, p=0·0008 vs WHZ ≥0). Stunting was not associated with reduced ACT efficacy.

▪ INTERPRETATION

Children younger than 5 years with acute malnutrition and presenting with uncomplicated falciparum malaria were at higher risk of delayed parasite clearance, ACT treatment failure, and reinfections. Stunting was more prevalent, but not associated with changes in ACT efficacy. Acute malnutrition is known to impact medicine absorption and metabolism. Further study to inform dose optimisation of ACTs in wasted children is urgently needed.

Virology

Characteristics and outcomes of COVID-19 patients admitted to hospital with and without respiratory symptoms. Citarella BW, Kartsonaki C, Ibáñez-Prada ED, Gonçalves BP, Baruch J, Escher M, Pritchard MG, Wei J, Philippy F, Dagens A, Hall M, Lee J, Kutsogiannis DJ, Wils EJ, Fernandes MA, Tirupakuzhi Vijayaraghavan BK, Panda PK, Martin-Loeches I, Ohshimo S, Fatoni AZ, Horby P, Dunning J, Rello J, Merson L, Rojek A, Vaillant M, Olliaro P, Reyes LF; ISARIC Clinical Characterisation Group. *Heliyon*. 2024 **10**(10): e29591. DOI: 10.1016/j.heliyon.2024.e29591. PMID: 38779000. PMCID: PMC11109728.

Analysis of the ISARIC database shows that 13.6% of patients with COVID-19 presented without respiratory symptoms. These patients had a higher crude in-hospital mortality rate (41%) compared to those patients who presented with respiratory symptoms (32%), but the risk of death was lower when adjusting for confounding factors (hazard ratio = 0.88 [0.83-0.93]).

▪ BACKGROUND

COVID-19 is primarily known as a respiratory illness; however, many patients present to hospital without respiratory symptoms. The association between non-respiratory presentations of COVID-19 and outcomes remains unclear. We investigated risk factors and clinical outcomes in patients with no respiratory symptoms (NRS) and respiratory symptoms (RS) at hospital admission.

▪ METHODS

This study describes clinical features, physiological parameters, and outcomes of hospitalised COVID-19 patients, stratified by the presence or absence of respiratory symptoms at hospital admission. RS patients had one or more of: cough, shortness of breath, sore throat, runny nose or wheezing, while NRS patients did not.

▪ RESULTS

Of 178,640 patients in the study, 86.4 % presented with RS, while 13.6 % had NRS. NRS patients were older (median age: NRS: 74 vs RS: 65) and less likely to be admitted to the ICU (NRS: 36.7 % vs RS: 37.5 %). NRS patients had a higher crude in-hospital case-fatality ratio (NRS 41.1 % vs. RS 32.0 %), but a lower risk of death after adjusting for confounders (HR 0.88 [0.83-0.93]).

▪ CONCLUSION

Approximately one in seven COVID-19 patients presented at hospital admission without respiratory symptoms. These patients were older, had lower ICU admission rates, and had a lower risk of in-hospital mortality after adjusting for confounders.

Direct-acting antiviral therapies for hepatitis C infection: global registration, reimbursement, and restrictions. Marshall AD, Willing AR, Kairouz A, Cunningham EB, Wheeler A, O'Brien N, Perera V, Ward JW, Hiebert L, Degenhardt L, Hajarizadeh B, Colledge S, Hickman M, Jawad D, Lazarus JV, Matthews GV, Scheibe A, Vickerman P, Dore GJ, Grebely J; Global HCV and HIV Treatment Restrictions Group. *Lancet Gastroenterol Hepatol*. 2024 **9**(4): 366-382. DOI: 10.1016/s2468-1253(23)00335-7. PMID: 38367631.

Direct acting antivirals (DAAs) have revolutionised hepatitis C treatment, which has a global prevalence of 57 million cases. This analysis describes country-level patterns of drug licensing, reimbursements and restrictions on use. 9% of countries currently licence no DAAs, and nearly half of all LMICs do not reimburse costs. Access to DAAs improves as costs fall.

Direct-acting antivirals (DAAs) for hepatitis C virus (HCV) infection have delivered high response rates (>95%) and simplified the management of HCV treatment, permitting non-specialists to manage patients without advanced liver disease. We collected and reviewed global data on the

registration and reimbursement (government subsidised) of HCV therapies, including restrictions on reimbursement. Primary data collection occurred between 15 Nov 2021, and 24 July 2023, through the assistance of a global network of 166 HCV experts. We retrieved data for 160 (77%) of 209 countries and jurisdictions. By mid-2023, 145 (91%) countries had registered at least one of the following DAA therapies: sofosbuvir-velpatasvir, sofosbuvir-velpatasvir-voxilaprevir, glecaprevir-pibrentasvir, sofosbuvir-daclatasvir, or sofosbuvir. 109 (68%) countries reimbursed at least one DAA therapy. Among 102 LMICs, 89 (87%) had registered at least one HCV DAA therapy and 53 (52%) reimbursed at least one DAA therapy. Among all countries with DAA therapy reimbursement (n=109), 66 (61%) required specialist prescribing, eight (7%) had retreatment restrictions, seven (6%) had an illicit drug use restriction, five (5%) had an alcohol use restriction, and three (3%) had liver disease restrictions. Global access to DAA reimbursement remains uneven, with LMICs having comparatively low reimbursement compared with high-income countries. To meet WHO goals for HCV elimination, efforts should be made to assist countries, particularly LMICs, to increase access to DAA reimbursement and remove reimbursement restrictions-especially prescriber-type restrictions-to ensure universal access.

At-admission prediction of mortality and pulmonary embolism in an international cohort of hospitalised patients with COVID-19 using statistical and machine learning methods. Mesinovic M, Wong XC, Rajahram GS, Citarella BW, Peariasamy KM, van Someren Greve F, Olliaro P, Merson L, Clifton L, Kartsonaki C; ISARIC Characterisation Group. *Sci Rep*. 2024 **14**(1): 16387. DOI: 10.1038/s41598-024-63212-7. PMID: 39013928. PMCID: PMC11252333.

Applying machine learning to the largest international dataset of hospitalised COVID-19 patients (>800,000 patients), prediction models for both death and occurrence of pulmonary embolism were determined. Pulmonary embolism occurred in 0.7% of the cohort. The prediction tool has an Area Under the Curve of ~75% for both PE and death – outperforming other models.

By September 2022, more than 600 million cases of SARS-CoV-2 infection had been reported globally, resulting in over 6.5 million deaths. COVID-19 mortality risk estimators are often, however, developed with small unrepresentative samples and with methodological limitations. It is highly important to develop predictive tools for pulmonary embolism (PE) in COVID-19 patients as one of the most severe preventable complications of COVID-19. Early recognition can help provide life-saving targeted anti-coagulation therapy right at admission. Using a dataset of more than 800,000 COVID-19 patients from an international cohort, we propose a cost-sensitive gradient-boosted machine learning model that predicts occurrence of PE and death at admission. Logistic regression, Cox proportional hazards models, and Shapley values were used to identify key predictors for PE and death. Our prediction model had a test AUROC of 75.9% and 74.2%, and sensitivities of 67.5% and 72.7% for PE and all-cause mortality respectively on a highly diverse and held-out test set. The PE prediction model was also evaluated on patients in UK and Spain separately with test results of 74.5% AUROC, 63.5% sensitivity and 78.9% AUROC, 95.7% sensitivity. Age, sex, region of admission, comorbidities (chronic cardiac and pulmonary disease, dementia, diabetes, hypertension, cancer, obesity, smoking), and symptoms (any, confusion, chest pain, fatigue, headache, fever, muscle or joint pain, shortness of breath) were the most important clinical predictors at admission. Age, overall presence of symptoms, shortness of breath, and hypertension were found to be key predictors for PE using our extreme gradient boosted model. This analysis based on the, until now, largest global dataset for this set of problems can inform hospital prioritisation policy and guide long term clinical research and decision-making for COVID-19 patients globally. Our machine learning model developed from an international cohort can serve to better regulate hospital risk prioritisation of at-risk patients.

Dry swabs and dried saliva as alternative samples for SARS-CoV-2 detection in remote areas in Lao PDR. Sibounheuang B, Boutthasavong L, Chommanam D, Phommasone K, Panapruksachat S, Praphasiri V, Bouttavong S, Sisavath H, Christy NCV, Letizia AG, Mayxay M, Vongsouvath M, Ashley EA, Dubot-Pérès A. *Open Forum Infect Dis*. 2024 **11**(8): ofae433. DOI: 10.1093/ofid/ofae433. PMID: 39145142. PMCID: PMC11322834.

SARS-CoV-2 detection was compared between swabs collected in viral transport medium (VTM), dry swabs, saliva and dried saliva spotted on filter paper. 60% of participants had a positive test on swabs in VTM. Cohen's kappa coefficients were calculated between VTM and saliva (0.74), dry swabs (0.71), and dried saliva (0.57). Dry swabs present multiple advantages, and may be suitable for surveillance in low-resource settings.

▪ **BACKGROUND**

Surveillance of SARS-CoV-2 circulation is mainly based on real-time reverse transcription-polymerase chain reaction, which requires laboratory facilities and cold chain for sample transportation. This is difficult to achieve in remote rural areas of resource-limited settings. The use of dried blood spots shipped at room temperature has shown good efficiency for the detection of arboviral RNA. Using a similar approach, we conducted a study at 3 provincial hospitals in Laos to compare the detection of SARS-CoV-2 from neat and dried spot samples.

▪ **METHODS**

Between January 2022 and March 2023, patients with respiratory symptoms were recruited. Nasopharyngeal/ oropharyngeal swabs in virus transport medium (VTM), dry swabs, saliva, and dried saliva spotted on filter paper were collected. All samples were tested by SARS-CoV-2 real-time reverse transcription-polymerase chain reaction.

▪ **RESULTS**

In total, 479 participants were included. The VTM samples tested positive for 288 (60.1%). High positive percent agreements were observed for dry swab (84.8%; 95% CI, 80.2%-88.8%) and saliva (89.2%; 95% CI, 85.1%-92.6%) as compared with VTM. There was a loss of sensitivity when saliva was dried on filter paper (73.6%; 95% CI, 68.1%-78.6%) as compared with saliva. SARS-CoV-2 variant (Delta or Omicron) had no significant impact on the performance of the different sample types.

▪ **CONCLUSION**

Our findings suggest that dry swabs could be a good alternative for sample collection and permit easy shipping at ambient temperature for subsequent viral SARS-CoV-2 RNA purification and molecular investigation. This is a useful tool to consider for a rapid implementation of large-scale surveillance of SARS-CoV-2 in remote areas, which could be extrapolated to other respiratory targets during routine surveillance or in the case of a novel emerging pandemic.

The COVID guidelines India project: A rapid living evidence synthesis during a pandemic in a LMIC setting. Singh B, Alexander H, Tharyan P, Mathew J, Garner P, Rupali P, et al. *Clinical Epidemiology and Global Health*. 2024 **28**:101548. DOI: 10.1016/j.cegh.2024.101548.

The COVID Guidelines India project was set up to synthesise evidence related to all aspects of COVID management, providing freely accessible clinical guidelines that are updated in real time, as new evidence emerges. The WHO Evidence to Decision framework was employed to ensure guidelines were contextually relevant.

▪ **BACKGROUND**

COVID-19 has had an unprecedented impact worldwide. Evidence for management interventions emerged rapidly but was difficult for clinicians and others to assess and decide how to use. Our team in India set up a national and international collaboration preparing guidance in real time to help guide clinical practice in the country during a pandemic setting. We describe our methods and the product in this paper.

▪ **METHODS**

Specialized groups comprising core, steering, methodology, evidence synthesis, dissemination and intervention expert working groups were formed. A Cochrane Rapid Review approach was used for prioritised questions in areas of clinical equipoise in management of COVID-19. GRADE methodology was incorporated into this process and expert working groups tailored guidelines for India using the WHO Evidence to Decision framework. This was then disseminated on a widely accessible platform indiacovidguidelines.org. A questionnaire was then used to obtain end-user feedback on the guidelines.

▪ **RESULTS**

Since May 2021, a total of 20 guidelines have been developed spanning pharmacological, respiratory and other supportive interventions for management of COVID-19, with over 83,600 unique page views up to December 2023. Results from a pilot survey suggest usefulness of the guidelines, but also highlighted areas for improvement. A key output was adoption of our anticoagulation recommendation in state level COVID-19 guidelines (Kerala, India). National and institutional capacity for evidence synthesis and guidelines was strengthened.

▪ **CONCLUSION**

The COVID Guidelines India project successfully developed contextually relevant, nationally applicable, evidence-based guidelines in a timely manner, and disseminated these freely through a dedicated website while successfully building capacity amongst Indian clinicians for evidence-based guideline development. Throughout the ongoing COVID Guidelines India project, the team has maintained a 'living' approach, continuously updating and refining recommendations in response to emerging evidence during the ever-evolving pandemic landscape.

Bayesian spatio-temporal analysis of dengue transmission in Lao PDR. Soukavong M, Thinkhamrop K, Pratumchart K, Soulaphy C, Xangsayarath P, Mayxay M, Phommachanh S, Kelly M, Wangdi K, Clements ACA, Suwannatrai AT. *Sci Rep*. 2024 **14**(1): 21327. DOI: 10.1038/s41598-024-71807-3. PMID: 39266587. PMCID: PMC11393087.

National dengue incidence is 174 per 100,000, and infection rates are significantly higher in the rainy season. This analysis calculates the risk in relation to rainfall, temperature, vegetation and location. With clear geographic hot-spots in the south and nuanced associations with climate, control strategies should be tailored to multi-dimensional models that predict increased infection rates.

Dengue, a zoonotic viral disease transmitted by *Aedes* mosquitoes, poses a significant public health concern throughout Lao PDR. This study aimed to describe spatial-temporal patterns and quantify the effects of environmental and climate variables on dengue transmission at the district level. The dengue data from 2015 to 2020 across 148 districts of Lao PDR were obtained from the Lao PDR National Center for Laboratory and Epidemiology (NCLE). The association between monthly dengue occurrences and environmental and climate variations was investigated using a multivariable Zero-inflated Poisson regression model developed in a Bayesian framework. The study analysed a total of 72,471 dengue cases with an incidence rate of 174 per 100,000 population. Each year, incidence peaked from June to September and a large spike was observed in 2019. The Bayesian spatio-temporal model revealed a 9.1% decrease (95% credible interval [CrI] 8.9%, 9.2%) in dengue incidence for a 0.1 unit increase in monthly normalized difference vegetation index at a 1-month lag and a 5.7% decrease (95% CrI 5.3%, 6.2%) for a 1 cm increase in monthly precipitation at a 6-month lag. Conversely, dengue incidence increased by 43% (95% CrI 41%, 45%) for a 1 °C increase in monthly mean temperature at a 3-month lag. After accounting for covariates, the most significant high-risk spatial clusters were detected in the southern regions of Laos. Probability analysis highlighted elevated trends in 45 districts, emphasizing the importance of targeted control strategies in high-risk areas. This research underscores the impact of climate and environmental factors on dengue transmission, emphasizing the need for proactive public health interventions tailored to specific contexts in Laos.

Hepatitis B virus exposure, seroprotection status, and susceptibility in health care workers from Lao People's Democratic Republic: cross-sectional study. Virachith S, Phakhounthong K, Khounvisith V, Mayxay M, Kounnavong S, Sayasone S, Hübschen JM, Black AP. *JMIR Public Health Surveill*. 2024 **10**: e65093. DOI: 10.2196/65093. PMID: 39689257. PMCID: 11683653.

In this cohort of healthcare workers from 5 provinces, seropositivity for hepatitis B core antibody was 40.1%. Current infection was demonstrated in 5.4%. 28.7% had serological evidence of protection due to immunisation, with over 30% remaining susceptible to infection. This represents an opportunity for intervention.

▪ **BACKGROUND**

Despite the high prevalence of chronic hepatitis B virus (HBV) infection in adults in Lao PDR, Lao health care workers (HCWs) have previously been shown to have low levels of protection against infection. Furthermore, the prevalence of hepatitis D virus (HDV), which increases disease severity in individuals infected with HBV, is not known in Laos.

▪ **OBJECTIVE**

This study aimed to estimate the exposure and seroprotection against HBV, as well as exposure to HDV, in Lao HCWs from 5 provinces.

▪ **METHODS**

In 2020, a total of 666 HCWs aged 20 to 65 years from 5 provinces of Lao PDR were recruited, and their sera were tested by enzyme-linked immunosorbent assay to determine their HBV and HDV coinfection status.

▪ **RESULTS**

HBV exposure, as indicated by the presence of anti-hepatitis B core antibodies, was 40.1% (267/666) overall and significantly higher for HCWs from Oudomxay province (21/31, 67.7%; adjusted odds ratio 3.69, 95% CI 1.68-8.12; P=.001). The prevalence of hepatitis B surface antigen was 5.4% (36/666) overall and increased with age, from 3.6% (9/248) in those aged ≤30 years to 6.8% (8/118) in those aged ≥50 years. Only 28.7% (191/666) of participants had serological indication of immunization. We could find no evidence for HDV exposure in this study.

▪ **CONCLUSIONS**

The study found intermediate hepatitis B surface antigen prevalence among HCWs in Lao PDR, with no evidence of HDV coinfection. Notably, a significant proportion of HCWs remains susceptible to HBV, indicating a substantial gap in seroprotection against the disease.

Temporal changes in SARS-CoV-2 clearance kinetics and the optimal design of antiviral pharmacodynamic studies: an individual patient data meta-analysis of a randomised, controlled, adaptive platform study (PLATCOV). Wongnak P, Schilling WHK, Jittamala P, Boyd S, Luvira V, Siripoon T, Ngamprasertchai T, Batty EM, Singh S, Kouhathong J, Pagornrat W, Khanthagan P, Hanboonkunupakarn B, Poovorawan K, Mayxay M, Chotivanich K, Imwong M, Pukrittayakamee S, Ashley EA, Dondorp AM, Day NPJ, Teixeira MM, Piyaphanee W, Phumratanaprapin W, White NJ, Watson JA; PLATCOV Collaborative Group. *Lancet Infect Dis*. 2024 **24**(9): 953-963. DOI: 10.1016/s1473-3099(24)00183-x. PMID: 38677300.

This initial phase of SARS-CoV-2 clearance is enhanced by effective anti-viral drugs, and has become more rapid over time. Therefore in vivo *studies of viral clearance cannot be directly compared across time. Currently, the rate of viral clearance over the first 5 days is an appropriate correlate for clinical efficacy of anti-viral drugs, best reflecting current viral dynamics.*

▪ **BACKGROUND**

Effective antiviral drugs prevent hospitalisation and death from COVID-19. Antiviral efficacy can be efficiently assessed *in vivo* by measuring rates of SARS-CoV-2 clearance estimated from serial

viral genome densities quantitated in nasopharyngeal or oropharyngeal swab eluates. We conducted an individual patient data meta-analysis of unblinded arms in the PLATCOV platform trial to characterise changes in viral clearance kinetics and infer optimal design and interpretation of antiviral pharmacometric evaluations.

▪ **METHODS**

Serial viral density data were analysed from symptomatic, previously healthy, adult patients (within 4 days of symptom onset) enrolled in a large multicentre, randomised, adaptive, pharmacodynamic, platform trial (PLATCOV) comparing antiviral interventions for SARS-CoV-2. Viral clearance rates over 1 week were estimated under a hierarchical Bayesian linear model with B-splines used to characterise temporal changes in enrolment viral densities and clearance rates. Bootstrap re-sampling was used to assess the optimal duration of follow-up for pharmacometric assessment, where optimal was defined as maximising the expected Z score when comparing effective antivirals with no treatment. PLATCOV is registered at ClinicalTrials.gov, NCT05041907.

▪ **FINDINGS**

Between 29 Sept 2021, and 20 Oct 2023, 1,262 patients were randomly assigned in the PLATCOV trial. Unblinded data were available from 800 patients (who provided 16,818 oropharyngeal viral quantitative PCR [qPCR] measurements), of whom 504 (63%) were female. 783 (98%) patients had received at least one vaccine dose and 703 (88%) were fully vaccinated. SARS-CoV-2 viral clearance was biphasic (bi-exponential). The first phase (α) was accelerated by effective interventions. For all the effective interventions studied, maximum discriminative power (maximum expected Z score) was obtained when evaluating serial data from the first 5 days after enrolment. Over the 2-year period studied, median viral clearance half-lives estimated over 7 days shortened from 16·6 h (IQR 15·3 to 18·2) in September 2021 to 9·2 h (8·0 to 10·6) in October 2023 in patients receiving no antiviral drugs, equivalent to a relative reduction of 44% (95% credible interval [CrI] 19 to 64). A parallel reduction in viral clearance half-lives over time was observed in patients receiving antiviral drugs. For example, in the 158 patients assigned to ritonavir-boosted nirmatrelvir (3380 qPCR measurements), the median viral clearance half-life reduced from 6·4 h (IQR 5·7 to 7.3) in June, 2022, to 4.8 h (4·2 to 5.5) in October 2023, a relative reduction of 26% (95% CrI -4 to 42).

▪ **INTERPRETATION**

SARS-CoV-2 viral clearance kinetics in symptomatic, vaccinated individuals accelerated substantially over 2 years of the pandemic, necessitating a change to how new SARS-CoV-2 antivirals are compared (ie, shortening the period of pharmacodynamic assessment). As of October 2023, antiviral efficacy in COVID-19 can be efficiently assessed *in vivo* using serial qPCRs from duplicate oropharyngeal swab eluates taken daily for 5 days after drug administration.

Other infectious diseases

Diagnostic accuracy of DPP Fever Panel II Asia tests for tropical fever diagnosis. Dhawan S, Dittrich S, Arafah S, Ongarello S, Mace A, Panapruksachat S, Boutthasavong L, Adsamouth A, Thongpaseuth S, Davong V, Vongsouvath M, Ashley EA, Robinson MT, Blacksell SD. *PLoS Negl Trop Dis*. 2024 **18**(4): e0012077. DOI: 10.1371/ journal.pntd.0012077. PMID: 38598549. PMCID: PMC11034646.

A quantitative, multiplex rapid diagnostic test (RDT) for seven tropical non-malaria infections was evaluated in Laos. These were scrub and murine typhus, leptospirosis, dengue, Zika, Chikungunya and melioidosis. Test accuracy varied between pathogen, whether whole blood or serum was used, and between automated readers. While further optimisation of the platform is desirable, it is an important step towards multi-pathogen detection in resource-limited settings.

Fever is the most frequent symptom in patients seeking care in South and Southeast Asia. The introduction of rapid diagnostic tests (RDTs) for malaria continues to drive patient management and care. Malaria-negative cases are commonly treated with antibiotics without confirmation of bacteraemia. Conventional laboratory tests for differential diagnosis require skilled staff and appropriate access to healthcare facilities. In addition, introducing single-disease RDTs instead of conventional laboratory tests remains costly. To overcome some of the delivery challenges of multiple separate tests, a multiplexed RDT with the capacity to diagnose a diverse range of tropical fevers would be a cost-effective solution. In this study, a multiplex lateral flow immunoassay (DPP Fever Panel II Assay) that can detect serum immunoglobulin M (IgM) and specific microbial antigens of common fever agents in Asia (*Orientia tsutsugamushi*, *Rickettsia typhi*, *Leptospira* spp., *Burkholderia pseudomallei*, dengue virus, Chikungunya virus, and Zika virus) was evaluated.

▪ **METHODOLOGY/PRINCIPAL FINDINGS**

Whole blood (WB) and serum samples from 300 patients with undefined febrile illness (UFI) recruited in Vientiane, Lao PDR were tested using the DPP Fever Panel II, which consists of an Antibody panel and Antigen panel. To compare reader performance, results were recorded using two DPP readers, DPP Micro Reader (Micro Reader 1) and DPP Micro Reader Next Generation (Micro Reader 2). WB and serum samples were run on the same fever panel and read on both micro readers to compare results. ROC analysis and equal variance analysis were performed to inform the diagnostic validity of the test compared against the respective reference standards of each fever agent (S1 Table). Overall better AUC values were observed in whole blood results. No significant difference in AUC performance was observed when comparing whole blood and serum sample testing, except for when testing for *R. typhi* IgM (p = 0.04), *Leptospira* IgM (p = 0.02), and dengue IgG (p = 0.03). Linear regression depicted R2 values had ~70% agreement across WB and serum samples, except when testing for leptospirosis and Zika, where the R2 values were 0.37 and 0.47, respectively. No significant difference was observed between the performance of Micro Reader 1 and Micro Reader 2, except when testing for the following pathogens: Zika IgM, Zika IgG, and *B pseudomallei* CPS Ag.

▪ **CONCLUSIONS/SIGNIFICANCE**

These results demonstrate that the diagnostic accuracy of the DPP Fever Panel II is comparable to that of commonly used RDTs. The optimal cut-off would depend on the use of the test and the desired sensitivity and specificity. Further studies are required to authenticate the use of these cut-offs in other endemic regions. This multiplex RDT offers diagnostic benefits in areas with limited access to healthcare and has the potential to improve field testing capacities. This could improve tropical fever management and reduce the public health burden in endemic low-resource areas.

Case Report: A case of disseminated cutaneous listeriosis following appendicitis from Lao PDR. Evans TJ, Siratana V, Venkatesan T, Davong V, Thanadabouth K, Ashley EA. *Wellcome Open Res*. 2024 **8**: 504. DOI: 10.12688/wellcomeopenres.20210.1. PMID: 38434737. PMCID: PMC10905163.

This case reports a rare syndrome of Listeria monocytogenes *bloodstream infection with dissemination to the skin, with widespread pustular lesions. The patient had recently had appendicitis – the likely portal of entry. While this is the first report of* Listeria *infection in Laos, the burden of contamination and infection in LMICs is probably vastly underestimated.*

▪ **BACKGROUND**

Listeria monocytogenes is a food-borne pathogen that is a rare cause of bacteraemia and meningitis in immunosuppressed patients, and carries a high mortality rate. Cutaneous manifestations of listeriosis are rare, and are usually associated with direct inoculation of the skin.

▪ **CASE**

A 41-year-old woman who initially presented to a hospital in Laos with appendicitis was diagnosed with disseminated cutaneous listeriosis without recognised risk factors. Intra-abdominal pathology probably contributed to bacterial bloodstream invasion. Initial treatment with meropenem was switched to ampicillin based on best practice; however our patient died 5 days after diagnosis.

▪ CONCLUSION

This case highlights listeriosis as an important cause of mortality in LMICs, exacerbated by poor availability of laboratory diagnostics and ineffective empiric antibiotic regimens. Improvements in food hygiene, surveillance, and increased laboratory capacity are important strategies to reduce rates of infection and clinical outcomes.

Global, regional, and national incidence and mortality burden of non-COVID-19 lower respiratory infections and aetiologies, 1990-2021: a systematic analysis from the Global Burden of Disease Study 2021. GBD 2021 Lower Respiratory Infections and Antimicrobial Resistance Collaborators. *Lancet Infect Dis*. 2024 **24(**9): 974-1002. DOI: 10.1016/s1473-3099(24)00176-2. PMID: 38636536. PMCID: PMC11339187.

This in-depth analysis ranks the causes of lower respiratory tract infections between 1990 and 2021 by prevalence and mortality rate. Streptococcus pneumoniae *remained the commonest cause of infections and deaths throughout this period. Mortality in under-5s has fallen dramatically, although remains above WHO targets in many LMICs. Strategies for continued improvement are discussed.*

▪ BACKGROUND

Lower respiratory infections (LRIs) are a major global contributor to morbidity and mortality. In 2020-21, non-pharmaceutical interventions associated with the COVID-19 pandemic reduced not only the transmission of SARS-CoV-2, but also the transmission of other LRI pathogens. Tracking LRI incidence and mortality, as well as the pathogens responsible, can guide health-system responses and funding priorities to reduce future burden. We present estimates from the Global Burden of Diseases, Injuries, and Risk Factors Study (GBD) 2021 of the burden of non-COVID-19 LRIs and corresponding aetiologies from 1990 to 2021, inclusive of pandemic effects on the incidence and mortality of select respiratory viruses, globally, regionally, and for 204 countries and territories.

▪ METHODS

We estimated mortality, incidence, and aetiology attribution for LRIs, defined by the GBD as pneumonia or bronchiolitis, not inclusive of COVID-19. We analysed 26,259 site-years of mortality data using the Cause of Death Ensemble model to estimate LRI mortality rates. We analysed all available age-specific and sex-specific data sources, including published literature identified by a systematic review, as well as household surveys, hospital admissions, health insurance claims, and LRI mortality estimates, to generate internally consistent estimates of incidence and prevalence using DisMod-MR 2.1. For aetiology estimation, we analysed multiple causes of death, vital registration, hospital discharge, microbial laboratory, and literature data using a network analysis model to produce the proportion of LRI deaths and episodes attributable to the following pathogens: *Acinetobacter baumannii*, *Chlamydia* spp, *Enterobacter* spp, *Escherichia coli*, fungi, group B *streptococcus*, *Haemophilus influenzae*, influenza viruses, *Klebsiella pneumoniae*, *Legionella* spp, *Mycoplasma* spp, polymicrobial infections, *Pseudomonas aeruginosa*, respiratory syncytial virus (RSV), *Staphylococcus aureus*, *Streptococcus pneumoniae*, and other viruses (ie, the aggregate of all viruses studied except influenza and RSV), as well as a residual category of other bacterial pathogens.

▪ FINDINGS

Globally, in 2021, we estimated 344 million (95% uncertainty interval [UI] 325-364) incident episodes of LRI, or 4,350 episodes (4,120-4,610) per 100,000 population, and 2.18 million deaths (1.98-2.36), or 27.7 deaths (25.1-29.9) per 100,000. 502,000 deaths (406,000-611,000) were in children younger than 5 years, among which 254,000 deaths (197,000-320,000) occurred in countries with a low Socio-demographic Index. Of the 18 modelled pathogen categories in 2021, *S pneumoniae* was responsible for the highest proportions of LRI episodes and deaths, with an estimated 97.9 million (92.1-104.0) episodes and 505,000 deaths (454,000-555,000) globally. The pathogens responsible for the second and third highest episode counts globally were other viral aetiologies (46.4 million [43.6-49.3] episodes) and *Mycoplasma* spp (25.3 million [23.5-27.2]), while those responsible for the second and third highest death counts were *S aureus* (424,000 [380,000-459,000]) and *K pneumoniae* (176,000 [158,000-194,000]). From 1990 to 2019, the global all-age non-COVID-19 LRI mortality rate declined by 41.7% (35.9-46.9), from 56.5 deaths (51.3-61.9) to 32.9 deaths (29.9-35.4) per 100,000. From 2019 to 2021, during the COVID-19 pandemic and implementation of associated non-pharmaceutical interventions, we estimated a 16.0% (13.1-18.6) decline in the global all-age non-COVID-19 LRI mortality rate, largely accounted for by a 71.8% (63.8-78.9) decline in the number of influenza deaths and a 66.7% (56.6-75·.3) decline in the number of RSV deaths.

▪ INTERPRETATION

Substantial progress has been made in reducing LRI mortality, but the burden remains high, especially in LMICs. During the COVID-19 pandemic, with its associated non-pharmaceutical interventions, global incident LRI cases and mortality attributable to influenza and RSV declined substantially. Expanding access to health-care services and vaccines, including *S pneumoniae*, *H influenzae* type B, and novel RSV vaccines, along with new low-cost interventions against *S aureus*, could mitigate the LRI burden and prevent transmission of LRI-causing pathogens.

Non-malarial febrile illness: a systematic review of published aetiological studies and case reports from China, 1980-2015. Ip DKM, Ng YY, Tam YH, Thomas NV, Dahal P, Stepniewska K, Newton PN, Guérin PJ, Hopkins H. *BMC Infect Dis*. 2024 **24**(1): 843. DOI: 10.1186/s12879-024-09542-3. PMID: 39164620. PMCID: PMC11334328.

A wide variety of infectious diseases cause non-malaria febrile illness in China, revealed by this systematic review that spans 1980-2015. Prevalent viral, bacterial and parasitic infections include vector-borne infections and zoonoses, and this understanding of febrile illness epidemiology is central to planning healthcare provision and delivering public health interventions.

▪ BACKGROUND

Rapid point-of-care tests for malaria are now widely used in many countries to guide the initial clinical management of patients presenting with febrile illness. With China having recently achieved malaria elimination, better understanding regarding the identity and distribution of major non-malarial causes of febrile illnesses is of particular importance to inform evidence-based empirical treatment policy.

▪ METHODS

A systematic review of published literature was undertaken to characterise the spectrum of pathogens causing non-malaria febrile illness in China (1980-2015). Literature searches were conducted in English and Chinese languages in six databases: Ovid MEDLINE, Global Health, EMBASE, Web of Science™ - Chinese Science Citation Database (SM), The China National Knowledge Infrastructure (CNKI), and WanFang Med Online. Selection criteria included reporting on an infection or infections with a confirmed diagnosis, defined as pathogens detected in or cultured from samples from normally sterile sites, or serological evidence of current or past infection. The number of published articles, reporting a given pathogen were presented, rather than incidence or prevalence of infection.

▪ RESULTS

A total of 57,181 records from 13 provinces of China where malaria used to be endemic were screened, of which 392 met selection criteria and were included in this review. The review includes 60 (15.3%) records published from 1980 to 2000, 211 (53.8%) from 2001 to 2010 and 121 (30.9%) from 2011 to 2015;. Of the 392 records, 166 (42.3%) were from the eastern region of China, 120 (30.6%) were from the south-west, 102 (26.0%) from south-central, and four (1.0%) were multi-

regional studies. Bacterial infections were reported in 154 (39.3%) records, viral infections in 219 (55.9%), parasitic infections in four (1.0%), fungal infections in one (0.3%), and 14 (3.6%) publications reported more than one pathogen group. Participants of all ages were included in 136 (34.7%) studies, only adults in 75 (19.1%), only children in 17 (4.3%), only neonates in two (0.5%) and the age distribution was not specified in 162 (41.3%) records. The most commonly reported bacterial pathogens included Typhoidal *Salmonella* (n = 30), *Orientia/ Rickettsia tsutsugamushi* (n = 31), *Coxiella burnetii* (n = 17), *Leptospira* spp. (n = 15) and *Brucella* spp. (n = 15). The most commonly reported viral pathogens included Hantavirus/Hantaan virus (n = 89), dengue virus (DENV) (n = 76 including those with unknown serovars), Japanese encephalitis virus (n = 21), and measles virus (n = 15). The relative lack of data in the western region of the country, as well as in in neonates and children, represented major gaps in the understanding of the aetiology of fever in China.

▪ CONCLUSION

This review presents a landscape of non-malaria pathogens causing febrile illness in China over 36 years as the country progressed toward malaria elimination. These findings can inform guidelines for clinical management of fever cases and infection surveillance and prevention, and highlight the need to standardize operational and reporting protocols for better understanding of fever aetiology in the country.

Which trial do we need? A pragmatic randomised trial of trimethoprim-sulfamethoxazole versus vancomycin for the treatment of methicillin-resistant *Staphylococcus aureus* bacteraemia in low-resource settings. Recht J, Evans TJ, Chansamouth V, Phommasone K, Mayxay M, Ashley EA. *Clin Microbiol Infect*. 2025 **31**(1): 13-17. DOI: 10.1016/j.cmi.2024.07.018. PMID: 39067512.

Improvements in mortality from MRSA bacteraemias in low-resource settings require evidence-based treatments that are affordable and accessible. This proposed clinical trial suggests a head-to-head comparison of co-trimoxazole, which is cheap and widely available, with vancomycin, which is expensive, often unavailable, and requires intravenous administration. MRSA is typically sensitive to co-trimoxazole, and existing data suggests it may be non-inferior to vancomycin in real-world settings.

Diagnosis of human leptospirosis: systematic review and meta-analysis of the diagnostic accuracy of the Leptospira microscopic agglutination test, PCR targeting *Lfb1*, and IgM ELISA to *Leptospira fainei* serovar Hurstbridge. Valente M, Bramugy J, Keddie SH, Hopkins H, Bassat Q, Baerenbold O, Bradley J, Falconer J, Keogh RH, Newton PN, Picardeau M, Crump JA. *BMC Infect Dis*. 2024 **24**(1): 168. DOI: 10.1186/s12879-023-08935-0. PMID: 38326762. PMCID: PMC10848445.

This meta-analysis of the diagnostic accuracy of various leptospirosis diagnostic tests uses Bayesian latent class modelling to account for imperfect comparator tests. Paired acute and convalescent microscopic agglutination tests remain the serological assay of choice, with pooled sensitivity of 68% and sensitivity of 75%. Few studies have assessed PCR or IgM, but these studies report sensitivities >90%.

▪ BACKGROUND

Leptospirosis is an underdiagnosed infectious disease with non-specific clinical presentation that requires laboratory confirmation for diagnosis. The serologic reference standard remains the microscopic agglutination test (MAT) on paired serum samples. However, reported estimates of MAT's sensitivity vary. We evaluated the accuracy of four index tests, MAT on paired samples as well as alternative standards for leptospirosis diagnosis MAT on single acute-phase samples, polymerase chain reaction (PCR) with the target gene *Lfb1*, and ELISA IgM with *Leptospira fainei* serovar Hurstbridge as an antigen.

▪ METHODS

We performed a systematic review of studies reporting results of leptospirosis diagnostic tests. We searched eight electronic databases and selected studies that tested human blood samples and compared index tests with blood culture and/or PCR and/or MAT (comparator tests). For MAT selection criteria we defined a threshold for single acute-phase samples according to a national classification of leptospirosis endemicity. We used a Bayesian random-effect meta-analysis to estimate the sensitivity and specificity of MAT in single acute-phase and paired samples separately, and assessed risk of bias using the Quality Assessment of Studies of Diagnostic Accuracy Approach- 2 (QUADAS-2) tool.

▪ RESULTS

For the MAT accuracy evaluation, 15 studies were included, 11 with single acute-phase serum, and 12 with paired sera. Two included studies used PCR targeting the *Lfb1* gene, and one included study used IgM ELISA with *Leptospira fainei* serovar Hurstbridge as antigen. For MAT in single acute-phase samples, the pooled sensitivity and specificity were 14% (95% credible interval [CrI] 3-38%) and 86% (95% CrI 59-96%), respectively, and the predicted sensitivity and specificity were 14% (95% CrI 0-90%) and 86% (95% CrI 9-100%). Among paired MAT samples, the pooled sensitivity and specificity were 68% (95% CrI 32-92%) and 75% (95% CrI 45-93%) respectively, and the predicted sensitivity and specificity were 69% (95% CrI 2-100%) and 75% (2-100%).

▪ CONCLUSION

Based on our analysis, the accuracy of MAT in paired samples was not high, but it remains the reference standard until a more accurate diagnostic test is developed. Future studies that include larger numbers of participants with paired samples will improve the certainty of accuracy estimates.

Zoonoses and animal health

Novel estimation of African swine fever transmission parameters within smallholder villages in Lao P.D.R. Matsumoto N, Ward MP, Halasa T, Schemann K, Khounsy S, Douangngeun B, Thepagna W, Phommachanh P, Siengsanan-Lamont J, Young JR, Toribio JLML, Bush RD, Blacksell SD. *Trop Anim Health Prod*. 2024 **56**(5): 166. DOI: 10.1007/s11250-024-04012-z. PMID: 38758410. PMCID: PMC11101325.

African Swine Fever (ASF) virus first appeared in Laos in 2019, causing a nationwide outbreak. Modelling demonstrated that some disease transmission parameters in Lao smallholder settings, such as the reproduction number of 3.08 – 7.80, are consistent with outbreaks in larger commercial settings; however unique management and behavioural differences may affect the rate of transmission. The assumptions made deriving these models are discussed, which may help guide future outbreak responses.

African Swine Fever (ASF) disease transmission parameters are crucial for making response and control decisions when faced with an outbreak, yet they are poorly quantified for smallholder and village contexts within Southeast Asia. Whilst disease-specific factors – such as latent and infectious periods – should remain reasonably consistent, host, environmental and management factors are likely to affect the rate of disease spread. These differences are investigated using Approximate Bayesian Computation with Sequential Monte-Carlo methods to provide disease parameter estimates in four naïve pig populations in villages of Lao PDR. The villages represent smallholder pig farmers of the northern province of Oudomxay and the southern province of Savannakhet, and the model utilised field mortality data to validate the transmission parameter estimates over the course of multiple model generations. The basic reproductive number between-pigs was estimated to range from 3.08 to 7.80, whilst the latent and infectious periods were consistent with those published in the literature for similar genotypes in the region (4.72 to 6.19 days and 2.63 to 5.50 days, respectively). These findings demonstrate that smallholder village pigs interact similarly to commercial pigs; however the spread of disease may occur slightly slower

than in commercial study groups. Furthermore, the findings demonstrate that despite diversity across the study groups, the disease behaved in a consistent manner. This data can be used in disease control programs or for future modelling of ASF in smallholder contexts.

Medicine quality

Repurposing rapid diagnostic tests to detect falsified vaccines in supply chains. Bharucha T, Gangadharan B, Clarke R, Fernandez LG, Arman BY, Walsby-Tickle J, Deats M, Mosca S, Lin Q, Stokes R, Dunachie S, Merchant HA, Dubot-Pérès A, Caillet C, McCullagh J, Matousek P, Zitzmann N, Newton PN. *Vaccine*. 2024. **42**(7): 1506-1511. DOI: 10.1016/j.vaccine.2024.01.019. PMID: 38355318.

Rapid diagnostic tests (lateral flow tests and latex agglutination tests) were successfully used to distinguish genuine from surrogate vaccines against several pathogens. Such point-of-care assays are easily deployable in a range of environments, including less-resourced healthcare settings. Validation for individual vaccine/assay combinations may be necessary, but this is a promising counter-attack against the large market of falsified vaccines.

Substandard (including degraded) and falsified (SF) vaccines are a relatively neglected issue with serious global implications for public health. This has been highlighted during the rapid and widespread rollout of COVID-19 vaccines. There has been increasing interest in devices to screen for SF non-vaccine medicines including tablets and capsules to empower inspectors and standardise surveillance. However, there has been very limited published research focussed on repurposing or developing new devices for screening for SF vaccines. To our knowledge, rapid diagnostic tests (RDTs) have not been used for this purpose but have important potential for detecting falsified vaccines. We performed a proof-in-principle study to investigate their diagnostic accuracy using a diverse range of RDT-vaccine/falsified vaccine surrogate pairs. In an initial assessment, we demonstrated the utility of four RDTs in detecting seven vaccines. Subsequently, the four RDTs were evaluated by three blinded assessors with seven vaccines and four falsified vaccines surrogates. The results provide preliminary data that RDTs could be used by multiple international organisations, national medicines regulators and vaccine manufacturers/distributors to screen for falsified vaccines in supply chains, aligned with the WHO global 'Prevent, Detect and Respond' strategy.

Forensic investigation of falsified antimalarials using isotope ratio mass spectrometry: a pilot investigation. Newton PN, Chesson LA, Mayxay M, Dondorp A, Tabernero P, Howa JD, Cerling TE. *Sci Rep*. 2024 **14**(1): 3995. DOI: 10.1038/s41598-024-54168-9. PMID: 38369604. PMCID: PMC10874941.

The carbon, nitrogen, and oxygen content in real and falsified antimalarial drugs was compared, alongside heavier:normal isotope ratios. Falsified medications had lower carbon content, suggesting added inorganic materials, and higher heavier carbon isotopes, indicating maize-derived starch. Oxygen isotopes in maize starch varied globally, and so oxygen isotope analysis of starch from falsified medications may reveal geographic origins.

We explored whether isotope ratio mass spectrometry (IRMS) is useful to investigate the origin of falsified antimalarials. Forty-four falsified and genuine antimalarial samples (artesunate, artemether-lumefantrine, dihydroartemisinin-piperaquine and sulphamethopyrazine-pyrimethamine) were analysed in bulk for carbon (C), nitrogen (N), and oxygen (O) element concentrations and stable isotope ratios. The insoluble fraction ("starch") was extracted from 26 samples and analysed. Samples of known geographical origin maize, a common source of excipient starch, were used to produce a comparison dataset to predict starch source. In both an initial (n = 18) and a follow-on set of samples that contained/claimed to contain artesunate/artemether (n = 26), falsified antimalarials had a range of C concentrations less than genuine comparator antimalarials and δ13C values higher than genuine comparators. The δ13C values of falsified antimalarials suggested that C4 plant-based organic material (e.g., starch derived from maize) had been included. Using the known-origin maize samples, predictions for growth water δ18O values for the extracted "starch" ranged from − 6.10 to − 1.62‰. These findings suggest that IRMS may be a useful tool for profiling falsified antimalarials. We found that C4 ingredients were exclusively used in falsified antimalarials versus genuine antimalarials, and that it may be possible to predict potential growth water δ18O values for the starch present in falsified antimalarials.

Other topics

Pathogen genomic surveillance status among lower resource settings in Asia. Getchell M, Wulandari S, de Alwis R, Agoramurthy S, Khoo YK, Mak TM, Moe L, Stona AC, Pang J, Momin MHFHA, Amir A, Andalucia LR, Azzam G, Chin S, Chookajorn T, Arunkumar G, Hung DT, Ikram A, Jha R, Karlsson EA, Le Thi MQ, Mahasirimongkol S, Malavige GN, Manning JE, Munira SL, Trung NV, Nisar I, Qadri F, Qamar FN, Robinson MT, Saloma CP, Setk S, Shirin T, Tan LV, Dizon TJR, Thayan R, Thu HM, Tissera H, Xangsayarath P, Zaini Z, Lim JCW, Maurer-Stroh S, Smith GJD, Wang LF, Pronyk P; Asia Pathogen Genomics Initiative (Asia PGI) consortium. *Nat Microbiol*. 2024 **9**(10): 2738-2747. DOI: 10.1038/s41564-024-01809-4. PMID: 39317773. PMCID: PMC11445059.

All 13 South and Southeast Asian countries surveyed successfully employ Next Generation Sequencing (NGS) for pathogen surveillance – both for outbreak response and for endemic infections. Major barriers exist to more extensive implementation, including financing, policy and guidelines, supply chain, and quality assurance. Further development of this infrastructure will enable more robust surveillance of emerging pathogens.

Asia remains vulnerable to new and emerging infectious diseases. Understanding how to improve next generation sequencing (NGS) use in pathogen surveillance is an urgent priority for regional health security. Here we developed a pathogen genomic surveillance assessment framework to assess capacity in low-resource settings in South and Southeast Asia. Data collected between June 2022 and March 2023 from 42 institutions in 13 countries showed pathogen genomics capacity exists, but use is limited and under-resourced. All countries had NGS capacity and seven countries had strategic plans integrating pathogen genomics into wider surveillance efforts. Several pathogens were prioritized for human surveillance, but NGS application to environmental and human-animal interface surveillance was limited. Barriers to NGS implementation include reliance on external funding, supply chain challenges, trained personnel shortages and limited quality assurance mechanisms. Coordinated efforts are required to support national planning, address capacity gaps, enhance quality assurance and facilitate data sharing for decision making.

Predicting mortality in febrile adults: comparative performance of the MEWS, qSOFA, and UVA scores using prospectively collected data among patients in four health-care sites in sub-Saharan Africa and South-Eastern Asia. Lal S, Luangraj M, Keddie SH, Ashley EA, Baerenbold O, Bassat Q, Bradley J, Crump JA, Feasey NA, Green EW, Kain KC, Olaru ID, Lalloo DG, Roberts CH, Mabey DCW, Moore CC, Hopkins H; Febrile Illness Evaluation in a Broad Range of Endemicities (FIEBRE) Study Consortium. *EClinicalMedicine*. 2024 **77**: 102856. DOI: 10.1016/j.eclinm.2024.102856. PMID: 39416389. PMCID: PMC11474423.

The article compares the performance of three clinical severity scores (MEWS, qSOFA, and UVA) in predicting mortality among febrile adults in resource-limited settings across sub-Saharan Africa and Southeast Asia. The UVA score was the most accurate predictor, with an AUC of 0.82, suggesting its value for early identification and treatment of high-risk patients.

▪ BACKGROUND

Clinical severity scores can identify patients at risk of severe disease and death, and improve patient management. The modified early warning score (MEWS), the quick Sequential (Sepsis-Related) Organ Failure Assessment (qSOFA), and the Universal Vital Assessment (UVA) were developed as risk-stratification tools, but they have not been fully validated in low-resource settings where fever and infectious diseases are frequent reasons for health care seeking. We assessed the performance of MEWS, qSOFA, and UVA in predicting mortality among febrile patients in Lao PDR, Malawi, Mozambique and Zimbabwe.

▪ METHODS

We prospectively enrolled in- and outpatients aged ≥ 15 years who presented with fever (≥37.5 °C) from June 2018-March 2021. We collected clinical data to calculate each severity score. The primary outcome was mortality 28 days after enrolment. The predictive performance of each score was determined using area under the receiver operating curve (AUC).

▪ FINDINGS

A total of 2,797 participants were included in this analysis. The median (IQR) age was 32 (24-43) years, 38% were inpatients, and 60% (1,684/2797) were female. By the time of follow-up, 7% (185/2,797) had died. The AUC (95% CI) for MEWS, qSOFA and UVA were 0.67 (0.63-0.71), 0.68 (0.64-0.72), and 0.82 (0.79-0.85), respectively. The AUC comparison found UVA outperformed both MEWS ($p < 0.001$) and qSOFA ($p < 0.001$).

▪ INTERPRETATION

We showed that the UVA score performed best in predicting mortality among febrile participants by the time follow-up compared with MEWS and qSOFA, across all four study sites. The UVA score could be a valuable tool for early identification, triage, and initial treatment guidance of high-risk patients in resource-limited clinical settings.

Prospects for the development of community-based care in remote rural areas: a stakeholder analysis in Laos. Liverani M, Phongluxa K, Phommasone K, Chew R, Chandna A, Pongvongsa T, Mayxay M, Kounnavong S, Ashley E, Lubell Y. *BMC Health Services Research*. 2024 **24**(1): 55. DOI: 10.1186/s12913-023-10523-6. PMID: 38212788. PMCID: PMC10782664.

Community-level provision continues to be the backbone of the Lao health system, but is facing rapidly shifting demands. Challenges identified by a wide range of stakeholders relate to the breadth of ethnic groups in the country, shifts in prominent causes of disease, the economy, and the interaction between domestic and donor priorities. Empowering and enabling community-led services will be essential to rectify faltering health outcomes.

Community-based health programmes have been a cornerstone of primary care in Laos for decades. This study aimed to document prospects for the development of current programmes, considering perceptions about health and health care priorities in the communities, implementation challenges, the policy landscape and opportunities associated with the availability of new technologies.

Metabolism and physiology of pathogenic bacterial obligate intracellular parasites. Mandel CG, Sanchez SE, Monahan CC, Phuklia W, Omsland A. *Frontiers in Cellular and Infection Microbiology*. 2024 **14**: 1284701. DOI: 10.3389/fcimb.2024.1284701. PMID: 38585652. PMCID: PMC10995305.

Obligate intracellular bacteria have numerous genetic and metabolic adaptations that optimize fitness. These are described in this review, highlighting commonalities between species, as well as species-specific features.

Bacterial obligate intracellular parasites (BOIPs) represent an exclusive group of bacterial pathogens that all depend on invasion of a eukaryotic host cell to reproduce. BOIPs are characterized by extensive adaptation to their respective replication niches, regardless of whether they replicate within the host cell cytoplasm or within specialized replication vacuoles. Genome reduction is also a hallmark of BOIPs that likely reflects streamlining of metabolic processes to reduce the need for de novo biosynthesis of energetically costly metabolic intermediates. Despite shared characteristics in lifestyle, BOIPs show considerable diversity in nutrient requirements, metabolic capabilities, and general physiology. In this review, we compare metabolic and physiological processes of prominent pathogenic BOIPs with special emphasis on carbon, energy, and amino acid metabolism. Recent advances are discussed in the context of historical views and opportunities for discovery.

The Selangor Consensus: strengthening clinical trials for local public health in the Western Pacific. Park K, Chen M, Shin J, Ong GX, Moorthy V, Zhang W, et al. *Lancet Regional Health – Western Pacific*. 2024 **48**: 101136. DOI: 10.1016/j.lanwpc.2024.101136. PMID: 39380745. PMCID: PMC11459399.

The Selangor Consensus was devised at the 75th World Health Assembly. It provides a framework to strengthen clinical trials in the Western Pacific region, recognising that trial infrastructure is not spread equitably. Focus should address local priorities and under-represented groups, ensuring context-appropriate ethical conduct, embedding trials into routine care, and bolstering local expertise.

Cost-utility analysis of radiofrequency ablation among facet joint-related chronic low back pain patients in Thailand. Sittimart M, Butani D, Poonsiri C, Korakot M, Nalongsack M, Chalermkitpanit P, Euasobhon P, Pasutharnchat K, Nimmaanrat S, Kanjanapanang N, Teerawattananon Y. *Pain Physician*. 2024 **27**(7): E761-E73. PMID: 39353124.

Health Technology Assessment (HTA) of radio frequency ablation for treatment of chronic back pain related to facet joints demonstrated lack of cost-effectiveness. Incremental cost-effectiveness ratios per quality-adjusted life year were I$52,380 – I$99,267 at the study timepoints – compared to an allowable threshold of I$13.652.

▪ BACKGROUND

Radiofrequency ablation (RFA) is a common secondary treatment recommended for facet joint-related chronic low back pain (CLBP). However, Thailand still lacks sufficient evidence of RFA's cost-effectiveness to support the decision to fund it.

▪ OBJECTIVE

To conduct a comparative economic evaluation of RFA and conservative treatment for CLBP patients over 16-month and 28-month time horizons in Thailand.

▪ STUDY DESIGN

A full economic evaluation encompassing measurements of both health utilities and health costs.

▪ SETTING

Data were collected from 3 university hospitals in Bangkok, Thailand: King Chulalongkorn Memorial Hospital, Siriraj Hospital and Ramathibodi Hospital.

▪ METHODS

The cost-utility analysis, which used the Markov model, was developed according to the Thai health technology assessment guidelines and compared RFA and the best supportive care from the societal perspective. In the study, the population consisted of patients who had endured low back pain for more than 3 months despite receiving conservative treatment. The results

were presented as an incremental cost-effective ratio (ICER) in Thai Baht (THB)/quality-adjusted life year (QALY). Scenario and sensitivity analyses were conducted.

▪ RESULTS

RFA was not cost-effective in Thailand when compared to conservative treatment, with a cost-effectiveness (CE) ratio of I$13,652 at all time horizons. The ICER of RFA was I$99,267 and I$52,380/QALY for the 16- and 28-month time horizons, respectively. In a scenario analysis in which RFA was repeated at 28 months and followed up at 52 months, the ICER was reduced to I$43,451. One-way sensitivity analysis showed that the ICER was most sensitive to the changes in utility parameters, the cost of RFA, and opportunity cost in the no-pain state.

▪ LIMITATIONS

The study uses primary data to derive the utility value and determine the costs. However, the limitation includes a relatively small sample size and a short follow-up time for parameter inputs.

▪ CONCLUSION

This study, the first economic evaluation of RFA for CLBP in Asia, showed that RFA was not cost-effective in Thailand. Price negotiation is recommended to make the intervention more cost-effective before it is included in the benefit package.

Impact of COVID-19 pandemic on HTAsiaLink network members. Sitanggang RJ, Chavarina KK, K C S, Wadhwa R, Wiweko B, Purba FD, Ghazali IMM, Jacobsen JHW, Dilokthornsakul P, Mayxay M, Isaranuwatchai W, Wang Y, Chen YL, Ong BSK, Kar S, Avdeyev A, Teerawattananon Y. *Int J Technol Assess Health Care*. 2024 **40**(1): e63. DOI: 10.1017/s0266462324000357. PMID: 39587775.

The COVID-19 pandemic disrupted the work of Health Technology Assessment (HTA) organisations, mitigated by increases to funding and staff. The number of research projects conducted generally rose during this time, demonstrating resilient organisations that could guide policy decisions. Most work focussed on COVID-19 itself, emphasising the importance of well-resourced HTAs to provide crucial evidence-based assessments during future pandemics.

▪ OBJECTIVES

This study investigates the impact of coronavirus disease 2019 (COVID-19) pandemic on HTAsiaLink members at the organizational level and provides recommendations for mitigating similar challenges in the future.

▪ METHODS

A survey was disseminated among HTAsiaLink members to assess the COVID-19 impact in three areas: (i) inputs, (ii) process, and (iii) outputs of the Health Technology Assessment organizations' (HTAOs) research operations and HTA processes in general.

▪ RESULTS

Survey results showed that most HTAOs hired more staff and secured similar or higher funding levels during COVID-19. Nevertheless, some organizations reported high staff turnover. COVID-19-relevant research was prioritized, and most of the organizations had to adapt their research design to meet the needs of policymakers. Time constraints in conducting research and inability to collect primary data were reported as impacts on the research process. Overall, the number of research projects and accessibility of respondents' publications increased during COVID-19.

▪ CONCLUSION

Research demand for HTAOs increased during COVID-19 and impacted their research process; however, they demonstrated resilience and adaptability to provide timely evidence for policymakers. With the growing reliance on HTA, HTAOs require adequate financial support, continuous capacity building, collaboration, and partnership, innovative HTA methods, and a pragmatic yet robust, evidence-to-policy process in preparation for future pandemics.

Development of an education intervention for parents to improve oral health of children in Vientiane Province, Lao P.D.R. Vongsa S, Chanbounmy K, Sihavong P, Phanpadith S, Sangvilay S, Sidanoumonh P, et al. *Asian Journal of Dental Sciences*. 2024 **7**(1):186-193.

69% of preschool children in this study had dental caries – fewer than 73% found in 2013. Following implementation of a dental education programme, parents' knowledge of oral health, along with their oral health practice, increased significantly. This demonstrates the value of ongoing education, and future evaluation is required to measure the effects of these interventions.

▪ BACKGROUND

Dental caries is a major problem in young children worldwide, particularly in Southeast Asia. The prevalence of dental caries among preschool children is very high. In addition, parents play an important role in the development of caries in children.

▪ OBJECTIVE

This study aimed to evaluate dental education intervention for parents to improve oral health of children in Vientiane Province, Lao PDR.

▪ METHODS

This is a cohort study with a follow-up period of 3 months in two kindergartens in Vientiane province. Using modified oral health literacy and behavioural questionnaires to interview the parent or guardian before and after giving the education intervention. The oral health examination of all preschoolers was observed to record the quantity and severity of dental caries.

▪ RESULTS

A total of 218 children aged 3-5 years old in two kindergartens in Vientiane province, 117 (53.70%) were boys and 101 (46.30%) were girls. The prevalence of dental caries was 69.30% and the decayed, missing and filled teeth (dmft) index was 3.88 at baseline, lastly increased to 4.67 in the subsequent examination at 3 months post-intervention. In comparison with the pulpal involvement, ulceration, fistula and abscess (pufa) index was decreasing from 1.56 to 1.31 after intervention. The guardians who participated in the survey were mostly father/mother (90.80%), their average age was 35.79 (± 6.70) years old. There was a significant difference in the level of oral health knowledge, behaviour and parental practices after intervention (t = 5.41, 95% CI = 2.10-4.50, p < 0.001).

▪ CONCLUSION

The findings of this investigation indicate that providing dental education to parents is an important way to improve oral health knowledge, behaviour, and parental practices. However, the severity of dental caries in young children remains high. Therefore, it is crucial to implement oral health education and prevention programs in kindergartens.

Conference and meeting abstracts

International Society for Thrombosis and Haemostasis (ISTH)
22-26 June 2024, Bangkok, Thailand
Current management and treatment of *Plasmodium vivax* malaria and the haemolytic effects of 8-aminoquinolines on G6PD deficiency.
Cindy Chu.

▪ ABSTRACT

Relapses caused by *Plasmodium vivax* malaria occur frequently and at short intervals in Southeast Asia and Oceania. Anti-relapse treatment with an 8-aminoquinoline agent reduces recurrences significantly. Primaquine is the most commonly used 8-aminoquinoline for *P. vivax* malaria however, it can cause haemolysis in persons with G6PD deficiency. G6PD phenotype can be tested with a semi-quantitative fluorescent spot test, or with a recently available quantitative point of care device (STANDARD G6PD Biosensor). A newer 8-aminoquinoline, tafenoquine, has received regulatory

Anisone Chanthongthip and Danoy Chommanam on the roof of the Infectious Diseases Building of Mahosot Hospital after a test landing on the helipad. © LOMWRU.

ນາງ ອານິສອນ ຈັນທອງທິບ ແລະ ດຣ ດານ້ອຍ ຈອມມະນາມ ເຊິ່ງໄດ້ຈັດມີການທົດສອບຍົນນ້ອຍລົງຈອດທີ່ຊັ້ນດາດຟ້າຂອງ ຕຶກຊຶມເຊື້ອ ໂຮງໝໍມະໂຫສົດ. © LOMWRU.

approval for anti-relapse treatment for *P. vivax* malaria. Although tafenoquine also causes haemolysis in G6PD deficient individuals, its single dose regimen is advantageous over the 14-day course of primaquine. Tafenoquine cannot be given to individuals with < 70% G6PD activity thus, should be used alongside the STANDARD G6PD Biosensor test. These new tools support the progress towards malaria elimination.

International Congress for Tropical Medicine & Malaria (ICTMM)
19-23 September 2024, Kuching, Malaysia
Dose optimisation of tafenoquine for radical cure of *Plasmodium vivax* malaria.
Cindy Chu.

▪ ABSTRACT

Tafenoquine (an 8-aminoquinoine) is an alternative radical curative treatment to primaquine acting against the dormant liver stage of *Plasmodium vivax* (the hypnozoite). Tafenoquine has the considerable advantage of single dosing as compared to a 7 or 14-day course of primaquine to achieve radical cure. The recommended tafenoquine dose of 300mg was shown to be inferior in radical curative efficacy to a total primaquine dose of 3.5mg/kg in Southeast Asia; 74% versus 93% respectively. The comparator 3.5mg/kg total primaquine dose is the standard and most commonly used dose globally, but in Southeast Asia and the Western Pacific, higher doses of primaquine are needed for radical cure. Pharmacometric re-analysis of data from the Phase 3 pre-registration trials support a 50% dose increase, which is predicted to more than halve the relapses. The Southeast Asia Dose Optimisation of Tafenoquine (SEADOT) trial aims to determine whether a 50% increase in tafenoquine dose provides better efficacy against recurrent *P. vivax* infection at 4 months than the currently recommended tafenoquine dose.

Asia Pacific Malaria Elimination Network (APMEN) meeting
24-25 September 2024, Kuching, Malaysia.
Southeast Asian Dose Optimisation of Tafenoquine (SEADOT).
Cindy Chu.

▪ ABSTRACT

For efficacious radical cure in Southeast Asia and Oceania, high dose primaquine (total dose 7mg/kg) is needed. The equivalent single dose tafenoquine dose is 600mg, but adverse effects are a concern. The current recommended tafenoquine dose is 300mg; however, the regulatory radical cure trials show low radical cure rates (60-80%) in Southeast Asia. The SEADOT study is an NIH funded multi-centre trial conducted in 4 countries and aims to determine whether a 50% increase in tafenoquine dose provides better radical cure efficacy than the currently recommended dose. The pharmacokinetics and metabolism of tafenoquine will also be characterised. This study is ongoing and anticipated to be completed in 2028.

Stakeholder meeting for the SEADOT study at Khammouan province, with attendees from the national Centre for Malariology, Parasitology, and Entomology (CMPE), the provincial public health department and communicable disease center (CDC), and LOMWRU. © LOMWRU. Photographer: Souksavanh Simanivong.

ກອງປະຊຸມພາກສ່ວນກ່ຽວຂ້ອງກັບການສຶກສາ SEADOT ທີ່ແຂວງຄຳມ່ວນ ໂດຍມີຕົວແທນຈາກສູນໄຂ້ຍຸງ ແມ່ກາຝາ ແລະ ແມງໄມ້, ສາທາລະນະສຸກແຂວງ, ສູນຄວບຄຸມ ແລະ ປ້ອງກັນພະຍາດ ແລະ ທິມງານ © LOMWRU. ຮູບພາບໂດຍ: ທ້າວ ສຸກ ສະຫວັນ ສີມະນີວົງ.

Tropical Science Foundation (TropSci)
16-17 October 2024, Kuching, Malaysia
Health Service Challenges in Tropical Medicine.
Cindy Chu.

▪ ABSTRACT

Patients face unique challenges when accessing health services in tropical settings. Geography and topography within a region can vary greatly and limit the ease of travel. Infrastructure affects what tools are available to support clinical diagnosis and management. Human resources with different skills are needed to support health education activities at the community level, maintain medical services, and contribute to continuous education. Both infrastructure and human resources affect the quality of health care. Patient access to primary care in remote settings is ideally at the community level. However, rapid changes such as severe weather or the economic development in previously rural areas are changing how individuals interact with health care services.

Joint International Tropical Medicine Meeting (JITMM)
11-13 December 2024, Eastin Grand Hotel, Bangkok, Thailand
Leishmania in Laos.
Roberts T, Douangnouvong A, Robinson MT, Phommasone K, Adsamouth A, Souksavanh M, Phaxayaseng S, Keoluangkhot V, Phoumin P, Simmalavong M, Newton PN, Mayxay M, Ashley EA.

▪ INTRODUCTION

Leishmaniasis is a vector-borne disease spread by the bite of sand flies. Visceral leishmaniasis is a systemic, potentially lethal disease and has emerged as an opportunistic infection associated with HIV. Leishmaniasis has been reported in Thailand since 1999 with >200 cases reported. To date, there have been no reported cases of leishmaniasis in Laos; however there is no diagnostic capacity in the country, clinical awareness of the disease is limited and there have been no previous prevalence studies on *Leishmania* carried out. Therefore, the aim of the study was to investigate whether leishmaniasis is present in Laos in order to improve diagnosis and management in at-risk groups.

▪ METHODS

There were two aspects of this study: 1. EDTA blood was collected from newly diagnosed HIV-positive patients presenting to two HIV clinics in Vientiane, Laos and DNA was extracted from the buffy coat and submitted to nested-PCR of the ITS1 region; 2. Stored serum samples from adult patients presenting with fever to Mahosot Hospital in Vientiane, Laos were tested by InBios Kalazar *Detect* rapid test.

▪ RESULTS

There were 1,015 EDTA blood samples collected from HIV-positive patients between May 2021 and January 2024. All samples were negative by PCR. There were 511 stored serum samples tested by rapid test collected between January 2005 and October 2023 and two samples were positive (0.39%).

▪ CONCLUSION

This is the first study to show evidence for *Leishmania* circulating in Laos. Further studies are required to confirm our findings and show the geographical distribution.

Joint International Tropical Medicine Meeting (JITMM)
11-13 December 2024, Eastin Grand Hotel, Bangkok, Thailand
Assessment of direct RT-PCR technique, without RNA extraction, for detection of dengue infection from clinical samples.
Vilayouth Phimolsarnnousith, poster presentation.

Dengue is a leading cause of hospitalization, with an estimated 500,000 cases classified as severe dengue, and over 20,000 deaths related to dengue occurring every year worldwide. Real-time reverse transcription PCR (RT-qPCR) is the gold standard technique to detect dengue virus (DENV) during the acute phase of the infection. However, it requires prior RNA purification which is costly and time consuming. We evaluated direct RT-qPCR using Luna Universal Probe One-Step RT-qPCR kit (Luna RT-qPCR) for the detection of DENV in sera. Luna RT-qPCR conditions were optimized using DENV2 isolates. The efficiency of direct Luna RT-qPCR was evaluated on a panel of 132 patient sera using RNA purification (EZ1&2 Virus Mini Kit) followed by RT-qPCR (SuperScript III Platinum One-Step qRT-PCR system) as reference standard. Sensitivity (95% CI) of direct Luna RT-qPCR was 86% (77-92) when using 1/10 diluted patient sera. Comparable results were obtained with direct Luna RT-qPCR and reference standard process for samples with Cq<35. The results obtained in this study are promising. The use of direct RT-qPCR for DENV detection in patient sera, could make the use of PCR for dengue diagnosis in LMICs more affordable. Further studies are needed to evaluate DENV direct RT-qPCR on prospective samples in diagnosis context.

Dr Vilayouth Phimolsarnnousith. Photographer: Tamalee Roberts. © LOMWRU.

ດຣ ວິລະຍຸດ ພິມົນສານນຸສິດ ແລະ ໂປສເຕີສະເໜີ ທີ່ງານ JITMM 2024. ຮູບພາບໂດຍ: Tamalee Roberts. © LOMWRU.

2024 Ecology and Evolution of Infectious Diseases (EEID) Conference
24 June 2024, Stanford University
Estimating anti-Hepatitis E Virus Immunoglobulin G Positive Rate and Mapping Seroprevalence in all 18 Provinces of Laos.
Miley Sinantha-Hu, poster presentation.

Hepatitis E virus (HEV) is one of the main viruses causing viral hepatitis. HEV is a prominent global health challenge, as the WHO estimates 20 million annual cases and 44,000 annual deaths. HEV transmission primarily occurs orofecally through contaminated drinking water, placing people living with inadequate sanitation at higher risk. HEV also spreads zoonotically via consumption of undercooked pork products and animal contact. Transmission via blood transfusion is a growing concern; thus several countries recently added HEV testing to routine blood donor screening. Lao PDR is a middle-income country located in a region of HEV endemicity in Southeast Asia. In Laos, environmental factors predispose the population to both waterborne and zoonotic environmental transmission pathways. Yet, there is limited literature on HEV epidemiology in Lao PDR. HEV is not currently included in routine plasma screening for blood donors in Lao PDR. Varied regional climates, geographies, and levels of urban development may lead to varied seroprevalence among Lao provinces. Thus, this study aimed to estimate HEV seroprevalence in a cross-section of blood donors from all 18 provinces of Lao PDR who gave samples between May 2023 to May 2024. We conducted enzyme-linked immunosorbent assay (ELISA) testing from donor plasma to estimate anti-HEV IgG positive rate and map HEV seroprevalence by province in Laos. Preliminary findings confirm HEV seroprevalence variation from 38.7% to 64.3% among 300 samples from each of five completed provinces which span the northern, central, and southern regions.

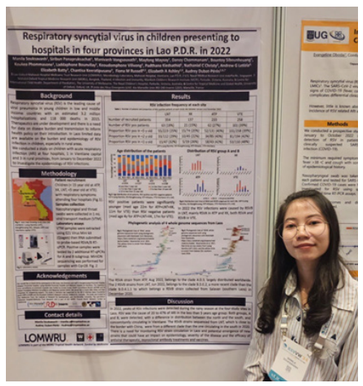
Lao National Health Research Forum
24-25 October, 2024, Vientiane
Hepatitis E Virus Seroprevalence in Blood Donations from 17 Provincial Blood Centers, Lao PDR.
Souksopha Banmanivong, poster presentation.

Hepatitis E virus (HEV) is one of the main viruses causing viral hepatitis globally. The WHO estimates 20 million HEV cases and 44,000 deaths, annually. Transmission via blood transfusion in places of known HEV circulation is a growing concern, particularly for immunocompromised or pregnant transfusion recipients for whom HEV can be fatal. Thus, several countries recently added HEV testing to routine blood donor screening. Lao PDR is a middle-income country located in a region of HEV endemicity in Southeast Asia. Yet, there is limited published data on HEV epidemiology in Lao PDR. HEV is not currently included in routine plasma screening for blood donors in Lao PDR. Varied regional climates, geographies, and levels of urban development may lead to varied seroprevalence among Lao provinces. Thus, this study aims to estimate HEV seroprevalence in a

cross-section of blood donors from all provinces of Lao PDR who gave samples between August 2023 to May 2024. 5,025 samples were received from 17 blood centre locations. Mean age: 29 years, range: 17 to 63 years. Overall, 2,413 (48.0%) donor samples were found positive by anti-HEV IgG ELISA. HEV seroprevalence ranged from 29.7% (Xiengkhuang) to 72.1% (Saravane) in the different provinces. These results indicate relatively high anti-HEV IgG seroprevalence compared to other nations in the Southeast Asia and Asia-Pacific. This suggests further investigation to estimate the risk of HEV transmission in Lao PDR is warranted.

8th RESVINET Conference RSVVW'24 – A Global Conference on Novel RSV Preventive and Therapeutic Interventions
13-16 February 2024, Mumbai
Respiratory Syncytial Virus In Children Presenting To Hospitals In Four Provinces In LAO P.D.R. In 2022.
Manila Souksavanh, poster presentation.

Respiratory syncytial virus (RSV) is the leading cause of viral pneumonia in young children in low income countries with an estimated 3.2 million hospitalizations and 118 000 deaths in 2015. In Laos limited data are available on the burden and epidemiology of RSV infection in children, especially in rural areas. We conducted a study on hospitalized children with acute respiratory infection (ARI) in four provinces in Laos from January to December 2022. RSV was tested by RT-PCR in upper respiratory tract sample from all recruited patients. In Vientiane capital, 101/258 (39.2%) children less than 5 year old were positive for RSV. 62/233 (27%), 63/354 (18%) and 21/137 (15%) children less than 15 year old were positive for RSV, in southern, northern and central provinces respectively. In all provinces, RSV epidemic was observed during rainy season. However, timing differences were observed. Whereas 97% of RSV infections were detected between April and July in the northern province, 90% of infections occurred between July to October in the southern and central provinces. The epidemic lasted longer in the southern province, from May to September, with few cases detected until December. Both groups, A and B, were detected; however, distribution differences between north and south were observed. Only RSVB was identified in the northern province, whereas mainly RSVA was identified in the southern and central provinces. In Vientiane capital, 63% were RSVB and 37% RSVA, with sequential circulation, RSVA appearing to replace RSVB over time. Whole genome sequencing will allow the characterization of circulating RSVA and RSVB strains.



Ms Manila Souksavanh, LOMWRU laboratory technician, and her poster at the 8th RESVINET Conference, Mumbai, India. © LOMWRU.

ນາງ ມະນີລາ ສຸກສະຫວັນ, ນັກວິເຄາະເຕັກນິກຂອງ LOMWRU ແລະ ໂປສເຕີ ສະເໜີ ທີ່ງານ RESVINET Conference, Mumbai, India. © LOMWRU.

ISPPD-13
17-20 March 2024, Cape Town, South Africa
What have we learnt from 10 years of sentinel site hospital-based acute respiratory infection surveillance in Lao PDR?
Keoudompone Vilivong, poster presentation.

Pneumonia surveillance is undertaken to characterize aetiology, quantify epidemiology and vaccine serotypes to inform vaccine introduction, monitor serotype replacement, evaluate vaccine impact, monitor AMR, identify outbreaks and immunisation programme gaps, and to support policy decisions on vaccine use. Here we describe the outcomes from 10 years of childhood acute respiratory infection (ARI) sentinel site hospital-based surveillance in Lao PDR. Surveillance at Mahosot Hospital, Vientiane commenced in 2013 and recruits 2-59-month-old children admitted with ≤14-day history of ARI. PCV13 status, clinical and demographic data are recorded, and swabs taken for pneumococcal detection by lytA qPCR, serotyping by microarray, AMR testing by WGS, and multiplex bacterial and viral assays. We found PCV13, introduced in 2013, to be effective against hypoxic pneumonia, a reduction in vaccine-serotype carriage, and evidence of indirect effects despite heterogeneous vaccine coverage. We found pneumococcal colonisation density to be associated with severe pneumonia. We found respiratory syncytial virus (RSV) to be a common cause of severe pneumonia in young children and that nasal or throat sampling are adequate for detection. We found some sustained improvements in pneumonia case management following the implementation of clinical guidelines. Our findings support the continued use of PCV and a change in its formulation, as well as the potential introduction of a future RSV vaccine. AMR results were presented at the meeting. We are also investigating the association between co-detection of common bacteria and viruses, pneumonia severity and pneumonia surveillance in Lao PDR (2013-2021) are forthcoming.

Conference on Medicines in the Algorithmized Era
26 April 2024, University of Lund, Lund, Sweden
Substandard and falsified medical products and innovation for prevent, detect and respond strategies.
Paul Newton (no abstract available).

World Health Summit
15 October 2024, Berlin, Germany
Choosing portable screening devices for the detection of substandard and falsified medicines - an online resource to guide national medicines regulators
Session title: *Instruments and methods for building trust in medicine quality in LMICs*. Céline Caillet and Gesa Gnegel.

▪ SESSION ABSTRACT

Up to two billion people around the world lack access to necessary medicines, and this vacuum is all too often filled by substandard and falsified (SF) products. WHO has identified this issue as one of the urgent global health challenges, given that more than one in ten medicines in LMICs are estimated to be SF. No country remains untouched. SF medical products may cause harm to patients, fail to treat the diseases for which they claim to be intended, lead to loss of confidence in the health systems, and contribute to AMR. Substandard medicines are 'genuine' (ie registered or licensed) medicines that fail to comply with adequate quality standards, while falsified medicines are often designed to appear identical to the genuine product. By their very nature, both substandard and falsified medicines are difficult to detect, even if for different reasons. However, many can be detected and identified by simple and inexpensive screening technologies which are currently emerging. This workshop will present both current technologies used for this purpose, and also new, emerging developments in this field. Experiences in the use of screening technologies, especially in LMICs, will be shared, and the training needs for the proper use of these technologies by researchers, regulators and other qualified stakeholders will be discussed.

LOMWRU team members join a walk in central Vientiane to mark World AMR Awareness Week 2024. Photographer: Elizabeth Ashley. © LOMWRU.

ທີມງານ LOMWRU ເຂົ້າຮ່ວມກິດຈະກຳຍ່າງເພື່ອສຸຂະພາບໃນງານສັບປະດາສາກົນໃນການປຸກຈິດສຳນຶກການນຳໃຊ້ຢາຕ້ານເຊື້ອ ທີ່ນະຄອນຫຼວງວຽງຈັນ. ຮູບພາບໂດຍ: Elizabeth Ashley. © LOMWRU.

Other activities in 2024

Public engagement & advocacy

Pint of Science Laos

Pint of Science Laos is fast becoming a major highlight in the annual science community calendar in Laos, and returned for the third year running in 2024. The international science festival was held simultaneously across 24 countries globally in May 2024. Building on the success of the previous years, this year Pint of Science Laos was held on 13-14 May 2024 at CoreBeer and attracted the biggest audience so far, with over 260 attendees over the two nights. Monday night was hosted by Vilaiphone Phomsisavath (Molecular Bacteriology) and Bountoy Sibounheuang (Microbiology/Virology Teams), and showcased conservation work by Anabel Lopez Perez of the Elephant Conservation Centre in Xayaboury, Sinongpheng Bouphanouvong from New Zealand-ASEAN Renewable Energy Facility and their work on improving energy efficiency and conservation in Laos, and Phonphachanh Sengmanikham (WWF Laos) who discussed fish welfare in Laos. On Tuesday night, hosted by Dr Vilayouth Phimolsarnnousith and Padthana Kiedsathid (Virology Team), David Viron of Dada Coffee gave a demonstration on coffee tasting, LOMWRU's very own Dr Manophab Luangraj discussed melioidosis in Laos, and Luckpanomphone Sinuanphao from The Makerbox Lao gave an insightful talk on her journey as a citizen scientist and working with NASA. Pint of Science Laos is organized and hosted by LOMWRU and an active team of volunteers: Tamalee Roberts, Vilaiphone Phomsisavath, Bountoy Sibounheuang, Vilayouth Phimolsarnnousith, Padthana Kiedsathid, Latsaniphone Boutthasavong, Vilason Souvannasen, Aphaphone Adsamouth, Mayulee Thalongsengchanh, Manila Souksavanh, Souksakhone Volavong, Anousone Douangnouvong, Danoy Chommanam, Vayouly Vidhamaly, Ooyanong Phonemeexay, Malavanh Vongsouvath and Matt Robinson.

World AMR Awareness Week 2024

World AMR Awareness Week (WAAW) 2024 emphasized the urgent need to tackle AMR globally and in Laos. Under the slogan *Educate. Advocate. Act now,* LOMWRU co-sponsored and joined a walk on 16 November 2024 from Patuxay Monument to the Presidential Palace, organized by the Department of Communicable Disease Control, MoH. Starting at 5 am, the event was attended by the Vice-Minister of Health and other distinguished guests. Continuing the week's activities, on 21 November, LOMWRU, the Fleming Fund, and WHO co-sponsored a meeting led by the Food and Drug Department, MoH, to raise awareness about AMR, antimicrobial consumption (AMC), and antimicrobial use (AMU) in Laos. The meeting brought together pharmacy owners, drug companies, and government representatives, where Dr Vilada Chansamouth presented key findings from the 2024 point prevalence surveys, highlighting critical insights into AMU practices.

Lao Medical Journal

LOMWRU continues to support publication of the Lao Medical Journal.

Farewells

Ms Sengmany Symanivong, Finance and HR Administrator at LOMWRU, who first joined in 2000, left LOMWRU to marry Lige Morris. Sengmany is now living in Ohio, USA. Mr Soulignasack Thongpaseuth retired after 21 (2003-2024) years working at LOMWRU. We thank them for so many years of dedicated service.

Leaving baci for Soulignasack Thongpaseuth and Sengmany Symanivong. Photographer: Elizabeth Ashley. © LOMWRU.

ພິທີບາສີສູ່ຂວັນອຳລາພະນັກງານ ທ່ານ ສຸລິຍະສັກ ທອງພະຈັນ ແລະ ນາງ ແສງມະນີ ສີມະນີວົງ
ຮູບພາບໂດຍ: Elizabeth Ashley. © LOMWRU.

Dr John Evans, LOMWRU Clinical Fellow. Photographer: Elizabeth Ashley. © LOMWRU.

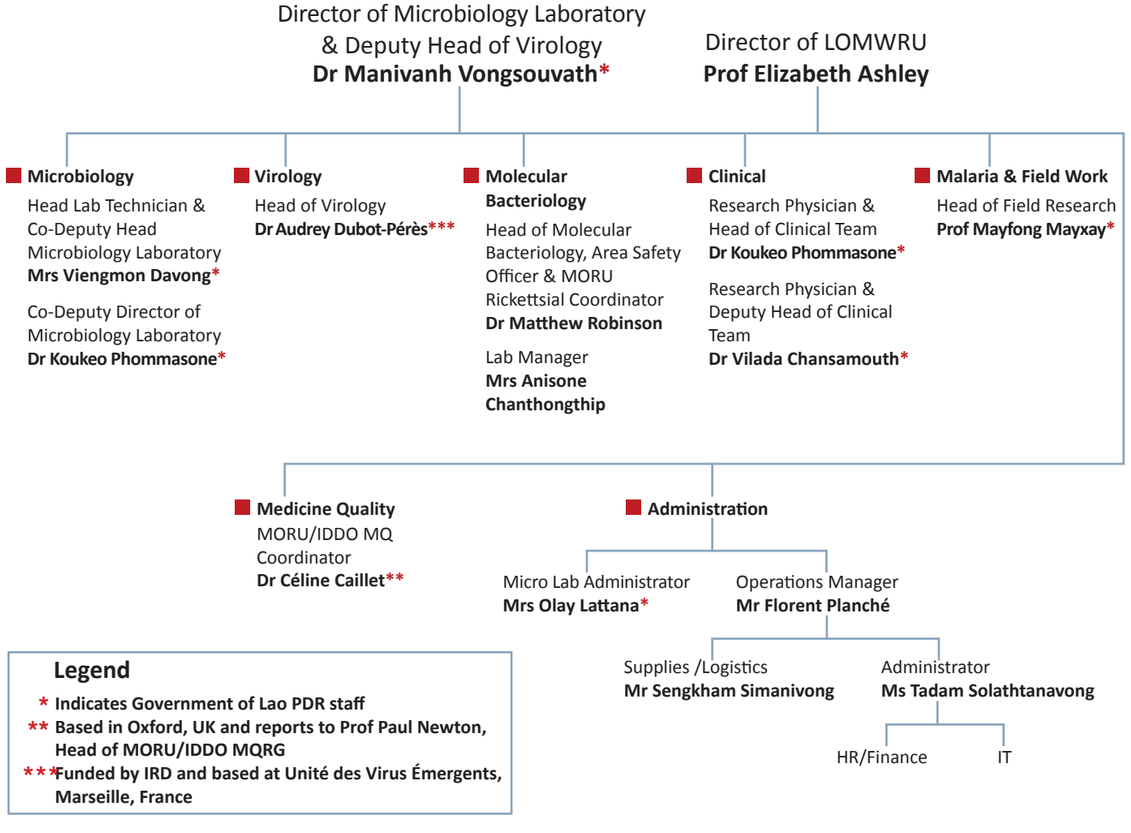
ດຣ John Evans, ທ່ານໝໍ LOMWRU fellow
ຮູບພາບໂດຍ: Elizabeth Ashley

Dr John Evans, Clinical Fellow, worked in Laos for 18 months and made a big impression on everyone. He returned to complete his training in Infectious Diseases & Microbiology in the UK.

Our thanks go to our other leavers in 2024: Ms Sompasong Soukhammala, Ms Nar Kingkeoudom, Dr Vannavong Siratana, Dr Mayulee Thalongsengchanh, Mr Khamxeng Khounpaseuth, Dr Sengdavanh Sydalay, Dr Soulichanya Phoutthavong, Dr Chom Phaiphichit, Dr Khambang Seevanhthong, Dr Viengsavanh Pimxaythong and Dr Xaipasong Xayaphet. We wish them the very best of luck with their future endeavours.

Finally, we would like to remember our colleague and friend, Mr Bounkhong Phommahasay, Laboratory Technician at Mahosot Hospital, who sadly passed away in 2024 after a long illness.

Annex A – LOMWRU organisational chart for 2024



Annex B – LOMWRU collaborators in 2024

1. Department of Communicable Disease Control (DCDC), Ministry of Health (MoH), Lao PDR
2. Department of Health Care and Rehabilitation (DHR), MoH, Lao PDR
3. Centre of Malariology, Parasitology & Entomology (CMPE), MoH, Lao PDR
4. National Centre for Laboratory & Epidemiology (NCLE), MoH, Lao PDR
5. Food and Drug Department (FDD), MoH, Lao PDR
6. University of Health Sciences (UHS), MoH, Lao PDR
7. Provincial Hospitals of Luang Namtha, Xieng Khouang, Salavan, Savannakhet, Attapeu and Vientiane, Lao PDR
8. Central Hospitals in Vientiane Capital: Mittaphab, Setthathirath, National Children's, Mother & Child, Police and Army Hospitals, Lao PDR
9. Lao Tropical and Public Health Institute
10. Food & Drug Quality Control Laboratory, MoH, Lao PDR
11. National Animal Health Laboratory (NAHL), Lao PDR
12. Bureau of Food and Drug Inspection, MoH, Lao PDR
13. Savannakhet Provincial Health Office, Lao PDR
14. WHO Lao Country Office, Vientiane, Lao PDR
15. Institut de Recherche pour le Développement (IRD), Lao PDR
16. Centre d'Infectiologie Christophe Mérieux du Laos, Lao PDR
17. Institut Pasteur du Laos (IPL), Lao PDR
18. Health Frontiers, Vientiane, Lao PDR
19. Dr Mathieu Picardeau, Unité de Biologie des Spirochètes, Institut Pasteur, Paris, France
20. Dr Alain Pierret and Dr Anne Pando, IRD, Lao PDR
21. Dr Olivier Ribolzi, Géosciences Environnement Toulouse, Université de Toulouse, France

22. Dr Lee Smythe and Dr Scott Craig, Leptospiral Reference Laboratory, Coopers Plains, Australia
23. London School of Hygiene and Tropical Medicine (LSHTM), London, UK
24. Prof Bart Currie, Menzies School of Health Research, Australia
25. Prof Al Richards, Rickettsial Diseases Research Program, Naval Medical Research Center, USA
26. Naval Medical Research Centre Asia Pacific, Singapore
27. Prof David Relman and Dr Stephen Popper, Department of Microbiology and Immunology, Stanford University, California, USA
28. Swiss Tropical and Public Health Institute, Basel/University of Basel, Switzerland
29. Dr Tim Barkham, Tan Tock Seng Hospital, Singapore
30. Dr Kate Bond, Dr Souly Phanouvong, Dr Jude Nwokike, Dr Victor Pribluda and Dr Mustapha Hajjou, United States Pharmacopeia, Rockville, Maryland, USA
31. Dr Todd French and Philip Bulterys, University of California - Los Angeles, USA
32. Dr Daniel Parker, University of California - Irvine, USA
33. Prof Fiona Russell, Murdoch Children's Research Institute (MCRI), University of Melbourne, Victoria, Australia
34. Prof John Crump, University of Otago, New Zealand
35. Prof Nicole Zitzmann and Dr Bevin Gangadharan, Department of Biochemistry, University of Oxford, UK
36. Infectious Diseases Data Observatory (IDDO), Centre for Tropical Medicine & Global Health, University of Oxford, UK
37. Dr Anders Omsland, Paul G Allen School for Global Health, Washington State University, WA, USA
38. Dr John Pettersson, University of Uppsala, Sweden
39. PATH, Seattle, USA
40. Prof Sabine Dittrich, Deggendorf Institute of Technology, Germany
41. Foundation for Innovative New Diagnostics (FIND), Geneva, Switzerland
42. Mathieu Pruvot and Amanda Fine, Wildlife Conservation Society, Wildlife Health Program, Bronx, New York, USA
43. Wildlife Conservation Society, Lao PDR Program, Vientiane, Lao PDR
44. Philippe Dussart and Paul Horwood, Institut Pasteur du Cambodge, Phnom Penh, Cambodia (now at Institut Pasteur du Madagascar, Antananarivo, Madagascar, and Australian Institute of Tropical Health and Medicine, James Cook University, Cairns, Australia, respectively)
45. Prof Xavier de Lamballerie, Unité des Virus Émergents, Aix-Marseille Université, Institut National de la Santé Et de la Recherche Médicale (INSERM), IRD, France
46. Institute of Medical Microbiology, University of Zurich, Switzerland
47. Institute for Health Metrics and Evaluation, USA
48. Médecins sans Frontières, France
49. Duke-NUS Medical School, Singapore
50. Clinton Health Access Initiative, Lao PDR
51. Dr Martine Barons, University of Warwick, UK
52. Health Intervention and Technology Assessment Program, Bangkok, Thailand
53. InBios International Inc. Innovative Diagnostics, USA
54. Global Access Diagnostics, UK and USA
55. Dr Chanthala Souksakhone, National Blood Transfusion Centre, Lao Red Cross, Vientiane, Lao PDR
56. Foundation Mérieux, Lao PDR
57. Prof David Denning, Manchester Fungal Infections Group, UK
58. Prof David Modrý, Dr Vojtech Baláž, and Jana Kacmarikova, University of Veterinary Sciences Brno, Czechia
59. Prof Mike Wiley, University of Nebraska, USA
60. Shoklo Malaria Research Unit (SMRU), Thailand
61. Mahidol Vivax Research Unit (MVRU), Thailand
62. Oxford University Clinical Research Unit (OUCRU), Viet Nam
63. Olivier Celhay, freelance consultant, Canada
64. MiraVista Diagnostics, Indianapolis, Indiana, USA
65. China Medical Board, Cambridge, MA, USA
66. National Dermatology Unit, MoH, Lao PDR
67. Cambodia-Oxford Medical Research Unit (COMRU), Cambodia
68. Department of Livestock and Fisheries (DLF), Ministry of Agriculture, Vientiane, Lao PDR
69. Dr Jemma Bergfeld and Dr Frank Wong, Australian Centre for Disease Preparedness (ACDP), CSIRO, Geelong, Australia
70. Asia Pathogen Genomics Initiative, Duke-NUS Medical School, Singapore
71. Dr Ahmar Hashmi, University of Texas, USA
72. Lao One Health University Network and Southeast Asia One Health University Network
73. Murdoch Children's Research Institute (Professor Fiona Russell), Melbourne, Australia
74. Dr Bhavin Rawal, Royal Brompton and Harefield NHS Foundation Trust, UK
75. Dr Kiattawee Chowongkomon, Department of Biochemistry, Faculty of Science, Kasetsart University, Bangkok, Thailand
76. Optimum Imaging Diagnostics (OIDx), Maine, USA
77. Prof Bayden Wood, Mr Aaron McLean: Centre of Biospectroscopy, Monash University, Melbourne, Australia
78. Dr Michael Edstein, Dr Marina Chavchich, Dr Wenjun Liu: Australian Defence Force Malaria and Infectious Disease Institute, Brisbane, Australia

Annex C – LOMWRU staff in 2024

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU)

Elizabeth Ashley – Unit Director

Atsamouth, Aphaphone	Laboratory Technician
Bellingham, Khonsavath	Research Scientist
Benjamin, Amelia Jane	Clinical Fellow in Microbiology
Boutthasavong, Latsaniphone	Senior Laboratory Technician/Deputy IDC lab Manager
Bounkhoun, Toukta	Research Physician
Banmanivong, Noy*	Cleaner
Caillet, Céline	Medicine Quality Research Group Coordinator/Research Scientist
Chu, Cindy	Senior Research Physician
Chansamouth, Vilada*	Senior Research Physician
Chanthaluanglath, Valin	Nurse, Patient Follow up
Chanthongthip, Anisone	Laboratory Manager
Chindavong, Touny	Senior Data Entry Officer
Chommanam, Danoy	Research Physician
Dadivong, Somxay	Junior Clinical Researcher
Davong, Viengmon*	Deputy Head of Microbiology Laboratory/Lab Manager
Duangmala, Souksavanh	Laboratory Technician - Follow up
Duangmala, Khuanta*	Laboratory Technician
Duangnouvong, Anousone	Research Physician
Dubot-Pérès, Audrey	Virology Group Head
Evans, Terry John	Clinical Fellow in Microbiology
Hanthongsay, Nilamith*	Specimens Storage Manager
Jaksuwan, Risara	Laboratory Management Advisor
Keodala, Malinar*	Laboratory Technician
Keokhamhoung, Dala	Patient Follow Up/Lab Technician
Keomeuangneua, Saisathit	HR and Administrative Officer
Keomoukda, Phatsalin	Laboratory Technician-Field
Khamsy, Chanthachone	Stock Officer
Khounpaseuth, Khamxeng	Laboratory Technician, Field
Kouaykesone, Phoudthasone	Data Quality Manager and Quality Support
Kiedsathid, Padthana	Laboratory Technician
Kingkeoudom, Nar	Data Entry Officer
Lathsachak, Thongsavanh	Laboratory Technician - Field
Lattana, Olay*	Head of Micro Lab Admin/Senior Laboratory Technician
Luangraj, Manophab	Research Physician
Mayxay, Mayfong*	Head of Field Research/President of University of Health Sciences
Nalongsack, Manilung	Research Pharmacist
Olinh, Thitthiphone	Research Pharmacist
Opphalavong, Somphone	Security Guard
Panapruksachat, Siribun	Molecular Bacteriologist
Panyanouvong, Phonepasith*	Senior Laboratory Technician
Pimmalath, Chanthalyphone	Finance Officer
Pimxaythong, Viengsavanh	Research Scientist
Phalivong, Sonexay	Project Coordinator (CMPE)
Phianthanom, Bountherng*	Laboratory Technician
Phimolsannousith, Vilayouth	Research Physician
Phommadeechack, Vanheuang	BSL3 Lab Manager/Research Scientist
Phommahasay, Bounkhong*	Laboratory Technician
Phommasone, Koukeo*	Deputy Head of Microbiology Laboratory and Senior Research Physician
Phonemixay, Ooyanong	Laboratory Technician
Phouminh, Phonelavanh*	Deputy Head of Micro Lab Administration & Senior Lab Technician
Padith, Kaisone	Laboratory Technician
Phuklia, Weerawat	Postdoctoral Scientist
Phakhounthong, Khanxayaphone	Research Physician, Field
Phommavanh, Xaykhamphet	Research Physician, Field
Phommavong, Touy	Research Physician- Field
Phomsisavath, Vilaiphone	Research Veterinarian
Phoutthavong, Soulichanya	Research Physician, Field
Planché, Florent Guillaume Yoann	Operations Manager
Roberts, Tamalee	Research Scientist
Robinson, Matthew	Group Head Molecular Bacteriology & Area Safety Advisor
Seevanhthong, Khambang	Research Physician - Field
Sengdatka, Davanh*	Laboratory Technician

Sengduangphachanh, Amphone-savanh*	Quality Control/Senior Laboratory Technician
Seubsanith, Amphaivanh*	Laboratory Technician
Sibounheuang, Bountoy*	Senior Laboratory Technician
Silichack, Lanoi*	Laboratory Technician
Silisouk, Joy*	Senior Laboratory Technician
Symanivong, Sengkham	Purchase & Supply Administrator
Symanivong, Souksavanh	Field Administrator/Logistician, Field
Simmalavong, Manivone*	Deputy Head of Micro Lab Administration/Laboratory Technician
Siratana, Vannavong	Research Physician
Singvongsa, Kikhamsen	IT Support Manager
Sihabout, Mongkhounthong	Facilities Officer
Souksavanh, Manila	Laboratory Technician
Solathtanavong, Tadam	Administrative and HR Officer
Soulivong, Ailatda	Research Physician, Field
Soukhammala, Sompasong	Finance and Admin Assistant
Souvannasen, Vilason	Laboratory Technician, Field
Syhalath, Somsavanh*	Laboratory Technician
Symanivong, Sengmany	Finance and HR Administrator
Sydalay, Sengdavanh	Research Physician
Thammavong, Sompong	Laboratory Technician
Thammavong, Amphaivanh	Research Pharmacist
Thammavongsa, Peeyanout	Research Physician
Thalongsengchan, Mayulee	Clinical Research Assistant
Thepbandith, Sompany	Senior Finance Officer
Thongpaseuth, Soulignasack	Senior Laboratory Technician
Vang, Sao*	Laboratory Technician
Vannachone, Souphaphone	Research Physician
Vidhamaly, Vayouly	Head of Clinical Trials Support Group
Vilayhong, Poukky	Research Physician
Vilivong, Keoudomphone	Study Coordinator
Volavong, Souksakhone	Specimens Storage Assistant
Vongratsavai, Aeo	HR and Administrative Assistant
Vongsouvath, Manivanh*	Director of Microbiology Laboratory/Deputy Virology Group Head
Vongsouvath, Viengsavanh	Administration Assistant
Vongsouvath, Malavanh*	Laboratory Technician
Xaithilath, Parnthong	Trainee Data Manager
Xayaphet, Xaipasong	Research Physician, Field
Xayalath, Somdy	Laboratory Technician, Field
Xongmalaythong, Khamthasone	Data Entry Officer
Xayvanghane, Saiamphone	Project Coordinator
Xayasit, Buasy*	Cleaner
Yiaye, Touxiong	Research Physician - Field

* Indicates Government of Lao PDR staff

Thank you, LOMWRU project funders in 2024!

We would like to thank our funders and partners for their very generous support of projects in 2024.

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CSIRO

NIH National Institute of Allergy and Infectious Diseases

National Health Foundation

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