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Robust mission-driven responses to infectious disease threats delivered by the Abbott pandemic defense coalition

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ABSTRACT

Objectives: Emerging infectious disease outbreaks present a continuous threat globally, and enhanced capacity to detect and mitigate these pathogens is urgently needed.
Design: The Abbott Pandemic Defense Coalition (APDC) launched in 2021 as a first of its kind global public-private partnership dedicated to early detection, characterization, and response to emerging disease threats with the mission to reduce the burden of existing epidemics and the risk of future pandemics. The APDC has the capacity to both detect emerging infectious agents and respond by rapidly developing and deploying prototype diagnostics to assist in assessing the magnitude of the threat.
Results: To date, the APDC network, with sites on 5 continents, has evaluated over 39,000 specimens from enrolled patients leading to the identification and characterization of 6 outbreaks and 23 previously unknown viruses that affect humans. The network has also trained 128 scientists in epidemiology, diag-

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nostics, sequencing, and bioinformatics. As a result, the APDC has published 113 manuscripts, which are highlighted herein.

Conclusions: As emerging pathogens present increasing challenges to public health in a closely connected global community, the APDC is uniquely positioned to continue to serve a key role in pandemic preparedness.

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Introduction

In the wake of the coronavirus disease 2019 (COVID-19) pandemic, emerging and re-emerging infectious diseases continue to pose a threat to humanity. Since the pandemic, the world has faced outbreaks of Ebola and Marburg viruses in Africa, the emergence of mpox as a global threat, a large outbreak of dengue in the Americas, the spread of H5N1 Highly Pathogenic Avian Influenza (HPAI) among dairy cows, poultry, and humans, and one of the largest measles outbreaks in the United States since achieving elimination status in 2000 [1–6].

Robust surveillance and pathogen discovery are the initial steps in an effective pandemic response cascade, followed by the development and deployment of sensitive and specific diagnostics. The successful development of critical countermeasures, such as vaccines and therapeutics, is predicated on these upstream efforts to detect and characterize the emerging threat. Although a survey of international infectious disease experts conducted in 2024 found that most (90%) believe the world is now better prepared for the next pandemic compared to before COVID-19, the same experts acknowledged that serious gaps in preparedness persist, with surveillance programs for early detection of emerging pathogens being the most urgent gap needing to be addressed [7].

The Abbott Pandemic Defense Coalition (APDC) was established in 2021 to meet these global needs as a first of its kind mission driven program dedicated to identifying and responding to infectious disease outbreaks to help end current epidemics and prevent future pandemics [8]. The APDC consists of partner sites located on five continents with expertise in infectious diseases, laboratory testing, genetic sequencing, immunology and epidemiology (Figure 1a). Each site contributes to the APDC mission through local infectious disease surveillance, novel pathogen discovery and investigation of the risks posed by a novel variant or pathogen to inform public health authorities (Figure 1b). Abbott equips APDC sites with diagnostic platforms, tests, personnel, and training to conduct surveillance and pathogen discovery in the host country and region. Importantly, each site is linked with their in-country Ministry of Health (MoH) to directly initiate communication when outbreaks and emerging infectious disease threats are detected. What truly sets the APDC apart as a unique program within the pandemic preparedness field are the focused standardized enrollment and testing of patients with acute febrile illness (AFI) and pathogen discovery through metagenomic next generation sequencing (mNGS) coupled with a robust bioinformatics tool. Further, the APDC has the capacity to develop and deliver industry-grade diagnostic prototypes and provide training for field epidemiologists as core components of the program. These defining attributes were all part of the five primary objectives that the APDC prioritized when it launched, as previously reviewed [8]:

1. Standardize case enrollment and clinical data collection at partner sites
2. Conduct surveillance of epidemic pathogens to track circulation and evolution of viral variants
3. Apply discovery sequencing and bioinformatics tools to identify novel and emerging pathogens
4. Develop and deploy prototype research use only (RUO) tests to evaluate the risk of novel and epidemic pathogens
5. Train the next generation of infectious disease epidemiologists

During the first 4 years of the program, the APDC has made substantial progress on all five objectives, which will be reviewed in the sections that follow.

Objective 1: standardize case enrollment and clinical data collection at partner sites

To achieve the APDC mission, the network applies a common workflow at partner sites that begins with enrollment of patients who are severely ill (Figure 1b). This is a critical step that concentrates downstream activities on optimal samples as fruitful sequencing efforts rely upon focused enrollment of patients who are at a higher risk of carrying a novel pathogen or variant. It is also important to ensure that sites are enrolling patients using the same criteria, making standardized case definitions a key feature of APDC. As the program launched, one of the first activities was to establish APDC case definitions for acute febrile illness (AFI), meningitis/encephalitis, acute hepatitis and severe acute respiratory illness (SARI) or influenza-like illness (ILI). All collections were approved by local ethics committees and all enrolled patients provided consent to participate in the study.

Effective application of these criteria was determined through analysis of the clinical data collected through a standardized electronic case reporting form (eCRF), which was implemented in 2023. The APDC eCRF database is a unique resource that is managed by Abbott and serves as a secure environment that restricts individual sites to only access their own data to maintain data privacy. As of June 2025, the APDC has enrolled and collected eCRF records from 24,683 acutely ill patients, comprised of 50.25% males, 49.74% females with an average age of 40 years (range of <1 month to 101 years) (Figure 2a). Notably, over half of all cases (13,477/24,683; 54.6%) were hospitalized and 61 deaths occurred following recruitment. A minority of enrolled participants, 714 (2.9%), reported occupational exposure to ill persons (healthcare workers) or animals (including domestic and wild animal) including veterinary workers ($N = 8$; 0.03%), wildlife workers ($N = 72$; 0.3%) and farm workers ($N = 1502$; 6.1%) (Figure 2b). In addition to the presence or history of a fever (≥ 38°C as determined by a healthcare professional), which is a criteria for enrollment, some of the most common reported symptoms include weakness, headache, malaise, fatigue and abdominal or joint pain (Figure 2c). Recent travel, a risk factor for exposure and spread of novel pathogens, was reported by 5523 (22.6%) of enrolled participants. Common co-morbidities in the cohort included: Human Immunodeficiency Virus (HIV) infection (4506/22,323; 20.2%), diabetes (897/22,323; 4.0%), and chronic lung disease (831/22,323; 3.7%) (Figure 2d). Many of the enrollees reported an exposure to animals (7168/24,084; 29.0%), including cats (1956/24,084; 8.1%) and dogs (4756/24,084; 19.7%), which

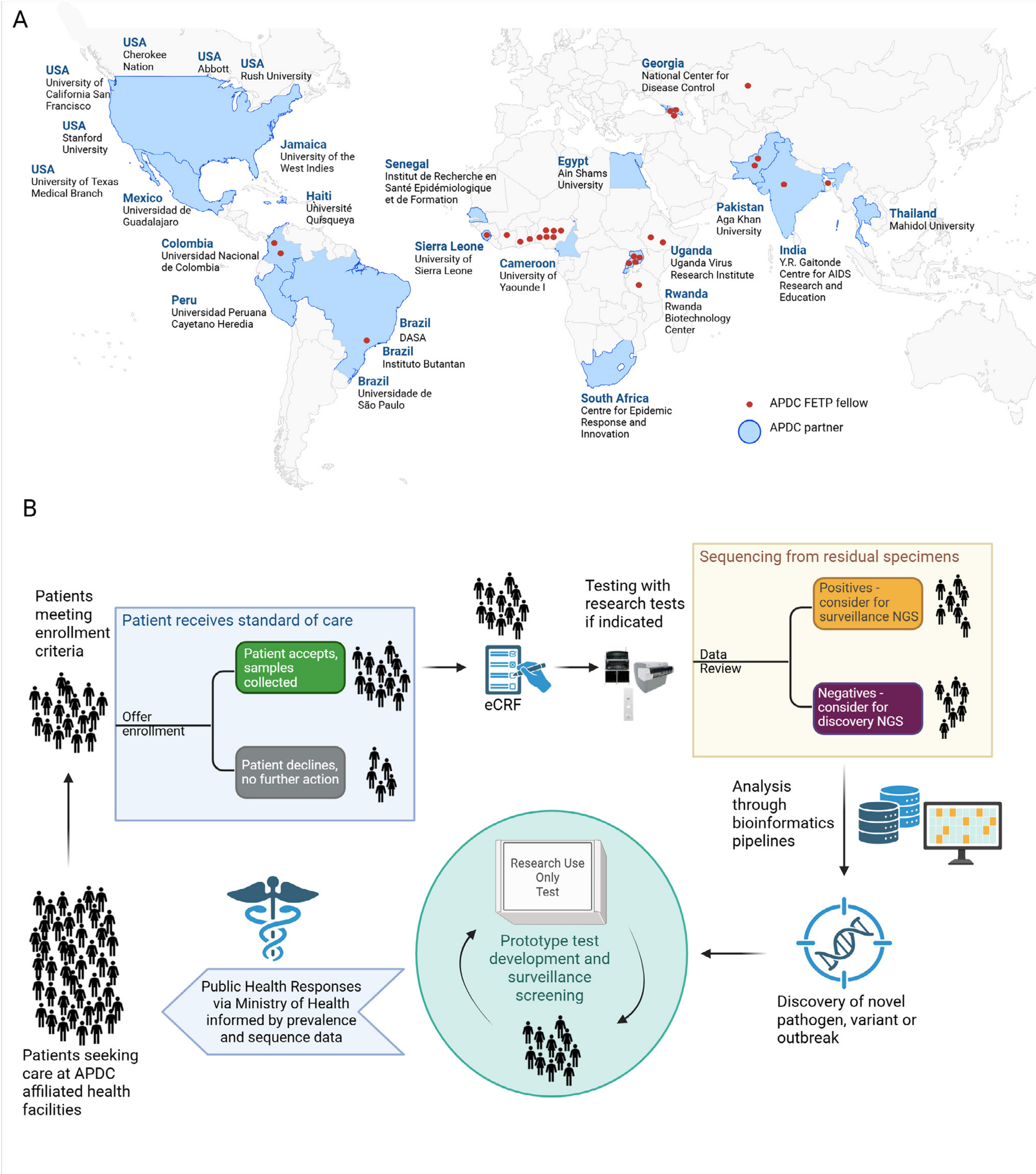

Figure 1. APDC Program Overview (a) APDC partner sites and Field Epidemiology Training Program fellow locations. Collectively, APDC partners include academic institutions, public health organizations, commercial laboratories, and nongovernmental organizations that each hold expertise in several areas of infectious diseases, epidemiology, laboratory testing and sequencing. APDC site recruitment and retention is a dynamic process; sites may be added or discontinued as the priorities and needs of the coalition evolve. New sites were integrated into APDC gradually over time, resulting in each operating at different stages of the APDC workflow today. In addition to sites actively recruiting patients, additional partner sites in the US and South Africa also contribute through analysis of study specimens. (b) The APDC surveillance and discovery workflow. Febrile patients meeting APDC case definitions are enrolled, and clinical data is collected through a standardized electronic case reporting form (eCRF). Collected specimens are screened with diagnostic tests to characterize the prevalence of circulating pathogens. A selection of cases that test negative for all pathogens tested are characterized by metagenomic next-generation sequencing (mNGS) with or without enrichment for processing through the APDC bioinformatics pipeline to quickly identify novel pathogens or variants [9]. Once a novel pathogen is identified, the index case serves as the foundation for the development of prototype molecular and serological research tests that are deployed to partner sites to conduct surveillance studies amongst at-risk populations. All key findings regarding the discovery, sequences and epidemiological data generated by APDC are shared directly with Ministries of Health and other public health agencies in the partner countries to improve the health of the communities involved in the study. *Created in BioRender. Rodgers, M. (2025)* https://BioRender.com/j6lceaz.

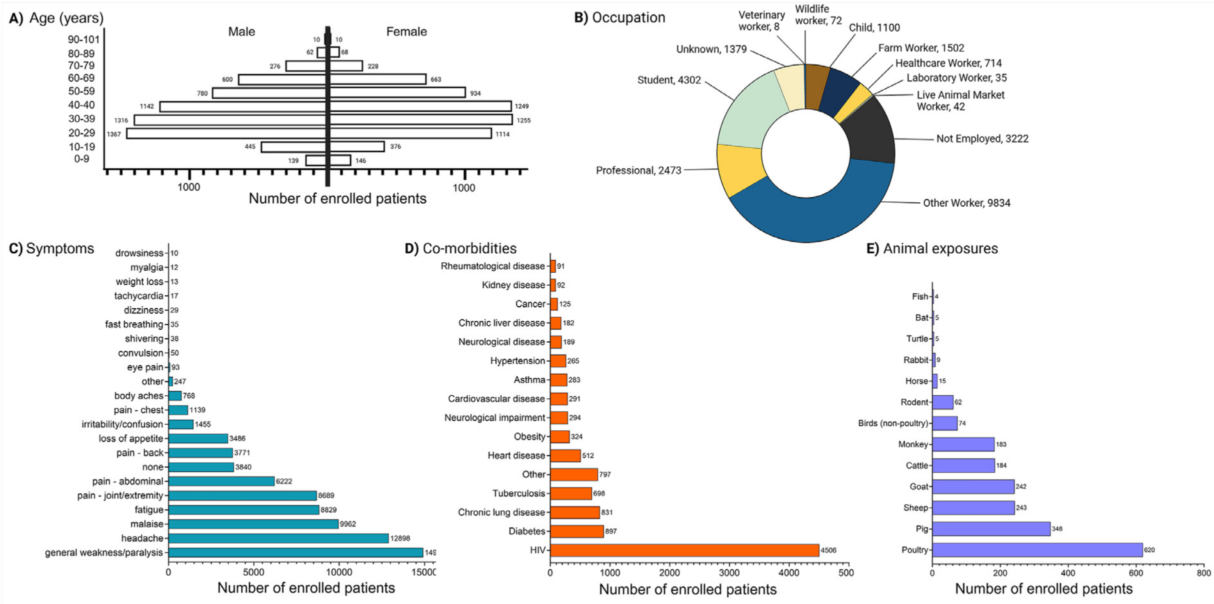

Figure 2. APDC study population characteristics. (a) The age and sex distribution is presented for $N = 12,180$ participants with complete eCRF records. (b) Participant occupations are presented from $N = 24,683$ eCRF records with responses in the eCRF, "other worker" category includes low risk professions like vendor, transporter and electrician. (c) The symptoms are presented as reported by $N = 22,988$ patients with responses in the eCRF, the "other" category includes symptoms that have fewer than 10 respondants, such as toothache, rashes, and seizure. (d) Participant co-morbidities indicated in the eCRF from $N = 22,323$ with eCRF responses, "other" category includes conditions with fewer than 10 responses, including malnutrition, renal impairment and neoplasm. (e) Participant animal exposures excluding cats and dogs are presented from $N = 7168$ eCRF entries that reported an exposure.

carry a lower risk of zoonotic transmission, as well as higher-risk animals such as monkeys (183/24,084; 0.75%), bats (5/24,084; 0.02%), and rodents (62/24,084; 0.25%) (Figure 2e). This metadata collection continues to grow as new patients are enrolled daily across the APDC, serving as a unique clinical database for monitoring infectious disease risks globally.

Objective 2: conduct surveillance of epidemic pathogens to track circulation and evolution of viral variants

The legacy Abbott Global Surveillance Program that has identified extremely rare Group P, Group N, and subtype L strains of HIV over 3 decades is an integrated pillar of the APDC, which has continued to monitor viral diversity at partner sites [10–14]. To conduct pathogen surveillance at APDC sites, samples collected from enrolled patients undergo routine testing according to the local standard of care and supplemental testing provided by the APDC for common pathogens. To date, over 700,000 molecular, serological and rapid tests have been delivered to APDC sites to analyze >39,000 specimens collected from enrolled patients on 20+ donated instruments, including freezers, hoods, an Illumina MiSeq, and high-throughput Abbott diagnostic automation (m2000, Alinity m, Architect, Alinity i) that are serviced and maintained by Abbott. Diagnostic testing frequently identified infectious pathogens including dengue virus (DENV), SARS coronavirus 2 (SARS-CoV-2) and hepatitis B virus (HBV) (Table 1). Further sequence characterization of the positive cases has led to new insights for each pathogen studied. Notably, the APDC has characterized emerging DENV strains in Colombia, Jamaica, and Thailand [15–17] as well as SARS-CoV-2 variants in Colombia and Senegal. The APDC SARS-CoV-2 seroprevalence studies in Senegal, India and Jamaica revealed a higher prevalence when viremic cases were underreported earlier in the pandemic and immunity studies in the US defined the development and duration of natural and vaccine-induced immune responses to SARS-CoV-2 [18–30]. Importantly, SARS-CoV-2 variants were continuously monitored throughout the pandemic for detection with Abbott's diagnostic tests with excellent detection and confirmation of conserved sequences in target gene regions [31,32].

Prevalence studies can also be used to measure the impact of public health programs. For example, the prevalence of hepatitis C virus (HCV) has been reduced by >80% through a successful elimination approach in the country of GA where APDC partners with the National Centers for Disease Control (NCDC) [33]. Part of this success is due to implementation of HCV core antigen reflex testing to identify viremic cases for treatment, which nearly doubled case finding in 2018 [34]. HCV testing algorithms have also been evaluated in Pakistan in studies that confirmed excellent performance for an HCV core antigen for the locally predominant genotype 3[40], followed by application of the HCV core antigen test as an effective confirmatory assay in a test and treat strategy [35,36]. APDC prevalence studies in vulnerable populations have also informed public health interventions in Jamaica and India for human T cell leukemia virus-1 (HTLV-1) and HBV, respectively [37,38].

Objective 3: apply discovery sequencing and bioinformatics tools to identify novel and emerging pathogens

Timely responses are best achieved through local sequencing and the APDC has steadily increased the proportion of sequences generated locally as the program has matured, growing from 29% in 2021 to 62% in 2025. The remainder have been sequenced at Abbott to increase overall coverage and to confirm local findings. Most enrolled cases tested negative for common pathogens after routine diagnostic testing at the time of enrollment; 10,398 out of 14,216 with initial results (73.1%). The majority of these cases and a portion of the cases that lacked initial diagnostic test results have been sequenced by APDC with metagenomic and/or enrichment next generation sequencing methods (12,368/24,683; 50.1%). Selective sequencing of a subset of the negative cases led to the identification of six significant outbreaks by the APDC: the 2022 Oropouche virus (OROV) outbreak in Colombia [39,40], the 2023 anthrax outbreak in Uganda [41], the 2025 Ebola outbreak in Uganda, the 2023 hepatitis E virus (HEV) outbreak in South

Table 1
Infections identified through specimen screening.

Pathogen	N Tested	N Positive (%)
Adenovirus	503	4 (0.80%)
Chlamydia pneumoniae	196	1 (0.51%)
Chikungunya virus	7992	8 (0.10%)
Coronavirus (non-SARS)	251	1 (0.40%)
Crimean-Congo Hemorrhagic Fever virus	124	5 (0.81%)
Cytomegalovirus	3879	464 (11.96%)
Dengue virus	12942	1479 (11.43%)
Entamoeba sp. (amebiasis)	1434	10 (0.70%)
Escherichia Coli	412	264 (64.08%)
Epstein-Barr virus	377	3 (0.80%)
Giardia sp.	1456	27 (1.85%)
Hepatitis A virus	1467	3 (0.20%)
Hepatitis B virus	8281	108 (1.30%)
Hepatitis C virus	5799	18 (0.31%)
Herpesviruses	375	4 (1.07%)
Human Immunodeficiency virus	8900	176 (1.98%)
Influenza A virus	8554	76 (0.89%)
Influenza B virus	8552	62 (0.72%)
Leptospira sp.	8075	10 (0.12%)
Mycobacterium Tuberculosis	333	12 (3.60%)
Miscellaneous bacterial/fungal[b]	230	41 (17.83%)
Miscellaneous viral[a]	9	6 (66.67%)
Norovirus	1427	6 (0.42%)
Oropouche virus	103	3 (2.91%)
Parainfluenza virus	502	6 (1.20%)
Plasmodium sp. (malaria)	12297	1035 (8.42%)
Respiratory Syncytial virus	328	9 (2.74%)
Rhinovirus/enterovirus	601	5 (0.83%)
Rickettsia typhi	48	10 (20.83%)
Rotavirus	76	3 (3.95%)
Streptococcus pneumoniae	315	1 (0.32%)
Salmonella typhi (typhoid)	725	9 (1.24%)
SARS-CoV-2	9775	151 (1.54%)
Treponema pallidum (syphilis)	279	18 (6.45%)
Vibrio cholerae (cholera)	80	5 (6.25%)
Varicella-Zoster virus	374	26 (6.95%)
Zika virus	6960	144 (2.07%)

[a]"Miscellaneous viral" includes cyclovirus, hepatitis E virus (HEV), human T Lymphotropic virus (HTLV), influenza C virus, Venezuelan equine encephalitis virus (VEEV), vientovirus.
[b]"Miscellaneous bacterial/fungal" includes *Helicobacter pylori, Mycoplasma pneumoniae, Pneumocystis jirovecii, Salmonella* sp.*, Shigella* sp.*, Staphylococcus aureus, Streptococcus pyogenes, Streptococcus milleri, Candida albicans, Cryptococcus neoformans, Corynebacterium* sp.*, Campylobacter* sp.*, Burkholderia pseudomallei, Aspergillus flavus,* and *Aspergillus niger.*

Sudan investigated with the Uganda site [42], and the 2023 Mayaro [43] and Yellow fever virus (YFV) [44] outbreaks in Colombia. Notably, the first cases of the YFV outbreak in Leticia were identified by APDC, which raised awareness about it re-emergence and ultimately led to public health interventions in Colombia in 2025 [44,45]. Importantly, phylogenetic characterization of the YFV cases identified the presence of potential vaccine escape mutations [44]. The index case of the 2025 Ebola outbreak in Uganda was discovered through a postmortem surveillance (PMS) study that involved recruitment, clinical data and specimen collection by an APDC-TEPHINET fellow at the MoH, and sequencing negative cases through the APDC Uganda site [46,47]. The outbreak was much smaller than past outbreaks, likely due to the establishment of PMS and VHF screening, which resulted in early detection of the outbreak, leading to a timely investigation and response. Collectively, these outbreak investigations illustrate the value of the APDC approach, from detection to characterization and mitigation of the threat for public health.

In addition to the identification of outbreaks, APDC has also identified novel and emerging pathogens through pathogen discovery studies. For example, the APDC PMS study in Uganda identified a cluster of recombinant Echovirus E7 cases in Kampala as well as a wide range of other pathogens, including Saffold virus, bufavirus, and *Cryptococcus neoformans* [48]. Discovery sequencing in Brazil to investigate meningoencephalitis infections identified a wide range of pathogens that were not detected by traditional means, including unexpected viruses like vesivirus and picobirnavirus [49]. In some cases, the identification of a novel virus was not deemed to immediately pose a threat to public health. For example, 9 novel divergent viruses that had previously only been seen in bats and insects were identified by APDC among HIV patients in Cameroon at a low prevalence, with only 1 or 2 patients harboring the virus [50]. The APDC also found a second case of a rare novel bunyavirus, Bangui virus, in a HIV patient from Democratic Republic of Congo [51]. Sequence comparison to the first case, reported 50 years earlier, revealed nearly identical viral genomes [51]. The high level of similarity and very low prevalence of cases are both consistent with extremely low circulation of this virus in the human population.

Monitoring the trends of common infectious diseases at APDC sites is also important, even when a new outbreak or emerging pathogen is not identified. By understanding the current landscape of circulating pathogens, global health communities can more quickly identify when an unusual trend emerges. For instance, the APDC Senegal site has been conducting AFI surveillance with very different findings than in Colombia or Uganda [9]. After ruling out malaria as the cause of illness for 17% of AFI cases, a subset of the remaining negative samples was sequenced, yielding detection of a variety of pathogens, including 8 viruses, 4 bacterial species, a fungus (*Aureobasidium pullulans*) and one nonmalaria parasite (Loa loa) [9]. The detected viruses ranged from common (HIV and HBV) to rare (Saffold virus and West Nile virus), and the list of bacteria included tick-borne *Borrelia crocidurae* and louse-borne *Rickettsia felis* [9]. The expected geographic range for these tickborne pathogens was expanded further in our study than had previously been seen in humans or animals. In a region where AFI is usually assumed to be malaria infection, the breadth of AFI pathogens is important to determine, particularly for informing appropriate management and treatment decisions and public health interventions.

Objective 4: develop and deploy prototype research use only (RUO) tests to evaluate the risk of novel and epidemic pathogens

RUO tests are critical tools for evaluating the potential risk posed by a pathogen—whether it is known or novel. Many diagnostic gaps exist for pathogens known to cause outbreaks and epidemics, making prototype tests for this category of pathogens immediately impactful. In the case of novel pathogens, prototype tests could shorten the timeline for access to diagnostics that would be urgently needed as part of a global response in a pandemic scenario. A cornerstone of the APDC is the capacity to rapidly develop and deploy prototype diagnostic tests at scale to evaluate the risk a pathogen may present to public health, including both known and novel pathogens. With a unique ability to develop robust prototypes with industrial rigor and scalability in mind, the APDC stands out as one of the only pandemic preparedness programs that can deliver high-throughput RUO tests to study circulating pathogens. Furthermore, the APDC has established mechanisms to ship RUO tests to sites on five continents, with >38,000 RUO tests delivered to date at partner sites for local research. The resulting studies that have utilized the first 15 new high throughput serological and molecular APDC RUO tests targeting novel pathogen and hepatitis biomarkers have demonstrated excellent performance (Table 2) 39,52–61. These RUO tests are just the beginning—with a pipeline of >30 additional RUOs in development, the APDC is continually contributing new tools for infectious disease surveillance and diagnostics.

Table 2
RUO tests developed by APDC.

RUO	ASSAY TYPE	SENSITIVITY	SPECIFICITY	STUDY REFERENCE(S)
MPOX (MPXVS)	Molecular	3.2 pfu/ml, 200 copies/ml	100% ($N = 53$)	Anderson et al.[51]
ORTHOPOX (MPXV+)	Molecular	3.2 pfu/ml, 200 copies/ml	100% ($N = 25$)	Anderson et al.[51]
PICOBIRNAVIRUS	Molecular	10-100 copies/ml	ND	Berg et al.[9]
OROV VIRUS	Molecular	0.6pfu/ml, 2.5 copies/rxn	100% ($N = 791$)	Ciouderis et al.[39]
OROV VIRUS	Serology - IgG	100% ($N = 92$)	99% ($N = 500$)	Ciouderis et al.[39]
OROV VIRUS	Serology - IgM	100% ($N = 27$)	99.8% ($N = 500$)	Ciouderis et al.[39]
HDV	Molecular	5 IU/ml	100% ($N = 68$)	Coller et al.[52], Qiu et al.[54], Butler et al.[53]
HDV	Serology –IgG	100% ($N = 16$)	100% ($N = 173$)	Coller et al.[52], Butler et al.[53]
HDV	Serology –Total Ig	95.2% (59/62)	99.5% (199/200)	Qiu et al.[54]
HBV RNA V1	Molecular	152 copies/ml	100% ($N = 103$)	Butler et al.[55]
HBV RNA V2	Molecular	22 copies/ml	ND	Anderson et al.[56]
HBcAg	Serology –Ag	4 pg/ml, 140,760 DNA IU/ml	99.4% (3/495)	Geissler et al.[57]
HBcAg-P	Serology –Ag	0.8 pg/ml, 28,150 DNA IU/ml	100% ($N = 495$)	Geissler et al.[57]
HBsAg ISOFORMS	Serology –Ag	ND	ND	Rodgers et al.[58], Bazinet et al.[59]
HBsAg IMMUNE COMPLEXES	Serology –Ag/Ab	ND	ND	Bazinet et al.[62]

The RUOs in Table 2 have already been useful during outbreak investigations, including the mpox assays, which have been used at APDC sites to respond to the recent clade IIb global outbreak of 2022 and the more virulent clade Ib African outbreak in 2024-2025. The first RUO is an mpox specific assay that can detect both clades I and II, called MPXVS (mpox specific) and the second was designed to detect a broader range of orthopox viruses, including mpox clades I and II, called MPXV+ [52]. Both MPXVS and MPXV+ are dual target assays with *E9L* and *B6R* regions targeted by MPXVS and the *J2L* and *B7R* regions targeted by MPXV+ [52]. The dual target design ensures that the assays remain robust in the face of continued viral diversification while maintaining 100% concordance with the Centers for Disease Control (CDC) assay. Notably, the Alinity m MPXV assay (MPXVS design) was the first test granted Emergency Use Listing (EUL) by the World Health Organization (WHO), demonstrating direct impact of the work by the APDC on the global availability of diagnostics for outbreak pathogens.

The APDC has also developed a panel of tests for novel hepatitis biomarkers to support research in the HBV cure field. As new therapeutics are developed to achieve a functional cure for HBV, defined as undetectable HBV surface antigen (HBsAg) and HBV DNA after 24 weeks in the absence of therapy, novel biomarkers are needed to monitor their effectiveness and mechanism of action in patients. Currently, the preferred therapy for HBV is nucleos(t)ide analogs that suppress genomic DNA release to the bloodstream without reducing the amount of chromosomal covalently closed circular DNA (cccDNA) in hepatocytes or HBsAg circulating in the blood. A portion of patients can achieve elimination of cccDNA over time and are able to safely stop therapy, which is currently evaluated by pausing treatment and monitoring the patient for rebound. As new therapies are developed that may increase the number of patients who will successfully eliminate their cccDNA reservoir, new biomarkers are needed to predict when treatment could be safely stopped. The APDC HBV RNA RUO is a strong candidate biomarker to evaluate cccDNA activity since pregenomic RNA (pgRNA) is produced from the cccDNA template, packaged into virions, and secreted into the bloodstream, even in the presence of nucleos(t)ide analogs. The HBV RNA RUO assay has a dual target format in the X and core regions and has recently been updated to a version 2 assay with approximately 10-fold improved sensitivity compared to the first version developed [58]. These assays have consistently demonstrated that patients are more likely to rebound upon cessation of several different classes of therapeutics if their HBV RNA levels are still detectable at the time that therapy ends [62–68]. Further research with the full suite of APDC hepatitis RUOs, including HBV RNA and others in Table 3, will continue to advance our understanding of the biology of HBV before, during and after treatment as they are applied to more patient cohorts around the world.

Table 3
APDC TEPHINET fellowship studies.

TOPIC	COUNTRIES	FELLOWS ($N = 34$)
ACUTE FEBRILE ILLNESS, DENGUE, AND HANTAVIRUS	Nigeria (4), Brazil, Kazakhstan, Côte d'Ivoire, Ethiopia, GA	9
HPV	Ghana, Togo, Pakistan, Uganda, Nigeria	5
BLACKWATER FEVER / MALARIA	Uganda (2)	2
HIV / HEPATITIS / LIVER CANCER	GA (2), Pakistan	3
LONG COVID-19	Pakistan	1
CRIMEAN-CONGO HEMORRHAGIC FEVER	GA, Nigeria	2
ENCEPHALITIS / WEST NILE VIRUS	Bangladesh	1
INFLUENZA-LIKE ILLNESS AND SEVERE ACUTE RESPIRATORY ILLNESS	Colombia (2), Tanzania	3
MORTUARY SURVEILLANCE	Uganda, Nigeria, Sierra Leone	3
MENINGITIS	Nigeria	1
EBOLA AND LASSA FEVER	Uganda	1
EARLY WARNING SURVEILLANCE SYSTEM	India	1
PARASITIC DX / REFUGEE HEALTH	Ethiopia (2)	2

Objective 5: train the next generation of infectious disease epidemiologists

Training is an essential component of the APDC. In addition to training in sequencing and bioinformatics, a major focus has been in training field epidemiologists. A collaboration with the Training in Epidemiology and Public Health Interventions Network (TEPHINET), a program within the Task Force for Global Health (TFGH), has resulted in a first-of-its-kind industry partnership with the TFGH/TEPHINET that began in 2022. The APDC-Field Epidemiology Training Program (FETP) Fellowship supports epidemiologists in-training to conduct surveillance and epidemiologic studies in infectious diseases in their home countries [69]. This unique program, where the APDC works closely with ministries of health, tackling priority public health issues while training the next generation of epidemiologists, has proven to be a model of the effectiveness of public-private partnerships in public health.

The fellows are selected from a network of 95 Field Epidemiology Training Programs (FETPs), associated with National Ministries of Health. Fellows apply to the APDC-FETP Fellowship and up to ten are selected annually through a competitive process. If selected, the Fellow is awarded a grant to fund their project implementation and, in addition, an international subject matter expert (SME) is identified to serve as a mentor to complement and strengthen the Fellows' experience. Abbott and APDC scientists also serve as mentors, collaborators, and co-investigators. In the first 4 years of the Fellowship, there have been 34 Fellows selected, and some have received a second-year award to continue their work. The 34 Fellows, from 15 countries (Figure 1b), have collectively screened > 18,000 patients and collected > 14,000 specimens for testing and pathogen discovery during 2022-2025 (Table 3).

These Fellowship projects extend the reach of APDC into countries without partner sites, enhancing the global understating of infectious disease threats. Epidemiologic studies conducted by APDC-FETP fellows have tracked and guided responses to emerging infectious disease threats in several countries. In a study conducted in West Kazakhstan, the seroprevalence of hantavirus was determined to be 3.1% in 2023, despite the absence of severe hantavirus hemorrhagic fever with renal syndrome (HFRS) cases reported during the previous 2 years [70]. Application of event-based surveillance in private hospitals in Kerala, India resulted in identification of nine outbreaks that were missed by the traditional indicator-based surveillance system [71]. In a study conducted in Colombia, adding multiplex PCR to the conventional immunofluorescence-based approach for investigation of acute respiratory infections greatly improved pathogen detection from 43.8% to over 90%, enabling a more detailed trend analysis from which outbreaks can be identified [72]. As more TEPHINET fellows conclude and publish their studies, a wealth of epidemiological insights will further expand the impact of the APDC on public health.

Limitations and challenges

The efforts of the APDC are not intended to serve as a comprehensive nationwide or global public health system. Instead, APDC serves as a supplemental resource to MoH efforts in each member country to assist with surveillance in a complimentary manner. Sites are selected after engagement with the Abbott team to evaluate a number of factors ranging from the local infectious disease risks to gaps in current surveillance efforts and capabilities of the team. Ultimately this limits APDC studies to patients who can access healthcare in the settings where the program operates. As an industry-led network, the APDC is challenged in working with groups like the World Health Organization due to restrictions that have been placed on working with industry [73], although increased engagement with industry has become a priority for improving global pandemic preparedness [74]. Logistic challenges in shipping materials across borders also presents a limitation for the APDC and any pandemic preparedness program.

APDC future work

The body of work that has been generated by the APDC serves as a solid foundation from which to build novel tools to address the infectious disease threats that we face as a global community. Studies conducted by the APDC to date have identified surveillance gaps in acute febrile illness, respiratory illness, HIV and viral hepatitis that need to be addressed. As infectious disease dynamics continue to evolve and global needs change, the work of the APDC will adapt, in line with our core mission. It will also be important to advance surveillance research from retrospective to prospective forecasts that can help communities to prepare appropriately and minimize the impact of both emerging infectious diseases and surges in existing epidemic pathogens. Through collaboration and its unique industry-led approach, the APDC is well-equipped to continue to support public health through its work in the years to come.

Ethical approval

This work has been approved by local ethics committees in all countries where patients were enrolled.

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Author contributions

MR, FA, GC, MA and MB conceived the manuscript. MR and FA wrote the manuscript. All authors contributed to the research and reviewed the manuscript.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Mary Rodgers, Francisco Averhoff, Michael Berg, Mark Anderson, Carolyn Strobel, Julissa Inostroza, and Gavin Cloherty are employees of Abbott Laboratories. This work was funded by Abbott Laboratories.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ijid.2025.108162.

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