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aggregation. This could be achieved by binding or wrapping of DNA amplicons onto GPNs to cause aggregation.

**Methods & Materials:** Asymmetric PCR amplification (As-PCR) technique was used to obtain ssDNA amplicons. Amplification was done using primers for RLEP gene as confirmed by gel electrophoresis. MTB and E. coli served as negative controls. Primer ratios were optimized for highest yield of ssDNA amplicons. Column purification was done to remove salts and primers. The purified amplicons were incubated with GPNs (20nm) in equal ratios followed by NaCl addition. The UV-visible spectral analysis of reaction mixture was performed.

**Results:** As-PCR using RLEP primers favourably amplified target sequences. Out of several primer combinations, the ratio 100:1 produced major ssDNA during As-PCR. After incubation with gold colloid and salt addition, the visible change in color from red to blue was observed indicating presence of amplified product that caused GNP aggregation while negative controls retain their color as verified by UV spectra showing a steep wavelength shift. The method showed high specificity with positive samples showing blue colored solution.

**Conclusion:** A simple colorimetric method for detection of *M. leprae* was demonstrated. Utilizing naked GPNs reduces steps, duration and complexity of the assays providing easy method for visible detection of infected sample without the need of labelling of GPNs. For leprosy being a neglected disease, this method would serve as an important tool to cater to the unmet needs of its rapid, simple and reliable diagnosis.

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The Use of Culture, Molecular Methods and Whole Genome Sequencing to Detect the Source of an Outbreak of Legionnaire’s Disease in New York State

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**Purpose:** Legionnaire’s disease (LD) is a systemic infection caused predominantly by *Legionella pneumophila* (Lp). Symptoms include fever, cough, headache, body aches and shortness of breath. *Legionella pneumophila* serogroup 1 (Lp1) is the main serogroup responsible for outbreaks in the United States. In August 2019, a community-associated outbreak of LD was identified in a New York county including 17 cases of Lp1. During this outbreak investigation, potential environmental sources within a 5-mile radius were tested. By using a combination of culture, molecular methods, and whole-genome sequencing (WGS) the Wadsworth Center laboratory (WC) was able to identify the outbreak source.

**Methods & Materials:** WC utilizes a streamlined testing algorithm that combines molecular screening of primary specimens followed by culture on PCR-positive samples. DNA was extracted from clinical and environmental samples using a manual procedure. Following the extraction, a multiplex real-time PCR was performed to detect Lp, Lp1 and other *Legionella* species. Samples that were positive for Lp1 were directly plated on BCYE, blood agar (TSA with sheep blood) and simultaneously set up using the IDEXX LegioListTM method. Colonies typical of Lp1 were confirmed by real-time PCR and subjected to WGS and analysis using the in-house developed *Legionella* clustering (LegioCluster) pipeline to determine isolate relatedness.