

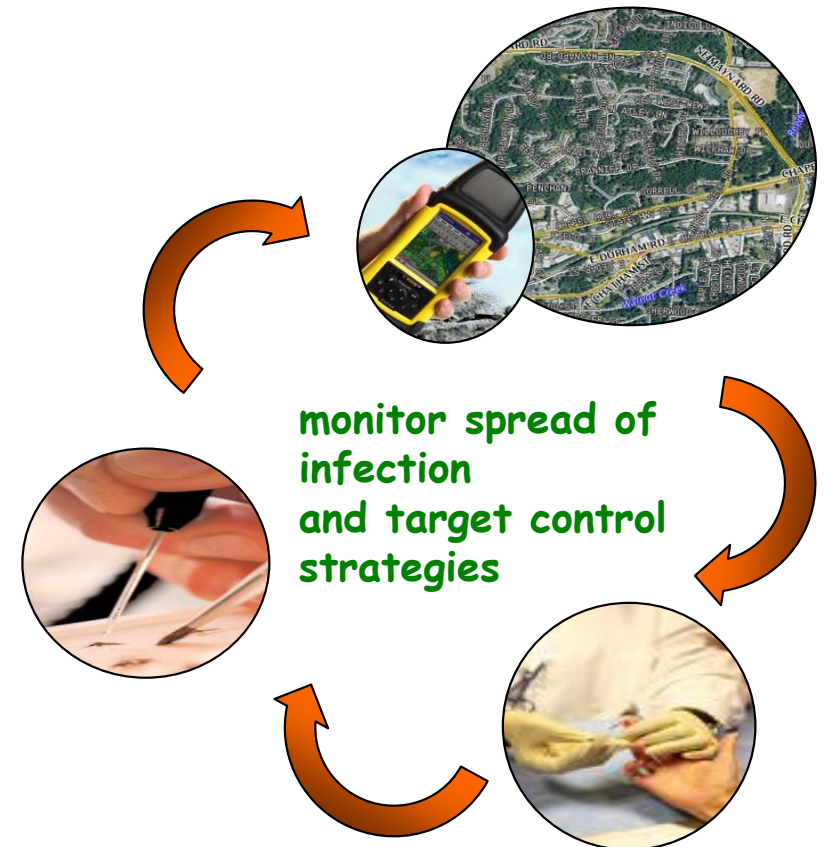
# **GIS Mapping of Lymphatic filariasis endemic areas in Gampaha district, Sri Lanka; based on the epidemiological and entomological screening**

*N.D.A.D. Wijegunawardana, Y.I.N. Silva Gunawardane,  
Aresha Manamperi and W. Abeyewickreme*

*Molecular Medicine Unit, Faculty of Medicine, University of Kelaniya, Ragama, Sri Lanka*

# Background

The health issues related to vector borne diseases appear always to be related to space and time.



# Objective



Development of a site directed GIS map for lymphatic filariasis (Lf) dispersed areas in Gampaha district, Sri Lanka as a guide to target control activities.

# Methodology

pre-identified 9 sites in Gampaha district, screening of Lf



and

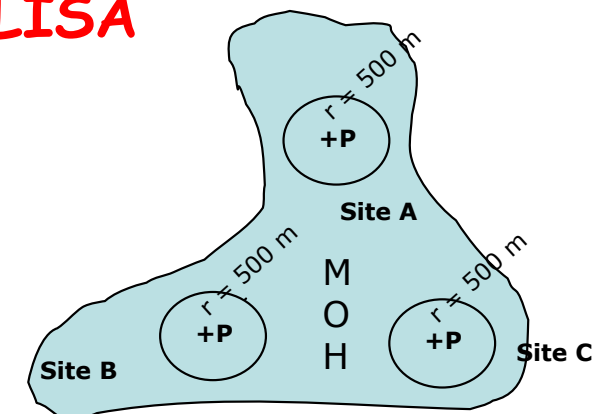


## Epidemiological

night blood  
screening

## Entomological

pool-screening  
PCR-ELISA



# Epidemiological Investigation

60  $\mu$ l of Finger pick blood was drawn from each individual



Thick blood films were prepared



Stained with 5% Giemsa stain



Observed under the microscope

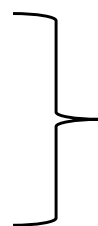


□ All participants were examined by a medical officer for **clinical manifestations** of lymphatic filariasis.

□ Questionnaire ;

Awareness

Practice



MDA



Indoor-resting mosquito collection (6 a.m. to 11a.m., manually)

Transportation to laboratory

Knocking down of mosquitoes (-20°C, 10 min)

Separation of female *Culex* mosquitoes

Sorting into 15 mosq/batch

Pools processing for  
DNA extraction (75%)

Pools processing for  
dissection (25%)

DNA extraction of  
pooled mosquitoes

collecting dissected body parts  
of the mosquitoes

PCR for extracted DNA

PCR-ELISA

Measurement of Absorbance

+ve samples

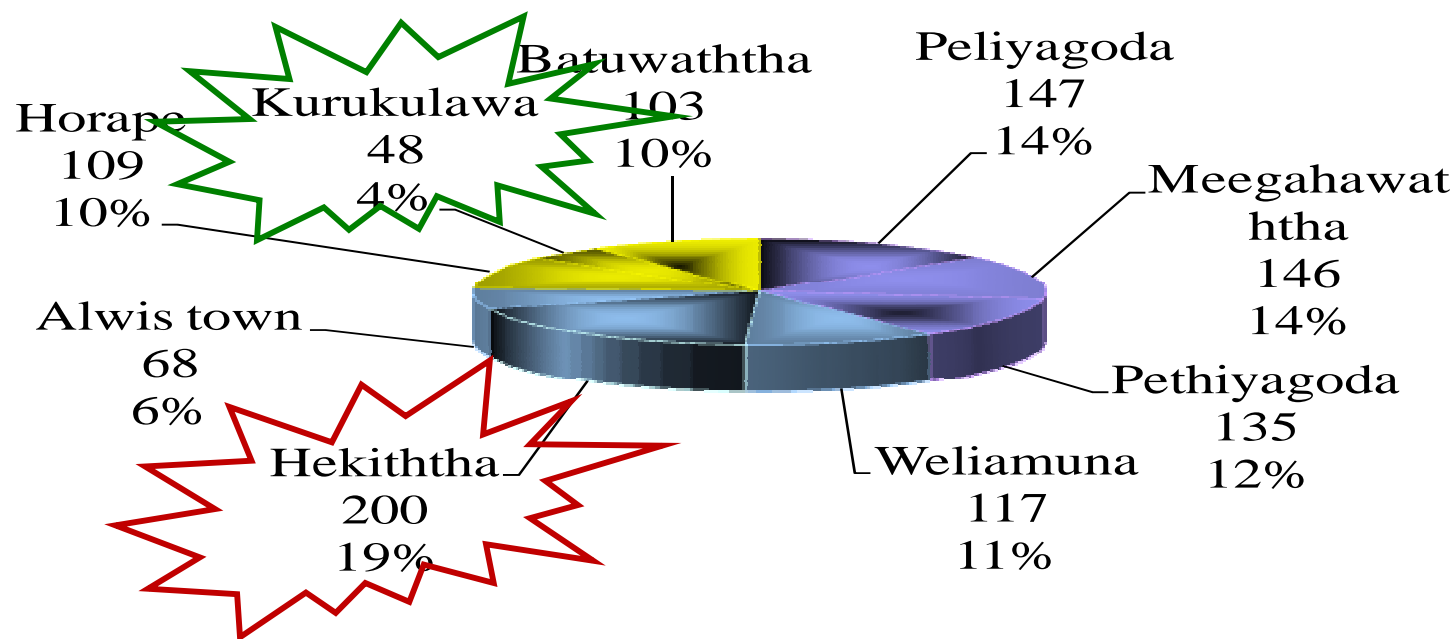
-ve samples

**Entomological  
Investigation**

**Figure 1:** Laboratory evaluation of transmission levels of vector mosquitoes

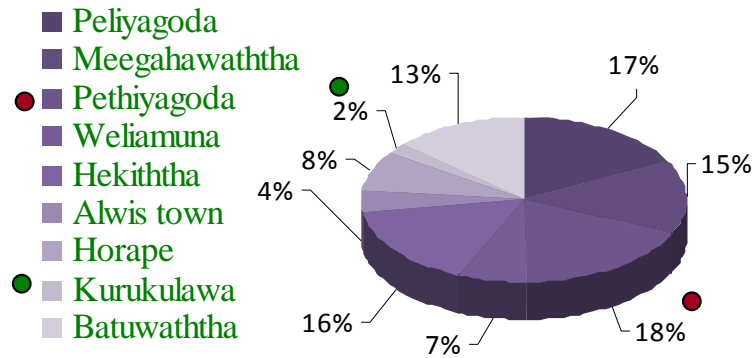
# Results

## Epidemiological Investigation

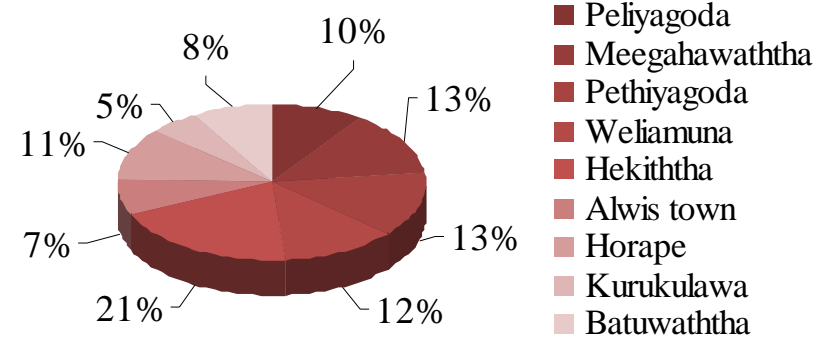


**Figure 02 :** Percentage and number of participants screened for Lf with respect to study sites

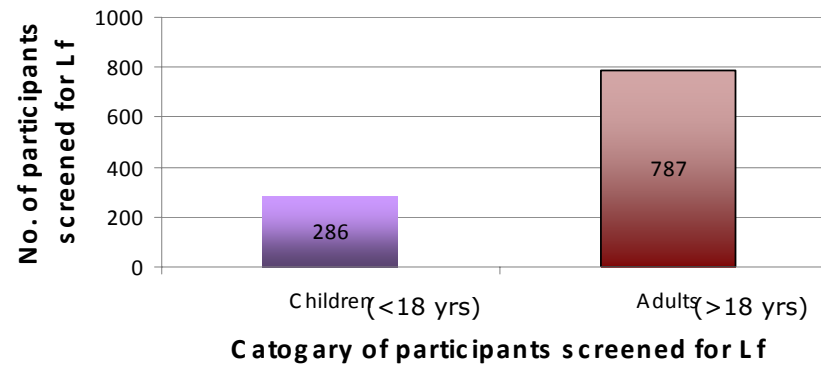
# Results



**Figure 3:** % of Adult vs. study sites

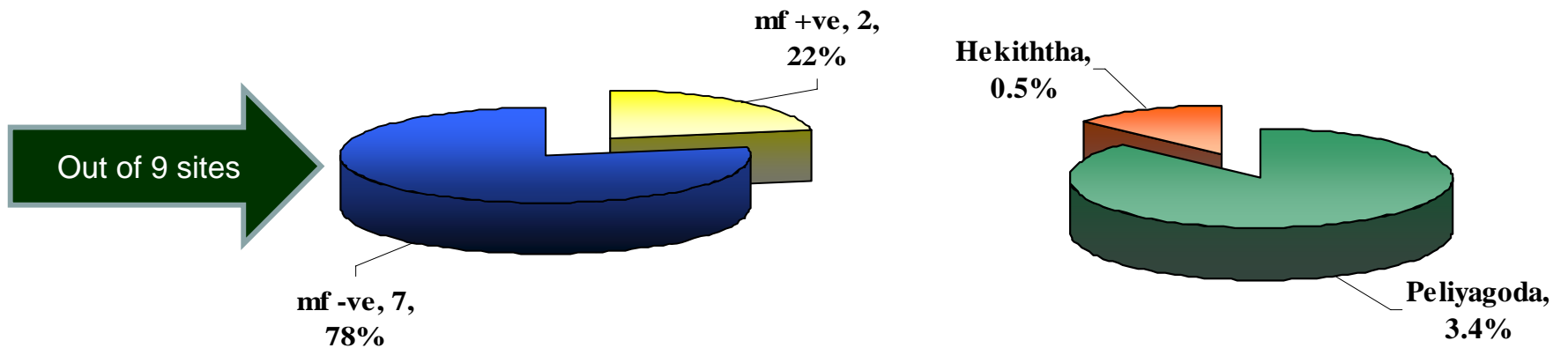


**Figure 4:** % of Children vs. study sites



**Total participants  
1073**

**Figure 5:** Number of participants screened for Lf in each category



**Figure 6:** Site level representation of mf positivity

**Figure 7:** % of mf prevalence in +ve sites



# Results

## Entomological Investigation

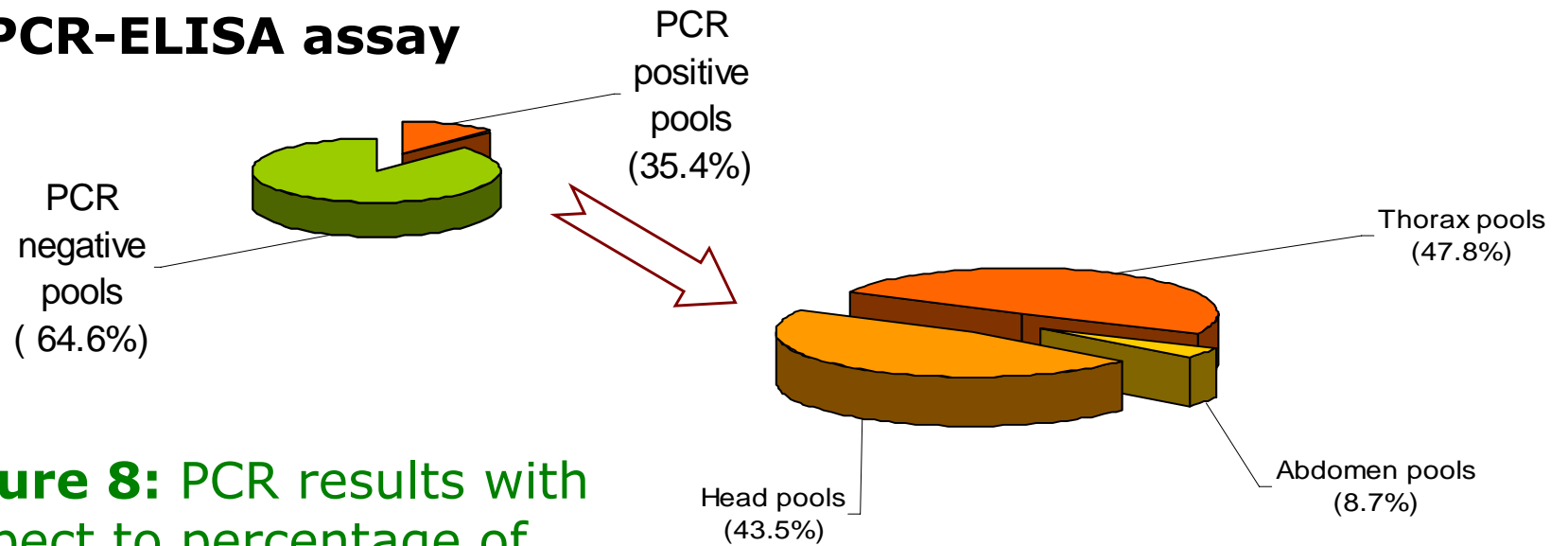
❖ **No. of mosquitoes collected;**  
varied from 0 - 45 per household

### 1. Conventional dissection and microscopic examination;

- ❖ **Rate of infestation** → **44.44%**
- ❖ **% of positive mosquitoes** → **8.54%**
- ❖ **L1 density** → **1 per +ve Mosq.**

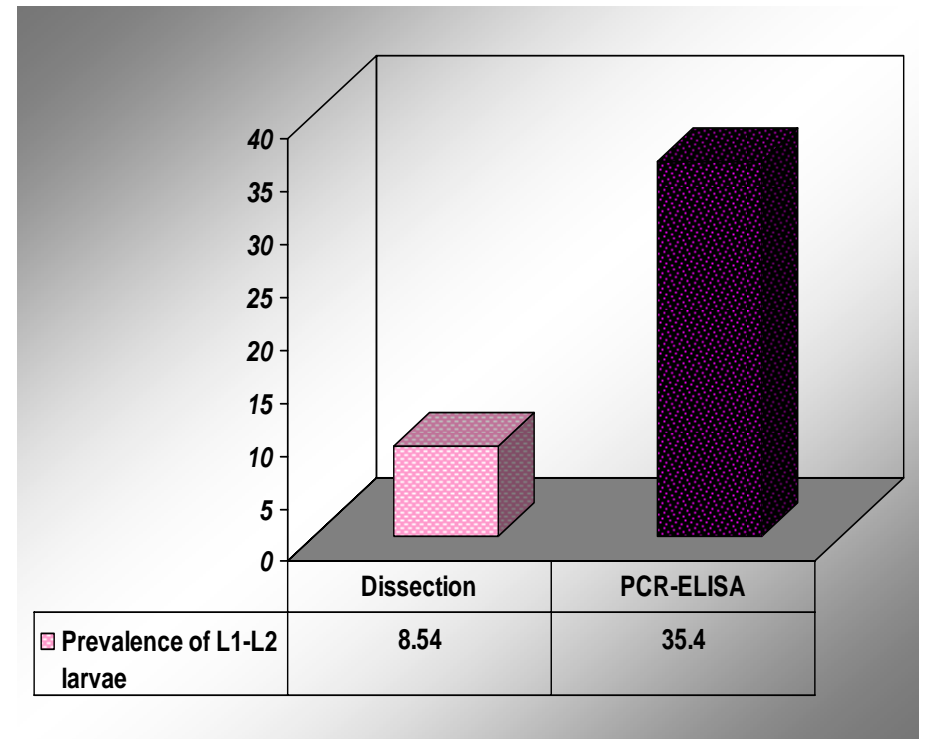
# Results

## 2. PCR-ELISA assay



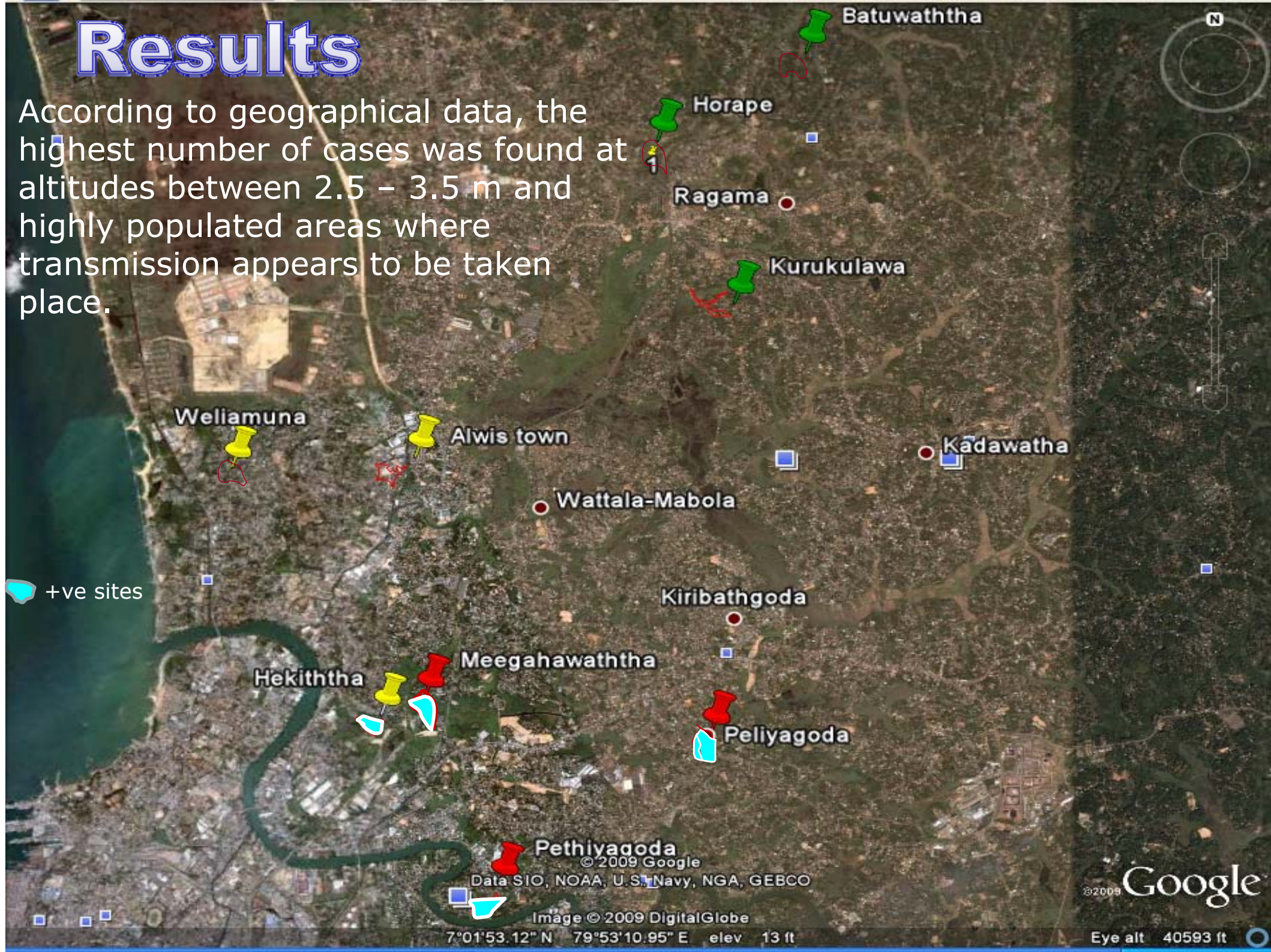
**Figure 8:** PCR results with respect to percentage of mosquito pools

**Figure 9:** Prevalence of L1 - L2 larvae from Dissection and PCR-ELISA



# Results

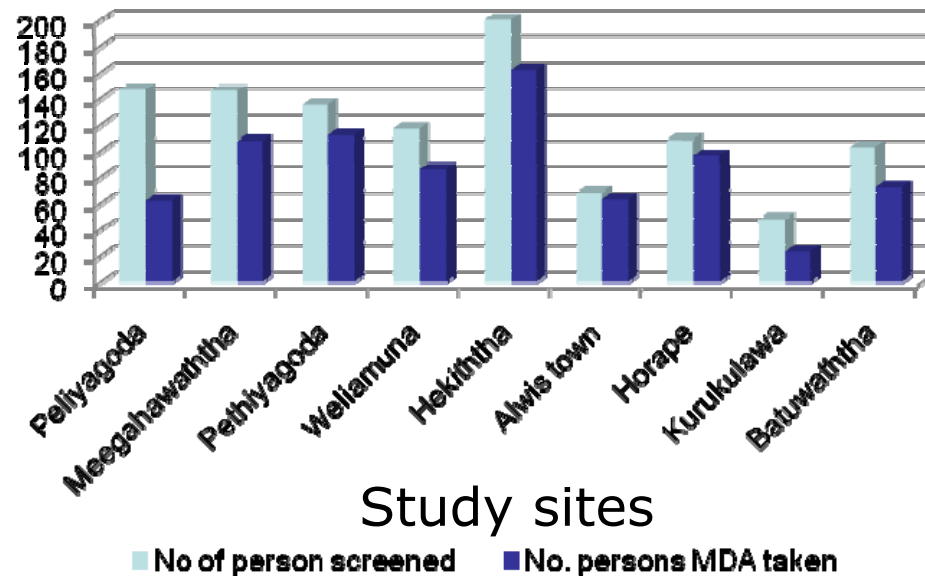
According to geographical data, the highest number of cases was found at altitudes between 2.5 – 3.5 m and highly populated areas where transmission appears to be taken place.



# Results

- **Of 1073 individuals;** 78% (837) - Aware of MDA, 65% (544) received MDA, 50% (272) had taken at least once, 34% (92) - 5-year MDA, **8.57%**

The rest did not give a clear answer to this question.

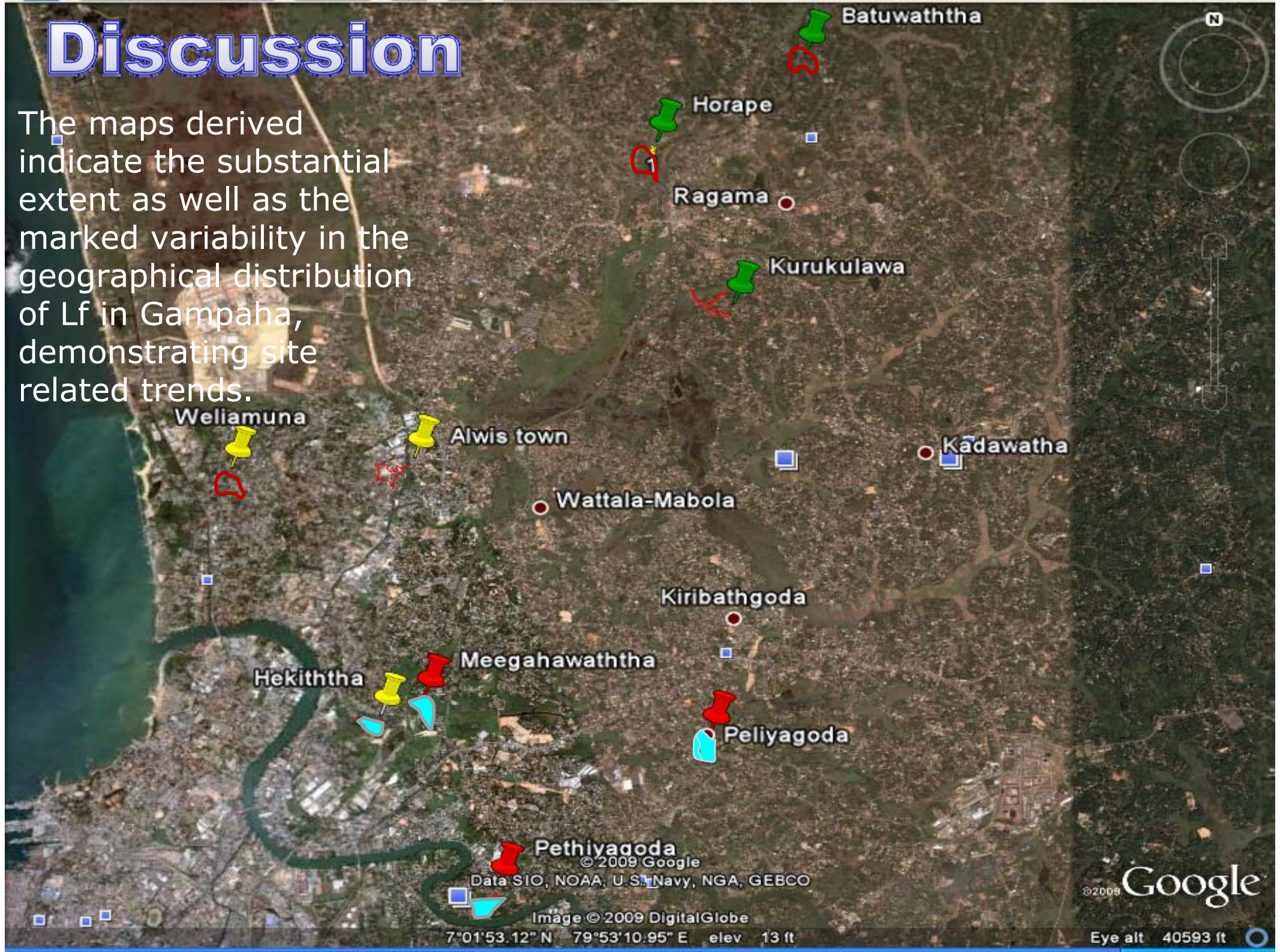


**Figure 10:** Questionnaire analysis data

Questionnaires indicated limited community awareness can be a reason for the fairly static infection rate prevalent in **Peliyagoda** sentinel site.

# Discussion

The maps derived indicate the substantial extent as well as the marked variability in the geographical distribution of Lf in Gampaha, demonstrating site related trends.

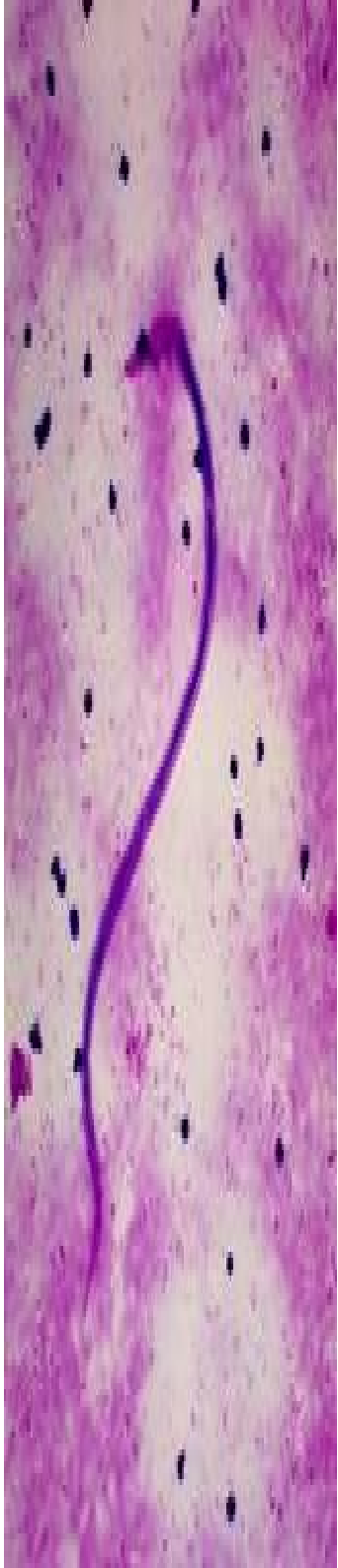


# Conclusion

According to the results of this study;

- mf rate of Lf in this study population is greater than the currently reported in the country (0.18%).
- Awareness of MDA was less compared to other countries.
- Confirmed that active transmission of *W. bancrofti* is currently taking place in the Gampaha district.

Therefore, an intensive MDA programme is recommended in selected highly infected areas to contain the spread of infection and also control programs to interrupt transmission need to be continued in this district.



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Sri Lanka**
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technical co-operation programme.**



**Thank you**

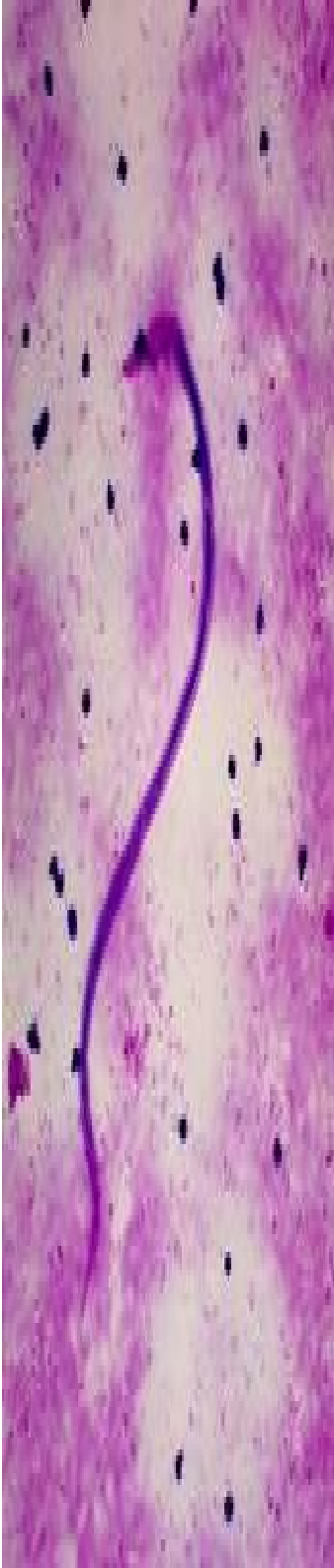


# Entomological Investigation

- **Mosquito collections;** 30 households/site
- **Collected mosquitoes;**
  - Knocked down in the laboratory
    - (-20°C, 10 min)
  - Separated - species and sex
  - Female *Culex* mosquitoes
    - \_ pooled by site of collection

## **1. Conventional dissection and microscopic examination**

- (25% of collected mosquito);
- Head, thorax and abdomen
  - dissected separately in a drop of 0.15% saline (1.5 g of NaCl in 1 L of H<sub>2</sub>O)



- **During dissections developing worms were classified as;**

- $L_1$  sausage stage ,
- $L_2$  motile short and
- $L_3$  motile, infective and with caudal papillae larvae

The number of larvae were counted to determine;

- the infection rate
- the no. of developing worms per mosquito



## **2. PCR Amplification and ELISA assay:**

### **➤ DNA extraction**

### **➤ PCR amplification**

**( NV-1 and NV-2 primers specific  
for the *Ssp I* repeat)**

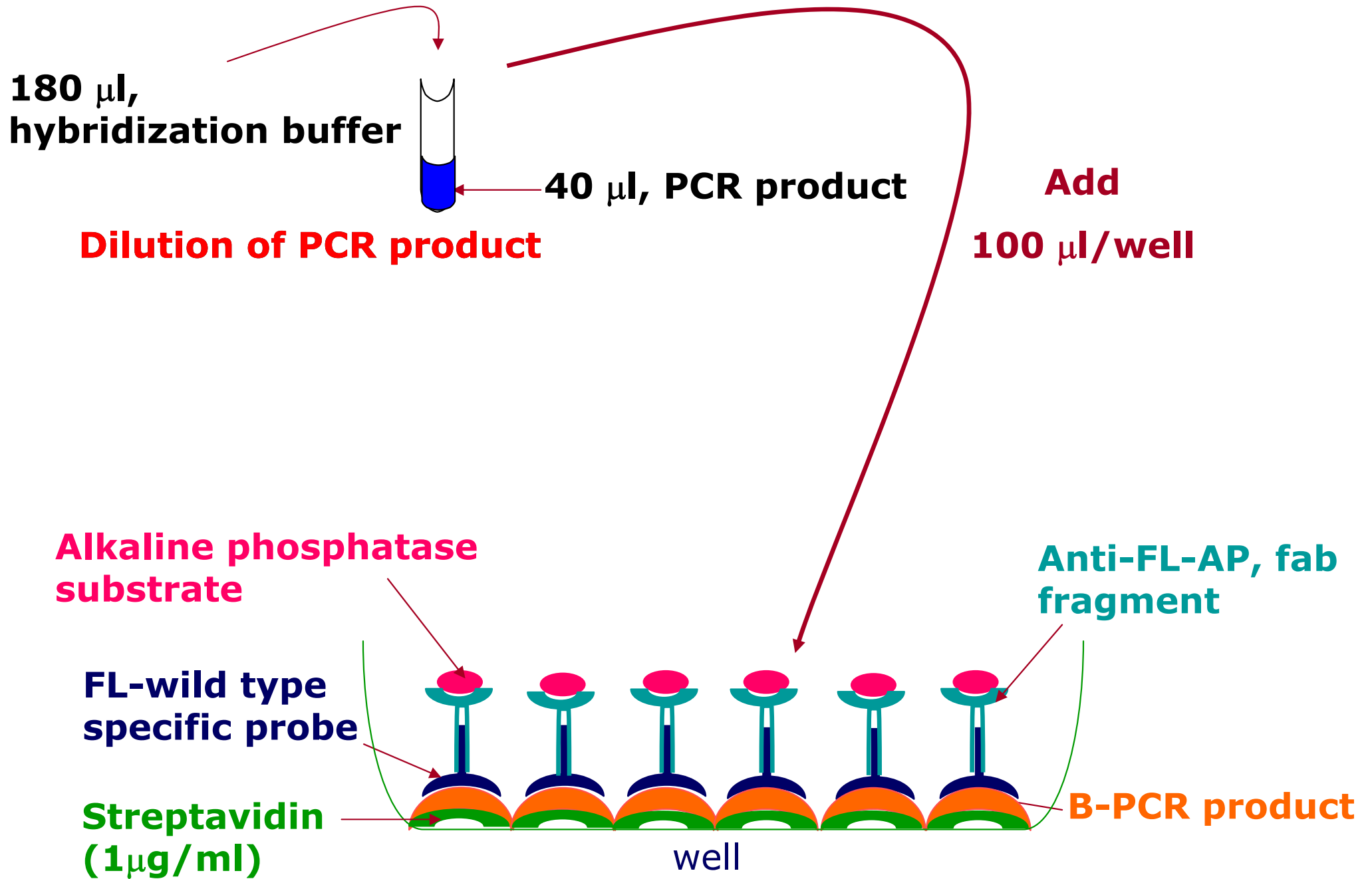
**Reaction volume - 50  $\mu$ l**

**Distilled water without internal  
control – (-ve control)**

**Pre-prepared *W. bancrofti* DNA  
– (+ve control)**

**Primer NV-2 was biotinylated to facilitate binding  
of the product to a 1  $\mu$ g/ml streptavidin-coated  
microtiter plate.**

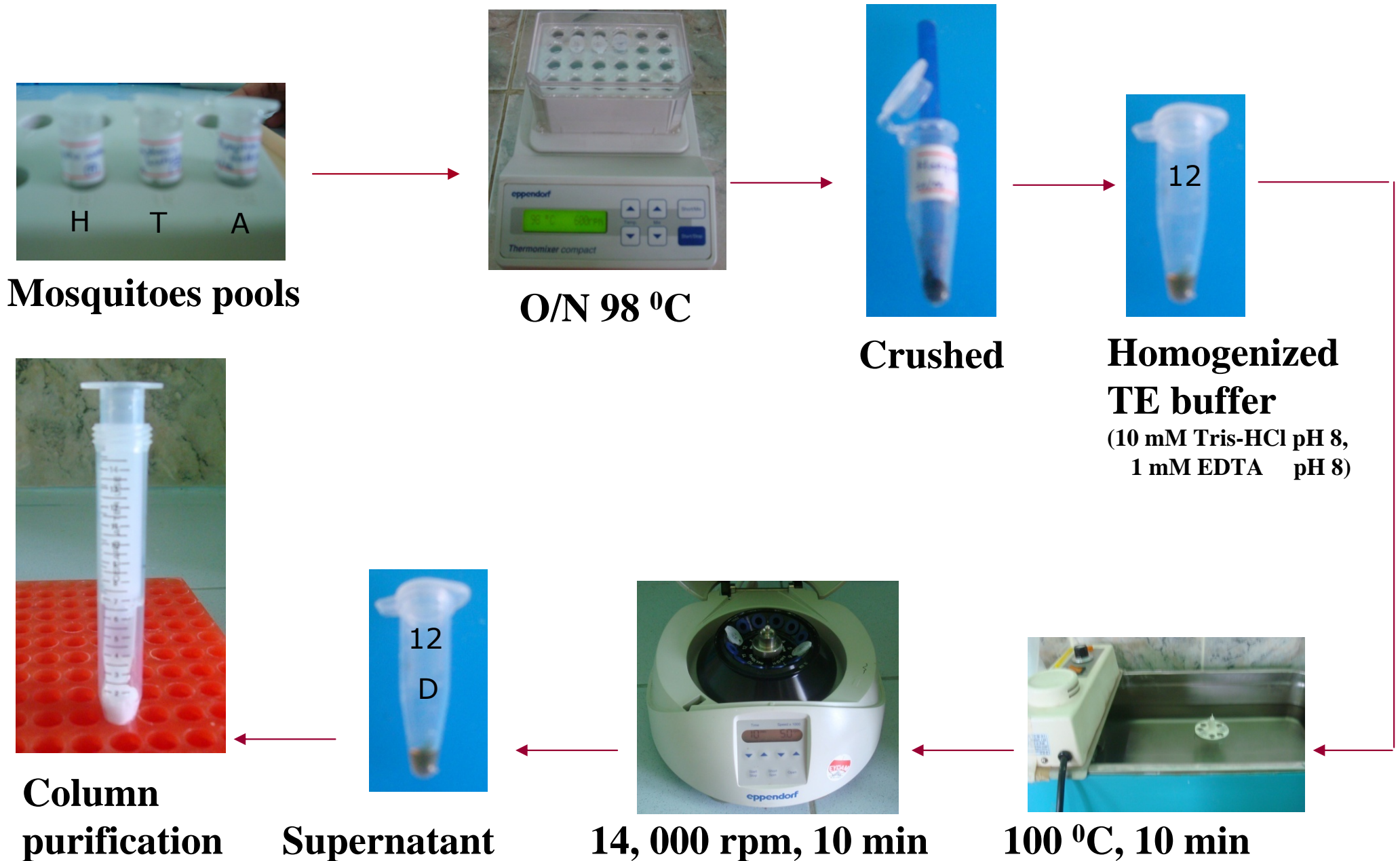
# PCR - ELISA assay:



- In ELISA assay,
  - ✓ amplified positive control DNA (0.1  $\mu\text{g}$  of extracted *W. bancrofti* DNA) was used as positive controls.
  - ✓ Negative controls included water and DNA extracted from a pool of 15 parasite-negative lab-reared mosquitoes.
  
- A positive sample was defined as 5 times the uncorrected optical density (OD) of a sample containing no template DNA.
  
- PCR\_ELISA point estimates were computed and compared using Poolscreen 2.0 software (The University of Alabama, Birmingham).

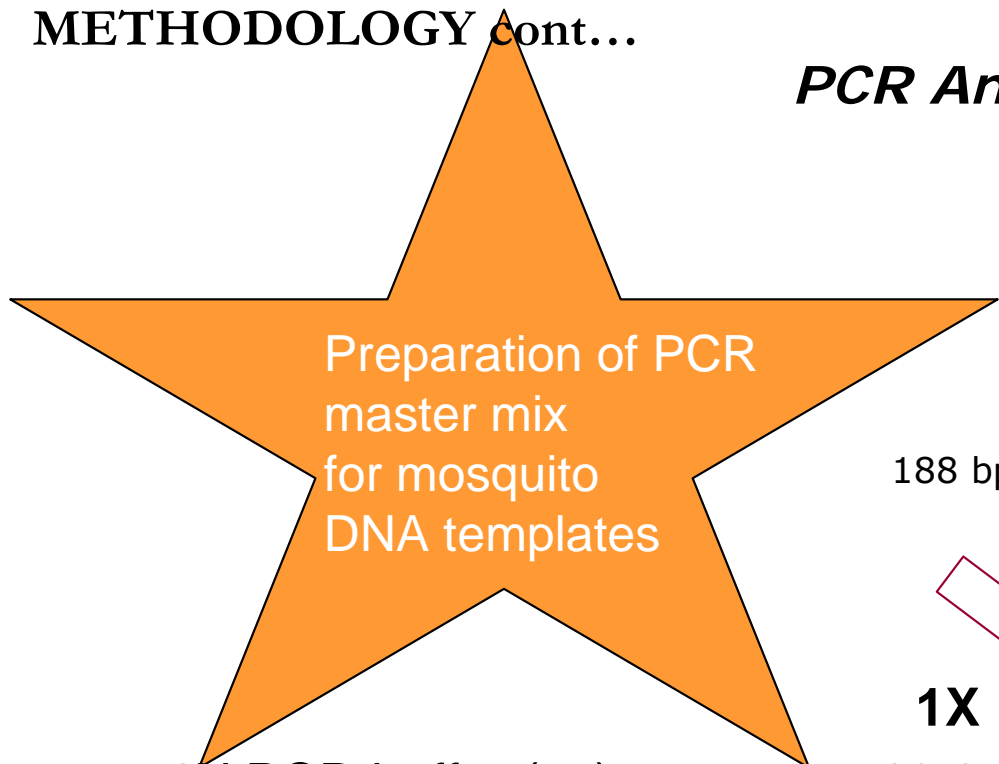
## 2. Polymerase Chain Reaction (PCR) assay

### *Extraction of DNA*

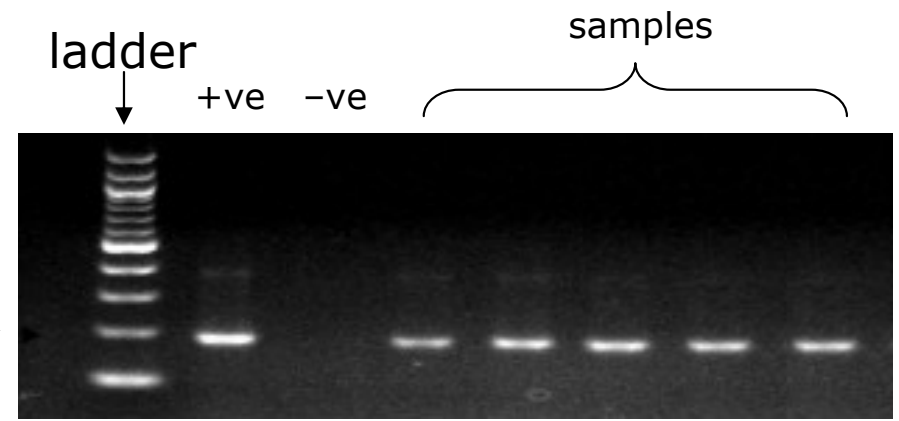




**PCR Amplification**



1X PCR buffer (5x)	10.0 µl
1.5 mM MgCl <sub>2</sub> (25 mM)	3.0 µl
1.25 mM dNTP (25 mM)	2.5 µl
10 pMol NV1 (10 pM/µl)	1.0 µl
10 pMol NV2 (10 pM/ml)	1.0 ml
2 U Taq (5 U/µl)	0.4 µl
H <sub>2</sub> O	27.1 µl
DNA	5.0 µl
<b>Total volume</b>	<b>50.0 µl</b>



**Qualitative analysis of PCR products**

5 min at 95 °C,  
1 min at 94 °C,  
1 min at 55 °C,  
1 min at 72 °C, } 35 cycles  
10 min at 72 °C

**PCR program**

**Dilution of PCR product  
(40  $\mu$ l, PCR product + 180  $\mu$ l, hybridization buffer)**



**100  $\mu$ l/well - added to streptavidin-coated plate**



**Hybridized with fluorescein-labeled wild-type  
specific probes - 55°C ,30 min**



**Incubated - alkaline phosphatase-labelled anti-  
fluorescein Fab fragment**



**Add substrate - 1 hr**



**Absorbance measured - 405 nm**