

# AN ALTERNATIVE SPATIAL ANALYSIS OF BREEDING SITES DISTRIBUTION TO SUPPORT CONTROL ACTIVITIES FOR DENGUE.

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**Background/aim** Dengue is an urban re-emerging infectious disease. In Cali-Colombia the disease is endemic and during the last years it has shown an increasing trend to larger outbreaks and more severe dengue cases. Control programs carry out actions to reduce populations of *Aedes aegypti* mosquitoes by detecting areas with high indexes of infestation (i.e.; more than 5% of recipients with *Aedes* pupae or larvae) and, subsequently, eliminating positive breeding sites. However, evaluations have not been developed about the role of negative, but potential, breeding sites in the dynamic of transmission. The objective of this study was to evaluate the distribution of positive and potential breeding sites inside households and in peri-domiciliar spaces.

**Methods** A geographic information systems (GIS) was implemented at a high space scale for storing, processing and analyzing data by using geo-statistical techniques (Kriging). We determined the spatial relationship between positive and potential breeding sites distributions.

**Results** Only 56% (R-squared) of the spatial variability of positive breeding sites distribution was associated to variability of potential breeding sites. 15,2% of the study area comprises zones with a simultaneous presence of high potential-high positive breeding sites and 64,2% of the area presented low potential-low positive breeding sites. However, 20,6% of the area presented a differential distribution of these types of breeding sites (5,1% high potential-low positive and 15,5% low potential-high positive). Maps were built to identify areas showing this lack of agreement in the distribution.

**Conclusion** Our results suggest that focusing interventions in areas only presenting high infestation with positive breeding sites might fail because they do not take into account the variability in breeding sites from potential to positive. Elimination and education activities could be better implemented taking into account the distribution of potential breeding sites.