Genetic connectivity plays a crucial role in maintaining the genetic variability, evolutionary potential, and the global biogeography of mangrove species. Mangroves plants are foundation species to unique tropical intertidal ecosystems, which are currently highly degraded. Therefore, fully understanding their patterns and drivers of genetic connectivity are crucial. The main objective of this project was to disentangle the different drivers and patterns of genetic connectivity at different geographical scales, i.e., at regional, local, and fine-scale levels, in the most abundant mangrove (*Rhizophora racemosa*) populations of the Cameroonian coastline.

Propagule dispersal modelling data, in congruence with genetic data, indicate that (historical) sea level rise and contemporary ocean current patterns have contrasting effects on regional-scale genetic connectivity. Local hydrodynamics and forest structure maintain local-scale genetic connectivity within the Cameroon Estuary Complex (CEC). Fine-scale genetic structure (FSGS) and signs of recent bottleneck events were observed in the CEC. Pollen dispersal potential was also low in the CEC, where a mixed mating system, i.e., outcrossing and a small level of selfing occur in these populations.

These findings support the need to investigate gene flow at multiple-geographical scales to identify the different drivers mediating connectivity at the different scales, and for holistic understanding of the drivers of species distribution.