CONCLUSION
6. Conclusion

Our study confirms that employing COI barcoding will help in the identification of the majority of fish species. Increasing application of DNA barcoding will overcome limitations of morphology based identifications and help identify previously undifferentiated species by revealing divergence of COI sequences within currently recognized species. DNA barcoding and morphological analysis should be complementary in such an endeavour. Establishment of reliable global COI barcode database for fishes will help anyone with sequencing facility to accurately identify, any fish or fish egg, larva or piece of tissue. The scientific and practical benefits of fish barcoding are manifold. This will be a valuable tool in the hands of fisheries managers, fisheries ecologists and fish retailers.

The conclusions about the Narmada, *M. armatus* and *C. catla* population are very clear, and results reported therein proves the genetic isolation of fish communities by dams. Fragmentation by dams and a water fall seems to participate in fish population isolation and differentiation. Preventing movements, totally from downstream to upstream, and partially from upstream to downstream, dams would enhance the natural isolation by distance effect and the asymmetry of the dispersal flows. Consequently, populations, and especially the most upstream, would have very
low immigration rates and are more subject to genetic impoverishment. Finally, even if this study brings few proven insights about the genetic and ecological characteristics of the Narmada fish population, one can pull out from it methodological guidance. Sampling a long river segment is certainly a more efficient way to assess fish dispersal behavior than only consider one obstacle, and use of isolation by distance such as the one developed in this study allow to assess cumulative and differential effects of multiples kinds of obstacles. However, in order to improve the power of the analyses, one should take care to sample nonrelated individuals by avoiding sample of grouped juveniles and an optimal sampling scheme would imply sampling directly upstream and downstream of all the obstacles.

Finally, our study suffers biases: Sampling size is low, no sampling between all the obstacles, nor directly upstream and downstream, no possibility of comparison of fragmented and un-fragmented segments, and disequilibrium in regard of the Hardy-Weinberg model which can have at least three non-excluding causes. Among them two do not rely on actual biological processes: null hypothesis, due to hyper variable region sequencing, and relatedness, likely due to non-efficient sampling strategy.