Dear Editor,

We have now revised our MS taking into account all comments. We thank the reviewers and editor for their constructive comments on this work.

Sincerely,

The authors

Comments of the editor (*Michelle DiLeo)*

- In particular, I share the concern that the site-level sampling strategy is perhaps not ideal, and that the implications of this should be discussed. It seems that MAPI is more suited to individual-based sampling (or at least finer-scale sampling) and I am interested to know if the results are sensitive to the resolution of the generated MAPI surface. How do the results of MAPI compare to analyses done with only the fourteen sampled sites?

=> Please, see also our answers to the comments from both reviewers.

In the new version of the MS, we added the population-based analysis approach implemented in the software GESTE (Foll & Gaggiotti 2006) to estimate specific local-FST values for each sampling site. Consistently with MAPI, this analysis also shows a gradient-like pattern from lower local-Fst values in the southeastern part of the study area to higher local-Fst values in the Northwestern part (see Fig 2 in the MS). Also, to determine whether the genetic structure retrieved from MAPI can be biased due to the smoothing of a relatively small spatial network (13 sampling sites in the peninsula) we performed both a simulation study and an analysis of subsampled datasets, as follow:

- Simulation (see Supplementary material, Section 4): datasets of individual microsatellite genotypes were simulated under a landscape configuration corresponding to a spatial gradient from a favorable to an unfavorable habitat, as described in Piry et al. (2016). 20 independent simulations were run and for each replicate, we sampled 10 times the individual genotypes in a way mimicking the sampling size and spatial coverage of our house mouse data set (i.e. 13 clumped sampling sites, with 40 individuals per site). On each of the 200 simulated datasets (20 replicates x 10 resampling) we used the approach combining MAPI and a CAR model to test the effect of the landscape features on the genetic pattern of differentiation (MAPI smoothed-Fst). The gradient-like pattern of genetic differentiation was observable from the MAPI outputs and for 95.5% of the simulated datasets, and we found a positive significant effect of the landscape as expected under the simulated scenario (see supplementary material, section 4).

- Resampling: we independently subsampled 100 times N (ranging from 6 to 12) sampling sites from the original dataset. We then analyzed each replicate of the different subsampling size (N) using the MAPI analysis and Bayesian CAR model. As different sampling sites were subsampled for each replicate of N, the MAPI grid resolution was

determined independently for each subsampling scheme by setting the 'beta' parameter to 0.25 in respect of the Nyquist-Shannon sampling theorem under a situation of random sampling (different samplings = different grids). The main effects observed from the complete dataset were observable even with N = 6 sampling sites: gradient-like pattern in genetic differentiation and high posterior probability for a negative effect of the variables "Connection" and "Industrial" and positive effect of the variables "Vegetation", "Residential" and "Built-up".

Although the sampling size and coverage of the house mouse dataset is not ideal, we believe that MAPI remains quite efficient in retrieving the main genetic structure because it is well-marked and quite simple: gradient-like pattern with a high level of genetic differentiation. Both the simulation and resampling analysis are mentioned in the Material and method and Results section of the new MS, and detailed in Supplementary material, section 4.

- Second, I echo the reviewer comment about the ability to tease apart the effects of historical versus contemporary aspects of the cityscape. It seems that these variables would be correlated, and it should be made abundantly clear to the reader how this problem was considered. I suspect that if there were no problems with collinearity, this might be easily addressed by reporting pairwise correlations and variance inflation factors for all variables.

=> We do agree that the intensity and meaning of the correlations between our explanatory variables was not properly addressed in the previous version of the MS. In the new version, we first analyzed the correlation between the land cover variables describing the current cityscape using a spatial PCA. This analysis was done using a 100m resolution raster derived from Borderon et al. 2014. We also provide historical information on the development of the city since the colonial period to these days (see Supplementary material, section 1). Based on both, we merged some classes of land cover as they are spatially highly imbricated (at a resolution finer that what can be retrieved from the MAPI analysis with the sampling size at hand) due to historic urbanization policies. Second, we also analyzed the relationships between genetic estimates (population-based and pairwise estimates - see our answer to the comment below) and cityscape features using a Random Forest approach. We used two different RF algorithms in order to test the significance of the most important predictors and to compute conditional permutation importance for each variable in order to account for potential multicollinearity effects. For the pairwise estimates (MAPI smoothed-Fst) we first trained the RF algorithm on 50% of the data (MAPI cells) and then used the resulting model to predict smoothed-Fst within the remaining 50% of the cells. The accuracy of the model was quite high supporting that, if not exhaustive, our cityscape variables are clearly important factors to understand the genetic structure of the house mouse. For all RF analyses, we used different parameter values (seeds for the computation in R and mtry value, which set the number of variable to use for splitting at each node) as recommended when dealing with correlated predictors. Results from RFs were very consistent with those from the CAR model and further allowed to discuss the role of each variable and pint point possible collinearity and/or local effects in the CAR model.

- Third, I agree that the discussion could use some work and that too much space is reserved for discussing the colonization history, which in my opinion is not the main or most interesting message of the paper.

=> We shortened the discussion on the colonization history and rewritten most of the discussion in the light of the new results.

Finally, I would be interested to see if genetic diversity correlates with the same aspects of the cityscape compared to genetic differentiation. Genetic diversity and differentiation can be driven by different processes and I think both are important when considering the practical applications of this work. I understand that with 14 sites you are limited to what can be included in a single model, but does genetic diversity show any strong univariate relationships with cityscape features beyond just the European settlement vs ancient village dichotomy?

=> We do agree that this is an important point. In the new version of the MS, we explored the relationships between local cityscape variables (current and historical) and population-based genetic estimates (allelic richness, expected heterozygosity and local-Fst (computed with the program GESTE) using: 1) Spearman pairwise coefficient for all pairs of variables and, 2) Random Forest approaches (including conditional RF that better handle multicollinearity). Local cityscape features were computed within nested circular buffers of radius equal to 300m, 600m, 1000m and 1500m and centered on the barycenter of the individual coordinates at each site. The variable values within any buffer "i" with a radius superior to 300m (smaller buffer) was computed as the difference between the values of the variables computed within the buffer "i" and within the buffer nested within "i". The historical variable "Connection" was among the best predictors for all buffer sizes for both the allelic richness and the local-Fst. Other important predictors included the variable "Vegetation" and "Built-up", the former being identified among the most important variables for buffer sizes of 600 and 1000m and the latter at 1000m only. For Hs, the best predictors included the variables "Industrial" (for the three largest buffers), "Vegetation" (for the two largest buffers) and "Residential" (for the 1000m buffer). We address possible explanations for this difference in the new version of the discussion.

Review 1

#1- my major concern is regarding the spatial distribution of sampling, which was focused in few sampling points giving a clustered sampling for a species that rather is likely found all over the city. I would like that the authors explain/address how their choice of sampling may bias results of an analysis that is based on building an spatial planar network that estimates spatial variations in pairwise genetic differentiation. The authors mentioned the challenges of sampling in this type of studies but did not mention the potential bias it can bring for landscape genetic analyses.

=> MAPI is a smoothing procedure, which, indeed, performs better when the sampling size and, more especially, the spatial coverage is high. The sensitivity of MAPI to the sampling scheme, especially spatial gaps and sampling size, was addressed in the paper describing the MAPI method (Piry et al. 2016) using individual genotypes data sets simulated considering various demographic models or landscape configurations. All results of these simulation studies are available at: https://www1.montpellier.inra.fr/CBGP/software/MAPI/index.html.

The main conclusions from this study were:

1) when analyzing highly irregular samplings (with large gaps), the method can detect a few areas of genetic discontinuity as the cells located within these spatial gaps are only informed from long-distance connections. However these "artifacts" are generally small in terms of surface and mainly located on the border of the study area.

2) when decreasing, the sampling size, the probability to detect a significant effect of landscape features also decreases (using a similar CAR model as for the house mouse dataset).

However, we do agree that the "population-based" sampling of 13 sampling sites (the island of Gorée was not included in the MAPI analysis) is lower, in terms of sampling size and spatial coverage that the situations of sub-sampling analyzed in Piry et al. (2016). In the new version of the MS, we evaluated whether the observed genetic structure can be biased due to the smoothing of a relatively small spatial network. To do so, we first compared the genetic structure retrieved from MAPI to the one obtained from the population-based approach implemented in the software GESTE, which estimates specific Fst values for each local population. Second, we used datasets of individual microsatellites genotypes simulated under a landscape configuration corresponding to a spatial gradient from a favorable to an unfavorable as described in Piry et al. (2016) (the simulation setting is presented section 4 of the new supplementary material). 20 independent simulations were run and for each replicate, we sampled 10 times the individual genotypes in a way mimicking the sampling size and spatial coverage of our house mouse data set (i.e. 13 clumped sampling sites, with 40 individuals per site – see Table 2). On each of the 200 simulated datasets, we applied the approach combining MAPI and a CAR model to test the effect of the landscape features on the genetic pattern of differentiation (MAPI smoothed-Fst). For 95.5% of the simulated datasets, we found a positive significant effect of the landscape as expected under the simulated scenario. None of the simulated datasets showed an unexpected significant negative effect. Third, we subsampled our dataset to

evaluate whether the observed genetic structure would change as a function of the number and localization of the sampling sites. To do so, we independently subsampled 100 times N (ranging from 6 to 12) sampling sites from the original dataset. We then analyzed each replicate of the different subsampling size (N) using the MAPI analysis and the Bayesian CAR model. As different sampling sites were subsampled for each replicate of N, the MAPI grid resolution was determined independently, which means that the shape and resolution of the grid varied across the replicates.

The main results of these new analyses are:

1) Similarly to MAPI, the mapping of local-Fst estimates from GESTE showed a gradient-like structure, from the lowest F_{ST} values estimated for the populations located in the South-Eastern part of the study area to the highest F_{ST} values estimated in the populations located in the North-Western part.

2) When combining MAPI and the CAR model to analyze the 200 simulated datasets considering a gradient from a favorable to an unfavorable habitat, we observed the expected significant positive effect of the landscape value for 95.5% of the replicates. None of the remaining datasets showed an unexpected negative effect.

3) The main effects retrieved from the CAR model (complete model with all variables – see Table 3 in the MS) applied the complete dataset were also observable when analyzing the subsampled datasets, even with N = 6 sampling sites: high posterior probability for a negative effect of "Connection" and "Industrial" and positive effect of "Vegetation", "Residential" and "Built-up".

We do agree that results should be interpreted very carefully when MAPI is run on datasets with low sampling size and spatial coverage. In such situations, carrying out a simulation study, as we have now done in the new version of the MS, is probably one of the most efficient ways to assess the robustness of the method. This being said, we do believe that, in the present study, MAPI is quite efficient despite the low sampling size and coverage because the level of genetic differentiation is high (as often observed for commensal rodents) and the main spatial structure of genetic variation is well-marked and quite simple (gradient-like pattern). MAPI would likely be a lot less efficient in retrieving more complicated or subtle genetic structure without increasing significantly the size and spatial coverage of the sampling. We now address this point in the discussion.

#2- Abstract: - Archetypal commensals: consider using other term, I don't think this is clear for everyone - Remove in mice - I think to be more precise instead of analyzing the influence of historical and current features on genetic structure, it`s on genetic differentiation as the analyses requires genetic distances which are a proxy of gene flow. I don't find the last sentences of the abstract regarding methods and results very useful, please be more specific on what type of analyses were carried and mention the most important results.

=> We replaced "archetypal commensals such as rodent pests" by "synanthropic rodents" and removed "in mice". We keep "genetic structure" as we know analyze the relationships

between cityscape feature and genetic diversity and differentiation. We have modified the last sentences of the abstract in order to be more specific about the analyses and about the results obtained.

#3- Introduction: - In the first it is mentioned that urbanization leads to genetic isolation, but there are already evidence showing that species can adapt and be benefited for urbanization processes, thus I think this paragraph needs a better overall framework, especially since the focus is on a species that has somehow benefited and demographically expanded due to urbanization.

=> We agree with the reviewer. The paragraph has been clarified.

Methods:

#4- The last paragraph of the section regarding classification of urban maps and cover classes can be shortened by omitting the details of all existing cover classes, which as explained later not all were explained. It would be more useful to know why the six-classes of urban habitats based on socioeconomic profiles were used, that is, which are the biological relevance for the dispersal or occurrence of the species? Also, I don't have much clear if all vegetation types were considered just as one class, and if it is, does it mean that the species does not have any preference for a specific type of vegetation?

=> We have now clarified how socio-economic features of the urban habitat may be related to rodent infestation in the introduction. The different classes of land cover used in the analyses are now more detailed in the method section and presented in Table 1 and Figure 1. We also provide complementary information on the urbanization process in the section 1 of the supplementary material. The different classes of "Vegetation" from Borderon et al. (2014) mainly distinguished between areas with dense vegetation and areas mixing vegetation and bare ground. These two types of habitats are not favorable to the house mouse, which is strictly commensal in Senegal, and are very likely to have the same effect on population dynamics (density gaps and/or dispersal barrier). This is why we merged these classes into a single class called "Vegetation" that we considered as a proxy of the localization of unfavorable habitats for the house mouse. For the sake of clarity, in the revised version, we simplified the description of this land cover class.

#5- Why the number of 20 samples as target?

=> In population genetics, a local sample size of 20 is often considered as the minimum number enabling to obtain valuable estimates of genetic diversity given the observed level of polymorphism. The target here was to try catching at least 20 individuals but in most cases this minimal number was largely exceeded (mean number of individual per locality = 37; see Table 2).

#6- Also, it is not specified if adults or juveniles were collected and if the species is easily distinguished from other rodent fauna in the city.

=> This has been specified in the revised version.

#7- Specify the base pairs amplified for the D-loop

=> Done

#8- Mitochondrial analysis: It is not clear with how many sequences the haplotype network was constructed. In the introduction it is mentioned that the D-loop data was also used to investigate the geographic origin of the house mouse with data from its entire distribution, so I don't have clear if the haplotype network was the only analyses performed to address this objective. I think performing phylogenetic trees are also needed for answering this.

=> As was indicated in the MS, the haplotype network was performed on haplotypes from Senegal exclusively (those obtained in this study and those of Lippens et al. 2017). We have now also specified in the revised version that the haplotypes found in this study were from the same haplogroups that those already evidenced for the house mouse in Senegal in Lippens et al. (2017). We thus refer to the haplotype tree already presented in Lippens et al. (2017), in order to discuss about the geographical origin of house mice from Dakar.

#9- Microsatellite analyses: (1) For what specific purpose the kinship coefficient was estimated? For performing landscape genetic analyses is important to eliminate related samples (sibs, half sibs), which I think can be better evaluated with other software, such as CERVUS.

=> CERVUS is dedicated to parentage analyses and it would require having a large proportion of putative parents and offspring in the dataset. The kinship coefficient was estimated to evaluate whether heterozygote deficiencies found in the dataset may be due to the oversampling of closely related individuals (i.e. family effect) or from the pooling (i.e, individuals sampled within a site are considered as a population in the sense of population genetic theory) of individuals sampled from different social groups. Such pooling for social species can lead to positive Fis values - see Parreira & Chikhi 2015). Here the observed within-site heterozygote deficiencies are more likely due to the second hypothesis as we do not observe high level of relatedness. We further detailed this point in the new version of the MS.

#10- (2) Accuracy of effective population size estimates depends highly on sample size, does n=20 is enough to obtain accurate estimates given than this species is quite abundant where it occurs?

=> Ne was estimated from more than 20 individuals for all but one locality (see Table 2). Although Ne estimates of a few dozen individuals is not unrealistic for the house mouse due to its social system (Linnenbrink et al. 2018), we do agree that the confidence intervals are quite large and that it is difficult to interpret the differences between the sampling sites. For these reasons we removed this analysis from the new version of the MS.

#11- (3) Sampling was not spatially uniform, but rather clustered in few sampling points within locations with different urban history. How does sampling bias or in this case, having very few points within a spatial grid where the species can occur everywhere may affect the results? This is because the hexagonal grid resulting from MAPI shows a fine mapping of

genetic discontinuities (gradient colors), but this the spacing between some sampling locations is not small.

=> Please see our answer to the comment #1 where we detail how we have assessed the possible bias that could results from the smoothing of a small spatial network of localities.

#12- Results: -The first sentence can be omitted.

=> Done

#13-Improve flow of the sentence about the number of D-loop haplotypes.

=> Done

#14-The information of haplotype frequency by city regions is hard to follow as it is mainly descriptive, I think a figure will help, figure S3 should be in the main text.

=> This has been done. Information on haplotypes is now presented Fig 1 in the MS.

#15- What does it mean to have a kinship value f 0.2 in terms of relatedness? I still think a more specific relatedness analysis is needed, to know if related samples were taken and if need to be omitted for further analyses.

=> Please see our answer to comment #9.

#16- Please mention the allelic richness values for the two groups: ancient villages and the European settlement, just mentioning they are significant different, does not tell much about the relative difference. And, for the other diversity measures? The trend was the same, higher in the first European settlements?

=> In the new version of the MS we removed this comparison and, following the suggestion of the Editor, we now further analyze the relationships between genetic estimates computed for each site (allelic richness, expected heterozygosity and local-Fst) and cityscape variables (including historical variables) using a buffer approach and Spearman correlation coefficient as well as Random Forest analyses. Please see our answer to the last comment of the editor.

#17- Ne values are not mentioned in results

=> This analysis has been removed in the revised version of the MS

#18- The removal or not of IDG was not mentioned in methods for the IBD test. Which is the explanation for performing this?

=> This point was clarified in the Method section of the revised version of the MS. As an island, IDG is clearly isolated from the rest of the peninsula (see results of the STRUCTURE analysis). As we were interested in analyzing and relating the genetic structure to the

structure of the cityscape, considering IDG in the MAPI analysis would only tell us that water acts like a barrier to gene flow, which we already knew from the clustering analysis.

#19- Discussion -I think results, discussion and the figure 2 will be easier to follow and understand if instead of naming urban 1 to urban 6, the name of what this classes represent is mentioned. For e.g, until discussion I knew that urban 5 refers to industrial areas.

=> We do agree and the land cover classes have been renamed as suggested. We also moved the Table presenting these different classes from the supplementary material to the main text (now Table 1).

#20- Conclusion. -In my opinion the conclusion should state only stress the main finding and the implication of the results. The statement about the challenges and limitation of sampling in this type of studies should go into discussion and also adding what type of implications may have on the type of analyses used and the results found.

=>The conclusion has been re-written as such.

Review 2 (Tuomas Aivelo)

I have two major issues with the manuscript.

#1- Firstly, it is unclear to me how the authors can differentiate between the effects of current urban structures and the historical structure of the urban landscape. I am not familiar with Dakar, but one would suspect that areas built at different time periods have different structural properties for house mouse and thus there would be correlation between time of urbanization and/or connection to urban area and the structural property of the area from the point of view of gene flow. Looking at the different patterns of prevalence of land covers, they do seem to partly correlate with the pattern of urban extension. It seems to me that the authors just assume that any genetic structure would be due to historic urban expansion. Why is that? Furthermore, the intriguing discrepancy between time since the connection to the early settlement and first occurrence of built-up areas suggests that there is more complex interplay of different aspects of urban structure than it first it seems.

=> Regarding the correlation between the historical development of the city and the spatial variation of the structural properties: in the new version of the MS, we analyzed the correlation between the land cover variables describing the current cityscape using a spatial PCA. This analysis was done using a 100m resolution raster derived from Borderon et al. 2014. We also provide historical information on the development of the city since the colonial period to these days (see Supplementary material, section 1). Based on both, we merged some classes of land cover are they are spatially highly imbricated (at a resolution finer that what can be retrieved from the MAPI analysis with the sampling size at hand) due to historic urbanization policies. We also present the Spearman correlation coefficient for all pairs of variables computed within the MAPI grid cells (Table S3.3 – Supplementary material, section 3). As could be expected, the historical variables "Built-up" and "Connection" are correlated between them and with the urban habitat "Old City" and "Industrial", which both rapidly expanded North to the first European settlement during the 40-50s (the class "Industrial" being other all less frequent than the class "Old_city"). We also use different approaches to investigate the relationships between the level of differentiation (MAPI smoothed-Fst) and the cityscape variables (current and historical) including Random Forest algorithms, which allow ranking the importance of each predictor variable using a permutation procedure that can be conditional to other variables (handling of multicollinearity). In RF, high correlation between variable predictors generally result in very similar importance values for these variables as one or the other can be used for splitting when building the tree.

The pattern of correlation between the current urban habitats and each of the historical variable is quite similar: highest level of correlations of both historical variables are with "Old_City" and "Industrial" and there is no or a very weak correlation with the variable "Spontaneous" and "Residential". Despite this similarity, the variable "Built-up" is not identified by the RF or the CAR model as an important variable to explain the global genetic pattern while the variable "Connection" is clearly one of the most significant predictor to explain the variation in MAPI smoothed-Fst values (Table 3 and supplementary material, section 3). If the structural properties of an area were mainly dependent on the time at which it has been built-up, we could expect to have a similar impact of both historical variables.

Regarding the comment about the discrepancy between the time since the connection to the early settlement and the first occurrence of built-up areas, as we did try to explain in the previous version of the MS, it results from the presence of the Lebou villages (Ouakam, Yoff and Ngor) in the North of the Peninsula. These villages were clearly identified as built-up areas in our early maps (see map of 1862 in Fig 1) while they have been among the last areas to be connected to the first European settlement connected (see maps of 1993 and 2001). These villages have now been absorbed in the city, however there are associated to high levels of differentiation, which suggest that even if the house mouse has been introduced in these village quite early, they have been quite isolated for a long time. This supports the hypothesis that historical gene flow intensity across the peninsula has been primarily dependent on the urban expansion. We now discuss this point in the discussion.

To summarize, we do not think that the observed genetic structure is only due to historic urban expansion but we do believe that this process still strongly reflects in the retrieved genetic structure, at least when using integrative genetic estimates such as Fst. The main message we wanted to pass was that the temporal dynamics of urban expansion and the current characteristics of the cityscape are likely to interplay in shaping the current genetic patterns of the house mouse in Dakar. We have tried to be more precise about this point in the new version of the MS and we also changed the title in this sense.

#2- Second issue is the structure and clarity of discussion: the authors now discuss in length the introduction of house mouse to Dakar, which seems secondary to what they have actually studied. It might make sense to just state that the genetic pattern is in line with the idea that mouse was introduced to first continental settlement at the south of Cap-Vert. In some parts of the discussion, the authors could make a clearer connection with their work and what they are arguing. For example, in the paragraph on trustworthiness the authors clearly have something important to say, specifically with their second point, but it is not clear how this is related the methods or results of this work. I would reorganize the contents of discussion and try to be more concise.

=> We agree with the reviewer and we have strongly reduced the part of the discussion concerning the introduction of the house mouse in the revised version. The discussion has also been re-written to account for new results.

Minor issues:
#3- In first paragraph of Introduction, the authors oppose "numerous species" and "commensal species". Arguably also some commensal species can be spatially isolated in cityscape. Thus I find introducing commensal species as those which can easily disperse in urban landscape a bit strange. Maybe just state that some species can disperse more easily than others in urban landscape?

=> We agree with the reviewer. The paragraph has been clarified.

#4- In second paragraph, yes, rodent control is costly (how costly?), but "weighs heavily on city's budget" sounds like an overkill. My hunch is that more often than not, rodent control is just seen as essential "this has to be paid" part of budgets.

=> We agree with the reviewer. The sentence has been modified.

#5- The first argument on the importance of spatiotemporal variation in gene flow seems to relate more actual movements of rodents than gene flow. If we know that rodents move from building to building, doing population genetics does not really give any additional help. The second and third argument are more on point.

=> We have deleted this first argument in the new version.

#6- In "Spatiotemporal pattern of urbanization": what is 'strict vegetation'?

=> We have now simplified the description of the land cover class "vegetation" as all the details presented were not needed to understand the typology. We initially wanted to explain that we had merged categories retrieved from Borderon al. (2014) that distinguished areas with vegetation only and areas where vegetation is mixed with bare ground (as can be identified from satellite image). The merging was based on the fact that both types of habitat are unfavorable for the house mouse and then are likely to affect population size and/or dispersal in the same way (e.g. desert resource areas).

#7- In "Mitochondrial sequence analysis" the authors outline how they consider urban areas linked. I do not disagree with their approach, but it would be good to argue how their approach suits for house mouse by outlining what do we know (or do not know!) about house mouse biology/dispersal in urban environment.

=> We do apologize as we do not understand the matter addressed by this comment. We did not relate the variability in mitochondrial sequences to the urban features but just pointed out that haplotype diversity was greater in sampling sites located in the southern part of the Cap-Vert Peninsula near to the first European settlement.

#8- The authors refer numerous times to applied aspects of their work, but it is not clear how straightforward it is. Is it sensible to have pretty much the whole downtown of Dakar as a simple target for eradication program, as I understood they are saying in the final paragraph of Discussion?

=> We agree with the reviewer that it would be great to have more straightforward recommendations in terms of rodent control. However, we think that we are yet hardly in a position to be able to do that as we now more clearly state at the end of the discussion.

We did not want to imply that the whole downtown of Dakar could constitute a unique target for eradication (supposing that eradication is even possible). We were suggesting that the large industrial area running along the railway is very likely to sustain a very dense and connected network, and that as such this particular area should probably be considered as a whole unit for control actions. The other suggestion was that in habitat that are less likely to sustain high densities more local actions of control could still be efficient, especially in a context where vegetation is abundant as it is likely to limit both population size and recolonization probability.

#9- In conclusion, you refer to challenges outlined in Parsons et al. (2017) and cite those as the reasons for low sample size. Which of these challenges did you encounter? It might make sense to shortly outline those in Methods? Furthermore you suggest that collaboration can be the way forward – maybe put this in the discussion as it is not really your conclusion.

=> As stated in Parson et al. 2017, it is not an easy task to sample rodents in private houses. We have permits from the Senegalese Head Office of Waters and Forests, the Ministry of Health and Social Action in Senegal, the National hygiene service, and the management director of the Dakar harbour (see acknowledgements). However, in each sampling site, we need to request the approval of the neighborhood leader, then of each inhabitant of the houses in which we want to set traps (about 20-30 persons in each sampling site). We need time to explain to each person the purpose of the study, and its requirements (avoid contact with trapped rodent, avoid moving of traps, be there for capture surveys, give access to the house early in the morning…). As such, a minimum of 7 days is necessary to prepare and perform the sampling in one district, sometimes up to 10 days, preceded by several months to obtain official permits from the different administrative services. We have deleted the sentence about collaborations in the new version of the MS.