2	"Phylogenetic patterns of extinction risk: the need for critical application of
3	appropriate datasets"
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15	ABSTRACT
16	Gereau et al. (2013) criticized our recent analysis on the phylogenetic patterns of
17	extinction risk in the Eastern Arc biodiversity hotspot (Yessoufou et al. 2012). However,
18	Gereau and colleagues based their critique on preconceptions and speculation rather than
19	data. Here we identify several shortfalls in their lines of argument, and suggest that, given
20	current rates of extinction, it is far more dangerous to wait for complete Red List
21	assessments than to explore patterns of threat using available data. Nonetheless, we agree
22	that all analyses should be based upon the best available data, and we encourage the rapid
23	releases of new data on threat status for the flora of the Eastern Arc.

Speculation versus data-driven conclusions: A response to Gereau et al.'s

25 Keywords: Eastern Arc, Gereau et al. (2013); Yessoufou et al. (2012)

26 Introduction

27 28 There is growing evidence indicating that we are entering a sixth mass extinction event 29 (Millennium Ecosystem Assessment 2005), driven by various pressures including 30 invasive species (Winter et al. 2009), habitat destruction (Vitousek et al. 1997; Haberl et 31 al. 2007), climate change and climate variability (Willis et al. 2008, 2010). It is estimated 32 that rates of species loss may be 1,000–10,000 times more rapid than background rates in 33 the paleontological past (Pimm et al. 1995; Millennium Ecosystem Assessment 2005), 34 and this loss is particularly pronounced in tropical biomes (Vamosi & Vamosi 2008). As 35 a consequence, $\sim 30\%$ of assessed species are considered threatened with extinction, and 36 a greater proportion is predicted to become threatened in the near future (Thomas et al. 2004; Mace et al. 2005). Biodiversity provides many ecosystem services that are 37 38 particularly crucial for rural communities in the developing world (e.g. food production, 39 medicinal plants, clean water, etc.), which is particularly vulnerable to the impacts of 40 global change (Mendelsohn 2006). There is therefore an urgent need for increased efforts 41 towards a better understanding of extinction risk to provide options for a better 42 management of the Earth's natural resources (McKinney 1997). 43

In a recent study (Yessoufou et al. 2012), we assessed the phylogenetic pattern of
extinction risk in an African biodiversity hotspot – the Eastern Arc Mountains. We used
publicly available data from the IUCN Red List database (www.iucnredlist.org), and
showed that the distribution of extinction risks is phylogenetically clustered, and

48 suggested that this pattern might be driven by vulnerable species. Gereau et al. (2013) challenge our conclusion along a number of lines: (i) inadequate knowledge of the study 49 50 area, its flora and relevant literature; (ii) lack of transparent or repeatable methods for the 51 data selection, compounded by inadequate sample size; and (iii) compilation and analysis 52 of an inconsistent dataset containing non-equivalent Red List assessments performed 53 under different criteria and at different times. However, Gereau and colleagues provide 54 no new evidence and present no additional analysis, but rather base their claims on 55 speculation and their own preconceptions. Here, we respond to the specific criticisms 56 raised by Gereau et al. and we request that if, as they claim, there is new data on 57 extinction risk for the Eastern Arc flora, it should be made available to the public rapidly. 58 The threats posed by the current extinction crisis are too urgent to be concerned about 59 data exclusivity. In our responses, we follow the structure used by Gereau et al. (2013). 60

61 **1.** Characterization and delimitation of study area

62 Gereau et al. (2013) suggested that we had "inadequate knowledge of the study area, its 63 flora and relevant literature". They justified this by claiming that we did not cite recent 64 literature on the study area, its ecosystems, flora, level of endemism, ecology and history. 65 Gereau et al. go on to list various references they considered important, including the 66 Critical Ecosystem Partnership Fund (2003). However, we did in fact use this database, 67 and it is cited on page six of our paper. Furthermore, we provided numerous references 68 on the Eastern Arc's ecosystems, its flora, endemism, ecology and history of the 69 ecosystems (e.g. Burgess et al. 2007; Fjeldså & Lovett 1997; Lovett 1988, 1993, 1998; 70 Trauth et al. 2005). Whilst there are of course many more references that could be cited,

the objective of our paper was not to provide a comprehensive review of the history of the Eastern Arc biodiversity of hotspot, but to present a timely analysis of the extinction risk of its flora. To the best of our knowledge, additional citations would not have changed our interpretations of results.

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76 Gereau et al. suggest that a lack of adequate context is reflected in our references to the 77 Eastern Arc Mountains as "woefully-understudied", and that this crucially undermines 78 their ability to interpret their findings accurately and objectively". We might debate 79 whether the Eastern Arc can be considered well studied or understudied in comparison to 80 other floras. We suggest that in comparison to the floras of much of the world, including 81 North America, Europe and most temperate biomes, our characterization of the Eastern 82 Arc Flora is wholly accurate. We additionally struggle to understand how this could in 83 any case change our interpretation of results; Gereau et al. remain somewhat vague about 84 this. We also found surprising that Gereau et al. suggest we did not focus on the 85 elevational distribution of extinction risk, as this is one of the key results of our paper, 86 and is clearly referred to in the abstract of the paper. We show that elevation range was 87 the best single predictor of threatened species richness, and could explain up to 42% of 88 threatened plant species richness.

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Gereau et al. also state that the criteria for selection of the 230 Eastern Arc plant species
that we analyzed were unclear, such that "the list cannot be tested nor a comparable list
compiled from other data or by other researchers". We cannot comprehend this statement
as we clearly state that "(w)e retrieved from the IUCN Red List database

94 (www.iucnredlist.org, accessed May 2012), assessment details for all angiosperm species 95 (about 5% of the total flora) that have been evaluated in the region". As for the Eastern 96 Arc, we state that we "also compiled a checklist of the Red-Listed flora within the 97 Eastern Arc forest blocks based upon a thorough literature survey [62,78] and 98 information extracted from the CEPF database (Critical Ecosystem Partnership Fund: 99 http://www.cepf.net, accessed 21st September 2011)". Finally, we include a complete list 100 of the threatened species included in our analyses in Table S2, making their criticism 101 particularly bizarre. We suggest that Gereau and coauthors might benefit from a closer 102 reading of our original paper. 103

104 Gereau et al.'s final criticism in this section is that we did not include the flora of the 105 Taita Hills of Kenya. It was not possible to simply generate a phylogenetic tree for the 106 floras of both Tanzania and Kenya because synonyms make combining published floras exceedingly complex. However, as 12 of the 13 forest plots were in Tanzania, it was not 107 108 clear how this limitation would bias our results on phylogenetic clustering. Further, when 109 exploring predictors of threatened species richness, we included all plots in our analyses, 110 so the criticism of Gereau and colleagues is unjustified here, and we could have easily 111 clarified this point if asked.

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113 2. Limitations and bias of the dataset

114 Gereau et al. suggest that our sample of 581 species that we analyzed for Tanzania

115 (representing all the Red Listed species for the region in the IUCN Red List database, but

116 only ~5% of the total flora of Tasmania, as we acknowledge in our paper) "is not

117 adequate or representative, either phylogenetically or phytogeographically, to address 118 patterns of extinction risk across any regional flora". This is a somewhat surprising 119 criticism of our paper as we state clearly that "(m)ost critically, there is an urgent need for 120 increased effort to evaluate threat status of unassessed species. Currently, only 5% of the 121 Tanzanian flora has been evaluated by the IUCN, and such lack of information could 122 itself pose a significant risk to the flora through under-informed management decisions [57–59]" (cf. last two sentences of the discussion of our paper). We can only conclude 123 124 that Gereau and colleagues must agree with us, or that perhaps they did not read to the 125 end of our paper.

127 Despite this admitted paucity of data, we argue strongly that we cannot afford to wait for 128 comprehensive data on extinction risks to become available before attempting to make 129 management decision. It is imperative that we draw attention now to the extinction crisis 130 that is impacting global hotspots of biodiversity. As we note above, it is increasingly 131 likely that we are on the verge of a sixth mass extinction event, and that impacts might be 132 particularly severe in the tropics (Vamosi & Vamosi 2008). In the Eastern Arc there is 133 already a growing body of work suggesting that the fauna and flora of the region are 134 severely threatened (Balmford et al. 2001a,b; Brooks et al. 2002; Burgess et al. 2004, 135 2007; Hall et al. 2009), and there has been at least one documented extinction 136 (Platypterocarpus tanganyikensis) (Lovett & Stuart 2001). Eastern Africa is one of the 137 most vulnerable regions to climate change in Africa (Trauth et al. 2005; Olwoch et al. 138 2007), which is considered a major driver of species to extinction (Willis et al. 2008). 139 More research in the region is urgently needed. We conducted the first study of the

phylogenetic structure of extinction risk in the region (Yessoufou et al. 2012), andencourage further research to be focused here.

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143 We used the best available data in our analysis. Of course we agree that more and better 144 quality data would be beneficial. However, the concerns raised by Gereau and colleagues 145 on the validity of our results perhaps reflect a poor understanding of our analysis and 146 phylogenetic methods in general. Gereau et al. suggest that "species are selected for (Red 147 List) assessment primarily due to other factors including rarity, restricted distribution, 148 extreme habitat specialization, and human exploitation (Gereau et al. 2009)", and that 149 "this creates an *a priori* bias toward inclusion on the Red List in the threatened 150 categories". This bias is a strong possibility, but our analyses indicated that vulnerable 151 species were more clustered than expected by chance. An operational bias towards 152 including species in the 'Vulnerable' category would not influence phylogenetic 153 clustering (there would simply be more vulnerable species included in the analysis). 154 What might drive phylogenetic clustering for vulnerable species, however, is shared traits 155 that confer sensitivity to particular extinction drivers, and/or taxonomic bias in the 156 assessment of Red Listed species, which we discuss in depth, but Gereau and colleagues 157 oddly dismiss.

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Gereau and colleagues also highlighted that "in a series of seven Red List workshops
conducted between 2006 and 2013, the Eastern African Plant Red List Authority
(EAPRLA) has reassessed many of these species under version 3.1 and has moved many
of them into higher threat categories or downgraded them to Near Threatened or Least

163 Concern". We do not find this result at all surprising, and we firmly support the 164 extremely valuable and ongoing efforts of these assessments. Over time, we would 165 (unfortunately) predict many susceptible species would move up the Red List categories, 166 and that assessments based on different criteria might place species in different 167 categories. We suggest that new analyses of extinction risks should be undertaken as new 168 data becomes available, but that this should not detract from the importance of 169 conducting research now, just as future Red List assessments do not devalue existing Red 170 List efforts.

172 3. Improvement of the dataset

173 Finally, Gereau and colleagues call upon us to use updated Red List assessments, but 174 these were still not available as of January 2014, and thus we do not find such 175 suggestions particularly helpful. Gereau et al. indicated that they had a checklist of 1142 176 species, subspecies and varieties for Eastern Arc flora using www.tropicos.org, and that 177 all these species have threat status on www.iucnredlistorg as for April 2013 (we 178 published our work in 2012). The first two authors of this paper met with Gereau in 179 January 2014, where it was confirmed that the data are still in process and not yet 180 available for public use. That the authors' claim that they downloaded data on the new 181 threat status for 1142 taxa in April 2013 is thus questionable. It might however suggest 182 that they have access to unpublished IUCN data. We would urge them to make these data 183 available. Although we are not able to verify these data, the authors state that of species 184 that are threatened, 14% = CR, 45% = EN and 41% = VU, a distribution they describe 185 somewhat disingenuously as relatively balanced, and thus suggest that "any statistical

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groupings of families based on the admixture of assessments performed under versions
2.3 and 3.1 are unlikely to have phylogenetic relevance". We are not entirely clear as to
their meaning, but if their intention was to imply that it is unlikely that there will be
similar phylogenetic structure in the new threat status (i.e. that revealed under version
3.1), we do not see any logical link. There is growing evidence that extinction risk is
phylogenetically non-random (e.g. Purvis 2008; Davies et al. 2011), and we might expect
this pattern to become more pronounced as better data becomes available.

194 4. Conclusion

195 In summary, we reaffirm that our methods were robust, transparent and reproducible. We 196 do not see any justification for the criticism levelled at our analysis by Gereau and 197 colleagues, and perhaps they reveal a lack of understanding of phylogenetic methods. Gereau et al. call upon us to use more recent Red List assessment data, but they were not 198 199 able to provide us with access; we therefore find this suggestion particularly unhelpful. 200 Nonetheless, I am sure we agree with Gereau and colleagues that new analyses will be 201 valuable as and when new data become available, a point we made clearly in our original 202 manuscript.

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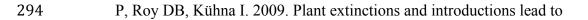
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