Scientific publication of georeferenced molecular data as an adequate guide to delimit the range of Korean *Hynobius* salamanders through citizen science

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Abstract. Despite the importance of clearly assessing the distribution boundaries of species, it is not possible for scientists to acquire genetic information and conduct molecular analysis for all populations. Consequently, citizen science is of increasing importance for large scale data collection. In this study, we described the range boundaries of the four *Hynobius* species occurring in Korea based on genetic identification and refined their distribution through citizen science data. The genetic identification of individuals was extracted from the literature, while the citizen science data were extracted from iNaturalist through GBIF. Distribution boundary lines were drawn from the genetic data and consistency with citizen science datapoints was assessed through a comparative analysis with the points found beyond the established boundary lines. Depending on the species, 1.43 to 25.00% of the observations extracted from the citizen science data were located beyond the boundaries suggested by the molecular analyses, with average distances ranging from 3.51 ± 2.97 to 51.47 ± 30.87 km (mean ± SD). We considered these variations negligible in the view of the whole distribution of these species. In general, the distributions extracted from iNaturalist were accurate and adequately representative of the distribution of the species, with the exception of the recently split *H. quelpaertensis*. Additionally, citizen science data highlighted the absence of gaps in the distribution of these species. In conclusion, given the good accuracy of citizen science data, we recommend the publication of molecular based data so that citizen science platforms could help define accurately the range of species for which data is missing or outdated.

Keywords. *Hynobius*, range description, population presence, public engagement, iNaturalist, Republic of Korea, North East Asia, citizen science.

INTRODUCTION

Despite a newly renewed interest in citizen science over the last decades (Reed, 2008; Crain et al., 2014; Jordan et al., 2015), citizen science has been playing a major role in the advancement of natural and ecological sciences over the last centuries (Gray et al., 2017; McKinley et al., 2017), with demonstrated benefit to biodiversity conservation (Newman et al., 2012, 2017; McKinley et al., 2017). Because of the ubiquitous impact of human activities on biodiversity (Pimm and Raven, 2000; Steffen et al., 2011) and the species extinction rate, which could be a thousand

times higher with respect to pre-human levels (Pimm et al., 1995; Scheffers et al., 2012), large-scale data collection is becoming more and more urgent. Since one of the strengths of citizen science is the quantity of datapoints collectable over a short period of time (Lintott et al., 2010), relying on this discipline to create conservation policies for the remaining species, through ever more convenient and accurate technologies (Sullivan et al., 2009; Joppa et al., 2012; Bowser et al., 2014) is therefore one of the potential ways to breach the wave of destruction.

Citizen science involvement takes several forms and it is assessed to be extremely efficient when conducted with clear protocols and objectives (Shirk et al., 2012; Gray et al., 2017), or combined with molecular analysis (Silvertown et al., 2011). Conversely, not everyone is satisfied by the quality of data collected through citizen science, as discussed by Cohn (2008), Conrad and Hilchey (2011) and Dickinson et al. (2010). It is however impossible for a single researcher to conduct large scale field surveys on the totality of a species' range. For instance, it took four years of field work to describe the comparatively small range of the Suweon Treefrog (*Dryophytes suweonensis*), a non-cryptic and highly detectable species, via a study conducted almost every day of the species' breeding season (Borzée et al., 2017). In comparison, as of 1 February 2018, the totality of the species' range, minus a single location, is available from the citizen science website iNaturalist (https://www.inaturalist.org). The species used as an example is comparatively well studied (Borzée, 2018) but there are other well-studied species which geographic ranges are poorly described (Jetz et al., 2012; Meyer et al., 2015). Additionally, ranges are dynamic and need regular updates, as they can show geographic shifts in response to climate change (Chen et al., 2011).

Given that technologies become increasingly user-friendly and convenient for citizen science, an increase in the quality and resolution of the data uploaded is expected. For instance, it is common to upload datapoints directly from the observation site, including GPS coordinates at the cm resolution, pictures and other metadata. A rising platform for the upload of observations is iNaturalist (www.inaturalist.org), and the platform success in recording species is demonstrated by the presence of data for about 75% of bird species and 35% of amphibian species (as of 1 February 2018). The particularity of iNaturalist is that, despite anyone being able to upload any observation, classified as "Need ID" if fulfilling minimum requirements, the observations are then cross-validated to obtain a "research grade". This requires the ID to be confirmed by at least two-thirds of the identifiers (i.e. anyone interested in confirming or reassigning the species/genera/clade ID of the observation). Therefore, the ID provided does not reflect the knowledge of a single person but that of the community, and therefore of a meta-brain, including scientist expert in their field (Joppa et al., 2012; He and Wiggins, 2015).

Here, we first defined the range of the four *Hynobius* salamander species occurring in Korea through traditional molecular tools, and then refined range and presence within ranges through the platform iNaturalist. The four species are *Hynobius leechii*, *H. quelpaertensis*, *H. yangi* and *H. unisacculus*. The secondary purpose of this work was to highlight the accuracy of citizen science in a region where it is still comparatively under-used (Roh et al., 2014).

MATERIALS AND METHODS

Species

Four of the described *Hynobius* species are present in the Republic of Korea, and three of these species are endemic (Min et al., 2016). *Hynobius leechii* is widespread on the Korean peninsula and North-East China, while *H. quelpaertensis*, *H. yangi* and *H. unisacculus* are restricted to the southern coastal area of the peninsula (Yang et al., 1997, 2001, 2005; Kim et al., 2003; Min et al., 2016). This coastal area is also populated by three candidate species (Baek et al., 2011a, 2011b), although these were not included in our analyses as the clades have not yet been given the species status. The species breed between February and May, both in natural streams and modified landscapes in the form of rice paddies. They are locally abundant species present under vegetation and litter of forested hills outside of the breeding season.

Molecular assessment

The *Hynobius* sequences used here were extracted from the literature (Kim et al., 2003; Yang et al., 2005, 2007; Baek et al., 2011a, 2011b; Min et al., 2016). Each data point for which molecular identification was available, based on any gene sequence, was incorporated in the dataset, resulting on N = 270 for molecular-based species assignment.

Citizen science data

Prior to data download, the citizen science data on iNaturalist (https://www.inaturalist.org) were curated on 15 October 2017 for obvious errors. A query for observations was created with the filters "*Hynobius*" and "South Korea", and a few observations were flagged as "captive" when coming from zoos or private collections, based on GPS coordinates. The citizen science datapoints were then downloaded through GBIF. org (https://doi.org/10.15468/dl.tb0v6j; accessed 5 February 2018), filtered for *Hynobius* observations in the Republic of

Korea and from iNaturalist only, dated up to 15 October 2017. Only the observations reaching "Research Grade" on iNaturalist are transferred to GBIF, and the research grade can only be reached when more than two-thirds of the identifiers agree on a taxon. The original download included 852 datapoints, but all the observations with known issues flagged by GBIF were removed, and duplicated records were deleted. Additionally, only datapoints geolocated with an accuracy of at least three decimal places (100 m resolution) were maintained. Finally, to avoid spatial autocorrelation, any point within 200 m of another point from the same dataset was deleted, in correspondence to the core range of several salamander species (Semlitsch, 1998; Semlitsch and Bodie, 2003). This selection resulted in 468 datapoints, collected between 18 April 2005 and 26 August 2017.

Spatial and statistical analysis

The two datasets where then uploaded on ArcMap 10.5 (Environmental Systems Resource Institute, Redlands, California, USA) and each species was colour coded (Fig. 1). Based on the genetic analyses data, we drew lines joining the border localities of each species. For localities close to the seashore, border lines which guaranteed the smallest distance between the locality and the coast were drawn. Given the geographically representative sampling, in relation to the low vagility of the species and of salamanders in general (Semlitsch, 1998; Semlitsch and Bodie, 2003), we can consider the drawn lines as adequate estimates of each species' range. In addition, since no large-scale hybrid zones are expected between the species in this study (Baek et al., 2011a; Min et al., 2016), we excluded the possibility of a significant misidentifications because of cytonuclear disequilibrium.

Once the boundary of the four species were established, here referred to as "distribution boundary lines", we counted for each species the number of localities identified by citizen science which were external to the distribution boundary lines and measured the distance between the focal locality and the closest distribution boundary line. We did not include datapoints located between DNA identified localities and the sea shore, as not all islands were genetically tested.

The presence points within the species boundary lines were then investigated in GIS through the distance tool for clear gaps in distribution. For this purpose, a gap was defined as one tenth of the longest diagonal crossing the range of the species, here limited to the Republic of Korea.

The distance between datapoints and distribution boundary lines was then statistically tested for differences between species. As the data was not normally distributed for each cell of the design (observation of Q-Q plots), and there were no significant correlations between the four species and distance to the boundary lines (Pearson Correlation; $r = 0.09$, $n = 27$, $P = 0.663$), we used an independent-samples Kruskal-Wallis test to assess the relationship among the distances between datapoints and distribution boundary lines. The statistical analyses were performed with SPSS v21.0 (SPSS, Inc., Chicago, USA).

RESULTS

The DNA based location map used to draw the distribution boundary lines included 270 samples (Fig. 1), divided into 164 datapoints for *H. leechii* (Fig. 2), 45 for *H. quelpaertensis* (Fig. 3), 19 for *H. unisacculus* (Fig. 4) and 43 for *H. yangi* (Fig. 5). The citizen science data included 468 samples, distributed into 350 datapoints for *H. leechii*, 92 for *H. quelpaertensis*, 12 for *H. unisacculus* and 14 for *H. yangi*. There were 27 (13.28%) citizen science datapoints that were external to the distribution boundary lines: 5 for *H. leechii* (1.43% of datapoints), 18 for *H. quelpaertensis* (19.57%), 3 for *H. unisacculus* (25.00%) and 1 for *H. yangi* (7.14%).
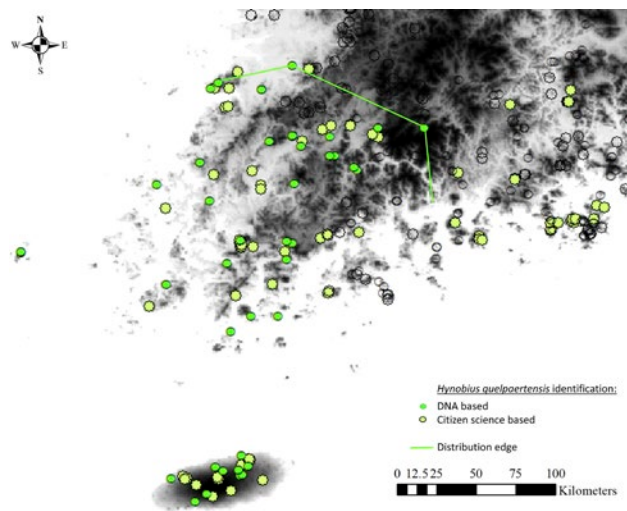
We did not find any gap in population presence that was higher than one tenth of the longest diagonal crossing the range of the species within the Republic of Korea. The average distance for datapoints beyond the distribution boundary lines was 37.17 ± 32.54 km (mean ± SD). *H. unisacculus* displayed the shortest average distance (3.51 ± 2.97; n = 3), followed by *H. leechii* (4.75 ± 2.99;
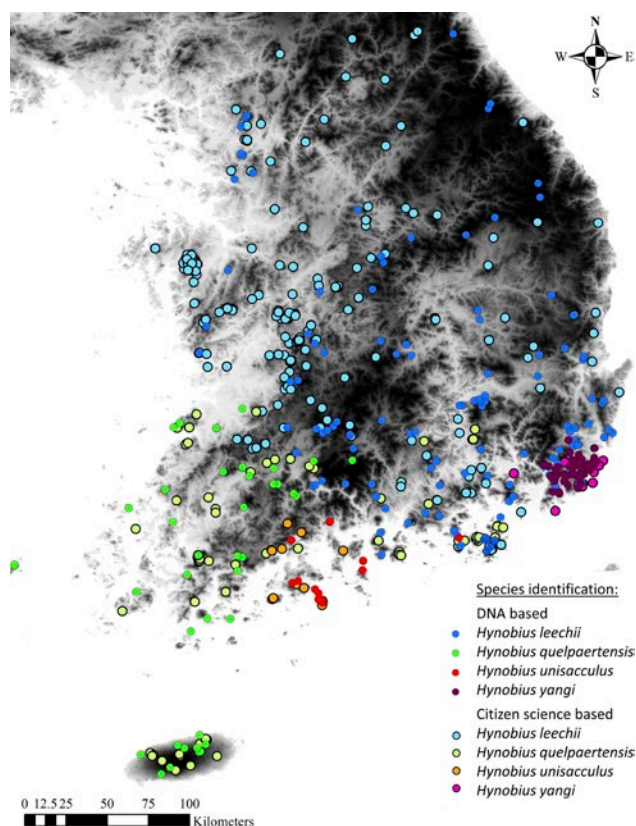
Fig. 1. Distribution of *Hynobius* spp. in the Republic of Korea. The map includes *H. leechii*, *H. quelpaertensis*, *H. unisacculus* and *H. yangi* data extracted from both mtDNA and citizen science (iNaturalist through GBIF; doi.org/10.15468/dl.tb0v6j).
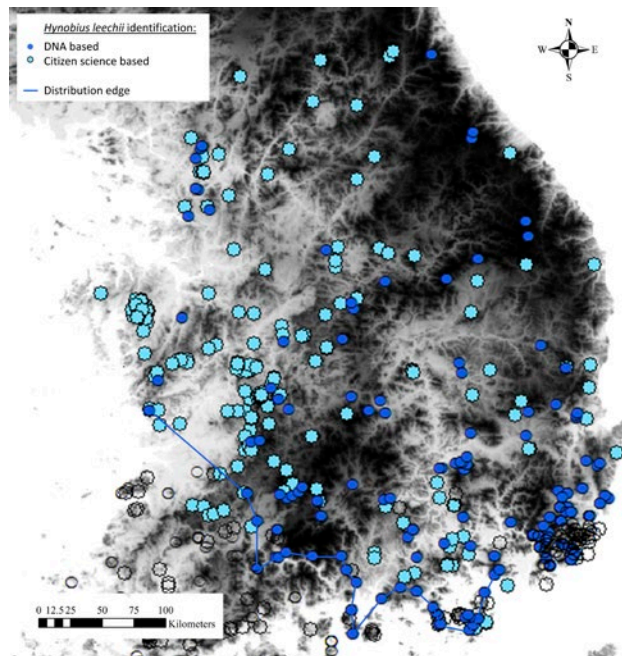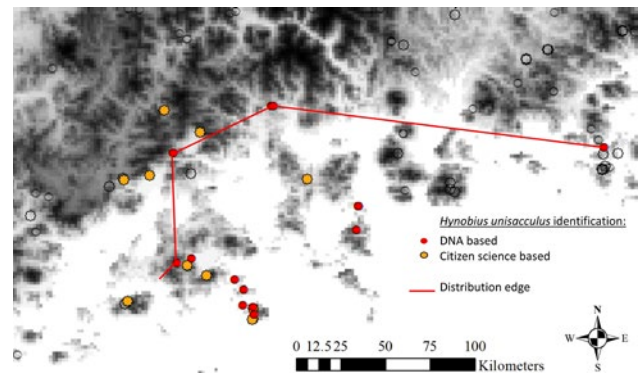
Fig. 2. Distribution of *Hynobius leechii* in the Republic of Korea. The map includes both mtDNA and citizen science datapoints (iNaturalist through GBIF; doi.org/10.15468/dl.tb0v6j), with the distribution boundary lines drawn from mtDNA data.

Fig. 4. Distribution of *Hynobius unisacculus* in the Republic of Korea. The map includes both mtDNA and citizen science datapoints (iNaturalist through GBIF; doi.org/10.15468/dl.tb0v6j), with the distribution boundary lines drawn from mtDNA data.
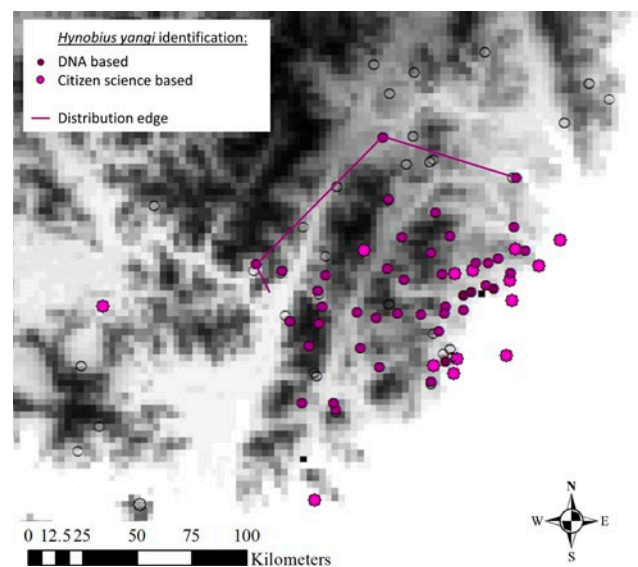

Fig. 3. Distribution of *Hynobius quelpaertensis* in the Republic of Korea. The map includes both mtDNA and citizen science datapoints (iNaturalist through GBIF; doi.org/10.15468/dl.tb0v6j), with the distribution boundary lines drawn from mtDNA data.
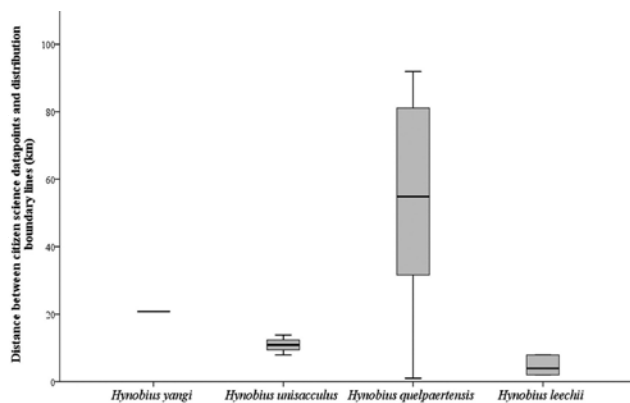

Fig. 5. Distribution of *Hynobius yangi* in the Republic of Korea. The map includes both mtDNA and citizen science datapoints (iNaturalist through GBIF; doi.org/10.15468/dl.tb0v6j), with the distribution boundary lines drawn from mtDNA data.

tribution boundary lines varied between species was significant (H = 1.49, df = 3, n = 27, P = 0.009). The largest divergence between distribution boundary lines and citizen science observation was observed for *H. quelpaertensis* (Fig. 6).

DISCUSSION

Through the integration of citizen science-based data collection following the guides provided by molecular tools, we refined the distribution of the four Korean

n = 5), by *H. yangi* (20.67 km; n = 1) and finally by *H. quelpaertensis* (51.47 ± 30.87; n = 18). The independent-samples Kruskal-Wallis test used to assess whether the distance between citizen science datapoints and the dis-

Fig. 6. Discrepancies between citizen science and mtDNA based range description for Korean *Hynobius*. The data presented here is the distance between the citizen science datapoints and the distribution boundary lines, for each Korean *Hynobius* species separately. The distance is significantly different between species.

as further genetic testing may narrow down the width of contact zones between species. Finally, we confirm that when citizen science data collection follows clear landmarks set by molecular analyses, the results provided are clear and accurate. However, we need to emphasize that citizen science is most efficient when conducted within a specified framework (Shirk et al., 2012; Gray et al., 2017). Our work follows the steps of other citizen science projects focused on amphibians (e.g., Mossman et al., 1998; Corn et al., 2000; Roh et al., 2014) and we recommend the broader development of this type of projects. If specific projects were set up for the distribution of *Hynobius*, instead of the opportunistic data collected here, even more precise results would be expected.

Regarding the discrepancy points between the two methods, the largest majority was located within the distribution range of *H. quelpaertensis* before the species was split into *H. quelpaertensis* and *H. unisacculus* (Min et al., 2016). Therefore, once these cases removed, only nine discrepancy points remained, highlighting the impact of recent taxonomic modifications onto natural science enthusiasts. Eventually, the combination of knowledgeable nature enthusiasts and the verification method for "Research Grade" on iNaturalist provides clear distribution patterns. Interestingly, the distribution patterns drawn here from citizen science are more accurate than the ones extracted from the red list of the International Union for Conservation of Nature (http://www.iucn-redlist.org; as of February 2018). We therefore recommend the use of citizen science platforms, such as iNaturalist, to assess the distribution of species that have not been assessed yet, or those in need of an updates, such as the Korean *Hynobius* species.

Our results however call for a resolution of the taxonomic question regarding the overlapping ranges and potential hybridisation between the different Korean *Hynobius* clades. For instance, the known subclades within *H. leechii*, geographically located between the distribution of *H. unisacculus* and *H. yangi* (Baek et al., 2011a, 2011b; Min et al., 2016) could not be used in this study. However, the taxonomic resolutions are also expected to cause confusion in the identification of *Hynobius* individuals by nature enthusiast when and if new species are described. For this reason, the involvement of experts on citizen science platforms is essential and the resulting general education, together with the development of interests, is one of the best ways to reach conservation purposes on the long term (Cooper et al., 2007; Marshall et al., 2012).

An important point that also needs to be raised here is that citizen science accuracy is directly related to the taxon studied (Cohn, 2008; Crall et al., 2011; Gardiner et al., 2012). The identification of *Hynobius* sp. based on morphology is not considered easy (Kim et al., 2003), even for experienced researchers, and the molecular identification available was the most important contributing factor for the refinement of the ranges presented here. Additionally, a small group of dedicated users on the citizen science platform could make a significant difference. Most observations used for this study were confirmed by a group of dedicated users, allowing the observations to reach the "Research Grade", or oppositely, downgraded to the genus identification because of disagreements with the original observer. These people are therefore important in their own rights for the accumulation of knowledge on species, as already observed by Rotman et al. (2012) and Johnston et al. (2017).

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