Fantastic beasts and how to diversify them

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Despite their secrecy, fantastic beasts are oftentimes noticed by muggles. Their diversity, however, was never subject of any study in order to understand what could have driven it. At least two groups of creatures show that both historical and environmental aspects played role on these organisms’ lineages’ splitting events, leading to their current distribution on the globe. Additionally, nonspecialist readers that enjoy Harry Potter culture might become interested in the topic and, as such, fictional content can represent an innovative tool of science outreach to introduce evolutionary biology and biogeography concepts to the general public.

WHERE AND WHO ARE THEY?

Not even special clauses (Scamander, 2001) prevented muggles of noticing fantastic beasts among them. They are part of our days probably since before we started creating tales about them (d’Huy, 2013). Present in all continents, except Antarctica, magical creatures occupy an unequal variety of niches, from herbivorous forms to fire-eating beasts (Scamander, 2001). All the main differences described for such creatures may reflect not just local traditions or modifications from oral stories, but actual lineage branching events (e.g., Hamilton et al., 2015).

Among such beasts, there are some groups in which well-known diversification processes can be exemplified, namely a clade of hominoid-related beasts, and a clade of insect-related creatures, both currently spread in the European and North American continents (Fig. 1; topology follows Gerelle et al., 2016). Basically, the appearance of natural barriers, as well as opportunistic exploitation of diverse ecological niches, could be the main causes explaining where such fantastic creatures currently inhabit (i.e., their geographic distribution); this would be in spite of the common explanation of climate change driving biodiversity dynamics (e.g., Janis, 1993; Alroy et al., 2000).

INSECT-RELATED HUMANOID BEASTS

According to Gerelle et al. (2016), Fairies, Imps, Pixies, Grindylows, and Doxies form the sister clade to butterflies (crown-Lepidoptera), making them a sort of ‘lepidopteran-like’ beasts. Despite being phylogenetically related to insects, all creatures in this clade possess humanoid traits, consisting of a remarkable case of evolutionary convergence. In addition,
the absence of wings in Grindylows and Imps is probably a case of reversion to the apterous plesiomorphic condition of insects (i.e., the insect lineage was originally wingless; Kukalová-Peck, 1991).

Figure 1. Current distribution of the groups discussed in the text with their phylogenetic relationships, based on Gerelle et al. (2016).

It is plausible to assume that the split between crown lepidopterans and lepidopteran-like fantastic beasts occurred back in the earliest Jurassic (Hettangian) of Britain (circa 200 Ma, i.e., 200 million years ago), as this is where the oldest fossil lepidopteran comes from (Whalley, 1986; Schachat & Gibbs, 2016). At that time, continents were united in a single land mass, called Pangaea, which would have allowed some populations of ‘Doxy-like’ beasts to migrate from British areas to what is now North America (Fig. 2A). This would explain why Doxies are present in both continents, but the remaining representatives of the group are not, demonstrating another case of disjunct distribution, as occurs, for example, with ratite birds, some pleurodiran turtles and flowering plants (Wen, 1999; de Queiroz, 2005). Otherwise, Doxies might have later migrated to North America through land continuities such as the De Geer Bridge (McKenna, 1975).
Grindylows branched early in this clade’s evolutionary history, “soon” after the Doxy lineage separated, likely dating to the Toarcian (late Early Jurassic; circa 180 to 175 Ma), when England was flooded by marine transgressions (Wignall, 1991). The populations occupying the deluged area probably vanished, while the ones remaining at its borders survived and later invaded the aquatic environment (organisms closely related to modern Grindylows). This is somewhat akin to the Pleistocene refuge hypothesis of Neotropical diversification (e.g., Vanzolini & Williams, 1981; Garzón-Orduña et al., 2014), but instead of forest retraction due to climate fluctuation, areas underwent fragmentation because of marine water incursion.

Like the other splitting events, Imps and Pixies diverged mainly due to historical causes. Both beasts share morphological and reproductive similarities (Scamander, 2001). Pixies are restricted to Cornwall, whereas Imps are distributed throughout Britain, living near river banks. In Cornwall, the River Tamar largely represents the boundary with the rest of England (Carey, 1911). The rise of sea-level (similar to that of the last interglacial period; Rohling et al., 2008), could have flooded the river region, isolating populations that lived near it (like modern Imps do). On the Cornish side of the river, a small population would have differentiated, preventing gene flow after the restoration of sea levels (Fig. 3). Despite

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**Figure 2.** Probable location of ancestors of (A) the lepidopteran-like beasts during the Hettangian (earliest Jurassic) of Britain, with posterior migration to North America, and (B) hominoid-related beasts, originating in Central Europe during the Paleogene, with subsequent migration to northern Europe and North America. Maps modified from the Paleobiology Database (PBDB; [www.paleobiodb.org](http://www.paleobiodb.org)).
capable of flying (and thus crossing the river), Pixies are not known to form hybrids with Imps.

According to folklore, Fairies are exclusively British creatures (Briggs, 1967; Silver, 1999), but the lack of information regarding ecological preferences (Scamander, 2001), as well as fossils, hinder speculation about their evolutionary history.

**Figure 3.** (A) Geographical distribution of ‘Pixie + Imp’ ancestor in southwestern England. (B) Vicariant event isolating two populations and preventing gene flow. (C) Current distribution of Imps and Pixies, the latter being restricted to Cornwall.

**HOMINOID-RELATED BEASTS**

It is likely that, instead of historical events causing populations to split, ecological constraints were mainly responsible for the current diversity of hominoid-related beasts. The first branching lineage to be analyzed is the clade formed by Gnomes, Red Caps, and Leprechauns. As hominoid-related beasts, the group probably originated at least before the Miocene (a period spanning roughly 23 to 5 Ma; Stevens et al., 2013) and later invaded European landmasses. The burrowing habit of Gnomes most likely resulted of selective pressure due to the predation by Jarveys, a large ferret-like beast present both in Europe and North America. As such, the plesiomorphic (i.e., ancestral) condition of the group was a non-burrowing habit, which might have evolved independently in Red Caps too (Scamander, 2001). The occurrence of Gnomes in both
Europe and North America depicts again a case of disjunct distribution, but the processes that drove such pattern probably differ from that of the Doxy. Rather than a vicariant event resulting from the split of Laurasia, climatological events could have created a passage that allowed them to reach North America (e.g., the Thulean Bridge; Brikiatis, 2014), as exemplified by marine diatoms during the Eocene (Bijl et al., 2013). As Jarveys intensively preyed on Gnomes, some populations likely sheltered in tunnels and acted as scavengers, feeding on the blood shed by their kin (similar to modern Red Caps).

In turn, Leprechauns likely represent a more recent lineage that migrated to Britain at first (still connected to the European mainland; Erlingsson, 2004) and then reached Ireland, probably across a land bridge before humans (Edwards & Brooks, 2008; Bower, 2016), being later included in Irish folklore (Winberry, 1976; Koch, 2006). However, Leprechauns (as all the exemplified beasts) lack a fossil record, which complicates the understanding of how and when such groups colonized the areas they currently live in (Crottini et al., 2012).

The other clade of hominoid-related beasts comprises Erklings, Trolls and Pogrebins, distributed in northern Europe (Fig. 4A). Modern representatives of the group are known to feed on flesh (especially human; Scamander, 2001), which evokes whether such beasts arose earlier or later than the Homo arrival to Europe (ca. 1.4–1.8 Ma; Parfitt et al., 2005; Toro-Moyano et al., 2013). Probably spread all over Europe originally, the competition for the same kind of resources (mostly raw flesh) with a distantly related clade

Figure 4. (A) Probable ancient distribution of Erklings, Trolls, and Pogrebins in Europe. (B) Arrival of Homo species in Europe, ca. 1.5 Ma. (C) Demise of original populations of fantastic creatures, showing their current relictual distribution in Europe.
(Homo species) may have constrained the range of the group (mainly inhabiting densely vegetated zones today), extinguishing ancient populations more widely distributed. This last example analogously illustrates a case (e.g., Silvestro et al., 2015) in which the later arrival of a phylogenetically distant (but ecologically similar) clade to an area triggered diversification shifts onto the previous occupiers, as well as the probable extinction of some forms.

**BIOGEOGRAPHICAL HISTORY OF FANTASTIC BEASTS**

In order to verify if there is a regionalization among the fantastic biota, their geographical distribution was compiled from Scamander (2001) and interpreted based on (i) six distinct geographical realms from Wallace (1876), and (ii) the recent division of Holt et al. (2013) in 13 domains. Each creature was plotted against the realm in a simple area vs. taxa matrix (e.g., Souza, 2005), scoring (0) if absent, and (1) if present in a determined locality. This gives us a diagram, called ‘area cladogram’, with the biogeographic history of the groups.

The area cladogram obtained with Wallace’s six biogeographic domains (Wallace, 1876) is partially consistent with the biogeographical history of the southern hemisphere (i.e., mostly Gondwanan-derived land masses), according to patterns observed in some plants and animals (e.g., Sanmartín & Ronquist, 2004), in which the Oriental biota (i.e., mainly Indian) is the sister group to the remaining areas (Fig. 5A). This could be reasonably expected, since India was the first land mass to branch in Gondwana breakup geological sequence (Barron, 1987; McLoughlin, 2001). The relationships of African, South American and Australian areas however disagree with Sanmartín & Ronquist (2004), in which it was expected that South American and Australian biotas were more closely related to one another than to the African biota. This result could imply a Pangean origin for these fantastic beasts, with subsequent vicariant events. However, this hierarchical pattern following the breakup sequence of Gondwana could also be a kind of ‘vicariance-mimicking’ phenomenon affecting the cladogram area topology (see Upchurch et al., 2002). Until fossils of fantastic beasts are found, knowledge about their past distribution remains obscured. On the other hand, when plotted according to the biogeographic realms of Holt et al. (2013) the Gondwanan-derived continents do not present such hierarchical relationship (Fig. 5B), resulting in a pectinate (i.e., comb-like) conformation within the area cladogram. Both results could also be influenced by the lack of data about the fantastic beasts, which may not follow the pattern of ordinary ones.

In sum, due to the incompatible results for Gondwanan continents, the fantastic biota could have had a hybrid, composed origin (Amorim, 2012), with both autochthonous and allochthonous elements. The Palearctic and Nearctic realms were recovered together in both analyses, although both regions are inhabited by most of the beasts, which could have biased the result. Despite of the apparently unarguable Laurasian distribution of such beasts, it has been historically difficult to depict the continents’ biogeographical scenario (Sanmartín et al., 2001; Wildman et al., 2007).
FICTION AS SCIENCE OUTREACH

Biogeography is an integrative science combining different sources of evidence to understand what caused organisms to be distributed the way they presently are – or were in the geological past (Lomolino et al., 2010). Despite of its relevance, the public knowledge (i.e., outside the academic environment) concerning this research area seems debilitated, even with the timid increase in electronic dissemination (Ladle, 2008). Present in both evolutionary approaches of Darwin (1859) and Wallace (1876), the spatial distribution of organisms offers an unparalleled tool to stimulate students to think about evolution and natural history (Rosenau, 2012; Allchin, 2014) – and not just to understand evolution, but to accept it as well (Lombrozo et al., 2008).

In this context, the teaching of biogeography (and evolution in general) could benefit from the use of fictional organisms with “real” distributions around the globe. Presenting the continents’ past and present arrangement, allied with the localities inhabited by the beasts and possible disjunction events, in a kind of inquiry-based approach (e.g., Robbins & Roy, 2007) would instigate students to formulate their own hypotheses. This, in turn, could lead them to more easily assimilate

Figure 5. Area cladograms obtained based on (A) Wallace’s zones (1876), and (B) Holt et al. (2013) new zones, subdividing those proposed by Wallace.
all these concepts. The specific use of the popular *Fantastic Beasts* of the *Harry Potter* franchise to canalize this is supported mostly by the interest of younger audiences (under 25 years old) in the recently released spin-off movie (over 50%; Lang, 2016). Actually, scientific scenarios were already present on several episodes from the *Harry Potter* books (e.g., Rowling, 1997; 1998; 1999; 2005), providing a larger background for people to get involved.

Moreover, this would not be the first time that a fictional universe was considered to engage younger people on scientific activities (e.g., Roque, 2016). J.K. Rowling’s fantasy novels are already proven as a promising and innovative background for scientific experiments (e.g., Vezzali et al., 2014). As such, the present work is hopefully in a good position to arouse at least a spark of interest among students to understand what made our beasts – fantastic or otherwise – to live where they do.

**REFERENCES**


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