



World Scientific News

WSN 57 (2016) 664-673

EISSN 2392-2192

Trying to solve current issues with invertebrate taxonomy – the conceptual web-based application

Jarosław Kur^{1,*}, Monika Mioduchowska², Matija Petković³

¹Empty Spaces Research, 14b/3 Miłosza Str., 83-000 Pruszcz Gdanski, Poland

²Department of Genetics, University of Gdansk, 59 Wita Stwosza Str., 80-308 Gdansk, Poland

³Institute of Zoology, Faculty of Biology, University of Belgrade, Studentski trg 3, 11000 Belgrade, Serbia

*E-mail address: jarek.kur@gmail.com

ABSTRACT

The information considering taxonomy of invertebrates is mostly comprised of scientific articles and few softwares which are comprehensible only for the specialists of a narrow field. Till now, new invertebrates species are being described on a daily basis by a means of morphological and molecular data. Emergence of comprehensive database which is updated regularly eases access to much more needed information. Any kind of means of identification by non-specialists are most welcome. The concept of integrative taxonomy is not new but the one proposed in our work idea of combination both morphology and DNA dates in web-based application which will be available for everyone, not only for specialists in this field, seems to be an invaluable. This is a conceptual multi platform web application based on a single determination step for each individual to the species level identification.

Keywords: invertebrate taxonomy; species identification; DNA barcoding; web-based application

1. INTRODUCTION

Taxonomy as “science” which originated in Greek hundred years BC. First known medical plant illustrations have been made about 1500 BC (Manktelow 2010). Generally, this

“old profession” was a part of all biological-medical research and is applied to different fields of studies (Tautz 2003).

The exact definition of taxonomy varies from source to source (Wilkins 2011). As points of reference, definitions of taxonomy were presented by Walker et al. (1988), Wheeler (2004), Lawrence (2005), Judd et al. (2007), Kirk et al. (2008) and Simpson (2010). Simply, it is the theory and the practice of grouping individuals into species, arranging species into larger groups, and giving those group names, thus producing a classification (Judd et al. 2007). Moreover, taxonomy is a part of the systematic study, similar to the identification and nomenclature of organisms (Wilkins 2011).

Nowadays taxonomy is divided into prelinnaean taxonomy – “traditional morphological nomenclature” system and postlinnaean taxonomy – most used morphological and molecular characters. However, the last decade is strongly influenced also by the Phylocode system (Manktelow 2010).

Linnaeus had introduced a binomial naming system about 1750 (Linnaeus 1753) and now the rules have been established for classifications, names and identification for all of biological sciences. The binomial naming system is very helpful in avoiding errors with descriptions or use same/similar names for describing more than one species.

Taxonomy becomes the science of defining groups of biological organisms on basic characteristics and giving name to the group. Organisms are grouped together into taxa (singular: taxon) and these groups are given a taxonomic rank; groups can be aggregated to form a super group of higher rank, thus creating a hierarchy (Judd et al. 2007, Simpson 2010).

In past two terms “alpha taxonomy” and “beta taxonomy” were introduced. Alpha was focused on the species level, beta described the classification of ranks higher than the species (Mayr 1968). Finally, it was introduced the term of macrotaxonomy for higher ranks than the species and microtaxonomy for practical and theoretical problems that are referred to as the species problem (Mayr 1982).

From 19th century the taxonomy rules were established and they are monitored by scientists from mentioned commission. In 1895 the International Commission on Zoological Nomenclature created the *International Code of Zoological Nomenclature* (see amendment in 2012 on electronic publications <http://www.iczn.org/node/40407>).

The amount of effort needed to determine one individual varies significantly between taxa. Size of animals is one of the factors that can remarkably contribute, or in case of small and fragile specimens, extremely complicate preparation of a material itself. Some animals do not demand any preparation while others, usually need some sort of treatment, for example, cleaning of exoskeleton from soft tissues and his enlightenment for microscopy. Number and stability of taxonomic characters also vary significantly. From Diplopods where size and shape of gonopods is main and very stable character to the Amphipods where there are more than 100 characters, some countable, other measurable and some regarding shape, which are highly variable and are used in combination.

There are a number of databases which are useful in the taxonomy of animals like www.faunaeur.org, and other relevant online databases within the Kingdom Animalia http://www.faunaeur.org/external_databases.php, however, they are not connected to GenBank <https://www.ncbi.nlm.nih.gov/genbank/>. The Linnaean system has progressed to a system of modern biological classification based on the evolutionary relationships between organisms, both living and extinct, example is ITIS date basis (The Integrated Taxonomic Information System) (<http://www.itis.gov/index.html>).

Places of conjuring scientist of specific taxes, such as <http://www.marinespecies.org/>, are crucial to the experts and enthusiast with similar topics. These kinds of platforms are offering spontaneous large scale collaboration and progress in solving present day issues in taxonomy as well as a faster flow of new informations.

One of the interesting taxonomic software named DELTA (DEscription Language for TAXonomy) is a data format used in taxonomy for recording descriptions of living things. It is designed for computer processing, allowing the generation of identification keys, diagnosis, etc. (<http://freedelta.sourceforge.net>), as described above, there is no connection to the database GenBank.

Invertebrate animals play an important role in world's entire biodiversity and perform a wide range of crucial functional roles in ecosystems. Correct species identification is the key that can help to overcome practical problems in creating a conservation strategy. There are large gaps in the investigation of invertebrate taxonomy. Unfortunately, the problems in proper identification of invertebrate species are common and experts in the field usually are able to identify only certain groups of species. Moreover, Linnaean taxonomy is opposed to a molecular taxonomy called „phylogenetic taxonomy” (de Queiroz and Gauthier 1994), which has contributed to the revolution in traditional taxonomy (Soltis and Soltis 2001). Resolving difficulties in taxonomic determinations of species are making good platform for further studies such as ecological, biogeographical, animal development, etc.

In the last decade a slight increase of productivity in this field has been noticed, but with also noticed "change of generation" and rapidly decreasing possibility for any permanent job in taxonomy for further young researchers further progress is under question.

This paper aims to combine different sources of data to the identification of invertebrate species. Integration of traditional taxonomy (based on morphology) and molecular taxonomy (based on DNA Barcoding) as an integrative taxonomy could be widely available as mobile web-based application tools.

2. RESULTS

Each species has unique mitochondrial DNA (mtDNA) sequences so that mitochondrial molecular markers can be viewed as genetic “barcodes”. This is a reliable species identification on a molecular level. The mitochondrial cytochrome c oxidase subunit I (*cox1*) gene fragment was proposed as the barcode source of invertebrate species identification (<http://www.barcoding.si.edu/DNABarCoding.htm>). Among molecular tools, DNA Barcoding is a simple and affordable method to species identification (Padial and De La Riva 2007, Evans and Paulay 2012). To amplify *cox1* gene fragment, a region of approximately 600 base pairs (bp), universal primers for diverse metazoan invertebrate species are available (Folmer et al 1994). Obtained in this simple way *cox1* gene fragment is then compared to other sequences which were deposited in a database. Finally, matching these sequences allows for species identification on a molecular level.

The additional advantage of using the molecular method is the possibility of species identification even on the basis of a small fragment of tissue without former species identification on morphological level. Moreover, molecular techniques allow individuals identification at any stage of their development in the life cycle.

Molecular tools are crucial in terms of difficulties in morphological taxonomy, identification of immature individuals and resolve status of cryptic species as well as

problems of synonymy and phenotypic plasticity. However, species should not be described on the basis of sequence data alone because using DNA Barcoding will never provide sufficient information to describe new species (Ebach and Holdrege 2005). Target sequences are of course suitable to look at the genetic distance between species, but the knowledge of its morphology as well as geographical distribution is also needed. Moreover, taxonomic species identification only on the bases on molecular data, without the knowledge of species morphology and its geographical distribution would lead to incomplete results.

Molecular taxonomy is based on other criterion of defining species than are commonly applied in Linnaean taxonomy. Firstly, the method of overall similarity is rejected. Secondly, the comparisons of evolutionary lineages on the bases on appropriate DNA sequences are applied. It should be mentioned that the rate of evolution for different molecular markers is varied which leads to a discrepancy in taxonomy in these both fields.

Some new species have been still described, both on the morphological and molecular level. Moreover, new records of knowing species and information about their changes in the geographical distribution range have also been updated. Without a complex study on invertebrate taxonomy, including species distribution, it is impossible to know which species are common or even under the threat of extinction in geographical area (Bachmann 1995). Presently, the information on invertebrate taxonomy is available, especially as scientific articles which are comprehensible only for the specialists of a narrow field. There is a real need for an easily found, comprehensive source of taxonomic information in a more available way also for non-specialists.

The conceptual web-based application consists of several pages. The first one is the login page and registration page to the system (Figure 1). After logging in to the application, the user is redirected to the next webpage. This part is a private user panel (Figure 2). The top of the page displays: the statistics, including, quantity followers of our publications, comments and dialogues, likes our work-publications. There is the possibility to edit and configure your own profile. Below the conceptual design includes: new identification process, your works progress, connection to social networks, preferences for own adjustment. A part of the page is placed by news feeds where you will be able to exchange your opinion and motivate people to work and learn. It also allows the supervision of student learning.

Next web page is focused on identification processing (Figure 3). The process is intended for the determination of individual organisms to the species level and focuses mainly on the last stage of taxonomic work. Determination of invertebrate animals is based on diagnosis of a number of morphological features, a set of specific characteristics will classify the invertebrate organism to the appropriate taxonomic group. On this page, we define the level of species determination by adding more characters added as a single or multiply photo. It is possible to add a large amount of morphological determination characteristics. Also, we consider adding here a text box where you will be able to describe morphological features of the picture. The lower part containing the navigation button transfers you to the description of the species.

The last page (Figure 4) contains a detailed description of the species introduced by the user. Another important part is the geolocation of each individual. Entering data will take place by selecting the online map or by entering GPS coordinates. The last part will include a section describing the molecular biology to this section, you will add a sequence in a variety of formats. Geolocation and genetic sequence is possible for linking data from different database.

3. CONCLUSIONS

As a means to revitalize traditional taxonomy - molecular taxonomy (Tautz et al. 2003) as well as increased utilization of cybertools (La Salle et al. 2009) - have been promoted as alternative approaches so that innovation technique is useful to develop the field of invertebrate taxonomy and resolve its serious problems. An ideal scenario to overcome these problems would be a simple platform where everyone can include some information about the investigated species. As computer technology plays a crucial role in scientific development, a suitable web application would be a perfect key to resolve current issues in invertebrate taxonomy. Tautuz et al (2003) agreed that web-based technology could be a great step towards a more accessible and universal platform for the deposition and retrieval of taxonomic information and it could speed up communication, and make species diagnoses and new descriptions more accessible as each web-based application can operate on mobile devices or computers such as PC or MAC. It does not depend on the user web browser or computer system platform. The most important feature of this application is archiving your work. You can view the history of others work and improve previous records.

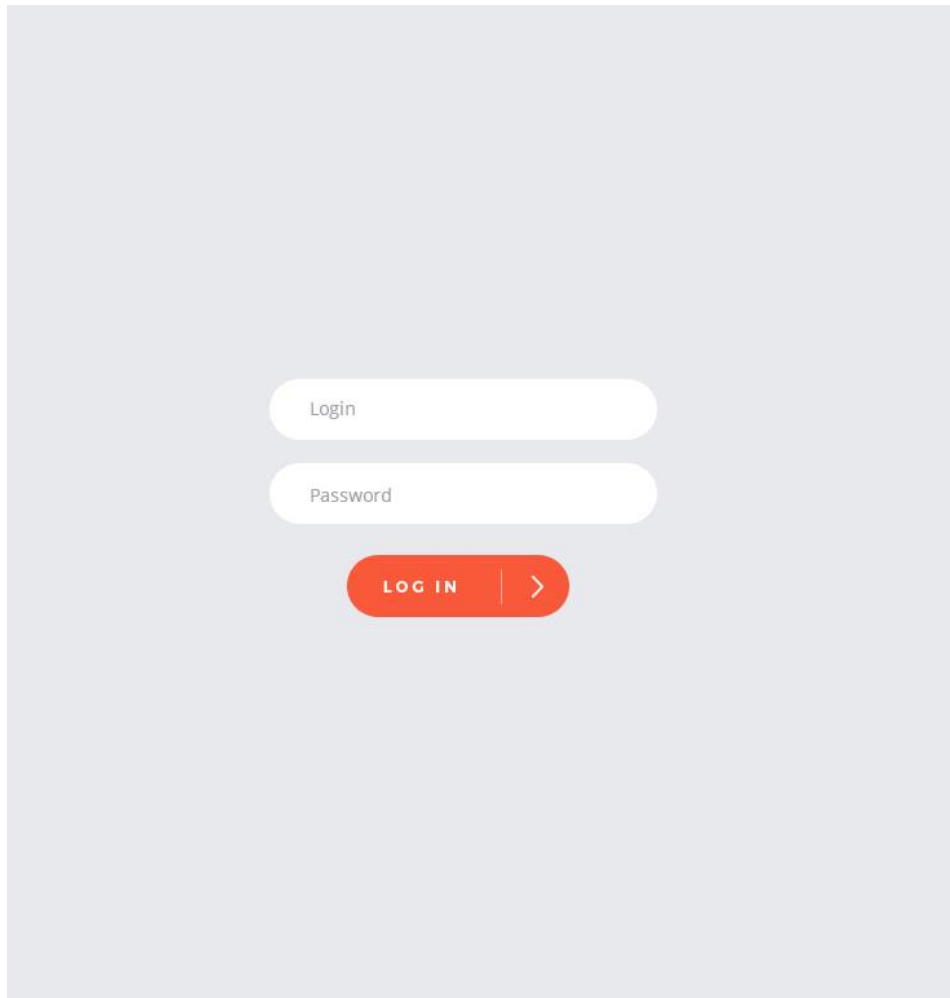


Figure 1. User login panel.

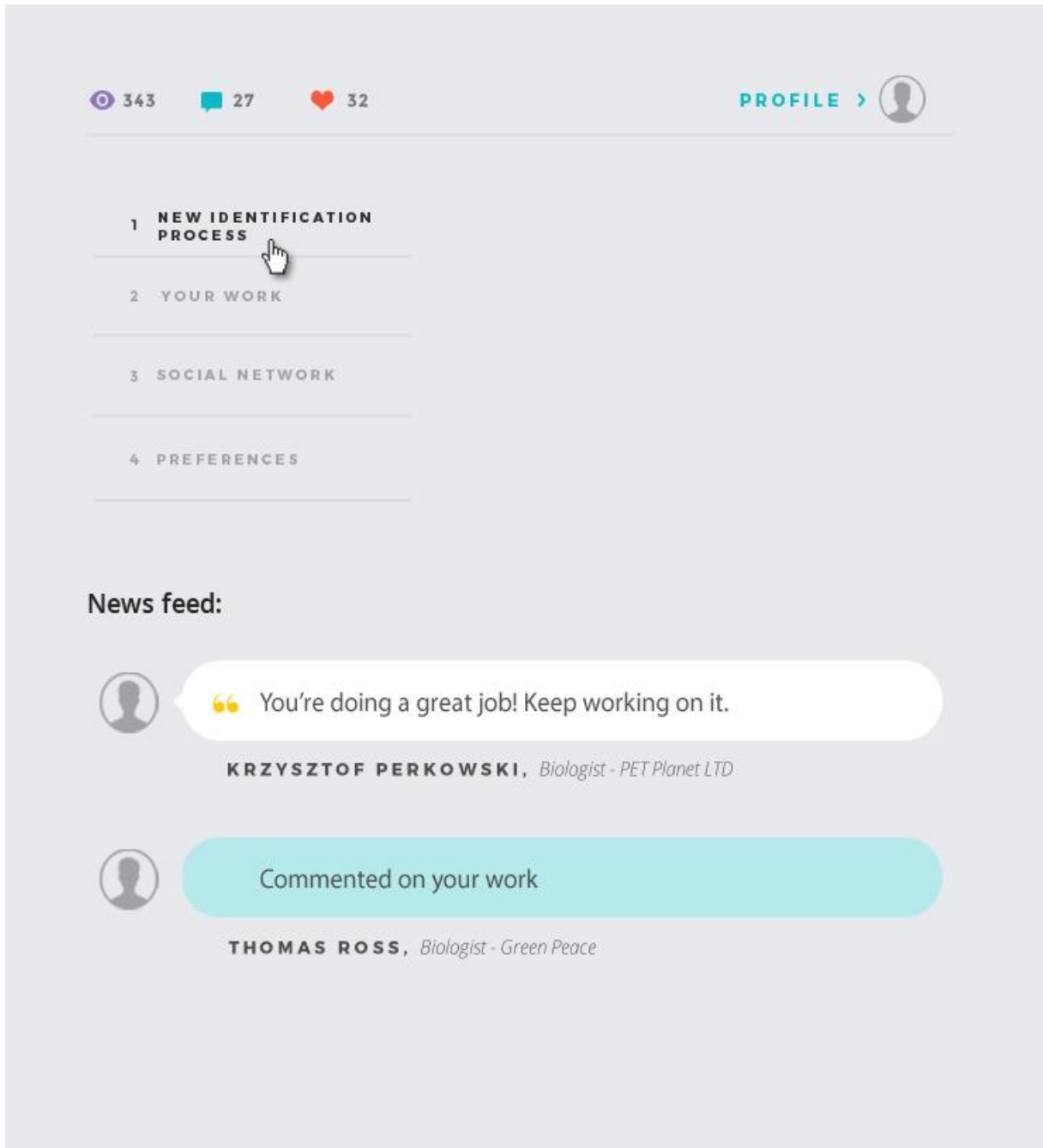


Figure 2. User preferences editor.

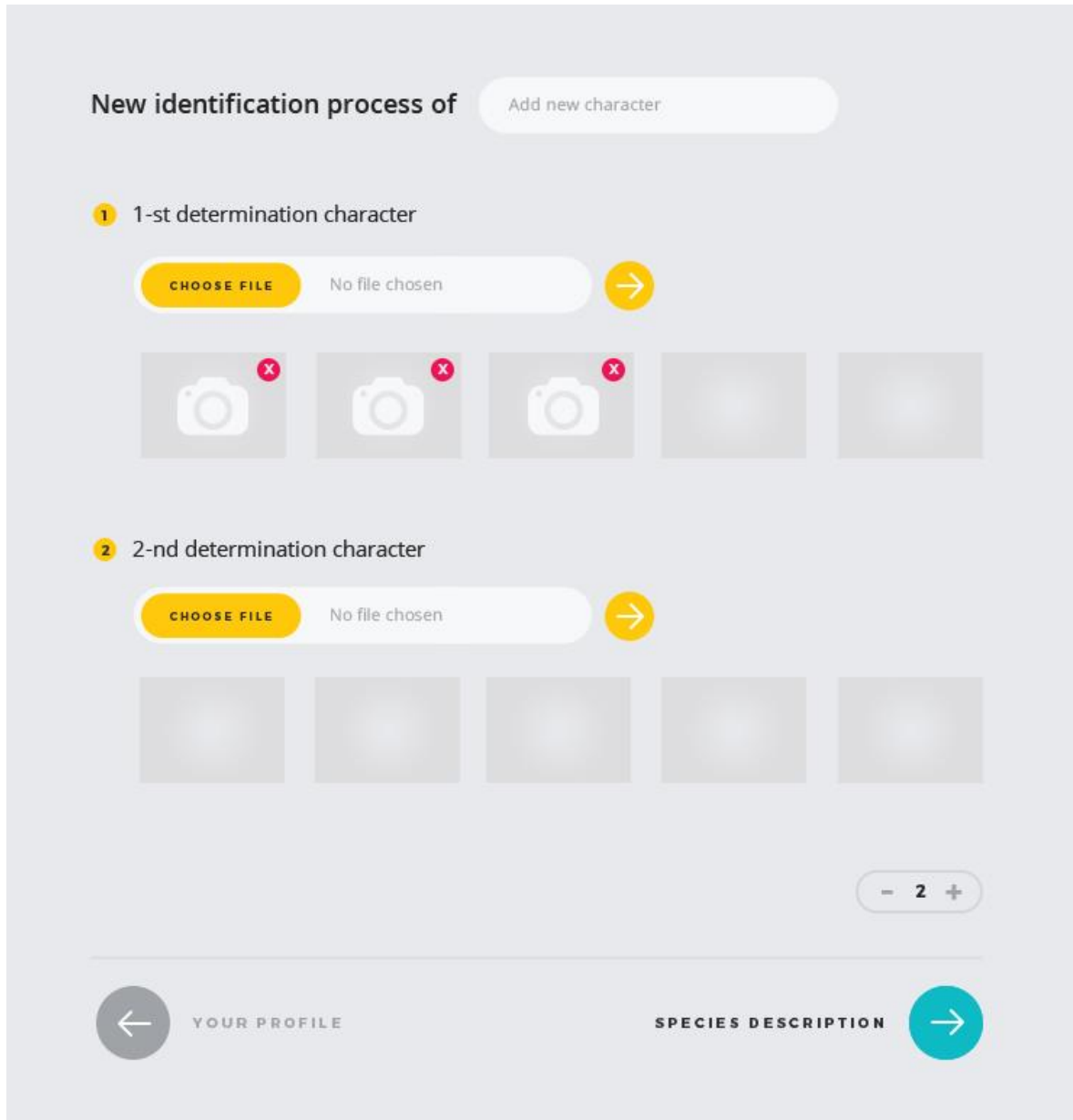


Figure 3. Page of the single identification process consists of new determination characters.

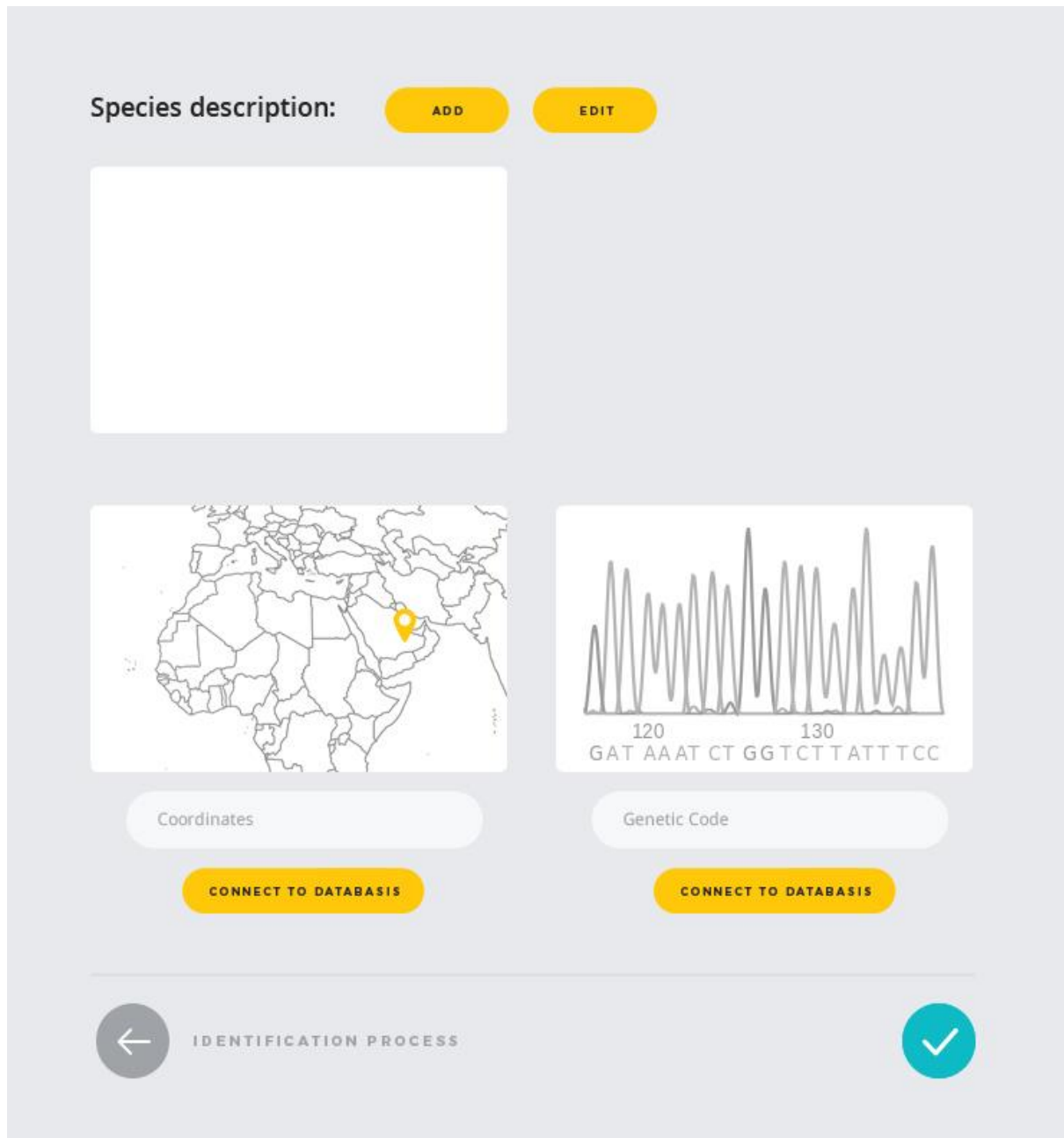


Figure 4. Page of detailed species description with database connection links.

References

- [1] K. Bachmann, Progress and pitfalls in systematics: cladistics, DNA and morphology, *Acta Botanica Neerlandica* 44 (1995) 403-419.
- [2] K. de Queiroz, J. Gauthier, Toward a phylogenetic system of biological nomenclature, *Trends in Ecology & Evolution* 9 (1994) 27-31.

- [3] M. C. Ebach, C. Holdrege, DNA barcoding is no substitute for taxonomy, *Nature* (2005) 434:697.
- [4] N. Evans, G. Paulay, DNA barcoding methods for invertebrates, *Methods in Molecular Biology* 858 (2012) 47-77.
- [5] O. Folmer, M. Black, W. Hoeh, R. Lutz, R. Vrijenhoek, DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates, *Molecular Marine Biology and Biotechnology* 3 (1994) 294–299.
- [6] W. S. Judd, C. S. Campbell, E. A. Kellogg, P. F. Stevens, M. J. Donoghue, Taxonomy [In:] *Plant Systematics – A Phylogenetic Approach, Third Edition*. Sinauer Associates, Sunderland, 2007.
- [7] P. M. Kirk, P. F. Cannon, D. W. Minter, J. A. Stalpers, Taxonomy [In:] *Dictionary of the Fungi*, 10th edition. CABI, Netherlands, 2008.
- [8] J. La Salle, Q. Wheeler, P. Jackway, S. Winterton, D. Hobern, D. Lovell, Accelerating taxonomic discovery through automated character extraction, *Zootaxa* 2217 (2009) 43-55.
- [9] E. Lawrence, Henderson's Dictionary Of Biology. Pearson/Prentice Hall, 2005. ISBN 9780131273849
- [10] C. Linnaeus, Species plantarum, exhibentes plantas rite cognitatas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas. Holmiae, Impensis Laurentii Salvii. [L. Salvius, Stockholm], 1 May 1753. Starting point for Spermatophyta, Pteridophyta, Sphagnaceae, Hepaticae, Fungi (incl. slime moulds and lichen-forming fungi) and Algae (pro parte). 1753.
- [11] M. Manktelow, History of taxonomy. Lecture from Dept. of Systematic Biology, Uppsala University DOI: http://atbi.eu/summerschool/files/summerschool/Manktelow_Syllabus.pdf. (2010)
- [12] E. Mayr, The Role of Systematics in Biology: The study of all aspects of the diversity of life is one of the most important concerns in biology, *Science* 159 (1968) 595-599.
- [13] E. Mayr, Chapter 6: Microtaxonomy, the science of species. *The Growth of Biological Thought: Diversity, Evolution, and Inheritance*. Belknap Press of Harvard University Press. ISBN 9780674364462 (1982)
- [14] J.M. Padial, I. De La Riva, Integrative taxonomists should use and produce DNA barcodes, *Zootaxa* 1586 (2007) 67-68.
- [15] M.G. Simpson, Chapter 1 Plant Systematics: an Overview. *Plant Systematics* (2nd ed.). Academic Press. ISBN 978-0-12-374380-0 (2010)
- [16] P.S. Soltis, D.E. Soltis, Molecular systematics: assembling and using the Tree of Life, *Taxon* 50 (2001) 663-677.
- [17] D. Tautz, P. Arctander, A. Minelli, R.H. Thomas, A.P. Vogler, A plea for DNA taxonomy, *Trends in Ecology & Evolution* 18 (2003) 70-74.

- [18] P. M. B. Walker (ed.) *The Wordsworth Dictionary of Science and Technology*. W. R. Chambers Ltd. and Cambridge University Press (1988)
- [19] Q. D. Wheeler, Taxonomic triage and the poverty of phylogeny [In:] H.C.J. Godfray, S. Knapp. *Taxonomy for the twenty-first century*. *Philosophical Transactions of the Royal Society* 359 (2004) 571-583.
- [20] J. S. Wilkins, What is systematics and what is taxonomy? 2011, <http://evolvingthoughts.net/2011/02/what-is-systematics-and-what-is-taxonomy/>

(Received 29 September 2016; accepted 10 October 2016)