Assembling a Virtual Weevils of North America Checklist with Symbiota – Preliminary Insights

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Abstract

We report on preliminary insights gained from the virtual Weevils of North America (WoNA) project. WoNA represents a novel, collaborative solution to the challenge of assembling monographs for taxonomically complex groups such as the weevils (Coleoptera: Curculionoidea) by leveraging the large-scale, specimen-level digitization efforts of thematic collection networks. The project has been developed on-line since 2012 within the framework of the Southwest Collections of Arthropods Network (SCAN). Current WoNA holdings include voucher-based data on more than 300 genera and 1000 species as well as high-resolution images for more than 400 species. Efforts to enrich these data with additional images, taxon profile pages, and interactive identification keys are underway. SCAN and WoNA are sustained by the Symbiota software platform which promotes diversified forms of engagement with research colllections, taxonomic experts, and the general user community. In each case the sources and actions related to data holdings are properly accredited. Future Symbiota modules will facilitate an increasingly monograph-like representation and publishable output under this approach. Integration of Filtered Push technology allows external users to submit annotations amounting to an open, distributed, and dynamic system of peer review that can increase support and trust in such virtual taxonomic knowledge environments.

Introduction

Specimen-based monography is transitioning from traditional, one-time publication in print media to the continuous assembly of dynamic, virtual environments (Smith, 2013). Large-scale investments into biodiversity data mobilization in North America and elsewhere are shifting the landscape (Baker, 2011). Such game-changing initiatives include the National Science Foundation's Advancing Digitization of Biological Collections program (NSF-ADBC, 2011) and the iDigBio HUB which jointly sustain 10 Thematic Collection Networks (TCNs) initiated since 2011. Virtual collections mobilization for research and outreach is also a central objective of the Network Integrated Biocollections Alliance (NIBA) and related initiatives (Wheeler and others, 2012; Hanken, 2013; Hardisty and Roberts, 2013). The natural history collections community is making a strong push to bring specimen data on-line at a global scale.

However, digitization of specimen data without further systematic synthesis and discovery is not optimal. Natural history collections require continuous growth and curation to best serve diverse user communities (Drew, 2011; Johnson and others, 2011). Curation, in turn, requires taxonomic experts who are distributed across many institutions and must also respond to pressures to produce peer-

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reviewed and highly cited research (Valdecasas, 2011). Thus digitization finds itself at a crossroads where trade-offs between investing into (1) data quantity versus quality, (2) build-up of research-supporting infrastructure versus genuine research and innovation, or (3) publication in on-line databases versus highly ranked journals, can present stark choices for taxonomic experts (Wägele and others, 2011; Costello and others, 2013). Moreover, *trust* in data *quality* is at the top level of the Semantic Web stack that specimen data sustain at lower levels (Berners-Lee and others, 2006). To earn that trust and maximize return on investment, we must offer experts new incentives to engage in the virtual curation of digitized specimen data (Vollmar and others, 2011).

Numerous efforts to bridge the divide between 'just digitization' of specimen data and accredited systematic publication are underway (e.g. Smith and others, 2013). Here we offer preliminary insights into one such effort intended to create a new model of collaborative virtual monography for a major lineage of North American insects – the weevils. The **Weevils of North America (WoNA)** project (Franz and others, 2014; *http://symbiota1.acis.ufl.edu/scan/portal/checklists/checklist.php?cl=1*) is the first to build directly upon an NSF-supported TCN, i.e. **SCAN – the Southwest Collections of Arthropods Network** (SCAN, 2014). SCAN came on-line in mid 2012 and has since (as of January, 2014) accumulated ~ 435,000 specimen occurrence records representing13,000 primarily North American arthropod species (excluding GBIF records and moth observations which are also hosted in SCAN). Of these specimen records, approximately 70% are georeferenced with decimal latitude/longitude data. A similar percentage is identified to the level of species.

SCAN and WoNA are hosted by the iDigBio HUB server infrastructure and sustained by the innovative, Open Source, and exclusively web-based **Symbiota software platform** (Gilbert and others, 2014; Gries and others, 2014). Symbiota facilitates the bottom-up assembly of voucher-based biodiversity information communities – called *portals* – of which the Southwest Environment Information Network (SEINet, 2014) is a primary example.

In the past 5-10 years, floristic treatments within SEINet have matured into monograph-like resources of high information density and accessibility (Gilbert and Licher, 2014; Makings, 2014). Such treatments include abundantly vouchered and searchable species lists, species profile pages with high-resolution images and descriptive data, interactive occurrence maps, and dynamic keys to identify taxa based on checklist- or map-driven entry points. Hence, many components for delivering a Symbiota-based WoNA monograph are already in place, as are platform-inherent advantages related to the continuous expansion, annotation, and enhancement of checklists by contributors and users.

Our interim review of assembling WoNA includes sections on special taxonomic challenges related to weevils, an overview Symbiota's design principles and checklist support functions, current data holdings, and future developments. Throughout, our motivation is to further promote this approach for adoption by diverse arthropod research communities.

Taxonomic Challenges and Opportunities

Weevils – Coleoptera: Curculionoidea in the sense of Bouchard and others (2011) – are among the most diverse, economically impacting, and taxonomically challenging lineages of arthropods globally (Oberprieler and others, 2007) and in North America (herein limited to Canada and the United States). Weevils are ubiquitous in all terrestrial habitats where they are major herbivores of naturally occurring or cultivated plants as well as premier control agents (O'Brien, 1995). Anderson's (2002) synopsis and other curculionoid treatments in the *American Beetles* (Arnett and others, 2002) account for seven families with 317 genera and 2728 species in the region. The fungus-cultivating bark and ambroisa beetles (Harrington, 2005), which are members of the Curculionoidea (Kuschel, 1995), add at least 77 genera and 532 species to this diversity (Rabaglia, 2002). Mananging such richness is

challenging enough when taxonomic groups are well circumscribed. However, in weevils this challenge is further amplified by an unnatural and impenetrable mid-level classification that limits the recognition of monophyletic lineages.

The taxonomic history of the weevil superfamily can be abridged into (1) a period of foundation laying by 19th century authors such as Schoenherr (1823, 1826, 1833–1845) and Lacordaire (1863, 1866), and (2) a prolonged period of incremental extensions of that basic framework throughout the 20th century. It is well known that Lacordaire's (1863, 1866) definitions of weevil groups are too simplistic to yield natural taxon circumscriptions (Kuschel, 1995; Anderson, 2002; Oberprieler and others, 2007). Nevertheless these definitions remain highly influential in modern classifications (Alonso-Zarazaga and Lyal, 1999) which recognize some 16 subfamilies, 195 tribes, and 5800 genera in the Curculionidae alone (again, excepting bark beetles). Molecular projects conducted over the past 15 years (e.g. Farell, 1998; McKenna and others, 2009; Bocak and others, 2013) have undersampled this diversity so dramatically as to yield only minimal classificatory realignments (Franz and Engel, 2010).

The Weevils of North America project represents a novel, bottom-up effort that emphasizes specimen-level data and phenotype-based taxonomy and thus critically complements parallel top-down phylogenetic efforts. Past decades have shown that major advances in weevil systematics exceed the abilities of individual researchers. No fruitful synthesis is possible unless both bottom-up and top-down components are covered and coordinated. Hence we require a better structured and distributed research and synthesis platform that (1) is up to date with developments and standards in biodiversity informatics and (2) can utilize these tools to scale up to the vast dimensions of the task.

Symbiota Design Principles

Symbiota portals embody several design principles (this section) and specific functions in support of creating checklists (subsequent section) that merit a brief review.

Themed Collaborations Yield Enhanced Information Quality

Symbiota portals provide a framework for collaboratively publishing biodiversity information. Regional checklists are built upon vouchered records with direct linkages to the source that manage the data and physical holdings (Fig. 1). This ensures that data *updates* undertaken within the source collections can *flow back* to the virtual checklists, and vice-versa (Vollmar and others, 2011).

Symbiota portals adhere to a particular regional and/or taxonomic *theme* and *scope*. A portal's full potential is reached if it is supported on a broad scale through numerous thematically interconnected data contributors. Portals promote a *positive feedback loop* that includes: (1) making data public instantaneously which can serve to expose errors; (2) using web-based editing tools and workflows that allow such errors to be resolved as they are identified; (3) redirecting data repairs back to a source collection's internally used platform; and (4) rendering repairs permanent with the subsequent data update. Thus Symbiota leverages the themed data mobilization approach towards improving the *quality* of the individual collections' datasets (Costello and others, 2013).

Portals Promote Diversified Forms of Engagement

Symbiota portals allow different of forms of engagement for contributing collections, research teams, individual experts, and public groups or citizens. In particular, collections and researchers have the option to contribute specimen information through either (1) direct "Live Data" management or (2) a "Data Snapshot" harvested periodically from another database system. In the former case, Symbiota's Collection Management System (CMS) is used to achieve day-to-day digitization and data assembly tasks; whereas in the latter case the portal merely exposes information generated in another (preferred)

environment. Symbiota has features to allow for such flexibility; including manual or API-supported data uploads using Darwin Core-compliant formats (Wieczorek and others, 2012). In addition, *any* user can readily access a portal's occurrence records by downloading auto-configured datasets in spreadsheet format. Users can submit *comments* to data owners following a simple login procedure. Jointly these features lower the threshold for engaging new member collections and taxonomic experts.

Functional Modularity, Data Integrity, and Customization

Symbiota allows communities to acquire distinct identities and functions while ensuring database integrity at a broad scale. The aim to integrate biodiversity information sets practical strictures on the degree to which configurations can vary. These limitations are most apparent in the format of the single **occurrence data table** (Fig. 2) which is furthermore linked to a portal's **taxonomic thesaurus.** The latter constitutes a continuously curated reference classification that subtends all taxonomically based search functions and output displays. Joining a Symbiota portal requires acceptance and coordination of these conventions (Scoble, 2004; Franz and others, 2008).

Beyond sharing data formats, Symbiota portals are customizable in numerous ways that suit specific community needs. *Modularity* is manifested at different levels: (1) application modularity – the modules for managing specimens, biotic inventories, identification keys, and taxon profile pages are designed to function independently of one another; (2) data modularity – collections are represented as independent units with their own management regimes; and (3) portal modularity – multiple Symbiota portals can maintain distinct front-end appearances while connecting to a single back-end database.

Modularity also means deploying existing web services optimized for specific functions. For instance, services related to mapping occurrence records are provided through Google Maps (*https://maps.google.com/*). Georeferencing tasks are supported by GEOLocate tools (Rios and Bart, 2010). Voucher images can be imported from external sites such as the Encyclopedia of Life (Wilson, 2003).

Checklist Assembly Functions – a Primer

We limit our Symbiota review to the creation of 'static' checklists, created by single or collaborating experts 'on top of' baseline digitizations efforts (see also *http://symbiota.org/tiki/tiki-index.php?page=Static+Species+Lists*). WoNA exemplifies this model.

Biotic Inventories. Once a portal and member collection nodes are established, contributing experts can author *regional checklists* by either (1) creating a species list within the network or (2) linking a group of species lists within a Symbiota *project.* Static checklists give researchers complete and continuous control over species composition, taxonomic placements, region specific comments, and voucher assignments. Additional partitioning of an all-inclusive list multiple smaller lists – e.g. for states, counties, or conservation areas – is also possible.

Symbiota offers a flexible user interface for exploring checklists (Fig. 1). Users can filter these lists by taxon and display results with author names, habitat information, and/or voucher details. Checklists can also be displayed as a set of thumbnail images, thus making it easier to visualize the taxa represented in the region (Fig. 3).

Interactive Keys. Symbiota's interactive keys are generated directly from descriptive data stored in a relational DELTA format (*http://delta-intkey.com/*). Such keys have many advantages over traditional, dichotomous keys (Hagedorn, 2007; Brach and Boufford, 2011). Computerized identification tools have advanced to the point where assessing only 2-5 characters often reduces a long list of candidate taxa to a manageable size. Subsequent browsing of taxon images, distribution maps, and descriptions can further speep up the process.

The Symbiota key editing interface is coordinated with the hierarchy defined within the taxonomic thesaurus, allowing for character inheritance and other efficient coding tools. If a large region or taxonomic group is treated, keys are usually broken down into several levels of complexity, and the user proceeds from one key to the next.

Taxon Profile Pages. Symbiota offers *taxon profile pages* that complement the aforementioned modules (Fig. 4). Natural language descriptions as well as images may be provided for each taxon. An occurrence map generator utilizes information from the collections records to dynamically produce a Google distribution map. The corresponding CMS includes separate tabs to: (1) provide synonyms and vernacular names; (2) view all annotated images; (3) specify the sequence in which images appear; (4) add new images; and (5) add natural language description(s) or notes on natural history and distribution. Links to source repositories for primary taxonomic literature such as the Biodiversity Heritage Library (*http://www.biodiversitylibrary.org/*) are supported.

Checklist Management. Symbiota's CMS for checklist management (Fig. 5) allows lead authors to manage contributor access rights and related checklists; add new taxa and images; and link new vouchers based on dynamic searches. Tabs to resolve conflicting voucher identifications and output reports round out the checklist CMS.

Current WoNA Holdings

From its beginnings in 2012, WoNA has been exclusively Symbiota-based (Fig. 1). The project has benefitted from donations of authoritately identified specimens of the CWOB collection (Green Valley, AZ; see O'Brien and Wibmer, 1982; Fig. 2). January 2014 searches for North American curculionoids in *SCAN* yielded > 14,500 specimens and > 1300 species; with a strong Southwest bias mirroring that of the source collections (i.e., ~ 6,500 specimens and 300 species are from Arizona alone). WoNA itself has 1-50 specimen occurrence records for > 300 genera (~ 85% genus-level coverage for North America) and > 1000 species (~ 30% species-level coverage for North America). High-resolution images (frequently with a scale bar) are available for more than 400 species (~ 12-15%; Fig. 3). Roughly 100 diagnoses, imported from the Biodiversity Heritage Library, have been added to WoNA (Fig. 4). The following URL for the cryptorhynchine genus *Acalles* Schoenherr (in the sense of O'Brien and Wibmer, 1982) illustrates how these components are integrated in Symbiota: *http://symbiota1.acis.ufl.edu/scan/portal/taxa/index.php?taxon=4682*.

WoNA's interactive key module is available at *http://symbiota1.acis.ufl.edu/scan/portal/ident/key.php?cl=1*. Basic functionality of this module is projected for mid 2014, although authoring a powerful tool will require considerable new taxonomic research. The SCAN identification module will include a new feature that allows authors to *illustrate specific characters* via voucher-based, SVG-highlighted detail images (Ramírez and others, 2007; Yoder and others, 2011). So far 50 multi-state characters for curculionoid families and subfamilies have been extracted from the *American Beetles* chapters (Anderson, 2002; Arnett and others, 2002) and reformulated for the WoNA key.

Conclusions – Prospects for Arthropod-Centric Symbiota Monographs

We close with discussing a broader question – what are the advantages and limitations of the WoNA approach to systematic 'monography', and under what circumstances should prospective authors make use of this approach?

Mayr and Ashlock (1991, p. 421) define a monograph as "an exhaustive treatment of a higher taxon in terms of all available information pertinent to taxonomic interpretation; [which] usually involves full systematic treatment of the comparative anatomy, biology, ecology, and detailed

distributional analyses of all included taxa". While WoNA fits this definition in a general sense, we acknowledge that publishing into Symbiota is not identical to a one-time submission of a manuscript to a traditional, peer-reviewed Journal. Academic recognition of new and significant systematic contributions in such a medium is arguably the greatest challenge.

However the landscape of acceptable models for publishing taxonomic information is changing (ICZN, 2012; Smith, 2013; Smith and others, 2013). There are many advantages inherent in shifting to a dynamic, collaborative monography model – especially for a project of WoNA's dimensions. For one, Symbiota – as a result of prior NSF awards and strong iDigBio/TCN community support (Gries and others, 2014) – is an immensely robust, production-level platform with some 250 collections, 2000 users, and 12-15 million specimen occurrence records managed in more than 18 portals including SCAN. SEINet alone has ~ 20,000 monthly site visits according to Google Analytics. Such widely distributed data input and institutional/user support are valuable assets to taxonomist authors. Additional synergy may be obtained through linking WoNA with the nationwide network of Symbiota vascular plant portals. Connecting weevil and plant specimen data at such a scale opens up new possibilities for analyses of co-occurrences and interactions.

Symbiota's capabilities to support monographic treatments can be further improved with **new modules** that allow (1) the citable exposition (author/year/reference URL) of 'Symbiota monographs' within existing portals; (2) custom-configurable (taxon-/region-specific) static output functions (e.g., "extract the checklist as a PDF; show taxa, images, and key for Arizona"); and (3) a standard-compliant reference module for taxon profile pages. These modules can mature as WoNA and similar treatments receive more authoritative input and weight. Integration with ZooBank (Krell and Pyle, 2010) would open up possibilities for publishing new nomenclatural actions.

Another advantage is the ability to accommodate different forms of institutional and author engagement with proper intellectual attribution. This allows WoNA to transparently accredit the provenance of each specimen, image, description, or key identification component (Figs. 1 and 4). Attribution of credit is critical for engaging additional collections and experts into such collaborative projects.

Lastly, Symbiota is developing tools to **promote peer review via expert annotations** using the novel Filtered Push technology (Morris and others, 2013; see *http://wiki.filteredpush.org/wiki/*). This technology amounts to an open, distributed, and dynamic system of contributor engagement and peer review. The coming years will reveal to what extent these developments contribute to altering the cost/benefit ratio for taxonomic experts interested in leveraging large-scale specimen-level digitization efforts towards monographic projects with Symbiota.

Acknowledgements

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Figure 1. Screenshot of Weevils of North America checklist homepage in SCAN; showing current occurrence record statistics (January, 2014) and taxa with "Taxon Authors" and "Notes & Vouchers" (see checkmarks in the Options/Filter box). Specimens are annotated with their collector and source collection (displayed in square brackets). The Options/Filter box includes a search function (with synonymy) to further narrow down the taxon list, as well as print and spreadsheet output options (icons to the right of "Rebuild List"). The top right corner includes icons for checklist administration ("A"), managing linked vouchers ("V"), and adding species ("Spp").

Figure 2. Screenshot of the SCAN occurrence data table (in part) for the 'live-managed' specimen ASUHIC0031908 (see also *http://symbiota.org/tiki/tiki-index.php?page=Occurrence+Fields*). Top-level tabs include screens for editing the specimen's identification (with options to submit to Filtered Push; see Conclusions), viewing annotations, adding images or GenBank links, and occurrence record administration. Switching from front-end (Fig. 1) to back-end (Fig. 2) displays of specimen-level data is instantaneous in Symbiota for users with the corresponding editor rights.
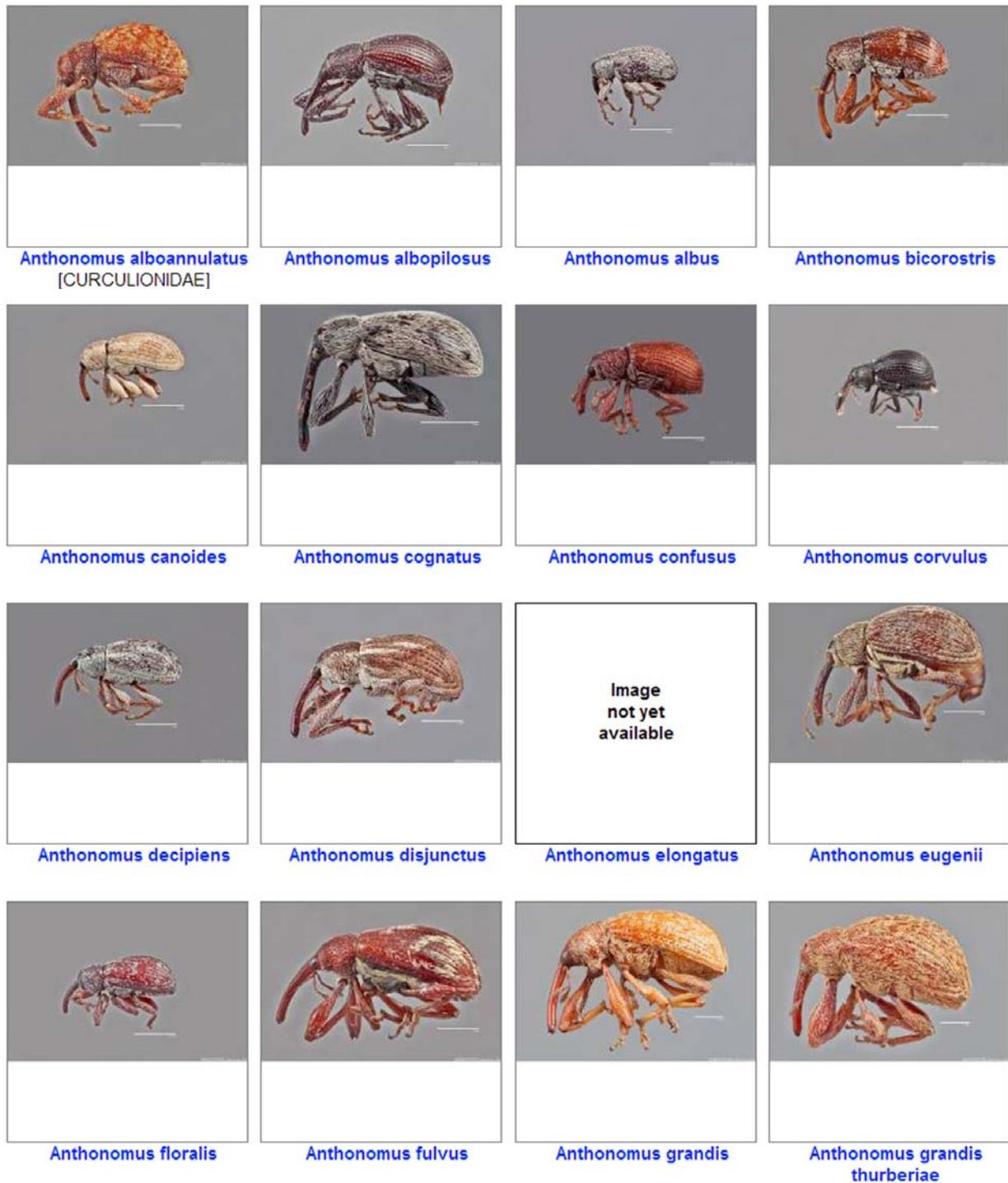
Figure 3. Screenshot with thumbnail view of species in the weevil genus *Anthonomus* Germar (in the sense of O'Brien and Wibmer, 1982) linked to WoNA. This view is produced by searching for "*Anthonomus*" in the checklist's Search/Filter box (Fig. 1) and then selecting "Display as Images" and "Rebuild List". Clicking on each thumbnail will lead to the corresponding taxon profile page where additional high-resolution images and specimen-data are available.

Figure 4. Screenshot of SCAN/WoNA species profile page for *Acalles sablensis* Blatchley; with link to the original description (Blatchley, 1920: 174) available through the Biodiversity Heritage Library, thumbnails of dorsal and lateral habitus photographs, and an interactive map to specimen occurrence records. The pen icon in the top right corner links to the taxon profile page CMS (see Fig. 5).

Figure 5. Screenshot of WoNA checklist administrator interface for managing linked vouchers. Checklist authors can create custom searches ("Create SQL Fragment") to identify vouchers recently added to the SCAN environment as potential candidates for inclusion in the checklist.