

Short communication

The identification aid Scramble version 2.1 and the *Xiphinema americanum* group (Nematoda: Longidoridae)

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'Scramble' is a computer software created to support identification of *Longidorus* and *Xiphinema* specimen and to simplify the handling with morphometrical data (TIEFENBRUNNER et al., 2002a und b). The last version 2.1 is adapted for the *X. americanum* group, too.

It is part of the philosophy behind 'Scramble' not to create new identification keys, but to support the most general existing ones, which are for *Longidorus*: CHEN et al. (1997) and Supplement 1 - LOOF and CHEN (1999) - and for *Xiphinema* with exclusion of *X. americanum sensu lato* LOOF and LUC (1990) and supplement 1 - LOOF and LUC (1993) - and supplement 2 - LOOF et al. (1996) -, and for *X. americanum*: LAMBERTI et al. (2000). Unfortunately there is a lack of agreement between the team of LAMBERTI, MOINARI, MOENS and BROWN, who realised regional polytomous identification keys of the *X. americanum* group (LAMBERTI et al., 2002) and the team of LOOF, LUC and BAUJARD, who created the most successful polytomous *Xiphinema* key (LOOF et al., 1996) and criticize (LUC and BAUJARD, 2001) the key of LAMBERTI et al. (2000). As they comment, in some species all characters taken from this key share the same state and hence it is not possible to distinguish between them.

On the other hand LAMBERTI et al. (2000) decided to use only morphological characters, especially morphometrical ones - this character restriction is a consequence of a 'morpho-species concept'. This makes the use of a computer identification aid, that simplifies the handling with this data type, useful. From our pragmatical point

of view it was therefore obvious to integrate the key of LAMBERTI et al. (2000) to the software 'Scramble'. Because we follow no own taxonomical opinion, we had to do this without changing this key or the key of LOOF and LUC (1990). Thus the lack of agreement causes troubles for the user of 'Scramble':

- 1) LUC et al. (1998) corrected *X. brevicolle* to *X. brevicollum* and declared *X. diffusum*, *X. incognitum*, *X. parvum*, *X. pseudoguirani*, *X. sheri* and *X. taylori* as junior synonyms of *X. brevicollum*. LAMBERTI et al. (2000) mentioned and seemed to accept this point of view but did not follow it ('This does not infer the rejection of these synonymies, but rather we considered it more useful to include all species until comparison can be made with the morphological and molecular data that is currently being accumulated as part of the EU funded project'). Therefore their key and its 'Scramble' version contain all these species. On the other hand because they did not reject the synonymisation we decided to use it in the textfiles (necessary for multivariate analysis) that are data containers for specimens of *Xiphinema* species (X_Ref_All.txt and Xa_Referenz.txt). So '*X. brevicollum* (L95)' ('L95' is a reference to the publication, where the data are from) of the reference files was originally described as *X. brevicolle* by LISKOVA (1995) and later on as *X. taylori* (LISKOVA, 1997).
- 2) There is no agreement about the species that belong to the *X. americanum* group. LOOF and LUC (1990)

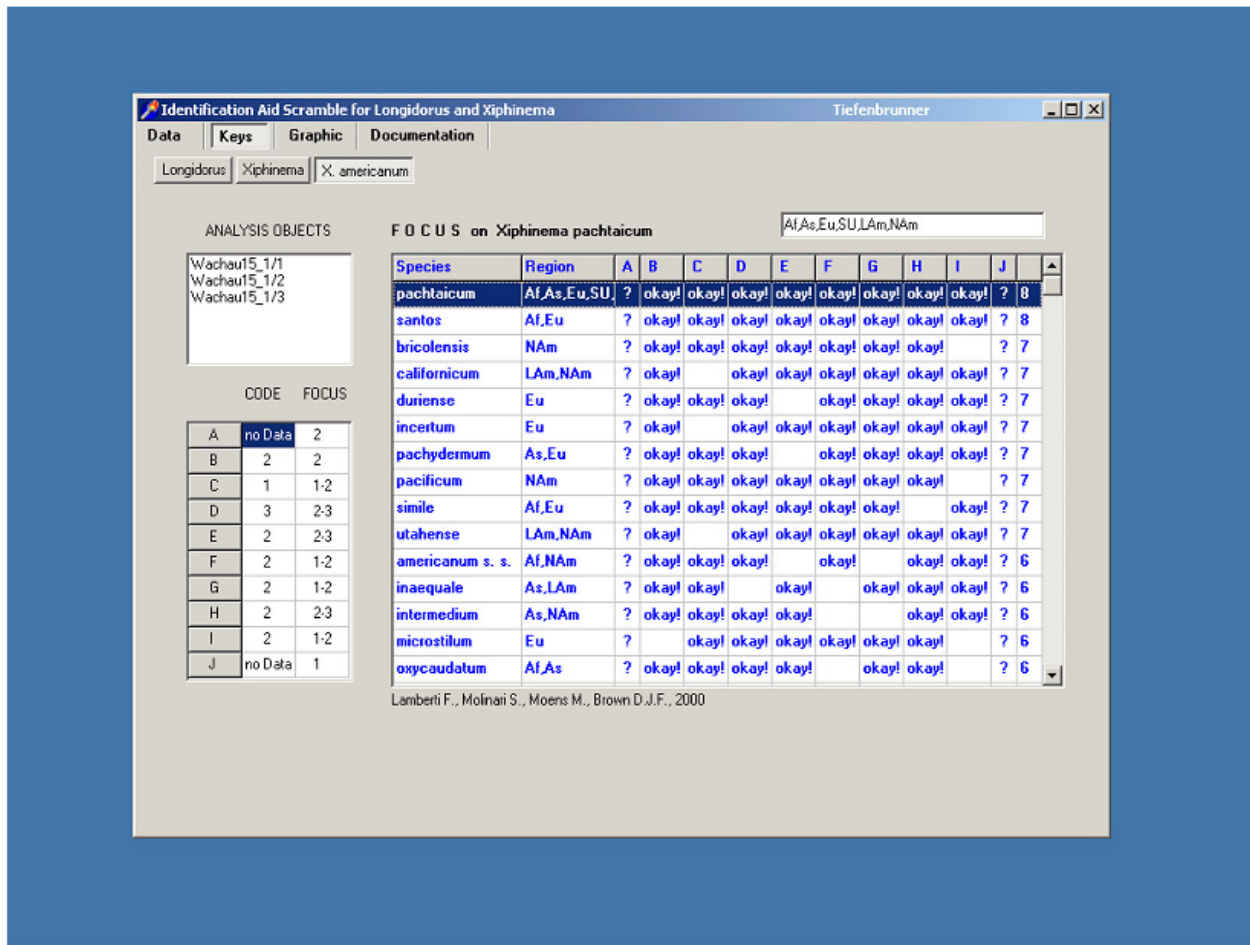


Fig. 1: *X. americanum* key page of Scramble 2.1. In mean the selected specimens (analysis objects) fulfill the codes of all 8 metrical characters of *X. pachtaicum* and *X. santos*. A focus is set on *X. pachtaicum* (by mouse clicking on the right grid), so geographical data to this species and the whole code (Lamberti et al. 2000) are presented.

excluded *X. pachydermum* from the *X. americanum* group and also *X. bacaniboia* is not included. Later (LUC et al., 1998) *X. bacaniboia* was included, but until now without changing the key (LOOF and LUC, 1990) or the character state description of *X. americanum sensu lato*. So in these two cases the computerized key will not lead to *X. americanum s. l.* but directly to the species names. More problematic are the species *X. brevisicum*, *X. mesostilum*, *X. microstilum* and *X. longistilum*, originally described by LAMBERTI et al. (1994). They are not recognized by the key of LOOF and LUC (1990) and Supplements 1 and 2, because LOOF et al. (1996) accepted them to belong to the *X. americanum* group. LUC et al. (1998) excluded them from *X. americanum s. l.*, but

did not include them to their key (*Xiphinema* without *X. americanum s. l.*). According to LAMBERTI et al. (2000) they are *X. americanum s. l.* and hence part of their key. In 'Scramble 2.1' the keys are hierarchically positioned: one first reaches the more general key of LOOF and LUC (1990) and then - by focusing *X. americanum s. l.* - the specialized one of LAMBERTI et al. (2000). *X. brevisicum* fulfills the character description of *X. americanum s. l.* (LOOF and LUC, 1990) and so one reaches the key of LAMBERTI et al. (2000) with the state description of the species, but note that LUC and BAUJARD (2001) recognized that *X. brevisicum* cannot be differentiated from *X. duriense* by this key. *X. mesostilum*, *X. microstilum* and *X. longistilum* do not fulfill the state description

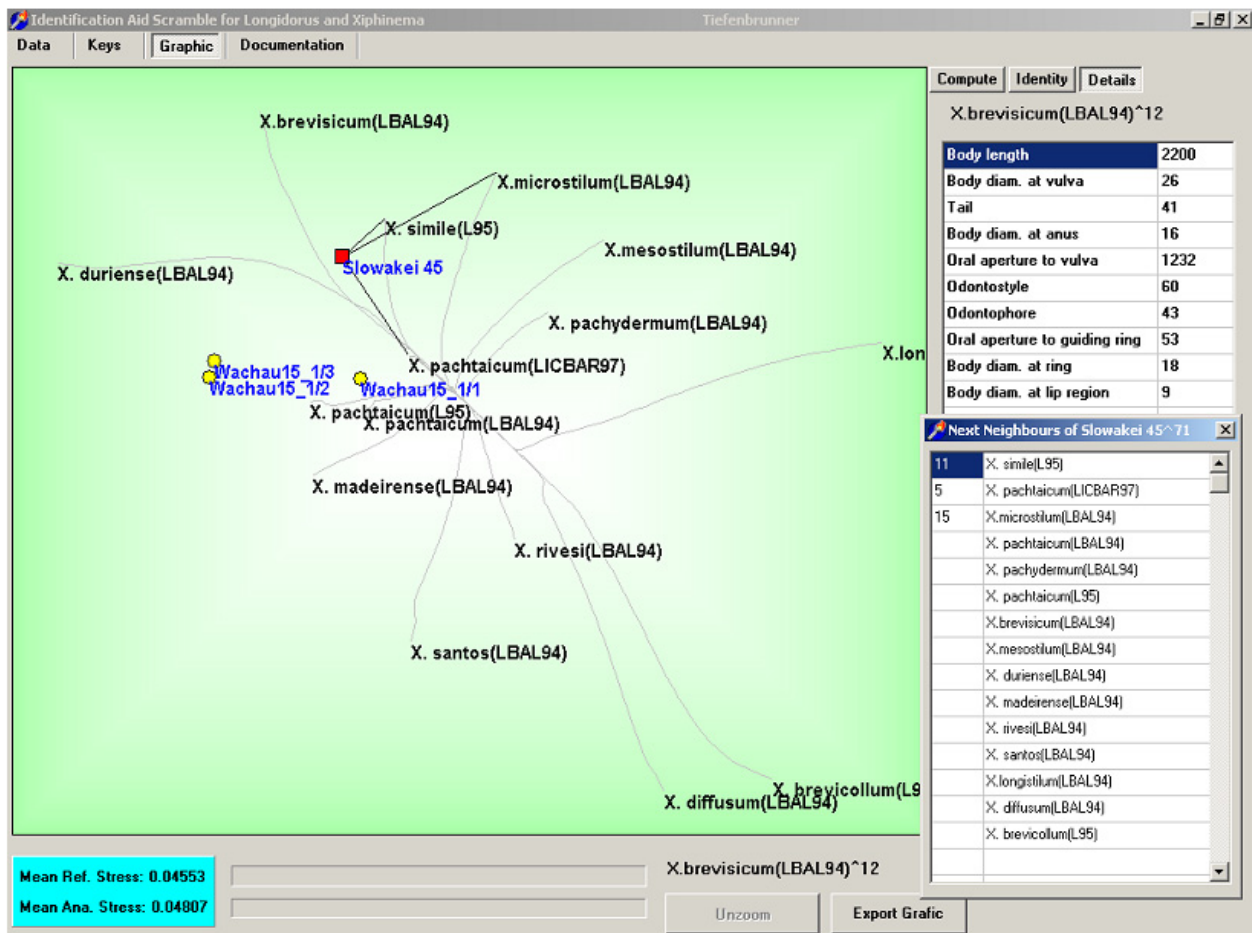


Fig. 2: Multivariate presentation using the reference file 'Xa_Referenz' that contains only data of species that are (or were once) recognized as *X. americanum* s.l. The 'Detail Information' page is activated, which presents the character states of that object in the graphic, that is nearest to the mouse position. A lot of other tools, useful for identification, can be used.

of *X. americanum* s. l. in the key of LOOF and LUC (1990) (F3 instead of F1/2), and are not included in it. So you neither get information about these species by this key nor do you see a reason to look to the one of LAMBERTI et al. (2000).

- 3) The description of some species does not fit to the key of LAMBERTI et al. (2000). For instance in *X. difusum* of LAMBERTI et al. (1994) character H does not fit (there is a coherence to point 1 - using the key of LAMBERTI et al. (2000) would lead to *X. brevicollum*, *X. incognitum* and *X. taylori*).
- 4) Troublesome for the programmers of 'Scramble' is the fact, that the codes of the keys of LOOF and LUC (1990) and LAMBERTI et al. (2000) contain non-defined areas. An example of LOOF and LUC (1990) are

the character state E5 (vulva position 45-49) and E6 (> 50). Vulva position 50 is not defined, see e.g. the description of *X. dentatum* by LISKOVA (1995). An example of LAMBERTI et al. (2000) is the code B, where a body length of 1.5 mm is not defined (also D and F). A correction would be useful.

In 'Scramble 2.1' there are two ways to handle the *X. americanum* group. After loading reference and analysis file and selecting one or more analysis specimen(s) (TIEFENBRUNNER et al., 2002a und b) the page expression 'Analysis' of the bottom page control (Fig. 1) must be pressed. Activating the button 'Xiphinema' opens the identification key page concerning this genus of the top page control and reads the data from the file 'Loof-

Luc.txt' to compare the selected object(s) from the analysis file with these data. The code of the selected specimen(s) is calculated, as long as the characters are metrical. The species with the best correspondence appear on the top of the right grid and furthermore they are alphabetically sorted. By mouse clicking on the right grid a species can be focused and normally the full code of this one is presented in the right column of the left grid. But if the focused species is '*americanum s.l.*' the data of 'LambEtAl.txt' are loaded and the analysis objects are compared with the key data of LAMBERTI et al. (2000) (Fig. 1).

The second way 'Scramble 2.1' supports the handling with the *X. americanum* group can be used by loading 'Xa_Referenz.txt' as reference file. It includes data from literature concerning some '*X. americanum s. l.*' specimens. It is easy to edit and to supply. Using it in the multivariate presentation procedure leads to a graphical presentation (for visual data exploration) of the similarity of the analysed specimen(s) to the data from literature (Fig. 2). Further procedures described earlier (TIEFENBRUNNER et al., 2002a und b) can be used to identify the specimen(s).

'Scramble 2.1' is available via www.visualdataflow.de/biologies as free beta version.

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