A novel alternative method for 3D visualisation in Parasitology: the construction of a 3D model of a parasite from 2D illustrations

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Abstract. Three-dimensional (3D) models of the marginal hooks, dorsal and ventral anchors, bars and haptoral reservoirs of a parasite, *Sundatrema langkawiense* Lim & Gibson, 2009 (Monogenea) were developed using the polygonal modelling method in Autodesk 3ds Max (Version 9) based on two-dimensional (2D) illustrations. Maxscripts were written to rotate the modelled 3D structures. Appropriately orientated 3D haptoral hard-parts were then selected and positioned within the transparent 3D outline of the haptor and grouped together to form a complete 3D haptoral entity. This technique is an inexpensive tool for constructing 3D models from 2D illustrations for 3D visualisation of the spatial relationships between the different structural parts within organisms.

INTRODUCTION

One of the problems encountered in studying structural and functional morphology of small organisms, in particular parasites such as the monogeneans (Platyhelminthes), is a lack of visualisation in three dimensions. Although the anatomical structures of all organisms are three dimensional (3D), images (line drawings and photographs) are usually two dimensional (2D) and thus provide an incomplete visualisation of their structural morphology. 3D visualisation has been successfully addressed in medicine and engineering using various hardware, e.g. magnetic resonance imaging (MRI) (Richard, 2000) and computed tomography (Mclntosh *et al.*, 2005), and related software (e.g. 3D Doctor) (Peña & Foote, 2008). Currently in the biological sciences there are dedicated CAD (computer aided design) software with the capability of producing 3D images from scanning electron microscopic (SEM), transmission electron microscopic (TEM) and confocal laser scanning microscopic images; this has been done for invertebrates (Semmler *et al.*, 2009), fungi (Dickson & Kolesik, 1999), mammalian cells (Ikonomov *et al.*, 2001), and recently for hard parts of monogeneans (Galli *et al.*, 2007). 3D models and 3D animations of the male and female human anatomy have also been developed for medical education as exemplified by the visible human project (VPH) (National Library of Medicine, 2009). The current 3D biological images were obtained from expensive electron and confocal microscopes which are not readily available to many researchers. Hence there is a need for an alternative method to develop 3D models of biological specimens in particular micro-organisms for 3D visualisation. Most of the structural information of micro-organisms are usually derived from light microscopy studies and the images obtained (line drawings, photographs) are 2D in nature. We are currently exploring the use of 3D software

to construct 3D models from 2D illustrations. To date, there is a paucity of published records on the use of 2D illustrations as the input image for constructing 3D models of biological materials despite the fact that 2-D illustrations are common forms of visual presentations in Biology, particularly in Taxonomy and 3D modelling softwares have been around for many years and widely used in architecture, engineering and in the entertainment industry (see above and below). Murakawa *et al.* (2006) also used 2D images but as subjects to guide deformation of selected previously developed generic 3D models in developing 3D model of an ant.

The aim of this project is to develop a 3D model prototype of the haptor (attachment organ) of a monogenean parasite of fish, which will allow us to study and understand the structural and functional morphology as well as the spatial relationships of diagnostic features (structural components) of the haptor. In this paper, we present the methods used in constructing 3D models of the hard and soft haptoral structures of the monogenean, *Sundatrema langkawiense* Lim & Gibson, 2009 and the assembly of the modelled 3D parts to form a complete 3D haptor based on existing 2D illustrations of *S. langkawiense*.

Technique

Choice of software

Various 3D software products, such as NewTek LightWave, Caligari Truespace, Google SketchUP Pro, Autodesk Autocad, Autodesk 3ds Max and Autodesk Maya, have the capabilities to construct 3D models from 2D illustrations for engineering (Fang *et al.*, 1996), architecture (Clayton *et al.*, 2002), cartoons and movies (Tuncay, 2001). As already noted, in biological and biomedical sciences, electron microscopic (EM) and confocal microscopic images are currently used as inputs for 3D model development (see above). In this project, our image sources are not images from EM

and confocal microscope, but 2D illustrations, so we have confined our choice of software to the software that are able to use 2D illustrations as input to develop the 3D models. After evaluating some of the available 3D software such as Autodesk AutoCAD, Autodesk 3ds Max and Autodesk Maya and their various modelling shape options, we decided to use Autodesk 3ds Max (version 9) mainly because this software supports imported digitised 2D Adobe Illustrator images. Unlike AutoCAD, which uses geometric shapes, 3ds Max uses polygonal shapes and a smoothing modifier to construct natural shapes. Polygonal modelling enables the designer to push, pull or extrude primitive shapes (cylinder, cube, cone, pyramid and spheres) to quickly fashion the desired form (Murdock, 2007).

The 3D modelling process

It should be noted that each Figure has axes (showing direction particularly rotational direction and orientation of the object in 3D space) associated with it to denote whether they are 2D image (indicated by x-y axes) or 3D models (indicated by x-y-z axes).

1. Preparing and importing 2D illustration into Autodesk 3ds Max (Version 9)

The monogenean, *S. langkawiense*, was chosen because it has a typical yet simple haptor. Images of the shape of the haptor and the hard and soft haptoral parts of *S. langkawiense* were captured using a Leica digital camera and image analysis software (QWin Plus) and were drawn on a digitising tablet (WACOM) using Adobe Illustrator software (Lim & Gibson, 2009). The resulting 2D illustrations of the haptor and haptoral parts of *S. langkawiense* (Fig. 1) serve as the template for the 3D constructions. Each of the illustrated hard parts (anchors, bars and marginal hooks), the haptoral reservoirs and the outline of the haptor was selected individually, converted to JPEG format and imported into Autodesk 3ds Max (Version 9) for 3D modelling.
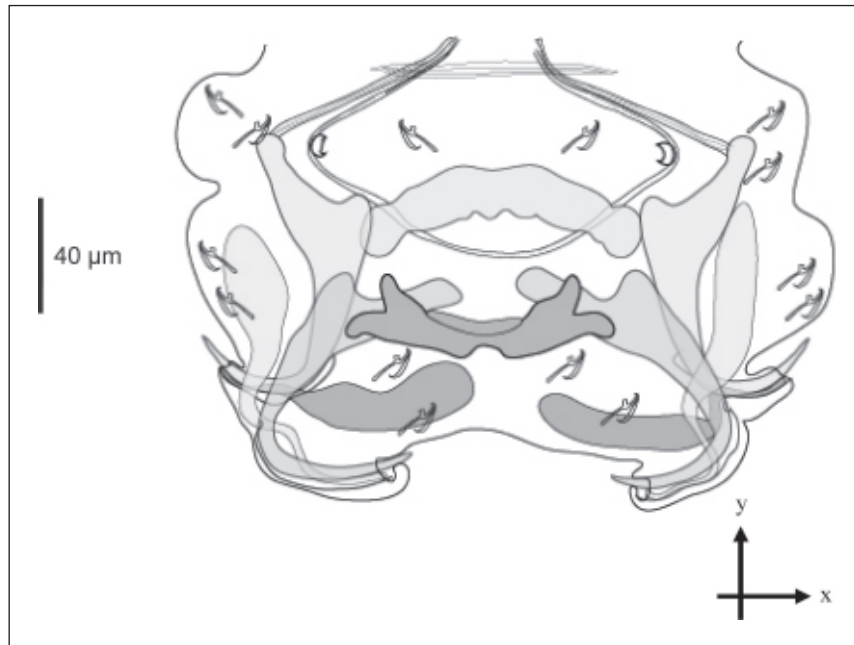
Figure 1. 2D image of the entire haptor of *Sundatrema langkawiense* Lim & Gibson, 2009, showing the arrangement of the diagnostic hard and soft parts

2.   Polygonal modelling of haptoral parts using selected primitive shapes

The polygonal modelling method was used to develop 3D models of the different haptoral parts (see above). Three of the available primitive polygonal shapes in the 3ds Max software, cylinder, plane and cube, were used to model rounded objects (Murdock, 2007). The selected shapes were aligned onto the selected hard parts. The process of polygonal modelling of a marginal hook is as follows. The cylinder shape was aligned onto the sickle and handle of the marginal hook (Fig. 2a). The edges of cylinder were extruded, by elongating, rotating and scaling, until the whole marginal hook was filled (Fig. 2b). Next, the cylinder-filled part was smoothened using TurboSmooth, the smoothing modifier (Fig. 2c). The plane shape was used to create the 3D domus (filament loop), and the transparency parameter for the domus was adjusted to reduce its opacity in order to produce a thin, transparent effect. Next, the modelled domus was attached to the sickle of the 3D model of the marginal hook (Fig. 2d). The same polygonal modelling procedure was repeated for the dorsal and ventral anchors, dorsal and ventral bars, and the haptoral reservoirs (Figs. 3-6).

3.   Polygonal modelling of the haptor body outline

Prior to the actual 3D modelling of the haptor body outline, a 3D template of its outline was modelled from the 2D illustration of the haptor using the polygonal cube shape (Fig. 7a). A 3D template is necessary in order to construct a more realistic and natural 3D model because the structure of the haptor is more complicated than that of the haptoral parts. Once this was done, the primitive plane shape was selected and aligned on to the 3D haptor template (Fig. 7b). The edges of the plane were extruded by elongating, rotating and scaling, until the entire haptor outline was filled (Fig. 7c). The upper part of the model was then elongated to form the peduncle. Next, the modelled haptor was smoothened using TurboSmooth (Fig. 7d) and the transparency parameter was adjusted to reduce its opacity (Fig. 7e).
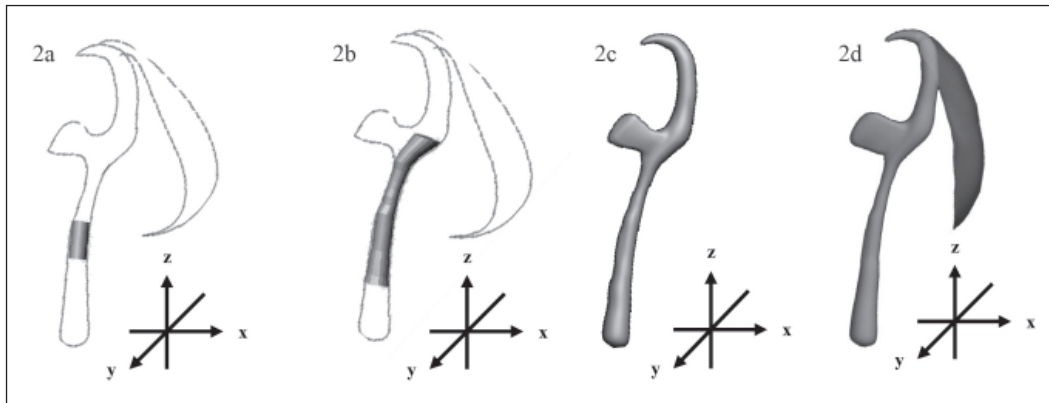
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Figure 2. Polygonal modelling procedure for a marginal hook: a, 3D cylinder aligned on the 2D illustration of handle; b, 3D cylinder extruded to fill the 2D illustration of marginal hook; c, smoothened 3D model; d, 3D marginal hook with the domus
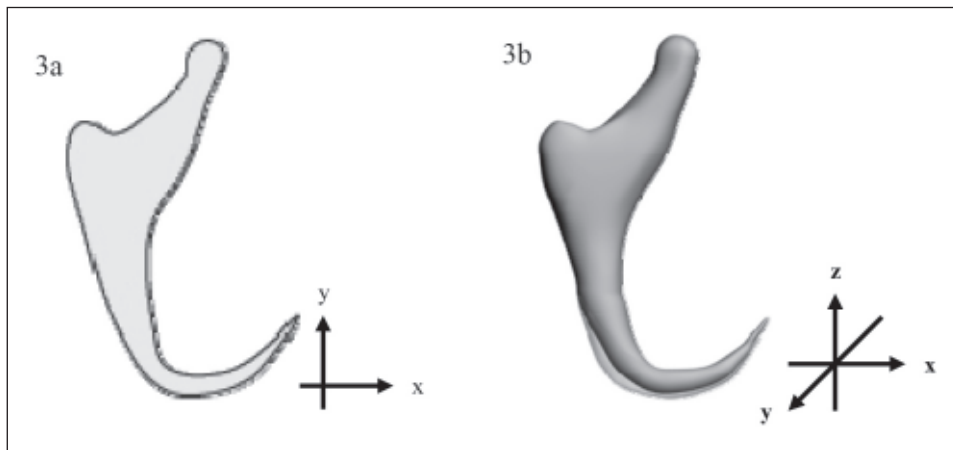

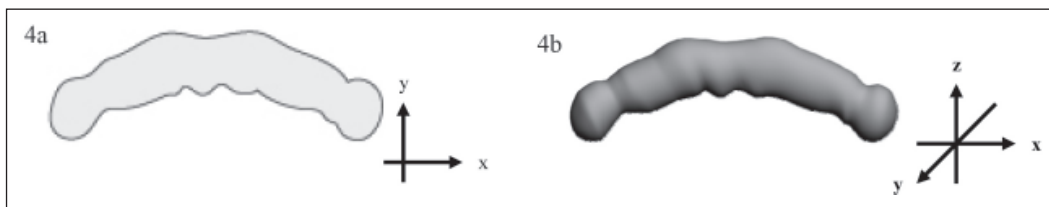Figure 3. Polygonal modelling for an anchor: a, 2D illustration; b, smoothened 3D model

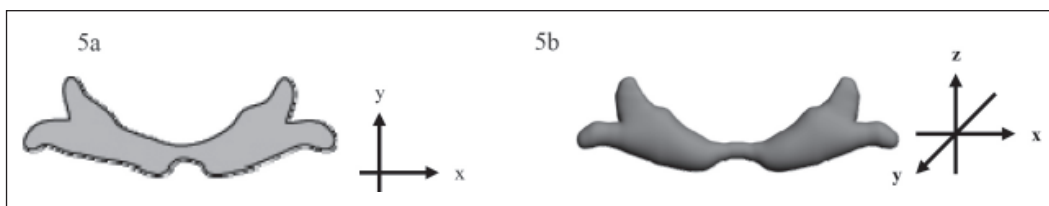Figure 4. Polygonal modelling for the dorsal bar: a, 2D illustration; b, smoothened 3D model

Figure 5. Polygonal modelling for the ventral bar: a, 2D illustration; b, smoothened 3D model
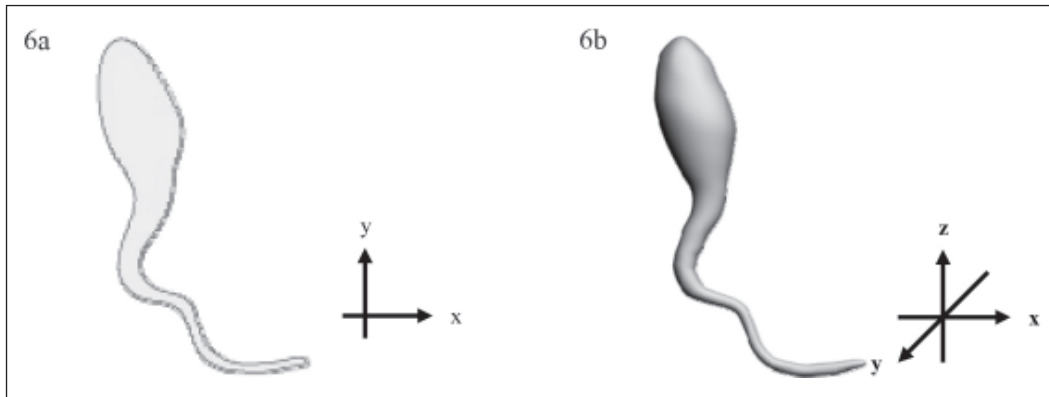
Figure 6. Polygonal modelling for a haptoral reservoir: a, 2D illustration; b, smoothened 3D model
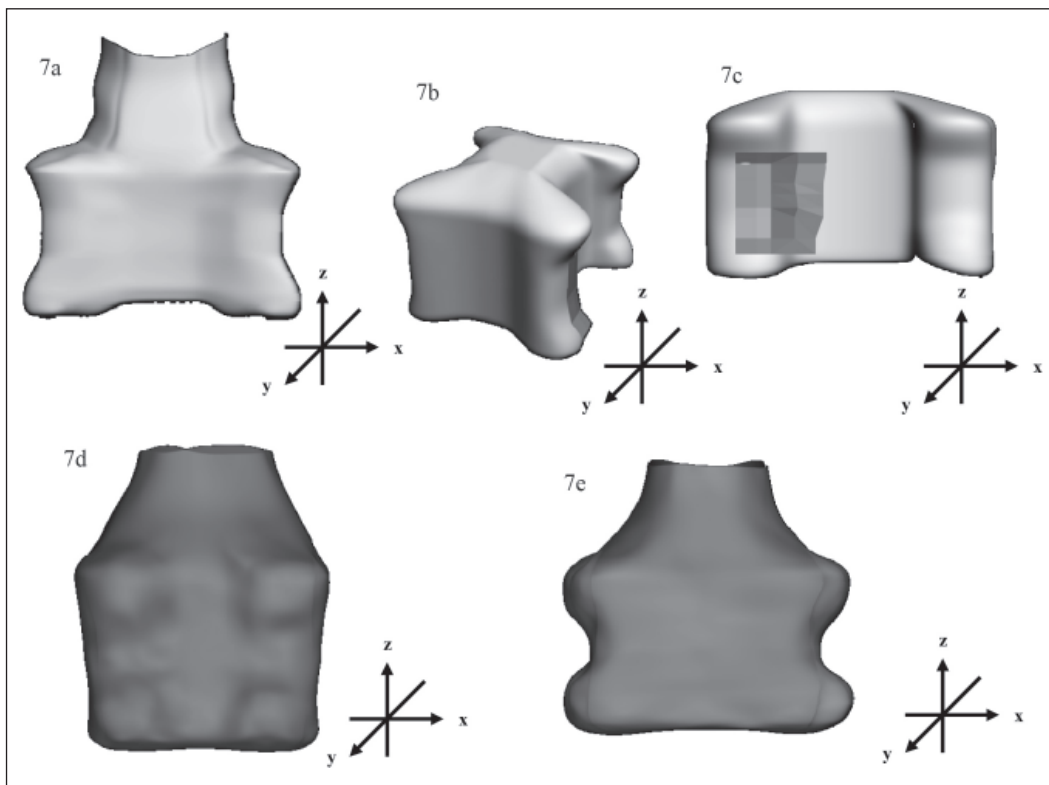

Figure 7. Polygonal modelling procedure for the haptoral outline: a, 3D template; b, 2D plane aligned on the 3D template; c, plane extruded to fill 3D haptoral template; d, smoothened 3D model of haptor shape; e, transparent 3D modelled outline

4. MaxScripts for the rotation of the modelled 3D parts

In order to correctly orientate the modelled 3D haptoral parts prior to assembling them into the modelled 3D haptor body outline, Maxscript (scripting language for 3ds Max) was written to create a graphical user interface (GUI) for controlling the rotation of the 3D models. The GUI includes four buttons that will control rotation in four different directions: left, right, up and down. The first part of the Maxscript defines the

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EulerAngle, a value that represent the rotation degree along x and z axes of the model.

```
euAngle3=eulerAngles -10 0  0
euAngle4=eulerAngles  10 0  0
euAngle1=eulerAngles  0 0 -10
euAngle2=eulerAngles  0 0  10
```

The second part labels the four buttons as "Left Rotation", "Right Rotation", "Up Rotation" and "Down Rotation".

```
button rotation1 "Left Rotation"
button rotation2 "Right Rotation"
button rotation3 "Up Rotation"
button rotation4 "Down Rotation
```

Finally, the third part assigns EulerAngle values defined in the first part to each of the four buttons in order to rotate the 3D models. The correctly orientated 3D modelled hard parts were then positioned in their specific locations within the 3D haptor outline and grouped together to form the complete 3D haptor model and to enable the 3D haptor to be rotated as a single entity (Fig. 13).

```
on rotation1 pressed do
(
    rotate $Group02 euAngle1
    )
on rotation2 pressed do
(
    rotate $Group02 euAngle2
)
on rotation3 pressed do
(
     rotate $Group02 euAngle3
     )
on rotation4 pressed do
(
    rotate $Group02 euAngle4
    )
```

5. Assembling the 3D haptor

The constructed 3D haptoral parts were rotated through various degrees using the MaxScripts (see above). The appropriate orientations were then selected and the 3D parts assembled in their respective positions in the transparent 3D haptor outline (Fig. 13) and grouped together as a 3D entity (whole haptor). The positions and orientations of the various 3D parts were checked and compared against the 2D illustration as well as the actual specimens of *S. langkawiense* deposited in the Zoological Museum in the University of Malaya, Kuala Lumpur to ensure that the 3D parts are properly assembled.

RESULTS

The results of the 3D modelling and the different views of the 3D models of the different hard parts rotated in x and z axes using the Maxscripts are shown in Figs. 2-7 and Figs. 8-12, respectively. Fig. 8c shows the domus or filament loop as a thin hood-like sheet covering the dorsal part of the marginal hooks rather than just a stringy loop as in its 2D illustration (Fig. 2a). In the 3D model of the anchor the 'filament' of the anchor is shown as a thin elongate sheet enveloping the dorso-lateral region of the anchor point (cf Fig. 9a and 9d). The shapes of the anchors and marginal hooks vary when rotated as shown in Figs. 9 and Figs. 8, respectively.

The 3D model of the whole haptor (Fig. 13) shows the spatial relationships of the various haptoral elements in a transparent 3D haptor. The 3D parts are positioned in the transparent 3D haptor (Fig. 13) as in the 2D illustration (Fig. 1) and their relative positions were checked against the specimens of *S. langkawiense* deposited in the UM parasite collection. The 3D model of the whole haptor (Fig. 13) can be rotated 360º in 3D space to show the lateral, dorsal and ventral views (Figs. 14a-14d).

DISCUSSION

The main reason for this present study is to determine whether it is possible to construct 3D models from 2D illustrations that will enable 3D visualisations of the shapes of haptoral parts and their spatial relationships within the haptor. The resulting graphics above show that it is
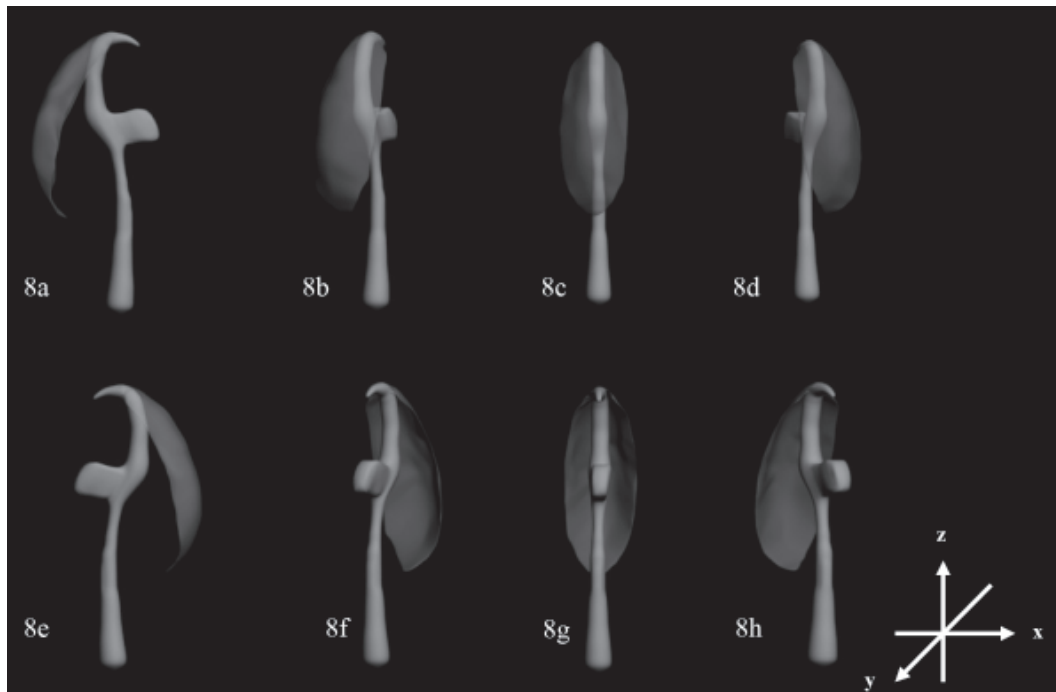
Figure 8. Views of a 3D marginal hook at different degrees of rotation (anti-clockwise) in the x-axis: a, side view at 0º rotation; b, at 60º; c, at 90º; d, at 120º; e, at 180º; f, at 240º; g, at 270º; h, at 300º
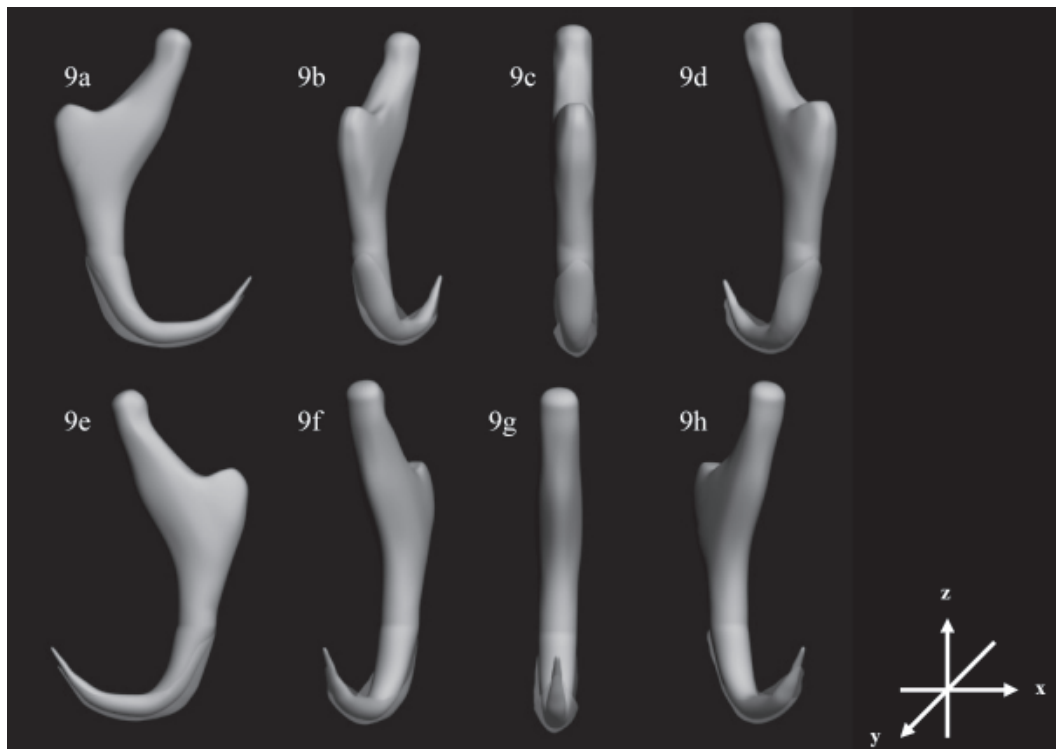

Figure 9. Views of a 3D dorsal anchor at different degrees of rotation (anti-clockwise) in the x-axis: a, side view at 0º rotation; b, at 60º; c, at 90º; d, at 120º; e, at 180º; f, at 240º; g, at 270º; h, at 300º
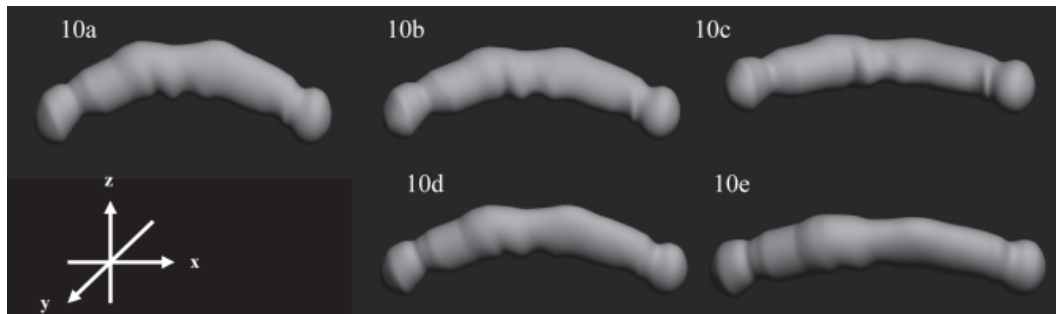
Figure 10. Views of a 3D dorsal bar at different degrees of rotation in the z-axis: a, frontal view at 0º rotation; b, at 30º (anti-clockwise); c, at 60º (anti-clockwise); d, at 30º (clockwise); e, at 60º (clockwise)
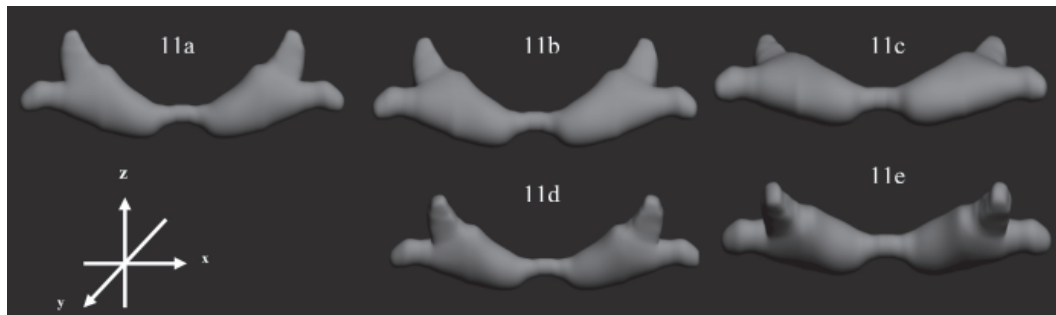

Figure 11. Views of the 3D ventral bar at different degrees of rotation in the z axis: a, frontal view at 0º rotation; b, at 30º (anti-clockwise); c, at 60º (anti-clockwise); d, at 30º (clockwise); e, at 60º (clockwise)

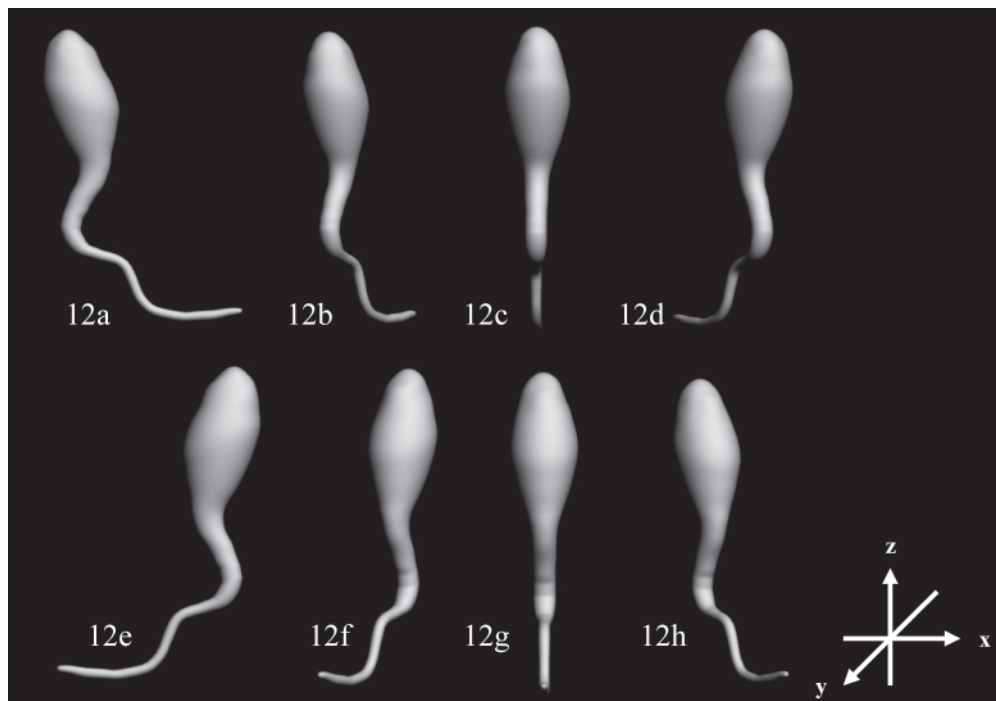

Figure 12. Views of the 3D haptoral reservoir at different degrees of rotation (anti-clockwise) in the x axis: a, side view at 0º rotation; b, at 60º; c, at 90º; d, at 120º; e, at 180º; f, at 240º; g, at 270º; h, haptoral reservoir at 300º
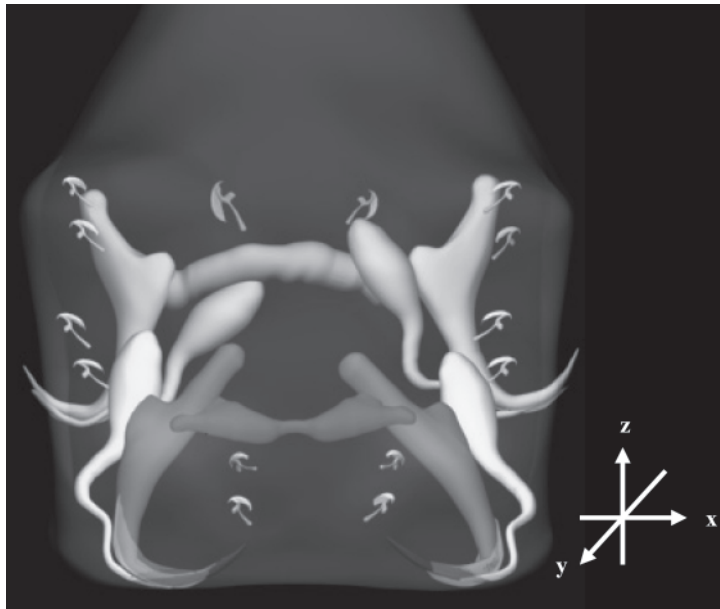
Figure 13. Assembly of 3D haptoral parts into 3D haptor Outline

possible to use 3ds Max software to construct 3D models from 2D illustrations (cf Fig. 1 and Fig. 13) thus providing researchers and students of parasitology with a tool to construct 3D models of their specimens from 2D illustrations for 3D visualisation.

Using the Maxscripts the 3D models of the marginal hooks and anchors are rotated through 360° and the resulting rotated images show that the shapes of the anchors, bars, haptoral reservoirs and marginal hooks are dependent on their orientations (Figs. 8-12). The resulting views of the rotated 3D hard-parts (Figs. 8-12 and Fig. 14) show that the orientations of the hard parts can affect their shapes. This confirms that the orientation of the worm at the time of preservation will affect the shape and perhaps also morphometric measurements of the hard parts of the parasites, thus supporting the need to flatten the worms in such a way as to have a horizontally disposed anchor, which gives the best view for measurement and taxonomic comparison (Lim & Gibson, 2009). In the future, it is likely that more advanced 3D techniques might obviate the need for such flattening. It is important to orientate the component parts correctly prior to assembling them in their correct ventral or dorsal positions in the haptor, since faulty orientation will cause erroneous results in terms of spatial relationships. The rotation of the whole 3D haptor as an entity allows us to visualize the spatial relationships of the diagnostic haptoral hard-parts within the haptor (Figs. 14). Compared with 2D images, 3D models provide additional visualisation capabilities for the study of organisms. 3D models and 3D visualisation will be extremely helpful to explain how component parts are able to function synergistically in a complex haptor.

This method of constructing 3D models is a relatively fast and an inexpensive way to study organisms compared to the expensive and tedious confocal and EM technologies. Although the developed 3D prototype has been shown to be a useful alternative to 3D images developed from confocal and TEM images, there are various limitations in the present modelling procedures that have to be rectified before the resulting models match the information from 3D models from confocal and TEM images. However it should be noted that the 3D models constructed from 2D
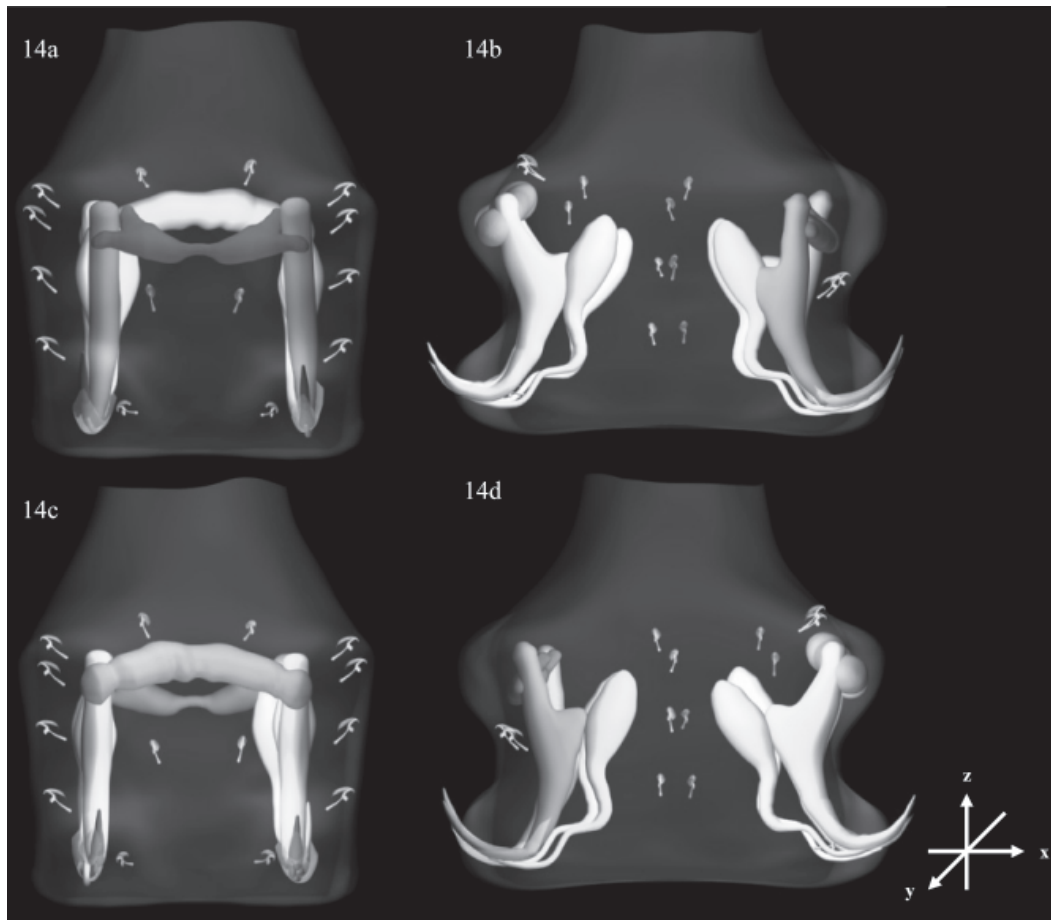
Figure 14. Views of the entire 3D haptor model in different degrees of rotation (anticlockwise): a, ventral view; b, at 90º (lateral view); c, at 180º (dorsal view); d, at 270º

illustrations have the advantage of being more versatile and the researchers can interactively manipulate and orientate the different constructed 3D parts for a better understanding of how the different structures function. On the other hand, 3D images developed from serial confocal or TEM images cannot be manipulated in the same manner. More work is needed to refine the present procedures and techniques in 3D modelling particularly in the transparency parameter adjustment and rendering processes. It is also necessary to explore and test different modelling tools and polygonal shapes to further improve the constructed 3D models.

Although we have constructed the shapes of the 3D models as accurately as possible based on the 2D illustrations, we did not include their morphometric dimensions mainly because data on the thickness of the different hard parts are not available from the 2D illustration nor in the species descriptions (Lim & Gibson, 2009) but might be useful in 3D models. We are currently looking at obtaining thickness information from histological sections and this parameter will be incorporated in our 3D modelling procedures in the future 3D modelling of the whole worm. We also plan to test the accuracy and compare the 3D haptors of monogeneans developed from 2D illustrations with corresponding 3D model from confocal and TEM microscopic images.

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