Fig. 1 shows the partitioning dimension of objects (subpart links for disjoint classes). For some of them (i.e. septa), other dimensions such as multi-instantiation (x symbol) and specialization (^ symbol) of objects can be seen. The former enables users to describe several sorts of the same object by descriptive iteration (there are 4 possible instances for septa in Fig. 1) and the latter lets users name each sort with the help of the following classification tree of objects (specialization links in Fig. 2).

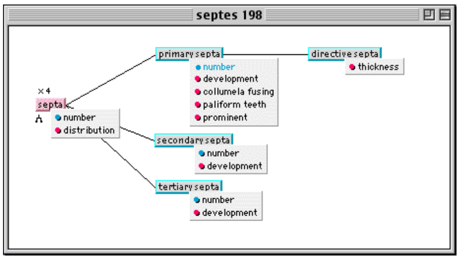

Fig. 2. Classification tree of object "septa"

In fact, one of the roles of the descriptive model is to bring an observation guide for the end-user: the objects are linked together by relations that go from the most general to the most specific (from left to right), making the next description process easier for the non specialist (see below).

3.2 The descriptions

Starting from the selection of a descriptive model, the program automatically generates a questionnaire [4]. It permits the less informed biologists, as the expert, to acquire personal descriptions and create a case base. An identification name is associated to each observation in order to form a description or a case (Fig. 3).

The description process generates sub-trees of the descriptive model (Fig. 1 and Fig. 3). Therefore, observed descriptions can be directly compared to one another by leafing through page by page: this navigation process is easier than viewing different lists of attribute-value pairs.

In Fig. 3, we illustrate possibilities of IKBS for rendering complete and comprehensive descriptions of a given sample.

Different types of attribute are used: taxonomic ones (e.g. general shape of object colony), numerical intervals (e.g. diameter of apical parts) and multi-nominal values (e.g. section of apical parts). The latter shows variation in objects displaying a set of multiple elements.

The visualization of objects differs graphically according to their status: black if present, black with a cross if absent, dimmed if unknown (see object "hood" at the bottom-right side of Fig. 1 and Fig. 3).

At last, an object can be specialized (e.g. the septa of calices from apical parts, see Fig. 1): the result is a substitution of its name by a more precise one (e.g. primary septa, see Fig. 3) with its associated attributes (inherited or not, see Fig. 2).

It is important for the user to visualize structured descriptions: so doing brings better clarity and comprehensibility to the acquisition phase. This is the most important part of our methodology for acquiring good results of classification and identification.