OBJECTIVES

To determine the risk of malignancy (ROM) in atypia of undetermined significance (AUS) and to assess which cytomorphologic features can be triaged to either benign or malignant category.

METHODOLOGY

Seventy seven (77) AUS cases with subsequent surgical follow-up from three tertiary hospitals from 2014 – 2018 were included. Smears were reviewed based on cellularity, and cytologic and architectural atypia. Cellularity was classified as mild (6 to 9 cell clusters), moderate (10 to 12 cell clusters), and marked (more than 12 cell clusters). Cytologic atypia included enlarged nuclei and/or pale chromatin, irregular nuclear contour, nuclear pseudoinclusions and/or grooves, atypical cist lining cells, histiocytoid cells, hurthle cells, paxilloma bodies, and atypical lymphoid cells. For architectural atypia, microfollicles, branching sheets and/or monolayers were used. Overall and subgroup ROMs were computed. Classification tree analysis using “rpart” and “partyplot” packages in “R” programming language was performed to identify which parameter/s of AUS can separate benign from malignant smears.

RESULTS

Overall ROM was 52%. Malignancy rate with mild, moderate, and marked cellularity did not differ much at 50%, 60%, and 48%, respectively. In the presence or absence of nuclear pseudoinclusions and/or grooves and presence or absence of irregular nuclear contour, ROM was 60%, 45%, 53%, and 50% respectively. Classification tree analysis showed that presence of nuclear pseudoinclusions and/or grooves yielded an ROM of 60%. In their absence, markedly cellular smears tend to be benign with ROM of 33.3%. Mildly to moderately cellular smears without nuclear pseudoinclusions but with nuclear contour irregularity tend to be malignant with ROM of 53%. Other parameters as predictors of malignancy could not be reliably assessed with their limited numbers.

CONCLUSIONS

Overall malignancy rate of 52% is higher than the Bethesda System reference rate of 10.30%. Nuclear pseudoinclusions, nuclear contour irregularity, and assessment of cellularity are useful AUS parameters that would help differentiate benign from malignant categories.

REFERENCES


Table 1. The rates of malignancy in cases with mild, moderate, and marked cellularity did not differ much at 50, 60, and 48% respectively. The number of cases with inadequate cellularity is too small (1 case only) to make a confident interpretation.

Table 2. Rate of malignancy in cases with nuclear pseudoinclusion and/or grooves is higher (60%) than in cases without them (45%).

Figure 1. Classification tree analysis using the “rpart” and “partyplot” packages in “R” programming language. Decision tree first classifies the smear according to the presence of nuclear pseudoinclusions and/or grooves. If present, ROM is 60% and the decision tree classifies the smear as malignant. If absent, decision tree classifies the smear according to cellularity. If there is marked cellularity, decision tree classifies the smear as benign with ROM of 33.3%. If the smear is inadequate, or there is only mild to moderate cellularity, decision tree uses presence of nuclear contour irregularity. If present, the smear is classified as malignant, with ROM of 53%.