# Comparison of different methods in order to identify Proteus spp

**Castro S.T., Rodriguez C.R., Perazzi B.E., Radice M., Paz S., Muzio H., Juarez J., Gutkind G., Famiglietti A.M., Santini P.I., Vay C.A.**
Cátedra de Análisis Clínicos I, Laboratorio de Bacteriología, Departamento de Bioquímica Clínica, Facultad de Farmacia y Bioquímica, Hospital de Clínicas Jose de San Martin, Universidad de Buenos Aires, Ciudad Autónoma de Buenos Aires, Argentina.

Comparison of different methods in order to identify Proteus spp. The objectives were: (a) to identify Proteus strains to species level, following Farmer's and O'Hara's conventional biochemical reactions; b) to evaluate the sensitivity and specificity of both the API 20E method and a schema of reduced reactions (TSI and MIO agar: motility, indole and ornithine) comparing them with conventional methodology, and c) to evaluate the utility of SDS-PAGE (total proteins) in order to identify Proteus strains to species level. Two hundred and five Proteus spp. clinical isolates, were collected between January 1998 and September 2004, from inpatients and outpatients at Hospital de Clinicas. Strains were identified by means of conventional methodology, the API 20E method, and a schema of reduced reactions. SDS-PAGE (total proteins) was used in 48 out of the 205 strains. The API 20E method identified 79 out of 87 (90.8%) strains of P. mirabilis, 103 out of 103 P. vulgaris complex, and 15 out of 15 P. penneri. Eight strains of P. mirabilis were identified as Proteus spp., the acid production from maltose being necessary to identify them to species level. The schema of reduced reactions identified 205 out of 205 (100%) strains, that is, this schema of reduced reactions identified all the strains to species level without any additional tests, in marked contrast to the API 20E method. The SDS-PAGE (total proteins) identified the three species of the genus, even if the strains of P. mirabilis showed different biochemical reactions.