

ABIS online - Advanced Bacterial Identification Software, an original tool for phenotypic bacterial identification

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ABSTRACT

Microorganisms' phenotypic identification to species level is, sometimes, one of the most difficult stages of bacteriological examination. For this purpose, many identification systems become available in recent years, from commercial identification kits, to online software. Each of these systems has its limitations: constraining the user to a predefined set of tests, limited interactivity, no relations to the ecological significance and pathology of the isolated strains. To tackle these problems we have created ABIS online, a laboratory tool for bacterial identification, based on morphology, biochemical characters, cultural characteristics, ecology and pathogenicity data. The aim of the study was to present and validate ABIS software by comparison to a commercially available identification system (API strips and *apiweb*[™] bioMerieux software), testing 16 reference strains and 123 wild isolates. *apiweb*[™] confirmed ABIS's results with a high percentage, showing a very good taxa identification by ABIS software.

INTRODUCTION

In the fields of applied bacteriology, human and veterinary clinic, phytopathology and also in environmental microbiology, bacterial strains from various sources are routinely isolated and phenotypically identified. Beside a properly equipped laboratory, this activity, on the edge between science, technique, craftsmanship and art, requires specific culture media, reagents, experienced specialists in bacteriology, and a bacterial identification system. The identification systems may be the manuals of bacteriology (1-4), Bergey's Manuals of Determinative (5, 6) and Systematic (7-9) Bacteriology, review articles on specific bacteria categories (10), commercial systems like *apiweb*[™] (bioMerieux), Biolog, and online systems. Each of these systems has its limitations, well-known by the specialists (no interactivity, no updating for the newly described taxa, constraining the user to a predefined set of

tests, no instant connection to a database of ecological significance and pathology of the isolated strains). To tackle these problems we created ABIS online - Advanced Bacterial Identification Software (<http://www.tgw1916.net>), a laboratory tool for bacterial identification, based on morphology, biochemical characters, cultural characteristics, ecology and pathogenicity data. The program allows a great flexibility in choosing biochemical tests and it is an alternative to commercial systems, code-books or identification tables. It is a free software, available on World Wide Web since 2007, being increasingly used by students, young researches, biologists and human and veterinary clinicians.

The aim of the study was to present and validate ABIS software by comparison to a commercially available, standardized identification system.

MATERIALS AND METHODS

ABIS online (*ABIS online - bacterial identification software* version 12, <http://www.tgw1916.net>) is a free bacterial identification software available on World Wide Web. The identification scheme is based on the comparison between the morphological and biochemical character values of the isolated strain and standard values of taxa contained in the database. Thirteen databases are currently available, covering areas of *Enterobacteriaceae*, *Pasteurellaceae*, *Campylobacteraceae*, *Bacillaceae*, *Lactobacillaceae*, *Staphylococcaceae*, *Streptococcaceae*, *Clostridium*, *Vibrio* and *Aeromonas*, *Listeriaceae*, *Neisseriaceae*, *Corynebacterium*, and Non-fermenters.

The databases were created taking into consideration the characteristics of type strains of each species, the characteristics of strains existing in international collections and rigorously characterized strains, generally described in Bergey's Manual of Systematic Bacteriology (7-9), Bergey's Manual of Determinative Bacteriology (5, 6), International Journal of Systematic and Evolutionary Microbiology, Topley & Wilson's Manual (1), as well as review articles (10).

ABIS is not an annex of an identification kit, so the type and number of the required tests are not limited by a pattern and can vary by lab availabilities. Depending on the number of the introduced tests, ABIS calculates the percentage of similarity with taxa from the database and the accuracy of identification. The quality of results

depends on the number of tests entered by the user. At least 8 tests are required, and the maximum depends on laboratory capacity and database limitations. ABIS databases contain an average of 40-50 tests from which the user can choose.

The most important feature of ABIS is that it allows the user to instantly access data from Encyclopedia about morpho-biochemical characters, cultural characteristics, ecology and pathogenicity of the identified taxa, leaving the final decision to the human factor, not to the machine.

The morphological and biochemical characters of 16 reference strains and 123 wild isolates were tested by ABIS online and apiweb™ software (bioMerieux) using all laboratory available tests (classical tests and API bioMerieux strips). The reference strains were derived from ROMVAC Company and Cantacuzino Institute Bacterial Collections. The wild strains were isolated from various human, animal and environmental sources: milk, urine, pus, vaginal secretion, ear secretion, skin, internal organs from deceased animals (liver, kidney, lungs, bone marrow, salpinx), yolk sac, sanitation tests and animal feed.

Commercially available tests (Gram staining, oxidase, Simmons citrate, Triple Sugars Iron -TSI-, Motility Indole Urea -MIU-, hemolysis on sheep blood agar), together with commercially available API bioMerieux kits (API 20E, API 20 NE, API Staph, API Strep, API Campy, API 20A and API 50CHB/CHL) were used for identification.

RESULTS

Table 1 shows the tested reference strains and results of comparative identification with ABIS online and apiweb™ software.

Table 1. Comparative reference strains identification between ABIS online and apiweb™ software

#	Strain name and code	ABIS results id % ^a	apiweb™ results id % ^b
1.	<i>Staphylococcus aureus</i> ATCC 25293	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 99%	<i>Staphylococcus aureus</i> 97.8%
2.	<i>Helicobacter pylori</i> ATCC 43504	<i>Helicobacter pylori</i> 94%	<i>Helicobacter pylori</i> 99.9%
3.	<i>Bacillus thuringiensis</i> NCIMB 9134	<i>Bacillus thuringiensis</i> 93%	<i>Bacillus cereus</i> , possibility of <i>B. thuringiensis</i> 98.9%
4.	<i>Bacillus megaterium</i> NCIMB 8508	<i>Bacillus megaterium</i> 90%	<i>Bacillus megaterium</i> 99.6%
5.	<i>Clostridium tetani</i> RO-2009	<i>Clostridium tetani</i> 97%	<i>Clostridium tetani</i> (no id%)

6.	<i>Salmonella Choleraesuis</i> RO-014	<i>Salmonella spp.</i> 87%	<i>Salmonella choleraesuis</i> 99.7%
7.	<i>Salmonella Typhimurium</i> ATCC 14028	<i>Salmonella spp.</i> 94%	<i>Salmonella spp.</i> 99.9%
8.	<i>Salmonella Typhimurium</i> RO-TM2	<i>Salmonella spp.</i> 89%	<i>Salmonella spp.</i> 99.0%
9.	<i>Proteus hauseri</i> ATCC 13315	<i>Proteus vulgaris / P. hauseri</i> 95%	<i>Proteus vulgaris</i> group 99.8%
10.	<i>Escherichia coli</i> ATCC 8739	<i>Escherichia coli</i> 98%	<i>Escherichia coli</i> 99.9%
11.	<i>Streptococcus mutans</i> ATCC 55677	<i>Streptococcus mutans</i> 98%	<i>Streptococcus mutans</i> 99.9%
12.	<i>Enterococcus faecium</i> NCIMB 10415	<i>Enterococcus faecium</i> 97%	<i>Enterococcus faecium</i> 93.9%
13.	<i>Enterococcus faecium</i> NCIMB 11181	<i>Enterococcus faecium</i> 92%	<i>Enterococcus faecium</i> 99.2%
14.	<i>Pseudomonas aeruginosa</i> ATCC 15442	<i>Pseudomonas aeruginosa</i> 92%	<i>Pseudomonas aeruginosa</i> 98.1%
15.	<i>Lactobacillus plantarum</i> ATCC 8014	<i>Lactobacillus plantarum</i> 91%	<i>Lactobacillus plantarum</i> 1 99.9%
16.	<i>Lactobacillus paracasei</i> CCM 1837	<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i> 94%	<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i> 1 / 3 48.0 / 51.0%

Legend: a- ABIS %id represents the percentage of similarity with taxa from the database, all databases containing a matrix where probabilistic incidence values are allocated for every taxon and their corresponding morpho-biochemical characters; b- apiweb™ %id is a probabilistic calculation using bioMerieux own system procedure.

Very closed results (same taxa, with low difference, $\leq 10\%$, in id%) were obtained for reference strains in comparative identification with ABIS online and apiweb™ software.

Table 2 shows the tested wild strains together with their source of isolation and results of comparative identification with ABIS online and apiweb™ software.

Table 2. Comparative wild strains identification between ABIS online and apiweb™ software.

#	Code of strains	Source	Nr. of tested strains	ABIS results Average id% ^a	apiweb™ results Average id% ^b
1.	CSCT2013, 4295, NA10001, 8004, 10296/2, 6860, 5005, 3483, 10618, 7983 M2/4, 10241	Goat mastitis, chicken arthritis, dog skin, cat skin, cow milk, chicken liver and bone	11	<i>Staphylococcus aureus</i> 94.9%	<i>Staphylococcus aureus</i> 94.8%

marrow					
2.	10697/2G	Cow milk	1	<i>Staphylococcus chromogenes</i> 93%	<i>Staphylococcus chromogenes</i> 86.7%
3.	10177/1, 6C, 10035/2, B	Sheep and cow milk, vaccine contaminant	4	<i>Staphylococcus epidermidis</i> 96%	<i>Staphylococcus epidermidis</i> 94.4%
4.	7292, 1577, 1122M, 468	Dog and cat skin	4	<i>Staphylococcus intermedius</i> 96%	<i>Staphylococcus intermedius</i> 62.1%
5.	3460, 7038	Dog skin	2	<i>Staphylococcus haemolyticus</i> 91%	<i>Staphylococcus haemolyticus</i> 62%
6.	2826	Dog otitis	1	<i>Staphylococcus schleiferi</i> 93%	<i>Staphylococcus schleiferi</i> 44.7%
7.	7066	Dog skin	1	<i>Staphylococcus simulans</i> 89%	<i>Staphylococcus simulans</i> 96.0%
8.	10101/2, 10070/3, 10070/2	Goat and cow milk	3	<i>Staphylococcus xylosus</i> 95% (alternatives: <i>S. gallinarum</i> 93%, <i>S. nepalensis</i> 99%, <i>S. equorum</i> 98%)	<i>Staphylococcus xylosus</i> 98.4%
9.	5997	Environment	1	<i>Staphylococcus carnosus</i> 88%	<i>Staphylococcus carnosus</i> (no id%)
10.	StrM, 10201/4.1, 10324/3	Human skin lesion pus, goat and sheep milk	3	<i>Streptococcus agalactiae</i> 92.6%	<i>Streptococcus agalactiae</i> 99.7%
11.	NA10002	Sheep intestine	1	<i>Streptococcus bovis</i> 96%	<i>Streptococcus bovis</i> 67%
12.	85, 15040	Swine lungs	2	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> 84%	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> 92.5%
13.	10245/2.3	Goat milk	1	<i>Streptococcus mutans</i> 83%	<i>Streptococcus mutans</i> 99.7%
14.	10078, NA10003	Rabbit lungs, human throat	2	<i>Streptococcus pyogenes</i> 88% (alternative: <i>Gemella palaticanis</i> 86%)	<i>Streptococcus pyogenes</i> 43.9% (alternative: <i>S. oralis</i> 88.3%)
15.	1560/2pl, 10568	Pig lungs, pig arthritis	2	<i>Streptococcus suis</i> 90%	<i>Streptococcus suis</i> 98.8%
16.	10101/3	Bovine vaginal secretion	1	<i>Enterococcus durans</i> 98%	<i>Enterococcus durans</i> 99.4%
17.	10706 5sv, 10462, 7307, 1961/4 sv	Chicken yolk sac, chicken feces, dog skin pus	4	<i>Enterococcus faecalis</i> 93%	<i>Enterococcus faecalis</i> 99.1%
18.	10101/1, 10497-2R	Bovine vaginal secretion, goat kidney	2	<i>Enterococcus faecium</i> 92%	<i>Enterococcus faecium</i> 95.7%
19.	10234	Cow milk	1	<i>Lactococcus lactis</i> , subsp. <i>lactis</i> 90%	<i>Lactococcus lactis</i> , subsp. <i>lactis</i> 90.4%
20.	5265	Sanitation test from swine farm	1	<i>Stenotrophomonas maltophilia</i> 91%	<i>Stenotrophomonas maltophilia</i> 45%
21.	7292, 10535	Chicken yolk sac, water	2	<i>Pseudomonas aeruginosa</i> 88.5%	<i>Pseudomonas aeruginosa</i> 98.8%

22.	4209 10765	Dog urinary infection, cat vaginal secretion	2	<i>Chryseomonas luteola</i> 91%	<i>Chryseomonas luteola</i> 99.8% (no id% for 1 strain)
23.	1924/7	Chicken feces	1	<i>Moraxella lacunata</i> 96%	<i>Moraxella lacunata</i> 85.7%
24.	10826/8sv	Chicken yolk sac	1	<i>Acinetobacter baumannii</i> / <i>A. calcoaceticus</i> 91%	<i>Acinetobacter baumannii</i> / <i>A. calcoaceticus</i> 91%
25.	1509	Chicken intestine	1	<i>Campylobacter jejuni subsp. jejuni biotype</i> 1 86%	<i>Campylobacter jejuni subsp. jejuni biotype</i> 1 99.4%
26.	1821pl, 10828/1	Chicken salpinx, guinea pig lungs	2	<i>Mannheimia haemolytica</i> 85% (alternative: <i>M. glucosida</i> 77% - 1 strain)	<i>Mannheimia haemolytica</i> / <i>Pasteurella trehalosi</i> 77.5%
27.	1560/1pl, CS-G, 10154, 7844	Swine lungs with pneumonia, chicken liver and bone marrow	4	<i>Pasteurella multocida</i> 89%	<i>Pasteurella multocida</i> 95.0%
28.	10163	Goat vaginal secretion	1	<i>Vibrio parahaemolyticus</i> 77%	<i>Vibrio parahaemolyticus</i> 98.9%
29.	518F, 518I	Guinea pig intestine and liver	2	<i>Aeromonas hydrophila</i> 86%	<i>Aeromonas hydrophila</i> 97.9%
30.	10008/2lp	Cow milk	1	<i>Bacillus licheniformis</i> 85%	<i>Bacillus licheniformis</i> 99.9%
31.	10201/2.1	Cow milk	1	<i>Bacillus pumilus</i> 80%	<i>Bacillus pumilus</i> 99.9%
32.	309 op, 309 tr, 10896/2CL	Pig and chicken intestine	3	<i>Lactobacillus fermentum</i> 89.6%	<i>Lactobacillus fermentum</i> 71.7%
33.	IBNA02	Bovine intestine	1	<i>Lactobacillus rhamnosus</i> 84%	<i>Lactobacillus rhamnosus</i> 99.9%
34.	IBNA01	Bovine intestine	1	<i>Lactobacillus paracasei subsp. paracasei</i> 98%	<i>Lactobacillus paracasei subsp. paracasei</i> 99.8%
35.	NA10006, 3043, 10047	Vaccine and medical product contaminants	3	<i>Citrobacter freundii</i> 96.5%	<i>Citrobacter freundii</i> 99.8% (no id% for 2 strains)
36.	10040/2VAC, 10040/4CSC, 1924/1	Chicken feces	3	<i>Citrobacter youngae</i> 91.6%	<i>Citrobacter youngae</i> 99.6%
37.	3879	Dog conjunctivitis	1	<i>Enterobacter amnigenus biotype II</i> 96%	<i>Enterobacter amnigenus biotype II</i> 96%
38.	040905, 1989, 10398/2sv, 10659/8c, 10234, 10392E2col1, 10658sv	Chicken feces, yolk sac, and heart, animal feed, cow milk, dog otitis	8	<i>Enterobacter cloacae</i> 94.7%	<i>Enterobacter cloacae</i> 95.2% (no id% for 1 strain)
39.	10401/2os, 1os, 10272/4sv	Chicken bone marrow (2) and yolk sac	3	<i>Escherichia coli</i> 90.6%	<i>Escherichia coli</i> 99.9%

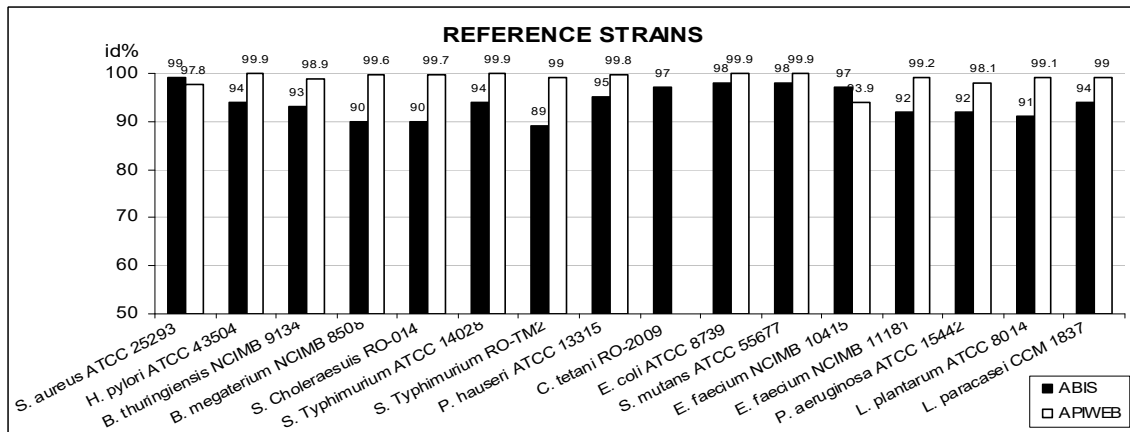
40.	10275/24ou	Chicken egg	1	<i>Escherichia hermannii</i> 96%	<i>Escherichia hermannii</i> 97.7%
41.	NA10004, NA10005	Canary leg necrosis, human urine	2	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> 94.5%	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> 98.2%
42.	3160	Guinea pig	1	<i>Morganella morganii</i> 94%	<i>Morganella morganii</i> 99.9%
43.	1272, 6528 RV, 10531	Pork meat, animal feed, chicken feces	3	<i>Proteus mirabilis</i> 92%	<i>Proteus mirabilis</i> 99.9%
44.	197	Chicken feces	1	<i>Providencia rettgeri</i> 92%	<i>Providencia rettgeri</i> (no id%)
45.	10190/2	Chicken feces	1	<i>Rahnella aquatilis</i> 95%	<i>Rahnella aquatilis</i> (no id%)
46.	10051/1, 3338	Human skin, shampoo sample	2	<i>Serratia marcescens</i> 88.5%	<i>Serratia marcescens</i> 97.4% (no id% for 1 strain)
47.	10234A	Cow milk	1	<i>Serratia liquefaciens</i> 82%	<i>Serratia liquefaciens</i> 99.8%
48.	2946, 8943, 10910, NA10007, 4753, 5276, 6032, 834, 10875, 10298, 10040/5OMV, 10550, 10685, 3269, 6075, 1015art, 1924/9, F8H5, 1676, Buc1F, 3740L-	Chicken liver and feces, pigeon bone marrow, arthritis and intestine, guinea pig bone marrow, animal feed, wild boar liver, pig feces, lungs, liver, and heart	21	<i>Salmonella</i> spp. 91.3%	<i>Salmonella</i> spp. 91.1% (no id% for 8 strains)
49.	10168	Chicken feces	1	<i>Shigella sonnei</i> 94%	<i>Shigella sonnei</i> 48.6%

Legend: a- ABIS %id represents the percentage of similarity with taxa from the database, all databases containing a matrix where probabilistic incidence values are allocated for every taxon and their corresponding morpho-biochemical characters; b- apiweb™ %id is a probabilistic calculation using bioMerieux own system procedure.

Comparable results (same taxa), but with important difference in the average id% for *Staphylococcus* spp. ($\leq 48.3\%$), *Streptococcus* spp. ($\leq 29\%$) and *Stenotrophomonas maltophilia* (46%), were obtained for wild strains in comparative identification with ABIS online and apiweb™ software.

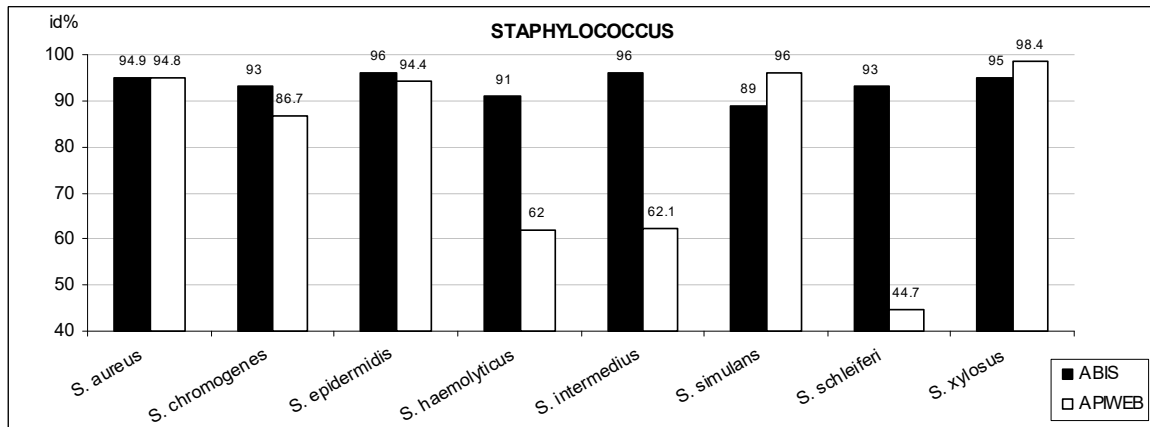
The ABIS online and apiweb™ software comparative identification results of reference strains and wild strains are graphically represented in figures 1 to 5.

Figure 1. Graphic comparison between ABIS (id%, black) and apiweb™ (id%, white) identification of reference strains.



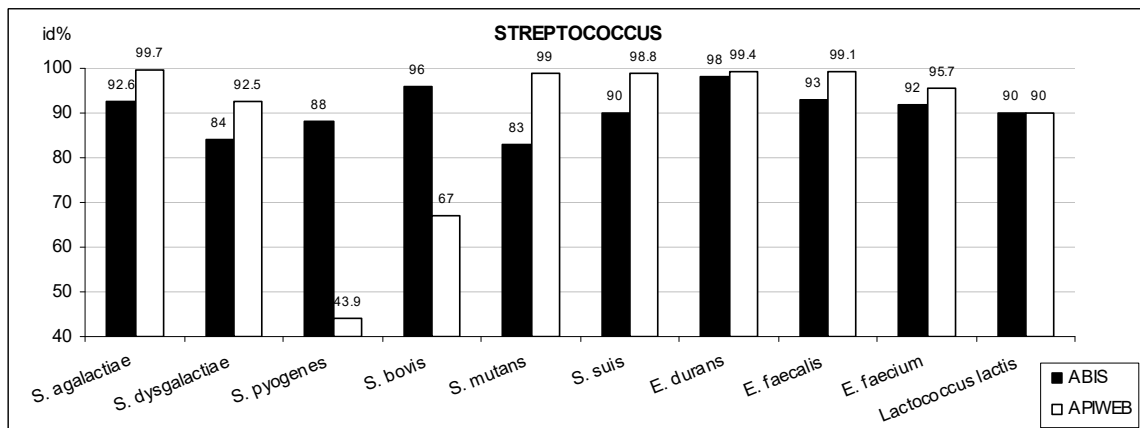
Both software programs returned the same taxa with a close identification percent for reference strains. For the *Clostridium tetani* RO-2009 strain, apiweb™ returned *Clostridium tetani* identity without an id%.

Figure 2. Graphic comparison between ABIS (id%, black) and apiweb™ (id%, white) identification of *Staphylococcus* spp., wild strains.



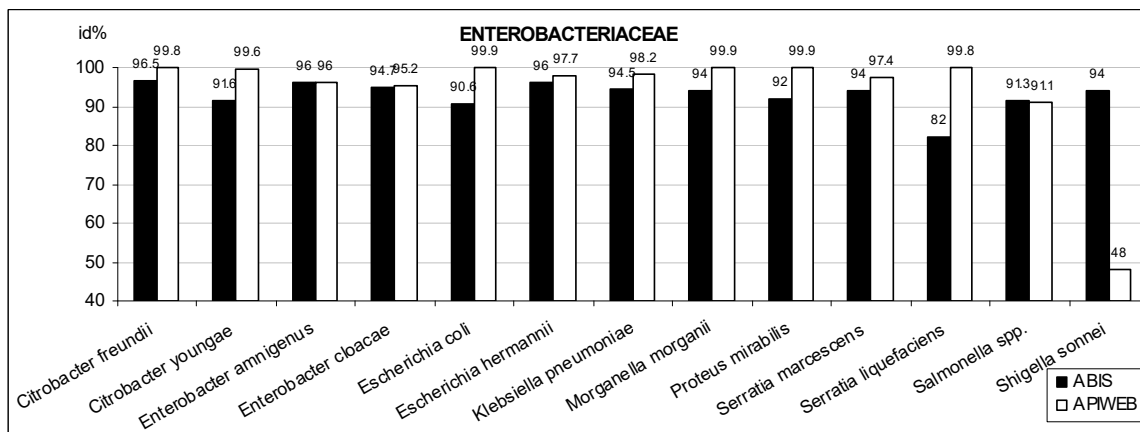
Apiweb™ returned low id% for the wild strains of *Staphylococcus haemolyticus* (62%), *S. intermedius* (62.1%) and *S. schleiferi* (44.7%). ABIS returned high id% (≥ 89%) for all wild strains of *Staphylococcus* spp.

Figure 3. Graphic comparison between ABIS (id%, black) and apiweb™ (id%, white) identification of *Streptococcus spp.* and related taxa, wild strains.



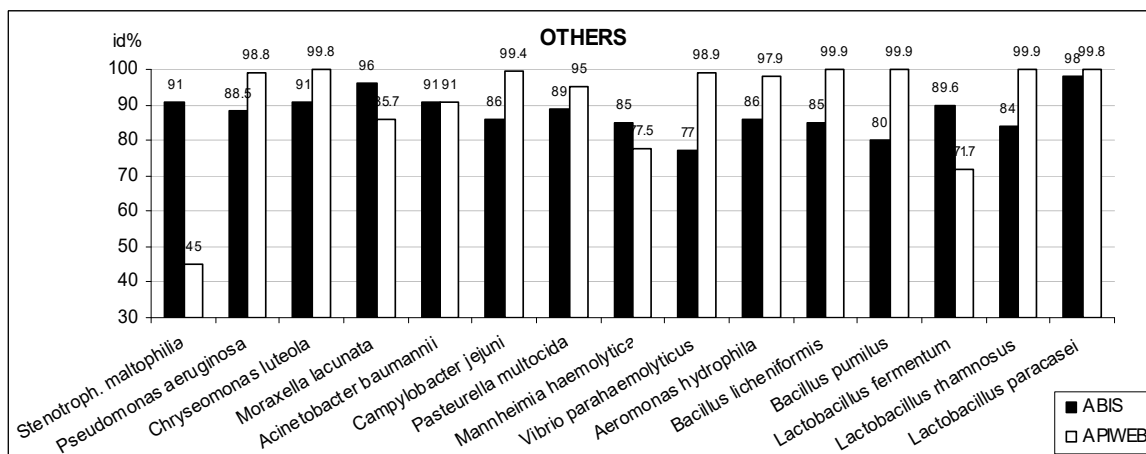
Apiweb™ returned low id% for the wild strains of *Streptococcus pyogenes* (43.9%) and *S. bovis* (67%). ABIS returned high id% ($\geq 83\%$) for all wild strains of *Streptococcus spp.* and related taxa.

Figure 4. Graphic comparison between ABIS (id%, black) and apiweb™ (id%, white) identification of *Enterobacteriaceae*, wild strains.



Apiweb™ returned low id% for the wild strain of *Shigella sonnei* (48%) only. ABIS returned high id% ($\geq 82\%$) for all wild strains of *Enterobacteriaceae*.

Figure 5. Graphic comparison between ABIS (id%, black) and apiweb™ (id%, white) identification of other bacteria, wild strains.



Apiweb™ returned low id% for the wild strains of *Stenotrophomonas maltophilia* (45%), *Lactobacillus fermentum* (71.7%) and *Mannheimia haemolytica* (77.5%). ABIS returned 77% for a strain of *Vibrio parahaemolyticus*, 80% for a strain of *Bacillus pumilus* and 84% or higher for rest of wild strains of other bacteria.

Apiweb™ “unacceptable” profiles and species not included in apiweb™ database are not represented in these charts.

DISCUSSIONS

Comparable results were obtained in ABIS and apiweb™ bacterial identification systems, both for reference and wild strains. In most cases both software programs returned the same taxa and a close identification percent.

For 16 strains apiweb™ considered the profile to be “unacceptable”, thus returned a suggested taxon without calculating the id% and without validating its results. In all these cases ABIS confirmed apiweb's suggested taxa with a high id%.

Apiweb™ returned an id% lower than 80% for 9 species (*Staphylococcus schleiferi*, *S. haemolyticus*, *Stenotrophomonas maltophilia*, *Salmonella spp.*, *Shigella sonnei*, *Streptococcus pyogenes*, *Streptococcus bovis*, *Mannheimia haemolytica*, and *Lactobacillus fermentum*), while ABIS returned low id% for 2 species (*Bacillus pumilus* and *Vibrio parahaemolyticus*).

For the reference strain *Clostridium tetani* RO-2009 apiweb™ returned *Clostridium tetani* without calculating an id%, as an alternative result after *Egerthella lenta* 75%, *Clostridium spp.* 16.9% and *Clostridium hystolyticum* 3%, while ABIS result was *Clostridium tetani* 97%.

Proteus hauseri is biochemically similar to strains commonly identified as *Proteus vulgaris*, but esculin and salicin negative. Since these tests were not available neither in lab, nor in API galleries, the ATCC 13315 - *Proteus hauseri* strain was identified by ABIS as “P. vulgaris / P. hauseri”, and by apiweb™ as “P. vulgaris group”.

When identifying *Salmonella*, results were almost similar, the id% differing only by 0.2%. Moreover, 17 *Salmonella* strains were serologically confirmed by “O”-antisera agglutination, 1 strain was confirmed by a national reference lab as *Salmonella* Typhimurium, and 1 strain was confirmed by a national reference lab as *Salmonella* Kottbus.

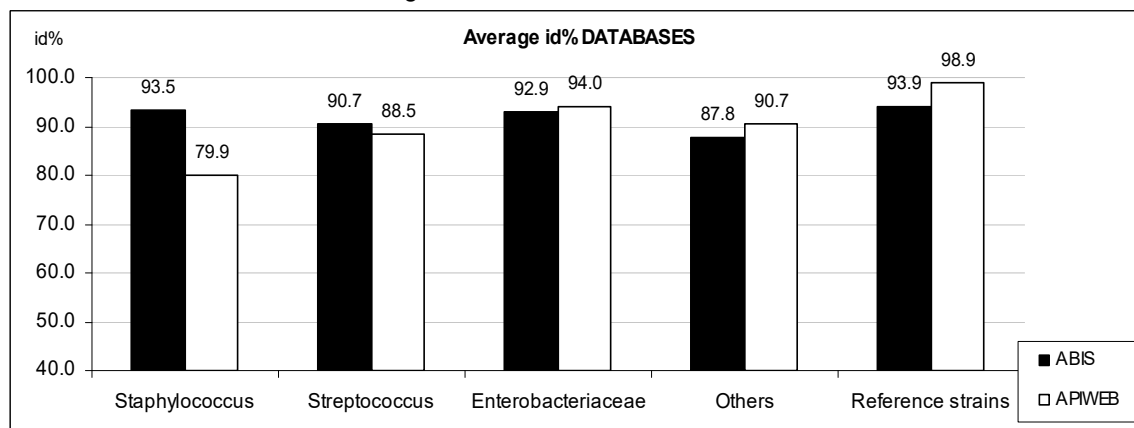
When identifying *Mannheimia haemolytica*, apiweb™ could not differentiate *M. haemolytica* from *Pasteurella trehalosi*. In one case ABIS returned *Mannheimia glucosida* as an alternative result. The validated result was *M. haemolytica* regarding ecology and pathogenicity.

When identifying *Streptococcus pyogenes*, for one strain apiweb™ returned an alternative option: *Streptococcus oralis*, while ABIS returned *Gemella palaticanis* as an alternative. In both cases the final result was *S. pyogenes* regarding strain’s ecology and pathogenicity.

When identifying *Staphylococcus xylosus*, ABIS returned multiple choices including: *S. gallinarum*, *S. nepalensis* and *S. equorum*. The validation of *S. xylosus* as final result is doubtful since apiweb™ database does not include the above taxa.

Comparison of the average id% of wild strains per ABIS and apiweb™ databases shows that ABIS got 13.6% higher identification score for staphylococci (93.5% vs 79.9%), 2.2% higher for streptococci (90.7% vs 88.5%), 1.1% lower for *Enterobacteriaceae* (92.9% vs 94.0%) and 2.9% lower for other bacteria (87.8% vs 90.7%). ABIS’s average id% of reference strains was 5.0% lower than apiweb’s (93.9% vs 98.9%) (fig. 6).

Figure 6. Graphic comparison between ABIS (id%, black) and apiweb™ (id%, white) database average id% for wild and reference strains.



Overall, ABIS achieved an average id% of 91.8% and apiweb™ 90.4%, ABIS showing an identification percent higher by 1.4%. Moreover, ABIS results have been correlated with ecological, morphological, biochemical and pathological characters of the identified taxa.

The variation range of apiweb™ id% (43.9 to 99%) was wider than ABIS (77 to 99%) which shows that the ABIS system is more homogenous and consistent.

CONCLUSION

Apiweb™ confirmed ABIS's results with a high id%, proving very good taxa identification by ABIS program. ABIS online (*ABIS online - bacterial identification software* version 12, <http://www.tgw1916.net>) is capable of correct phenotypical species identification, generates reliable results, is a powerful tool for microbiology lab and the Encyclopedia connection provides essential information about the ecological significance, pathology and other features of the identified strains.

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