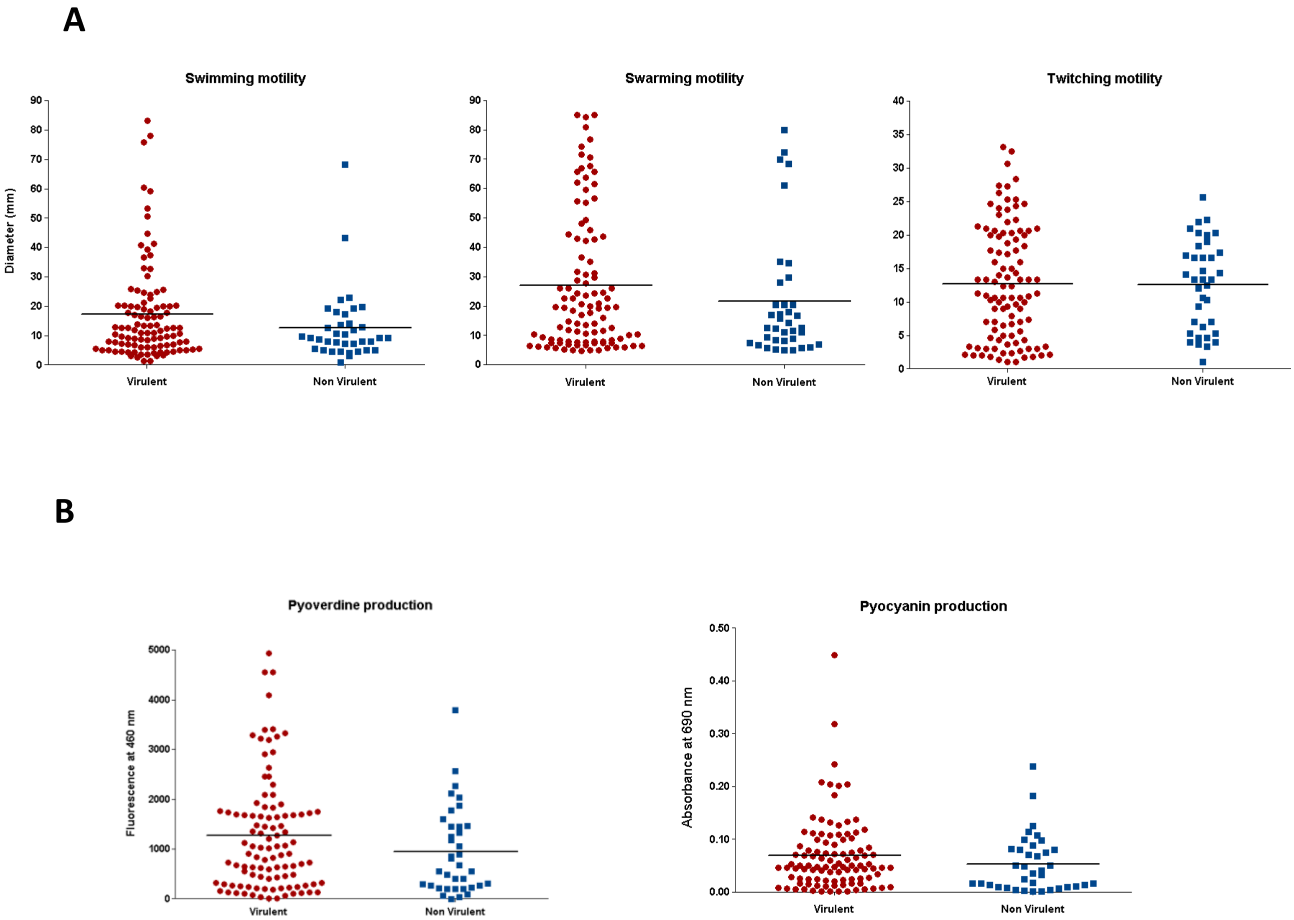
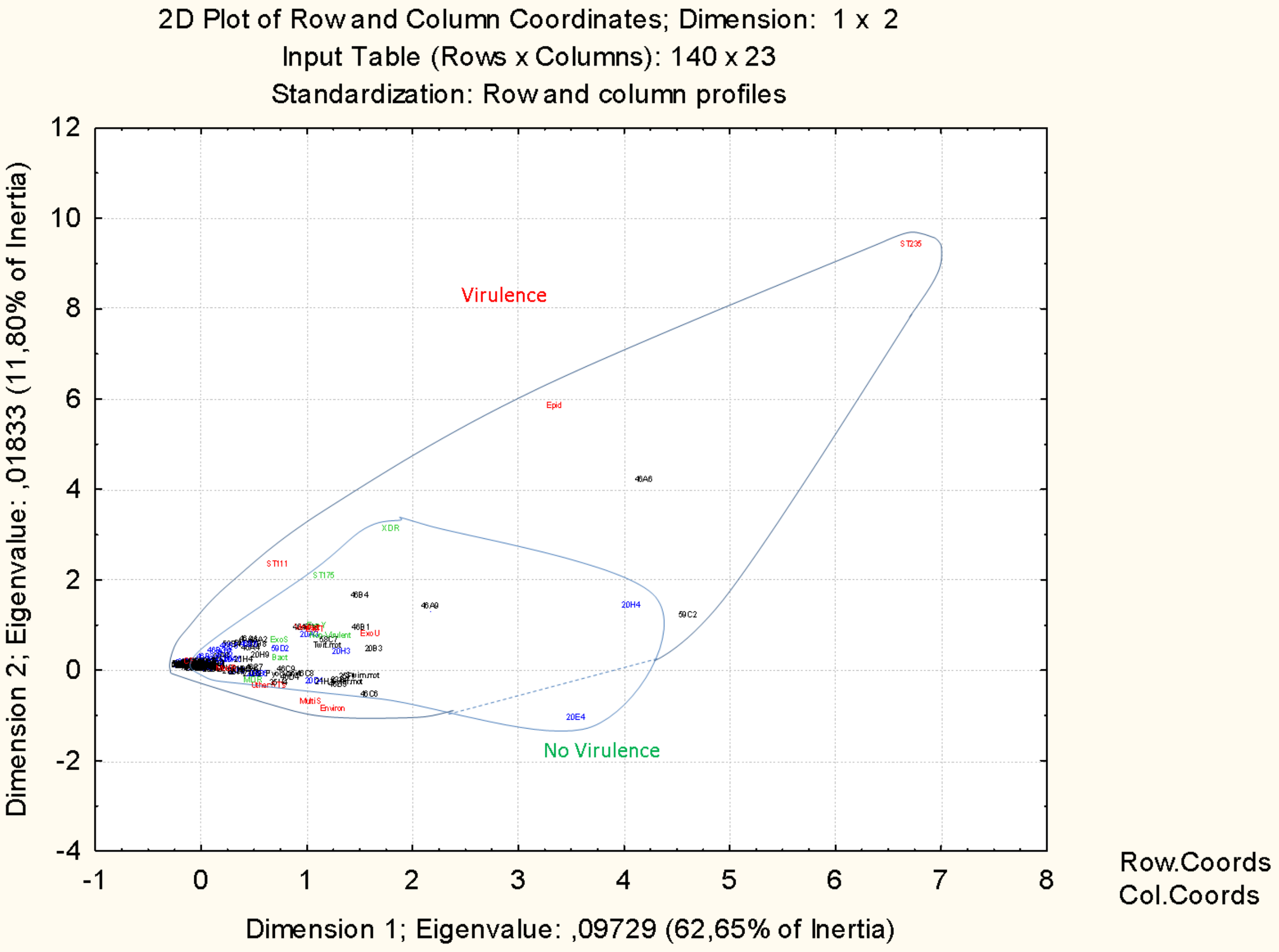
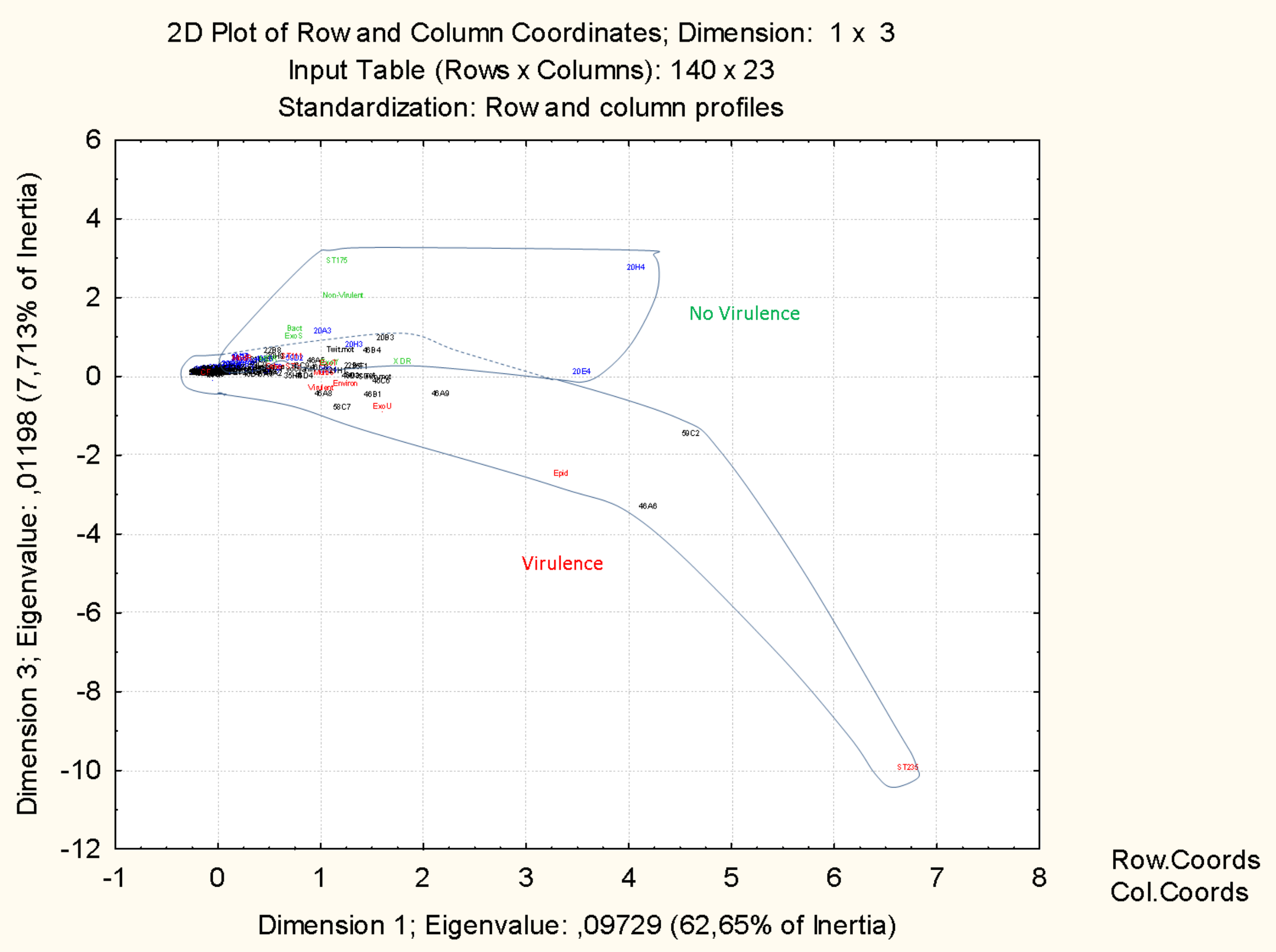


Figure S1. Comparative analyses of swimming, swarming and twitching motility assays (**A**) and pyoverdine and pyocyanin production assays (**B**) in virulent (CEVS 3-5) versus non-virulent (CEVS 1-2) isolates in the *C. elegans* model.


2D Plot of Row and Column Coordinates; Dimension: 1 x 2
Input Table (Rows x Columns): 140 x 23
Standardization: Row and column profiles
Dimension 2; Eigenvalue: ,01833 (11,80% of Inertia)
Dimension 1; Eigenvalue: ,09729 (62,65% of Inertia)
12
10
8
6
4
2
0
-2
-4
-1
0
1
2
3
4
5
6
7
8
Row.Coords
Col.Coords
Virulence
No Virulence
ST235
Epid
46A6
XDR
ST111
ST175
46B4
46A9
20H4
59C2
46B1
ExoY
ExoT
Non-Virulent
ExoU
58C7
Twit.mot
20H3
20B3
ExoS
59D2
Bact
20H9
20H4
46C9
46C8
Swim.mot
MDR
Other STs
46C6
MultiS
Environ
20E4



2D Plot of Row and Column Coordinates; Dimension: 1 x 3
Input Table (Rows x Columns): 140 x 23
Standardization: Row and column profiles
Dimension 3; Eigenvalue: ,01198 (7,713% of Inertia)
Dimension 1; Eigenvalue: ,09729 (62,65% of Inertia)
6
4
2
0
-2
-4
-6
-8
-10
-12
-1
0
1
2
3
4
5
6
7
8
Row.Coords
Col.Coords
No Virulence
Virulence
ST175
Non-Virulent
Bact
Exo S
20A3
20H3
20B3
20H4
Twit.mot
46B4
22B8
XDR
46A5
ExoT
22B5F1
35H6D4
20E4
Virulent
Environ
46A8
46C6
46B1
46A9
58C7
Exo U
CF
59C2
Epid
46A6
ST235

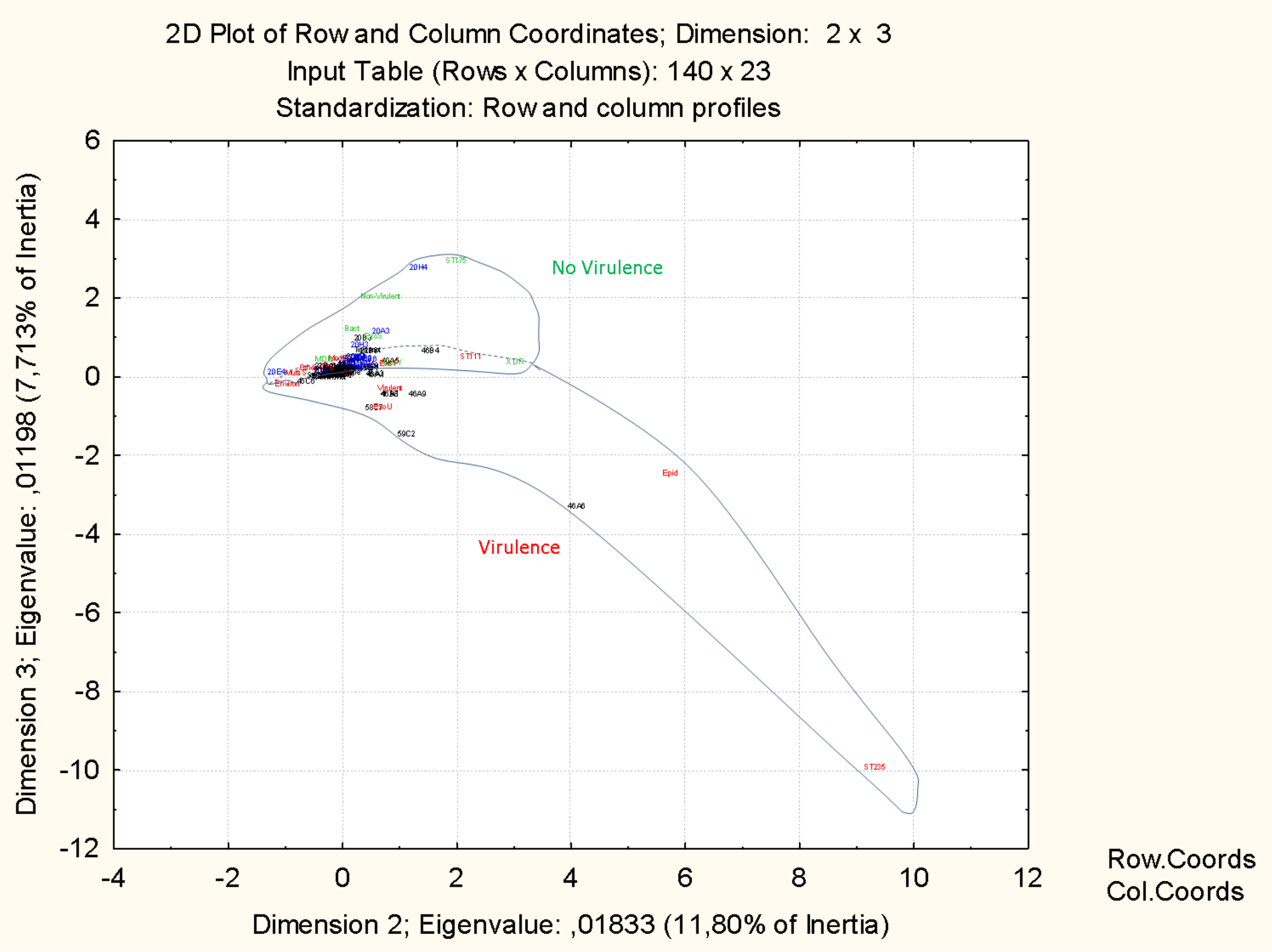
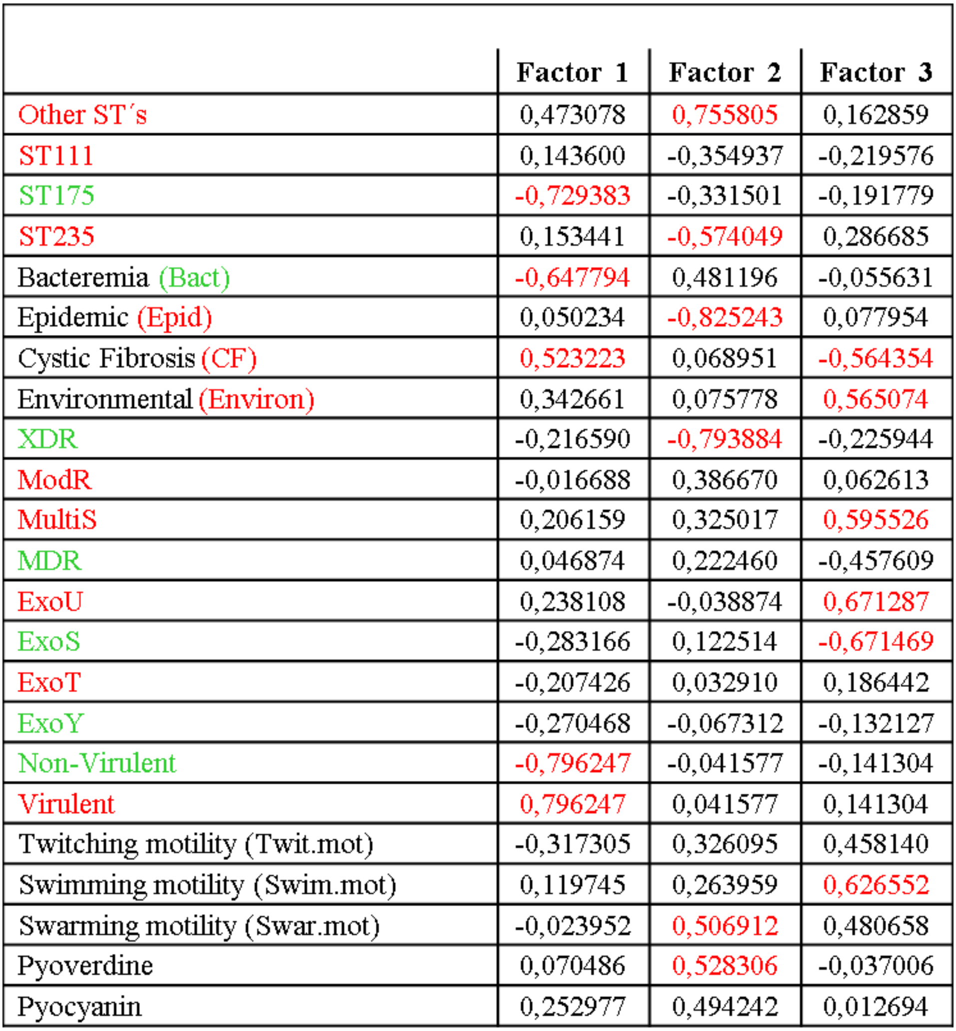


Figure S2. Disposition of clones and variables in the Factorial Space according to the Correspondence Analysis. The three first axis explain the 82.16% of total variation or inertia. Over the general background it is possible to infer the virulent and non-virulent structure based in those inferred by Factorial Analysis (Fig. 4).



	Factor 1	Factor 2	Factor 3
Other ST´s	0,473078	0,755805	0,162859
ST111	0,143600	-0,354937	-0,219576
ST175	-0,729383	-0,331501	-0,191779
ST235	0,153441	-0,574049	0,286685
Bacteremia (Bact)	-0,647794	0,481196	-0,055631
Epidemic (Epid)	0,050234	-0,825243	0,077954
Cystic Fibrosis (CF)	0,523223	0,068951	-0,564354
Environmental (Environ)	0,342661	0,075778	0,565074
XDR	-0,216590	-0,793884	-0,225944
ModR	-0,016688	0,386670	0,062613
MultiS	0,206159	0,325017	0,595526
MDR	0,046874	0,222460	-0,457609
ExoU	0,238108	-0,038874	0,671287
ExoS	-0,283166	0,122514	-0,671469
ExoT	-0,207426	0,032910	0,186442
ExoY	-0,270468	-0,067312	-0,132127
Non-Virulent	-0,796247	-0,041577	-0,141304
Virulent	0,796247	0,041577	0,141304
Twitching motility (Twit.mot)	-0,317305	0,326095	0,458140
Swimming motility (Swim.mot)	0,119745	0,263959	0,626552
Swarming motility (Swar.mot)	-0,023952	0,506912	0,480658
Pyoverdine	0,070486	0,528306	-0,037006
Pyocyanin	0,252977	0,494242	0,012694

Table S1. Factor Analysis for studied variables. The numbers represent the factor loadings (relative explanation) of the variables according the three main factors which were extracted by Principal components approach. Factor Loadings were Varimax normalized (Marked loadings are >,50). Most of variables are also well represented in the factorial space which link strains and variables (Fig. S2). Variables negatively or positively associated with virulence are shown in green or red color, respectively. Red data indicates the most important factors.