Does Integron-Coded Protein structure Depicts Simplicifolious and Non Simplicifolious Relationship?

[1]B.T. Thomas, [2]D.S.K. Olanrewaju-Kehinde, [3]E.S James, [4]A. Davies, [1]R.M. Kolawole and [2]O.D. Popoola

[1]Department of Cell Biology and Genetics, University of Lagos, Akoka, Lagos, Nigeria
[2]Department of Microbiology, Olabisi Onabanjo University, Ago-Iwoye, Ogun State, Nigeria
[3]Department of Clinical Pharmacy, Olabisi Onabanjo University, Sagamu, Ogun State, Nigeria
[4]Department of Medical Microbiology and Parasitology, Babcock University, Ilisan-Remo, Ogun State, Nigeria
benthoa2013@gmail.com

Abstract: The study evaluated the association between evolutionary relationship and the protein structure of class 1 integron-coded proteins of *Citrobacter freundii* and *Serratia marcenscens*. The prediction of the secondary structure of the class 1 integron coded protein was carried out using SOPMA tool. Results of the NCBI queries revealed significant identity with class 1 integron of the studied Organisms. The nucleotide sequence alignment depicted lesser numbers of conserved regions with varying degree of transitions, transversions, insertions and deletions. The isolates contained comparatively higher random coils and alpha helix than both extended strands and the Beta turn which were present in less percentages ranging from 17.46-22.42% and 11.48-8.56% respectively. In conclusion, this study confirmed a very strong association between the protein structure and the simplificifolius relationship observed in this study

[B.T. Thomas, D.S.K. Olanrewaju-Kehinde, E.S James, A. Davies, R.M. Kolawole and O.D. Popoola. **Does Integron Coded Protein structure Depicts Simplicifolious and Non Simplicifolious Relationship?** *Biomedicine and Nursing* 2016;2(1):1-3]. ISSN 2379-8211 (print); ISSN 2379-8203 (online). http://www.nbmedicine.org. 1. doi:10.7537/marsbnj02011601

Keywords: Integron; Protein Structure; Simplicifolious, Relationship

1. Introduction

Integrons are genetic elements that contain the component of a site-specific recombination system which recognizes and captures mobile gene cassettes [1]. These bacterial genetic elements allows the shuffling of smaller mobile elements called gene cassettes and so they are called genetic construction kit for bacteria [2]. They usually harbor antibiotic resistance genes and hence play a vital role in the emergence of new multidrug resistant bacteria [3].

These class 1 integrons tend to share certain levels of similarities at the nucleotides level while some levels of variation also occurred due to different types of nucleotides substitution in form of transition, transversion, deletion and insertion. Integrons by themselves are not mobile [4, 5], but they may be part of a mobile elements like transposons and plasmids [6, 7] which further enhance the spread of antibiotic resistance genes. Large conjugative plasmids harbouring both class 1 and class 2 integrons have been reported from *Salmonella* [8]. There are at least eight classes of integrons [9, 10], but those found in clinical isolates belong to four main classes according to their integrases and associated cassettes [11, 12].

Class 1 integrons have been described as the main mobilizers of antibiotic-resistance genes amongst enteric bacteria and according to Thomas *et al.*, [13], the phylogenetic analysis of the class one integron of some GNEB retrieved from NCBI gene bank revealed significant evolutionary relationships despite being from different enteric organisms. They further stressed that Class 1 integrons shared several conserved regions except in few organisms with lesser levels of conserved regions. However, how these nucleotides conservation level transforms into a common or different evolutionary ancestry in terms of being simplicifolious or not remain a topical question to be answered. This study was therefore aimed at evaluating the association between simplicifolious relationship and evolutionary ancestry using *Citrobacter freundii* and *Serratia marcenscens* as research specimens.

2. Material and Methods

In Silico:

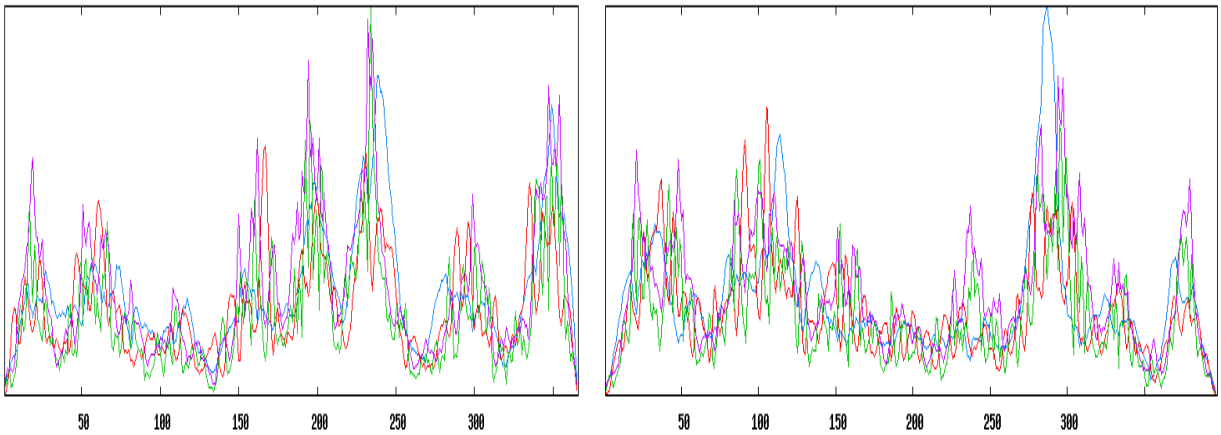
The sequences AY069972, DQ402098 were obtained using nucleotide BLAST (http:// blast.ncbi.nlm.nih.gov/ Blast.cgi) [14] and subjected to evolutionary analysis using the MEGA explorer [15]. Pairwise distances were calculated using Kimura 2 parameter. In MEGA explorer, translate option was used for converting the gene sequence into amino acid sequence. Sequence similarity search with BLASTP and best homologous protein was found using the multiple sequence alignment. Secondary structure of the protein sequences were predicted using SOPMA tool [16].

3. Results

The above table reveals the protein structure of the studied class 1 integrons. As shown in this table, the class 1 integron coded protein contain comparatively higher random coils and alpha helix than both the extended strands and the Beta turn which were present in less percentages ranging from 17.46-22.42% and 11.48-8.56% respectively. The amino acid sequences length for DQ402098 was 397bp while that of AY069972 was 366bp. The protein sequence when queried against the protein database, depicts no significant relationship with the other protein sequences. The nucleotide sequences prior to translating it using Mega Software were queried against the nucleotide database using the basic local alignment search tool (BLAST) and it was found that these sequences showed maximum identity of 100% for both DQ402098 and AY069972 respectively. The sequence alignment of these class I integron-coded protein reveals a simplicifolious relationship between the integrons.

Table 3.4: The protein structure the studied class 1 integrons

SOPMA PARAMETERS	The protein structure of the studied class 1 integrons	
	AY069972 (%)	DQ402098(%)
Alpha helix	34.43	31.74
Extended strand	17.76	22.42
Beta turns	11.48	8.56
Random coil	36.34	37.28



KEYS:
DQ402098 = *Citrobacter freundii*
AY069972 = *Serratia marcenscens*

Fig. 1: Chromatographical representation of the secondary structure of DQ402098 and AY069972

4. Discussion And Conclusion

The use of protein structure and nucleotide sequences to understand evolution of cell and function of genes cannot be overemphasized. According to Zuckerkandl and Pauling [17], evolutionary relationships between organisms can be studied by comparing their DNA sequences. The fact that two organisms namely *Citrobacter freundii* and *Serratia marscencens* connoted themselves differently on a simplicifolious clade is an indication that the distribution of their nucleotide sequence are substantially different from that of the other organisms. However, such observation may not be unconnected to the fact that such acquired class I integron has rearranged due to different levels of mutation resulting from substitution in form of transition, tranversion, deletion and even insertions. The class 1 integron coded protein contain comparatively higher random coils and alpha helix than both extended strands and the Beta turn which are present in less percentages ranging from 17.46-22.42% and 11.48-8.56% respectively. This knowledge is important as it helps us design low-molecular-weight synthetic agents that reproduce their essential features [18] by using synthetic agents to mimic the helices. In conclusion, this study confirmed a very strong association between protein

structure and simplificifolius organismal relationship for the studied class 1 integrons.

Corresponding Author:
Thomas, Benjamin Thoha
Department of Cell Biology and Genetics
University of Lagos, Akoka, Lagos, Nigeria
Telephone: +234 -806- 401-1412
E-mail: benthoa2013@gmail.com

References

1. Hall, R.M., 1997. Mobile gene cassettes and integrons: moving antibiotic resistance genes in gram negative bacteria. Ciba Found. Symp., 207:192-202.
2. Bennett, P. M., 1999. Integrons and gene cassettes: a genetic construction kit for bacteria. J Antimicrob Chemother., 43:1–4.
3. Hall, R.M., G.D. Recchia, C.M. Collis, H.J. Brown and H.W. Stokes, 1996. Gene cassettes and integrons: moving antibiotic resistance genes in Gram-negative bacteria. In: Antibiotic Resistance: from Molecular Basics to Therapeutic Options, pp. 19–34. Ed., Ama´bile-Cuevas, C.F. New York: Chapman and Hall.
4. Nield, B. S., A.J. Holmes, M.R. Gillings, G.D. Recchia, B.C. Mabbutt, K.M. Nevalainen and H.W. Stokes, 2001. Recovery of new integron classes from environmental DNA. FEMS Microbiol Lett., 195:59–65.
5. Boucher, Y., M. Labbate, J.E. Koenig, H.W. Stokes, 2007. Integrons: mobilizable platforms that promote genetic diversity in bacteria. Trends Microbiol., 15:301–309.
6. Greenberg, B., J.A. Kowalski, M.J. Klowden, 1970. Factors affecting the transmission of Salmonella by flies: natural resistance to colonization and bacterial interference. Infect Immun., 2: 800-809.
7. Holt, P.S., C.J. Geden, R.W. Moore, R.K. Gast, 2007. Isolation of Salmonella enterica serovar enteritidis from houseflies (*Musca domestica*) found in rooms containing *Salmonella* serovar enteritidis-challenged hens. Appl Environ Microbiol., 73: 6030-6035.
8. Arrow, K., C. Panosian, H. Gelband, 2004. Saving lives, buying time. Economics of malaria drugs in an age of resistance. Washington: National Academies Press.
9. Martinez, E. and F. De la Cruz, 1990. Genetic elements involved in Tn*21* site-specific integration, a novel mechanism for the dissemination of antibiotic resistance genes. EMBO Journal, 9:1275–1281.
10. Zuhlsdorf, M. T. and B. Wiedemann, 1992. Tn*21*-specific structures in Gram-negative bacteria from clinical isolates. Antimicrobial Agents and Chemotherapy, 36:1915–21.
11. Levesque, C., L. Piche, C. Larose and P.H. Roy, 1995. PCR mapping of integrons reveals several novel combinations of resistance genes. Antimicrobial Agents and Chemotherapy, 39:185–191.
12. Sallen, B., A. Rajoharison, S. Desvarenne and C. Mabilat, 1995. Molecular epidemiology of integron-associated antibiotic-resistance genes in clinical isolates of *Enterobacteriaceae.* Microbial Drug Resistance, 1:195–202.
13. Thomas, B.T., G.C. Agu, O.A. Oso, E.S. James, A. Davies and T.A. Dele-Osinbanjo (2016). Evolutionary and Secondary Structure of Multi Drug Resistance Class 1 Integron from Gram Negative Bacteria. International Journal of Microbiology Research (In press).
14. Wang, M., D.F. Sahm, G.A. Jacoby, Y. Zhang, D.C. Hooper, 2004. Activities of newer quinolones against *Escherichia coli* and *Klebsiella pneumoniae* containing the plasmid mediated quinolone resistance determinant qnr. Antimicrob Agents Chemother., 48:1400-1401.
15. Musser, J.M., 1995. Antimicrobial agent resistance in mycobacteria: molecular genetic insights. Clin Microbiol Rev., 8(4):496-514.
16. Geourjon, C., G. Deleage, 1995. SOPMA: significant improvements in protein secondary structure prediction by consensus prediction from multiple alignments. Comput Appl Biosci., 11(6): 681-684.
17. Zuckerkandl, E. and L. Pauling, 1965. Molecules as documents of evolutionary history. J Theor Biol., 8(2): 357–366.
18. Teo, J., G. Ngan, M. Balm, R. Jureen, P. Krishnan, R. Lin, 2012. Molecular characterization of NDM-1 producing Enterobacteriaceae isolates in Singapore hospitals. Western Pac Surveill Response J., 3: 19-24.

2/1/2016