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## Research Article



### Detection of Neuroaminidase genes of *S. pneumoniae* isolated from patients with pneumonia in Najaf Province/ Iraq

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#### Abstract

*S.pneumoniae* expresses neuraminidase that cleaves sialic acid containing substrates and is thought to promote pneumococcal colonization by exposing host cell receptors. The *S. pneumoniae* genome codes for up to three NA proteins: NanA, NanB and NanC. In this study, three genes of neuraminidase enzyme were detected by using monoplex –PCR technique in 74 *P.aeruginosa* isolates that isolated from 600 patients with clinical symptoms of pneumonia. the *nanA* gene was found in all *S.pneumoniae* isolates (100%) , While the results amplification of *nanB* gene primer by PCR revealed that most (62.2%) of *S.pneumoniae* isolates have *nanB* gene, except four of isolates (S<sub>11</sub>, S<sub>12</sub>, S<sub>17</sub>, S<sub>20</sub>) gave negative result (37.8%).

**Keywords:** *S.pneumoniae*, neuraminidase, nana , nan B, nanC, monoplex –PCR, pneumonia.

#### Introduction

*Streptococcus pneumoniae* is globally a significant pathogen and causes a wide range of diseases such as pneumonia, meningitis, otitis media, bacteraemia, and other less-frequent infections such as endocarditis and arthritis (Hausdorff *et al.*, 2005). It's commonly called the pneumococcus, is responsible for high rates of morbidity and mortality worldwide (Rudan *et al.*, 2008). *S. pneumoniae* normally colonizes the human nasopharynx, nose, and throat asymptotically and such carriage is considered essential for subsequent development of disease in susceptible individuals (particularly infants, the elderly, and the immune-compromised (LeMessurier, *et al.*, 2006). The incidence of pneumococcal disease and the occurrence of antibiotic- resistant isolates have been positively correlated to the levels of carriage (Paul, 1997).

*S.pneumoniae* expresses a variety of protein virulence factors that allow colonization of different human mucosal surfaces. Among these factors are neuraminidases (NA), or sialidases, that cleave

terminal sialic acids from glycoconjugates. Based on substrate specificity and catalytic mechanism NAs can be separated into three different classes (Lue *et al.*, 1999).

NanA, which contributes to nasopharyngeal colonization and development of otitis media in a chinchilla animal model (Tong *et al.*, 2000), and respiratory tract infection and sepsis in mice (Manco *et al.*, 2006). NanA is proposed to aid pathogenesis by revealing carbohydrate receptors for adherence, providing a carbon source for the bacteria, modifying the surface of other bacteria in the same niche, and affecting the function of host defense molecules (King *et al.*, 2006 ; Burnaugh *et al.*, 2008 ; Yesilkaya *et al.*, 2008).

Influenza virus encodes the neuraminidase NA, which is similar to *S.pneumoniae* NanA in substrate specificity (Suzuki, 2005 ;Xu *et al.*, 2008). NanA cleaves N-acetylneurameric acid (sialic acid) residues

on red blood cells, platelets and endothelial cells leading to the exposure of the Thomsen–Friedenreich antigen (TA) and allowing normally circulating anti-T antigen antibodies to react with the exposed TA on cells (Cochran *et al.*, 2004 ; Scheiring *et al.*, 2010). NanA may help promote colonization through desialylation of host proteins that mediate bacterial clearance, such as lactoferrin or immunoglobulin A2 (King *et al.* 2004). NanA also has been shown to desialylate lipopolysaccharides of *Neisseria meningitidis* and *Haemophilus influenzae* strains (Shakhnovich *et al.*, 2002). The desialylation of lipopolysaccharide may give pneumococci a competitive advantage over *N. meningitidis* and *H.influenzae*, which reside in the same host niche, by making them more susceptible to complement mediated clearance.

Much less is known about the 78 kDa NanB protein, which has low sequence identity (24%) with NanA (Berry *et al.*, 1996). Recent investigations suggest that NanB plays an important role during pneumococcal infection of the respiratory tract and sepsis (Manco *et al.*, 2006) as well as playing a role in bacterial nutrition (Burnaugh *et al.*, 2008). The third putative NA, NanC, present in less than 50% of pneumococcal strains has high sequence identity to NanB (46%) but remains to be characterized (Pettigrew *et al.*, 2006).

Pneumococci have been shown to have at least two distinctly separated appearances when grown on a transparent medium, these two appearances are referred to as either transparent or opaque, how these different morphological appearances are accomplished remains to be explained, but is generally considered to depend on protein expression and capsular thickness. Transparent phenotypes have been demonstrated to express a higher amount of neuraminidase, a fact that has suggested this as an explanation for the observed enhanced adhesion of transparent phenotypes in colonization (Melegaro and Edmunds,2004 ; Millar *et al.*, 2006).

## Materials and Methods

### Sample collection and processing

Sputum samples were collected from 600 out- and inpatients suffering from lower respiratory tract infection (LRTI) attending to the Chest Unit in Al-Sadder Medical City, Al-Hakeem General Hospital and

Clinic Consultive Center for Chest Disease and Al-Zahra'a Hospital for Childbirth and Children in Al-Najaf province during the period from February 2013-Aprile 2014. The patients included both sex (male and female) and the age range (1-80 years).

### Pneumococcal Identification

Sputum Ziehl-Neelsen Stain Method was performed according to Macfaddin (2000). With a special care, sputum was homogenized for a few minutes with a clean wooden stick. Gram stained sputum preparations were used for polymorphonuclear neutrophils (PMNs) and epithelial cells. If the sputum contain too many squamous epithelial cells (more than 10 cells per lower powered field) (100x) the specimen was considered not useful , sputum samples were considered valuable if no more than 10 squamous epithelial cells and more than 20 neutrophils per low-power field were visible and were considered positive for pneumonia infections(Murray,1975; Miriam and Buenviaje,1988).

sputum cultures were made for each specimen according to sputum gram stain for pneumonia infections. Sputum specimens were homogenized with an equal volume of normal saline on a vortex mixer. Blood agar and Chocolate agar were inoculated with 0.1 ml of homogenized specimen. Plates were incubated in (5-10)% CO<sub>2</sub>candle jar at 37 C° overnight. The identification of *S.pneumoniae* was achieved according to morphological staining, culture characters and biochemical reactions that described in Macfaddin .biochemical tests that confirmed the identification of isolates *S. pneumoniae* such as optochin sensitivity , 2% deoxycholate solubility and α-haemolysis. STREPTO-SYSTEM 9R for *S.pneumoniae* identification was used according to the recommendation of company product (Liofilchem, England). The final identification of *S. pneumoniae* was performed with VITEK-2 compact system using GP cards which contained 43 biochemical tests and one negative control well . The results of this test have been showed to be compatible with results of STREPO-SYSTEM 9R test in which all 74 *S. pneumoniae* isolates that diagnosed in STREPO-SYSTEM 9R gave positive results in VITEK-2 test.

## Extraction and Isolation of DNA

*S.pneumoneae* isolates were cultured on tryptic soy agar supplemented with 5% sheep blood and inoculated individually into TSB and incubated at 37°C/24h. Genomic DNA Extraction Kit (Geneaid) was used for DNA extraction. Geneaid Mini kit (USA) include the following: Gram+ Buffer (30ml), GB Buffer (40ml), W1 Buffer (45ml), Elution Buffer (30ml), GD Column (100pcs), 2ml Collection Tube (200pcs), Wash Buffer (25ml) (add ethanol) (100ml), Loding dye, Nuclease Free water, Ethidium

bromide, TBE (Tris- Borate EDTA) buffer, TE (Tris – EDTA) buffer, Agarose, 1kb DNA Ladder (DNA marker), 100 bp DNA Ladder (DNA marker).

Gel electrophoresis was used for detection of DNA by UV transilluminator according to Sambrook *et al.* (2001).

PCR assay was performed in monoplex patterns in order to amplify three genes of neuraminidase (*nanA*, *nanB*, *nanC*) under study for detecting of Staphylococcal virulence factor genes.

## Monoplex Master Mix Mixture

Type	Description	Purpose	Origin
KABA2G FastHotStart Ready Mix (2x)	The 2X Ready Mix contains KABA2G Fast HotStartDNA polymerase, KABA2G Fast HotStart PCR buffer, dNTPs (0.2mM each dNTP at 1X), MgCl <sub>2</sub> (1.5mM at 1X) and stabilizers.	Monoplex PCR	KAPA Biosystem (USA)

## PCR Primers of neuraminidase

Target Gene	DNA sequence(5'-3')	Product Size (bp)	References
<i>nanA</i>	F:ATA GAC GTG CGC AAA ATA CAG AAT CA R:GTC GAA CTC CAA GCC AAT AAC TCC T	550	Pettigrew <i>et al.</i> (2006)
<i>nanB</i>	F:ACT ACG AGG TGT TAA TCG TGA AGG R:CCA ATA CCC GCA GGC ATA ACA TC	500	Pettigrew <i>et al.</i> (2006)
<i>nanC</i>	F:TGG GGT AAG TAC AAA CAA GAG G R:CTA ATG GTA CTG GCG AAA ATC A	500	Pettigrew <i>et al.</i> (2006)

## PCR Cycling Conditions

PCR reaction tubes were centrifuged briefly to mix and bring the contents to the bottom of the tubes, and

placed into thermocycler PCR instrument where DNA was amplified as indicating in below:

Table (3.7): Program used to amplify the *nanA* and *nanB*

Stage	Temperature (time)	
Initial denaturation	94°C for 3min	
Denaturation	94°C for 1min	
Annealing	52°C for 1min	35cycle
Extension	72°C for 1.5min	
Final extension	72°C for 10min	

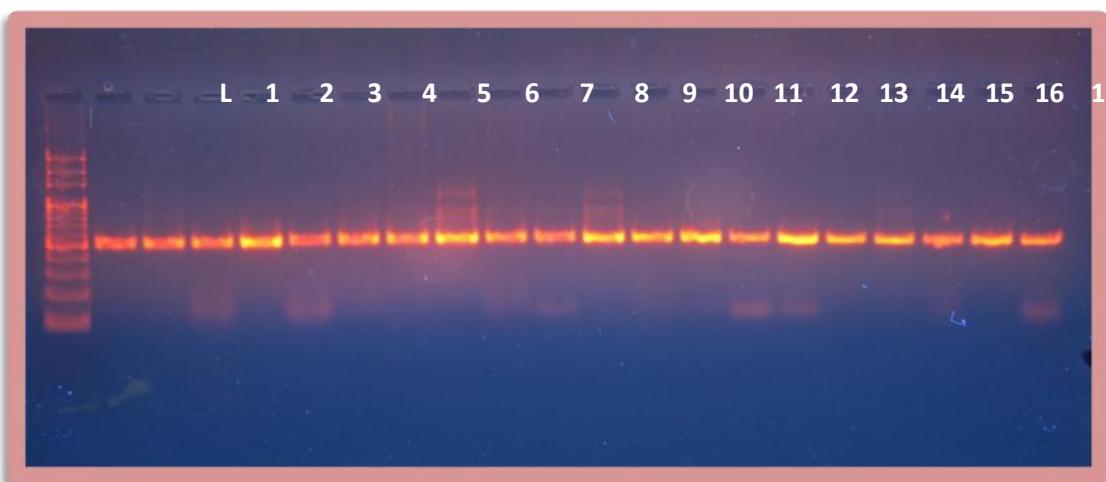
**Table (3.8): Program used to amplify the *nanC***

Stage	Temperature (time)
Initial denaturation	94°C for 5min
Denaturation	98°C for 30sec
Annealing	51°C for 30sec
Extension	72°C for 1min
Final extension	72°C for 10min

## Results and Discussion

In this study, the *nanA* gene was found in all *S. pneumoniae* isolates (100%) as shown in Figure (1).

While the results amplification of *nanB* gene primer by PCR revealed that most (62.2%) of *S. pneumoniae* isolates have *nanB* gene, except four of isolates ( $S_{11}$ ,  $S_{12}$ ,  $S_{17}$ ,  $S_{20}$ ) gave negative result (37.8%) figure (2).



**Figure (1): Gel electrophoresis of PCR product of *nanA* gene primers with product 550 bp.**  
Lane (L), DNA molecular size marker (2000-bp ladder), Lanes (1-20) show positive results with *nanA* gene.



**Figure (2): Gel electrophoresis of PCR product of *nanB* gene primers with product 500 bp.** Lane (L), DNA molecular size marker (2000-bp ladder), Lanes (11, 12, 17) show negative results with *nanB* gene.

*S. pneumoniae* is believed to produce more than one form of neuraminidase, but there has been uncertainty as to whether this is due to posttranslational modification of a single gene product or the existence of more than one neuraminidase-encoding gene. The pneumococcus genome encodes up to three neuraminidase proteins that have been shown to be important virulence factors: *NanA*, *NanB* and *NanC* (Berry *et al.*, 1988). Neuraminidase cleaves terminal sialic acid residues from a wide variety of glycolipids, glycoproteins, and oligosaccharides on cell surfaces or in body fluids, and such activity has the potential to cause great damage to the host (Krivan *et al.*, 1988). Histochemical studies of organs from mice dying after intraperitoneal administration of partially purified pneumococcal neuraminidase have indicated marked decreases in the sialic acid contents of the kidneys and liver compared with those of controls (Kelly *et al.*, 1970) and contributes to nasopharyngeal colonization and development of otitis media in a chinchilla animal model (Tong *et al.*, 2000) and respiratory tract infection and sepsis in mice (Manco *et al.*, 2006).

Two neuraminidases, encoded by *nanA* and *nanB*, have been described for *S. pneumoniae*. *NanA* is proposed to aid pathogenesis by revealing carbohydrate receptors for adherence, providing a carbon source for the bacteria and facilitating bacterial adherence by removing terminal sialic acid residues from glycoconjugates. Additionally, *NanA* also has been shown to desialylate lipopolysaccharides of *Neisseria meningitidis* and *Haemophilus influenzae* strains (King *et al.*, 2004). The desialylation of lipopolysaccharide may give pneumococci a competitive advantage over *N. meningitidis* and *H. influenzae*, which reside in the same host niche, by making them more susceptible to complement-mediated clearance. (Shakhnovich *et al.*, 2002), as well as antibacterial components of human airway secretions (King *et al.*, 2004), potentially reducing pneumococcal clearance whilst promoting the clearance of competing bacteria (affecting the function of host defense molecules) (Shakhnovich *et al.*, 2002 ; King *et al.*, 2006 ; Burnaugh *et al.*, 2008). *NanA* may help promote colonization through desialylation of host proteins that mediate bacterial clearance, such as lactoferrin or immunoglobulin A2 (Shakhnovich *et al.*, 2002). A *nanB* homolog, *nanC*, has also been identified, but its expression and activity have not been described. The third putative *NA*, *NanC*, present in less than 50% of pneumococcal strains has high

sequence identity to *NanB* (46%) but remains to be characterized (Chou *et al.*, 1996).

The benefits to a pneumococcus of production of two distinct neuraminidases are unclear. Apart from their difference in size, the two enzymes have widely different pH optima, which imply that these enzymes may assist exploitation of distinct environmental niches. Although a clear difference in specific activity was observed with MUAN as the substrate, this may not hold for other potential substrates. *NanA* and *NanB* are both exported proteins, with typical signal peptides, but unlike *NanB*, *NanA* contains a C-terminal cell surface anchorage domain.

Proteolytic cleavage without loss of enzymic activity may be important for controlled release of surface-bound *NanA*. The possible involvement of neuraminidase in pneumococcal pathogenesis has been suggested by Berry *et al.*, (2014) that purified *NanA* is a partially protective immunogen in mice (Lock *et al.*, 1988). However, it has not been possible to assess the contribution of neuraminidase to pneumococcal virulence by molecular genetic techniques, as *NanA* deficient mutants have residual enzymic activity because of production of *NanB*.

LeMessurier *et al.*, (2006) revealed that the expression of *nanA* was significantly elevated in the nasopharynx of infected mice compared to the other niches examined. And these results provide further support for an important role for *NanA* in colonization of the nasopharynx by pneumococci. Influenza virus encodes the neuraminidase *NA*, which is similar to *S. pneumoniae NanA* in substrate specificity (Xu *et al.*, 2008) *NanA* cleaves N-acetylneurameric acid (sialic acid) residues on red blood cells, platelets and endothelial cells leading to the exposure of the Thomsen–Friedenreich antigen (TA) and allowing normally circulating anti-T antigen antibodies to react with the exposed TA on cells (Scheiring *et al.*, 2010).

The results of the current study were compatible with Pettigrew *et al.*, (2012) results and found *nanA* was present in all strains of *S. pneumoniae* isolates, while *nanB* and *nanC* were present in 96% and 51% of isolates, respectively. The distribution of *nanC* varied among the strain collections from different tissue sources and suggested that the presence of *nanC* may be important for tissue-specific virulence. Studies that both incorporate MLST and take into account

additional virulence determinants will provide a greater understanding of the pneumococcal virulence potential.

Previously less is known about the 78 kDa NanB protein, which has low sequence identity (24%) with NanA. Recent investigations suggest that NanB plays an important role during pneumococcal infection of the respiratory tract and sepsis as well as playing a role in bacterial nutrition. Gut *et al.*, (2008) reported that the first structure of a neuraminidase from *S. pneumoniae*, the crystal structure of NanB in complex with its reaction product 2, 7-anhydro-Neu5Ac., and showed that NanB differs in its substrate specificity from the other pneumococcal neuraminidase NanA. Gut *et al.*, (2008) also, confirmed this finding and establish that free Neu5Ac (the reaction product of pneumococcal NanA) can act as a substrate for NanB. In addition, our biochemical assays clearly demonstrate the strict specificity of NanB towards a2-3 glycosidic substrate linkages and highlight the differences in substrate specificity between NanA and NanB.

Interestingly, hybridization analysis indicated that these two neuraminidase genes are different and that individual pneumococcal isolates contain both genes (Camara *et al.*, 1994). Berry *et al.*, (2014) demonstrated that *nanB*, a gene encoding a second *S. pneumoniae* neuraminidase, is located on the pneumococcal chromosome approximately 4.5 kb downstream of *nanA*. *nanB* appears to be part of a large operon consisting of at least six ORFs. Janapatla *et al.*, (2012) isolated and characterized a second neuraminidase gene (designated *nanB*), which is located close to *nanA* on the pneumococcal chromosome (approximately 4.5kb downstream). *nanB* was located on an operon separate from that of *nanA*, which includes at least five other open reading frames. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis suggested that NanB has a molecular size of approximately 65 kDa.

Pettigrew *et al.*, (2010) from USA reported that among the invasive isolates *nanB* and *nanC* were present in 95% and 58% of the isolates, respectively; Recently, Imai *et al.*, (Lami *et al.*, 2011) from Japan reported that among the 156 pneumococcal isolates recovered from adult patients with community-acquired pneumonia *nanC* was present in 35.9% of the isolates. A recent study showed that *NanA* but not *NanB* was

necessary for TA exposure on red blood cells in mice (Coats *et al.*, 2011). Nevertheless, Janapatla *et al.*, (2012) suggests that *NanC* could provide an additive effect to *NanA* and *NanB* in the overall activity of pneumococcal neuraminidases to expose Thomsen–Friedenreich antigen on various cells in patients with hemolytic uramic syndrome (complications of invasive pneumococcal infection).

In summary, the results of this study affirm that *nanA* is essential for virulence and that having *nanC* may predispose strains for invasion of the lung. Studies that incorporate MLST and take into account the presence or absence of additional virulence determinants will provide a greater understanding of the virulence potential of pneumococcal strains.

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