Activity of N-Acetylcysteine Alone and in Combination with Colistin against Pseudomonas aeruginosa Biofilms and Transcriptomic Response to N-Acetylcysteine Exposure

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ABSTRACT Chronic colonization by Pseudomonas aeruginosa is critical in cystic fibrosis (CF) and other chronic lung diseases, contributing to disease progression. Biofilm growth and a propensity to evolve multidrug resistance phenotypes drastically limit the available therapeutic options. In this perspective, there has been growing interest in evaluating combination therapies, especially for drugs that can be administered by nebulization, which allows high drug concentrations to be reached at the site of infections while limiting systemic toxicity. Here, we investigated the potential antibiofilm activity of N-acetylcysteine (NAC) alone and in combination with colistin against a panel of P. aeruginosa strains (most of which are from CF patients) and the transcriptomic response of a P. aeruginosa CF strain to NAC exposure. NAC alone (8,000 mg/L) showed a limited and strain-dependent antibiofilm activity. Nonetheless, a relevant antibiofilm synergism of NAC-colistin combinations (NAC at 8,000 mg/L plus colistin at 2 to 32 mg/L) was observed with all strains. Synergism was also confirmed with the artificial sputum medium model. RNA sequencing of NAC-exposed planktonic cultures revealed that NAC (8,000 mg/L) mainly induced (i) a Zn²⁺ starvation response (known to induce attenuation of P. aeruginosa virulence), (ii) downregulation of genes of the denitrification apparatus, and (iii) downregulation of flagellar biosynthesis pathway. NAC-mediated inhibition of P. aeruginosa denitrification pathway and flagellum-mediated motility were confirmed experimentally. These findings suggested that NAC-colistin combinations might contribute to the management of biofilm-associated P. aeruginosa lung infections. NAC might also have a role in reducing P. aeruginosa virulence, which could be relevant in the very early stages of lung colonization.

IMPORTANCE Pseudomonas aeruginosa biofilm-related chronic lung colonization contributes to cystic fibrosis (CF) disease progression. Colistin is often a last-resort antibiotic for the treatment of such P. aeruginosa infections, and it has been increasingly used in CF, especially by nebulization. N-acetylcysteine (NAC) is a mucolytic agent with antioxidant activity, commonly administered with antibiotics for the treatment of lower respiratory tract infections. Here, we show that NAC potentiated colistin activity against in vitro biofilms models of P. aeruginosa strains, with both drugs tested at the high concentrations achievable after nebulization. In addition, we report the first transcriptomic data on the P. aeruginosa response to NAC exposure.

KEYWORDS N-acetylcysteine, Pseudomonas aeruginosa, biofilms, colistin, cystic fibrosis, synergism, transcriptomic response
*Pseudomonas aeruginosa* is a leading pathogen infecting the airways of patients affected by cystic fibrosis (CF) and other chronic lung diseases (e.g., chronic obstructive pulmonary disease and non-CF bronchiectasis) (1). Once established in the CF airways, *P. aeruginosa* develops into chronic infections and generally persists indefinitely, contributing to frequent exacerbations, decline of pulmonary function, and higher rates of mortality (1, 2). Chronic infections by *P. aeruginosa* in CF lungs are associated with adaptive changes of the pathogen, such as conversion to a mucoid phenotype, switching to the biofilm mode of growth, and acquisition of antibiotic resistance (3). Cumulative exposure to antibiotics during treatment causes dissemination of multidrug-resistant (MDR) *P. aeruginosa* strains, leading to the ineffectiveness of the antibiotic therapy and consequently worse clinical outcomes (3).

Colistin is among the last-resort agents for the treatment of *P. aeruginosa* infections caused by MDR strains, with the advantage of being also administrable by nebulization, which allows the achieving of high lung concentrations while reducing systemic toxicity (4). In this perspective, inhaled colistin has been increasingly used for the treatment of difficult-to-treat respiratory tract infections, especially those related to biofilm formation (5).

*N*-acetylcysteine (NAC) is a mucolytic agent commonly administered with antibiotics for the treatment of lower respiratory tract infections, which has been demonstrated to exert also antimicrobial and antibiofilm activity against relevant respiratory pathogens (6–8). Recently, a potent *in vitro* antibiofilm synergism of NAC-colistin combinations was demonstrated against colistin-susceptible and colistin-resistant *Acinetobacter baumannii* and *Stenotrophomonas maltophilia* strains (9, 10).

NAC has been demonstrated to exert several heterogeneous biological activities (whose molecular bases have not always been clearly elucidated) and has recently been under extensive investigation for potential clinical applications beyond the approved therapeutic usage as an antidote in acetaminophen (paracetamol) overdose and as a mucolytic (11). Overall, NAC can act as a direct or indirect antioxidant, due to the ability of the free thiol group to react with reactive oxygen and nitrogen species and by constituting a precursor of intracellular glutathione (11). In addition, NAC can bind transition and heavy metal ions and act as a reducing agent of protein sulfhydryl groups involved in intracellular redox homeostasis (11). Despite several studies that have addressed the biological effects of NAC on planktonic and biofilm bacterial cultures (8), to the best of our knowledge, no data on bacterial transcriptomic response to NAC exposure have been reported so far.

In this study, we investigated the *in vitro* antibiofilm activities of NAC alone and in combination with colistin (at the high concentrations achievable by the inhalation route of administration) (8, 12) against a panel of *P. aeruginosa* strains (most of which are from CF patients) representative of different phenotypes (in terms of mucoidy, antimicrobial susceptibility pattern, and O type) and multilocus sequence type (MLST) genotypes. In addition, we provided original data on the transcriptomic response of *P. aeruginosa* planktonic cultures to NAC exposure.

**RESULTS AND DISCUSSION**

**Activity of NAC alone against preformed biofilm.** The antibiofilm activity of NAC alone was tested with 17 *P. aeruginosa* strains (Table 1), of which 15 were from CF patients, using the Nunc-TSP lid system.

NAC at 8,000 mg/L (i.e., a high concentration achievable after inhalation) showed limited and strain-dependent activity (Fig. 1 to 4). In particular, major effects were observed with *P. aeruginosa* Z154 (i.e., decrease of >1 log CFU/peg compared to the control) (Fig. 1) and *P. aeruginosa* PAO1 (i.e., increase of >1 log CFU/peg compared to the control) (Fig. 2). With an additional 7 strains, a very slight but statistically significant activity was observed (i.e., <0.5 log CFU/peg compared to the control), resulting in biofilm reduction in six cases (i.e., *P. aeruginosa* Z33, Z35, Z152, M13, M19, and M25) and biofilm increase in the remaining one (i.e., *P. aeruginosa* M42) (Fig. 2 and 3).

Overall, these results indicated that inhaled NAC alone might not have major effects on
P. aeruginosa biofilms already established in the lung and that the response to NAC was not related to phenotypic or genotypic features. The few previous studies that have addressed the activity of NAC against preformed P. aeruginosa biofilms have reported similar results (i.e., usually limited and strain-dependent effects), although a direct comparison of data is not straightforward due to different methodological approaches (e.g., different biofilm models and different NAC concentrations tested) and the low number of strains often tested in such studies (i.e., usually reference strains) (8, 13, 14). This study provided a wider picture on this topic by investigating a panel of characterized P. aeruginosa strains using a standardized in vitro biofilm model and in vivo achievable NAC concentrations.

Interestingly, NAC alone (at the concentration used in this study and the same biofilm model) did not exert any significant antibiofilm activity against P. aeruginosa Z154. However, a relevant potentiation of colistin antibiofilm activity was observed with all NAC-CST combinations tested. CST 2, colistin at 2 mg/L; CST 4, colistin at 4 mg/L; CST 8, colistin at 8 mg/L. Biofilms not exposed to NAC or CST represent the control. Black lines indicate median values. The x axis is set at the limit of detection (20 CFU/peg).

**FIG 1** Antibiofilm activity of N-acetylcysteine (NAC) at 8,000 mg/L, colistin (CST), and NAC-CST combinations against P. aeruginosa Z154 in the Nunc-TSP lid system. A relevant potentiation of colistin antibiofilm activity was observed with all NAC-CST combinations tested. CST 2, colistin at 2 mg/L; CST 4, colistin at 4 mg/L; CST 8, colistin at 8 mg/L. Biofilms not exposed to NAC or CST represent the control. Black lines indicate median values. The x axis is set at the limit of detection (20 CFU/peg).

**TABLE 1** Features of the 17 P. aeruginosa strains included in this study

| Strain | yr of | Phenotype | Origina | STb | O type | Resistance patternc | MIC (mg/L)d |
|--------|-------|-----------|---------|------|--------|---------------------|-------------|
| PAO1   | 1954  | Nonmucoid | Wound   | ST549| O5     | Wild type           | 2           |
| Z33    | 2005  | Nonmucoid | CST     | ST235| O11    | CP’, FQ’, AG’       | 1           |
| Z34    | 2006  | Nonmucoid | CST     | ST17 | O1     | CB’, CP’, FQ’, AG’  | 2           |
| Z35    | 2006  | Nonmucoid | CST     | ST235| O11    |                     | 1           |
| Z152   | 2013  | Mucoid    | CST     | ST155| O6     | CB’, FQ’, AG’       | 2           |
| Z154   | 2016  | Mucoid    | CST     | ST412| O6     | CP’, FQ’, AG’       | 2           |
| M7     | 2005  | Mucoid    | CST     | ST235| O10    | AG’                 | 2           |
| M13    | 2000  | Mucoid    | CST     | ST274| O3     | CB’, CP’, AG’       | 1           |
| M19    | 2006  | Mucoid    | CST     | ST3509| O7    |                     | 1           |
| M25    | 2002  | Mucoid    | CST     | ST235| O11    |                     | 2           |
| M32    | 2006  | Mucoid    | CST     | ST235| O11    |                     | 2           |
| M42    | 2007  | Mucoid    | CST     | ST2437| O6    | CB’, CP’, FQ’, AG’  | 2           |
| FC237  | 2007  | Nonmucoid | CST     | ST365| O3     | CB’, FQ’, AG’, CST  | 512         |
| FC238  | 2007  | Nonmucoid | CST     | ST910| O6     | CB’, CST           | 8           |
| FZ99   | 2018  | Nonmucoid | RTIICU  | ST111| O12    | CB’, CP’, FQ’, AG’, CST | 4        |

aCF, cystic fibrosis; RTIICU, respiratory tract infection in intensive care unit.
bAccording to the MLST Pasteur scheme.
cCB, resistance to carbapenems (imipenem and meropenem); CP, resistance to cephems (ceftazidime and cefepime); FQ, resistance to fluoroquinolones (ciprofloxacin); AG, resistance to aminoglycosides (amikacin and gentamicin); CST, resistance to colistin.
dCST, colistin; NAC, N-acetylcysteine.

P. aeruginosa biofilms already established in the lung and that the response to NAC was not related to phenotypic or genotypic features. The few previous studies that have addressed the activity of NAC against preformed P. aeruginosa biofilms have reported similar results (i.e., usually limited and strain-dependent effects), although a direct comparison of data is not straightforward due to different methodological approaches (e.g., different biofilm models and different NAC concentrations tested) and the low number of strains often tested in such studies (i.e., usually reference strains) (8, 13, 14). This study provided a wider picture on this topic by investigating a panel of characterized P. aeruginosa strains using a standardized in vitro biofilm model and in vivo achievable NAC concentrations. Interestingly, NAC alone (at the concentration used in this study and the same biofilm model) did not exert any significant antibiofilm activity against P. aeruginosa Z154. However, a relevant potentiation of colistin antibiofilm activity was observed with all NAC-CST combinations tested. CST 2, colistin at 2 mg/L; CST 4, colistin at 4 mg/L; CST 8, colistin at 8 mg/L. Biofilms not exposed to NAC or CST represent the control. Black lines indicate median values. The x axis is set at the limit of detection (20 CFU/peg).
** FIG 2 ** Antibiofilm activity of N-acetylcysteine (NAC) at 8,000 mg/L, colistin (CST), and NAC-CST combinations against *P. aeruginosa* PAO1 and three colistin-susceptible nonmucoid strains in the (Continued on next page)

** NAC-Colistin Synergism against *P. aeruginosa* Biofilms **

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** ** p<0.01, *** p<0.001, **** p<0.0001 (Kruskal-Wallis test with Dunn's correction)

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model) was recently shown to exert relevant activity against preformed biofilms of two relevant CF pathogens, namely, *S. maltophilia* and *Burkholderia cepacia* complex (BCC) (7). The reasons for such a diverse response of *P. aeruginosa* compared to *S. maltophilia* and BCC should deserve further attention, because they could possibly help identifying critical targets in the complex biofilm environments, to be used for the implementation of new antibiofilm strategies.

**Activity of NAC-colistin combinations against preformed biofilms.** *P. aeruginosa* Z154 (a mucoid, MDR, colistin-susceptible CF strain) was first used to test the potential antibiofilm synergism of NAC at 8,000 mg/L plus diverse colistin concentrations. As shown in Fig. 1, a relevant synergism was observed already with colistin at 2 mg/L (i.e., the colistin MIC for the tested strain), with a dose-dependent effect at increasing colistin concentrations, and complete biofilm eradication was achieved with the combination of NAC at 8,000 mg/L plus colistin at 8 mg/L (Fig. 1).

The remaining 16 strains were initially tested with the combination of NAC at 8,000 mg/L plus colistin at 8 mg/L. In order to detect a potential synergism, the concentration of colistin was then modified for strains forming biofilms highly susceptible to colistin (*n* = 7) or particularly resistant (*n* = 2) (Fig. 2 to 4). Overall, a relevant synergism of NAC-colistin combinations was observed with all tested strains (including the three colistin-resistant ones), although in two cases (i.e., *P. aeruginosa* M4 and M32), statistical significance was not achieved (Fig. 2 to 4). These latter strains were also tested with lower colistin concentrations (i.e., 2 and 4 mg/L, respectively), but synergism was not observed (data not shown). Concerning the synergism observed with the three colistin-resistant strains (Fig. 4), it is interesting to note that with strain FC237 (nonmucoid, MDR), an important decrease in viable biofilm cells was observed with a combination including a colistin concentration much lower than the colistin MIC for this strain (i.e., 1/64 MIC) (Fig. 4).

Overall, these data demonstrated that NAC could potentiate colistin activity against preformed biofilms of colistin-susceptible and colistin-resistant *P. aeruginosa* strains, regardless of the mucoid/nonmucoid phenotype, the resistance pattern, and the ST and O type. Present findings are consistent with the previously observed antibiofilm synergism of NAC-colistin combinations against colistin-susceptible and colistin-resistant strains of *A. baumannii* and *S. maltophilia* (9, 10). Further studies with a higher number of *P. aeruginosa* clinical isolates, especially with a colistin-resistant phenotype, are encouraged.

**Activity of NAC-colistin combinations in the ASM biofilm model.** Two *P. aeruginosa* CF strains exhibiting different phenotypes were selected for susceptibility assays with the artificial sputum medium (ASM) biofilm model: *P. aeruginosa* Z34 (nonmucoid, MDR, ST17, O1) and *P. aeruginosa* Z154 (mucoid, MDR, ST412, O6). Biofilms were grown in ASM, in order to mimic the *P. aeruginosa* biofilm environmental conditions experienced in the CF mucus. Preformed biofilms were then challenged in the same medium with NAC-colistin combinations.

As shown in Fig. 5, a clear synergism of NAC at 8,000 mg/L in combination with colistin at 64 mg/L was observed with both strains (Fig. 5). Compared to the experiments performed with the Nunc-TSP lid system, the concentration of colistin that allowed observation of a synergism was much higher (i.e., 32× the MIC), possibly due to colistin strong ionic interactions with ASM components (e.g., extracellular DNA and mucin) (15). Indeed, preliminary experiments carried out with lower colistin concentrations did not show either colistin antibiofilm activity or synergism with NAC (data not shown). In addition, the antibiofilm activity of NAC alone observed against *P. aeruginosa* Z154 in the Nunc-TSP lid system was not observed in the ASM model (Fig. 5), confirming that

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**FIG 2 Legend (Continued)**

**Nunc-TSP lid system.** A potentiation by NAC of colistin antibiofilm activity was observed with all tested strains. CST 4, colistin 4 mg/L; CST 8, colistin 8 mg/L. Biofilms not exposed to NAC or CST represented the control. Black lines indicate median values. The x axis is set at the limit of detection (20 CFU/peg).
FIG 3 Antibiofilm activity of N-acetylcysteine (NAC) at 8,000 mg/L, colistin (CST), and NAC-CST combinations against nine colistin-susceptible mucoid *P. aeruginosa* strains in the Nunc-TSP lid system. A potentiation by NAC-Colistin Synergism against *P. aeruginosa* Biofilms Microbiology Spectrum July/August 2022 Volume 10 Issue 4 10.1128/spectrum.01006-22

* *p*<0.05, **p*<0.01, ***p*<0.001, ****p*<0.0001 (Kruskal-Wallis test with Dunn’s correction)

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the efficacy of NAC alone against preformed *P. aeruginosa* biofilms could be limited in vivo.

Overall, these data demonstrated that the antibiotic synergy of NAC-colistin combinations against *P. aeruginosa* strains is preserved also under the environmental conditions mimicking the CF mucus, which is promising for clinical applications. Furthermore, the lower susceptibility to colistin of *P. aeruginosa* biofilms in the ASM model compared to biofilm susceptibility in standard media observed in this study is consistent with what was previously reported with *P. aeruginosa* (16).

**Transcriptomic response of *P. aeruginosa* Z154 to NAC exposure.** *P. aeruginosa* Z154 (i.e., colistin-susceptible CF strain, mucoid, MDR, ST412, O6) was selected for investigating the transcriptome response of planktonic cultures to NAC exposure (i.e., NAC at 8,000 mg/L). A total of 66 differentially expressed genes (DEGs) were identified (adjusted *P* value of <0.05 with 99% confidence interval [CI]), of which 46 were upregulated and 20 downregulated compared to the control (Table 2).

Analysis of DEGs revealed that NAC mainly acted as Zn\(^{2+}\) chelator, inducing a strong Zn\(^{2+}\) starvation response. DEGs associated with such response were consistent with data reported in previous studies addressing zinc homeostasis in *P. aeruginosa* and other bacteria (Table 2) (17–22). In particular, 31 of the 46 upregulated DEGs belonged to the zur regulon and are known to be activated in response to Zn\(^{2+}\) starvation (Table 2) (17–22). Such genes mainly included operons involved in zinc uptake (e.g., the PA4063-PA4064-PA4065-PA4066 operon, cntOLMI operon, and zurABC operon) and genes encoding zinc-independent paralogs of cellular proteins (i.e., type B 50S ribosomal proteins L31 and L36, RNA polymerase-binding protein DksA2, a GTP-cyclohydrolase FolE2) (Table 2) (17–23). Upregulated DEGs belonging to the zur regulon also included genes encoding an N-acetylmuramoyl-L-alanine amidase (AmiA, involved in splitting of septal peptidoglycan during cell division), a γ-carboxy anhydrase (Cam, involved in reversible hydration of carbon dioxide and important for growth under low-CO\(_2\) conditions), and three modulators of the membrane FtsH protease (i.e., HfIC and HfIK family modulators) (Table 2). The membrane FtsH zinc-dependent protease is required for the expression of diverse unrelated phenotypes (e.g., swimming and twitching motility, biofilm formation, autolysis, production of secondary metabolites, maintenance of plasma membrane integrity by degrading misfolded proteins), and it has been recently demonstrated to represent an important virulence factor in *P. aeruginosa* clone C (23). HfIC and HfIK family modulators interact with FtsH at the level of the plasma membrane, usually with an inhibitory effect (23). The NAC-mediated effects on the phenotypes related to FtsH would deserve further attention.

The remaining 15 upregulated DEGs included genes encoding a recently described transcriptional regulator, PA2100 (also named MdrR2) (24), an AhpC-like alkyl hydroperoxide reductase (involved in protection from oxidative stress) (25), and proteins possibly involved in copper and iron uptake (Table 2).

MdrR2, together with MdrR1, has been demonstrated to repress the mexAB-oprM operon (independently from the MexR repressor), activate the EmrAB efflux pump, and indirectly inhibit biofilm formation (Table 2) (24). The effect of NAC on the MdrR1-MdrR2 dual-regulation system should be further investigated. Nonetheless, a previous study aimed at investigating the potential antagonism of high NAC concentrations (i.e., as those tested in this study) on the activity of the major classes of antibiotics used in the clinical practice, did not show major effects (with the exception of carbapenems, due to a chemical instability of carbapenems in the presence of NAC) (26), suggesting that the activation of the EmrAB efflux could not be relevant or circumvented by compensatory mechanisms.

Analysis of downregulated DEGs identified genes involved in denitrification, in particular *norB* (encoding the nitric oxide reductase subunit NorB), *nosR* (encoding the...
**Fig 4** Antibiofilm activity of N-acetylcysteine (NAC) at 8,000 mg/L, colistin (CST), and NAC-CST combinations against three colistin-resistant nonmucoid *P. aeruginosa* strains in the Nunc-TSP lid (Continued on next page)

**p<0.01, ****p<0.0001** (Kruskal-Wallis test with Dunn's correction)
regulatory protein NosR), and nosZ (encoding the nitrous oxide reductase NosZ) (Table 2). These data suggested that NAC might affect *P. aeruginosa* anaerobic respiration (which is crucial in the deeper biofilm layers and in the CF mucus) (27), because the nitric oxide reductase NorBC and the regulatory protein NosR have been recently demonstrated to constitute the nucleus of the denitrification protein network (28). NAC-mediated inhibition of the *P. aeruginosa* denitrification pathway might be implicated in the observed antibiotic synergism of the NAC-colistin combination. Indeed, colistin has been demonstrated to exert increased antibiotic activity against *P. aeruginosa* under anaerobic conditions, possibly due to a lower ability to implement the tolerance mechanism (e.g., lipopolysaccharide [LPS] modification) because of the low metabolism accompanying anaerobic growth (29). In this perspective, the inhibition of anaerobic respiration by NAC would further inhibit a *P. aeruginosa* adaptive response to colistin toxicity. This could be particularly relevant in *P. aeruginosa* biofilm in the CF mucus, where the anoxic conditions of biofilm cells are related not only to the position of the bacteria within the biofilm (i.e., anoxic conditions in the deeper layers), but also to the intense O2 depletion caused by polymorphonuclear leukocytes (PMNs), determining entire biofilm growth without aerobic respiration (29).

Downregulated DEGs also included the following: (i) two genes involved in flagellar biosynthesis (i.e., flIF, encoding the flagellar M-ring protein FlIF, and flHF, encoding the flagellar biosynthesis protein FlhF); (ii) a NAD(P)H-quinone oxidoreductase protecting against ROS-induced oxidative stress, which was recently demonstrated to be part of the core biofilm transcriptome (PA1137) (30); and (iii) nalD, encoding a second repressor of the *mexAB-oprM* operon (31). Finally, consistent with previous studies on *Pseudomonas* response to zinc starvation, downregulation of *copA* and *copZ*, involved in copper efflux, was observed, suggesting interplay between zinc and copper homeostasis (Table 2) (32).

**NAC-mediated inhibition of *P. aeruginosa* denitrification pathway.** The role of NAC in the inhibition of the denitrification pathway was confirmed by measuring NO3− and NO2− concentrations during anaerobic growth of the *P. aeruginosa* Z154 strain (i.e., the strain used for transcriptomic analysis) in culture media supplemented with 10 mM NaNO3 or KNO2, in the presence or absence of NAC at 8,000 mg/L.

As expected from previous studies (33), in NaNO3-containing medium, the levels of NO3− and its reduction product, NO2−, fell below the detection limit after 24 h, in the absence of NAC (Fig. 6A). However, in the presence of NAC at 8,000 mg/L, the depletion of NO3− was followed by an accumulation of NO2− (evident at both 24 and 48 h), indicating that further reduction of NO2− was inhibited in the presence of NAC (Fig. 6A). In order to consolidate these data, the experiments were repeated using a medium supplemented with KNO2. In the absence on NAC, complete reduction of NO2 was observed after 48 h (Fig. 6B), as expected (33). On the contrary, in the presence of NAC at 8,000 mg/L, NO2 levels did not decrease (Fig. 6B).

These results were consistent with the transcriptomic data and showed that NAC was able to inhibit the denitrification pathway in anaerobic environments, such as those encountered in endobronchial CF mucus. This feature might contribute to the observed antibiotic synergism of NAC-colistin combinations, as previously discussed.

**Time-kill assays of the NAC-colistin combination against planktonic cultures grown under anaerobic and aerobic conditions.** Transcriptomic and biological data from this study suggested a role of NAC in inhibiting the *P. aeruginosa* denitrification apparatus, which could contribute to the observed antibiotic synergy of NAC-colistin combinations. In order to further investigate this issue, time-kill assays of the NAC-colistin combination were performed with *P. aeruginosa* Z154 (i.e., the strain used for transcriptomic analysis) planktonic cultures, under both anaerobic and aerobic conditions.

**FIG 4 Legend (Continued)**

system. A potentiation by NAC of colistin antibiotic activity was observed with all tested strains. CST 8, colistin at 8 mg/L; CST 32, colistin at 32 mg/L. Biofilms not exposed to NAC or CST represent the control. Black lines indicate median values. The x axis is set at the limit of detection (20 CFU/peg).
**P. aeruginosa Z154**
(NAC MIC = 16000 mg/L; CST MIC = 2 mg/L)

**P. aeruginosa Z34**
(NAC MIC = 64000 mg/L; CST MIC = 2 mg/L)

**p<0.01, *** p<0.001, **** p<0.0001** (Kruskal-Wallis test with Dunn's correction)

**FIG 5** Antibiofilm activity of N-acetylcysteine (NAC) at 8,000 mg/L, colistin at 64 mg/L (CST 64), and the NAC-CST combination against *P. aeruginosa* Z154 and *P. aeruginosa* Z34 in the ASM biofilm model. A potentiation by NAC of colistin antibiofilm activity was observed with both strains. Biofilms not exposed to NAC or CST represent the control. Black lines indicate median values. The x axis is set at the limit of detection (100 CFU/mL).
### TABLE 2

**DEGs in *P. aeruginosa* Z154 planktonic cultures exposed to 8,000 mg/L NAC compared to control**

| DEG      | Locus tag in *P. aeruginosa* strain | Gene Product (function) | Adjusted Log2 fold change | Zur regulon | Value | P value |
|----------|-------------------------------------|-------------------------|---------------------------|-------------|-------|---------|
| Upregulated | *Z154* | PA14_54180 | znuD | TBDR ZnuD (zinc uptake) | + | 4.6E–36 | 1.9 |
|          | PA14_39650 | PA14_39620 | cirA | TBDR CirA (iron and zinc uptake) | + | 0.0E+00 | 2.4 |
|          | PA14_39640 | PA14_39630 | exbD | ExbD proton channel family protein (energy support for TBDR, cotranscribed with PA1922) | + | 7.9E–36 | 1.9 |
|          | PA14_39620 | PA14_33110 | Hic family modulator of membrane FtsH protease | + | 1.7E–03 | 0.6 |
|          | PA14_33080 | PA14_33070 | hflK | HflK family modulator of membrane FtsH protease | + | 6.5E–03 | 0.6 |
|          | PA14_26420 | PA2101 | znuA | Transcriptional regulator for zinc homeostasis | + | 7.6E–03 | 0.6 |
|          | PA14_17710 | PA14_17700 | rpmJ2 | Zinc-independent paralog type B 50S ribosomal protein L36 | + | 2.0E–16 | 1.3 |
|          | PA14_17700 | PA14_17690 | rpmE2 | Zinc-independent paralog type B 50S ribosomal protein L31 | + | 1.2E–04 | 0.7 |
|          | PA14_11320 | PA14_11310 | sshC | Zinc ABC transporter, ATP-binding protein (zinc uptake) | + | 7.0E–41 | 2.0 |
|          | PA14_11300 | PA14_11290 | sshB | Zinc ABC transporter, permease (zinc uptake) | + | 4.2E–08 | 0.9 |
|          | PA14_11280 | PA14_11270 | sshA | Zinc SPB (zinc uptake) | + | 4.9E–13 | 1.2 |
|          | PA14_63910 | PA14_63900 | cntII | Pseudopaline transport plasma membrane protein Cntl (zinc uptake) | + | 6.1E–05 | 0.7 |
|          | PA14_63920 | PA14_63990 | cntM | Pseudopaline biosynthesis dehydrogenase CntM (zinc uptake) | + | 8.1E–26 | 1.7 |
|          | PA14_63940 | PA14_63930 | cntL | Pseudopaline biosynthesis enzyme Cntl (zinc uptake) | + | 9.3E–39 | 2.0 |
|          | PA14_63960 | PA14_63950 | cntO | Pseudopaline transport outer membrane protein CntO (zinc uptake) | + | 0.0E+00 | 2.5 |
|          | PA14_63970 | PA14_63960 | Hypothetical membrane protein | + | 8.0E–04 | 0.9 |
|          | PA14_72550 | PA14_72540 | znuA | Zinc soluble binding protein ZnuA (zinc uptake) | + | 9.0E–09 | 0.9 |
|          | PA14_72560 | PA14_72550 | zur | Transcriptional regulator for zinc homeostasis | + | 5.3E–10 | 1.0 |
|          | PA14_72580 | PA14_72570 | znuC | Zinc ABC transporter, ATP-binding protein ZnuC (zinc uptake) | + | 1.2E–07 | 0.9 |
|          | PA14_72590 | PA14_72580 | znuB | Zinc ABC transporter, ZnuB permease (zinc uptake) | + | 1.9E–03 | 0.6 |
|          | PA14_73000 | PA14_73000 | Hypothetical protein (unknown function, DUF1826 domain-containing protein) | + | 9.8E–23 | 1.5 |
|          | PA14_73010 | PA14_73010 | zigA | Zinc metallochaperone GTPase ZigA | + | 5.9E–42 | 2.1 |
|          | PA14_73020 | PA14_73015 | dksA2 | Zinc-independent paralog of RNA polymerase-binding protein DksA | + | 2.4E–23 | 1.5 |
|          | PA14_73030 | PA14_73025 | amiA | N-acetyluramoyl-l-alanine amidase (splitting of septal peptidoglycan during cell division) | + | 1.3E–08 | 1.0 |
|          | PA14_73040 | PA14_73035 | folE2 | Zinc-independent paralog of GTP-cyclohydrolase FoLE (folate biosynthesis) | + | 4.5E–28 | 1.7 |
|          | PA14_73050 | PA14_73040 | cam | γ-Carbonic anhydrase (reversible hydration of carbon dioxide) | + | 1.5E–24 | 1.6 |
|          | PA14_73060 | PA14_73050 | pyrC2 | Zinc-independent paralog of dihydroorotase PyrC (pyrimidine biosynthesis) | + | 3.1E–09 | 1.0 |
|          | PA14_73070 | PA14_73065 | Hypothetical protein (unknown function, DUF2946 domain-containing protein) | + | 1.3E–07 | 0.7 |
|          | PA14_05560 | PA14_05550 | TBDR for which the siderophore has not been identified | + | 1.5E–20 | 1.7 |
|          | PA14_06250 | PA14_06245 | furC | GNAT family N-acetyltransferase (release of iron from desferrioxime in the cytoplasm) | + | 3.9E–06 | 0.8 |
|          | PA14_53300 | PA14_53295 | atpB | AtpC-like alkaline hydroperoxide reductase (oxidative stress response and cell redox homeostasis) | + | 3.9E–16 | 1.3 |
|          | PA14_73010 | PA14_73005 | mdrR2 | Transcriptional regulator, regulatory partner of MdrR1 (regulator of efflux systems) | + | 6.3E–05 | 0.7 |
|          | PA14_15300 | PA14_15295 | conserved hypothetical protein (EamA-like transporter) | + | 1.7E–26 | 1.7 |
|          | PA14_15290 | PA14_15285 | Hypothetical protein (unknown function, Mov34/MPN/PAD-1 family protein) | + | 5.7E–13 | 1.2 |
|          | PA14_15280 | PA14_15275 | Hypothetical protein (unknown function) | + | 1.9E–06 | 0.8 |
|          | PA14_15270 | PA14_15265 | mdpR2 | Probable molybdopterin biosynthesis protein MoeB (ubiquitin-like modifier-activating activity) | + | 7.5E–06 | 0.8 |
|          | PA14_21530 | PA14_21525 | ankyrin repeat domain-containing protein (unknown function) | + | 1.9E–04 | 0.7 |
|          | PA14_17720 | PA14_17700 | Probable transcriptional regulator | + | 5.2E–12 | 1.1 |
|          | PA14_15120 | PA14_15110 | Hypothetical protein (unknown function) | + | 1.4E–05 | 0.8 |
|          | PA14_15110 | PA14_15100 | Copper chaperone PCuA(C) | + | 8.6E–07 | 0.9 |
|          | PA14_15070 | PA14_15060 | TBDR copper receptor OprC (copper uptake) | + | 1.0E–03 | 0.6 |
|          | PA14_62890 | PA14_62880 | Hypothetical protein (unknown function, BON domain-containing protein) | + | 9.8E–03 | 0.6 |

(Continued on next page)
| Locus tag in *P. aeruginosa* strain | Gene Product (function)                                                                 | Zur regulon | Adjusted P value | Log2 fold change |
|------------------------------------|----------------------------------------------------------------------------------------|-------------|------------------|-----------------|
| IS492_31510 PA5481 PA14_72360      | Hypothetical periplasmic protein (inhibitor of vertebrate lysozyme)                    | 3.9E-04     | 0.7              |
| IS492_00850 PA0164 PA14_02050      | γ-Glutamyltransferase family protein                                                  | 8.0E-04     | -0.6             |
| IS492_02660 PA0524 PA14_06830      | Nitric oxide reductase subunit NosB (denitrification)                                  | 3.9E-03     | -0.6             |
| IS492_02685 PA0529 PA14_06890      | Hypothetical protein (unknown function, MOSC domain-containing protein)              | 2.0E-05     | -0.7             |
| IS492_02690 PA0530 PA14_06900      | Probable class III pyridoxal phosphate-dependent aminotransferase (diverse metabolic pathways) | 5.7E-05     | -0.8             |
| IS492_02695 PA0531 PA14_06920      | Aspartate aminotransferase family protein                                            | 4.7E-03     | -0.6             |
| IS492_12670 PA1101 PA14_50140      | Flagellar M-ring protein FilF (motility)                                             | 7.6E-03     | -0.6             |
| IS492_12855 PA1136 PA14_49700      | Probable transcriptional regulator                                                   | 1.5E-12     | -1.1             |
| IS492_12860 PA1137 PA14_49690      | Oxidoreductase zinc-binding dehydrogenase family protein (protection from oxidative stress) | 0.0E+00     | -2.3             |
| IS492_14625 PA1453 PA14_45660      | Flagellar biosynthesis protein FilF (motility)                                      | 4.9E-05     | -0.7             |
| IS492_19230 PA2298 PA14_34900      | Probable oxidoreductase                                                              | 3.2E-04     | -0.7             |
| IS492_19235 PA2299 PA14_34880      | Probable transcriptional regulator                                                   | 3.2E-04     | -0.6             |
| IS492_26340 PA3391 PA14_20230      | Regulatory protein NosR (denitrification)                                            | 3.2E-04     | -0.6             |
| IS492_26345 PA3392 PA14_20200      | Nitrous oxide reductase (denitrification)                                            | 4.1E-05     | -0.8             |
| IS492_26895 PA3519 PA14_18810      | Iron-containing redox enzyme family protein                                         | 2.8E-05     | -0.3             |
| IS492_26920 PA3523 PA14_18760      | Resistance-nodulation-cell division (RND) efflux membrane fusion protein            | 3.2E-03     | -0.2             |
| IS492_27180 PA3574 PA14_18080      | Transcriptional regulator NalD (second repressor of MexAB-OprM)                     | 1.5E-19     | -1.3             |
| IS492_27185 PA3574 PA14_18070      | Copper chaperone CopZ (copper efflux)                                                | 9.1E-11     | -1.0             |
| IS492_27760 PA3690 PA14_16660      | Heavy metal-translocating P-type ATPase (efflux)                                     | 1.1E-08     | -1.0             |
| IS492_28975 PA3920 PA14_13170      | Copper-translocating P-type ATPase CopA1 (copper efflux)                             | 1.2E-27     | -1.2             |
| IS492_04870 PA5100 PA14_67350      | Urocanate hydratase (histidine catabolic process)                                    | 4.0E-04     | -0.6             |

*TBDR, TonB-dependent receptor; SBP, soluble binding protein; ABC, ATP-binding cassette. Protein functions were inferred from the literature and PseudoCAP ([https://www.Pseudomonas.com/pseudocap](https://www.Pseudomonas.com/pseudocap)).

ND, not determined.
Consistent with previous studies, anaerobic cultures were more susceptible to killing by colistin than aerobic cultures (34, 35) (Fig. 7A and B). Interestingly, a clear bactericidal effect of colistin at 0.25 mg/L (i.e., 1/8 MIC) in combination with NAC at 8,000 mg/L was observed in planktonic cultures grown under anaerobic conditions, with eradication achieved after 24 h of exposure (Fig. 7A). The wide error bars were due to the fact that in 2 out of 8 replicates (related to two independent experiments), no synergism was observed (Fig. 7A). This discrepancy was probably related to the low colistin concentration tested and the possible presence of heteroresistant subpopulations. On the contrary, cultures grown in the presence of oxygen were not affected by the NAC-colistin combination, demonstrating the influence of the growth conditions on the susceptibility of *P. aeruginosa* to such combination (Fig. 7B).

These results supported the hypothesis that, under anoxic conditions like those present in the deeper biofilm layers and in CF mucus, NAC-mediated inhibition of anaerobic respiration would prevent an adaptive response of *P. aeruginosa* to protect from colistin toxicity.

**NAC-mediated inhibition of *P. aeruginosa* swimming and swarming motility.**

Transcriptomic results indicated that NAC downregulated two genes belonging to *P. aeruginosa* flagellar apparatus (i.e., *flif* and *flhf*), which are necessary for the first step
of flagellum assembly (36). In order to confirm the potential NAC-induced inhibition of flagellum-mediated motility, we performed classical swimming and swarming tests with the reference strain *P. aeruginosa* PAO1 and the CF strain *P. aeruginosa* Z154 (i.e., the strain used for transcriptomic analysis). *P. aeruginosa* Z154 was not capable of swarming motility under our laboratory conditions, so only the effect of NAC on swimming motility could be tested with this strain.

Overall, the results showed a clear inhibition of both swimming and swarming motility in the presence of NAC at 8,000 mg/L (Fig. 8 and 9). Such inhibition could be related to the downregulation of crucial genes of the flagellar apparatus and/or the induction of a zinc starvation response. Indeed, zinc starvation has been demonstrated to affect the ability of *P. aeruginosa* to express several virulence phenotypes, crucial for the ability of this pathogen to colonize CF lung, including motility, biofilm formation and siderophore synthesis (37).

**Conclusions.** In conclusion, the results of this study demonstrated a relevant antibiofilm synergism of NAC-colistin combinations (at the high concentrations achievable by inhalation) against *P. aeruginosa*, which would deserve further investigation for potential clinical applications of inhaled formulations. Transcriptomic and biological experiments suggested that NAC inhibited *P. aeruginosa* anaerobic respiration, which could be relevant for the observed antibiofilm synergism with colistin.

![Graphs showing time-kill curves of *P. aeruginosa* Z154 planktonic cultures exposed to N-acetylcysteine (NAC) at 8,000 mg/L, colistin (CST) at 0.25 mg/L, and the NAC-CST combination under anaerobic (A) and aerobic (B) conditions. NAC potentiated the bactericidal activity of colistin only under anaerobic conditions. Data are plotted as the median values of CFU per milliliter for each time point. Dotted lines indicate the detection limit (17 CFU/mL).](image-url)
In addition, although NAC alone was not demonstrated to be effective against preformed *P. aeruginosa* biofilms, transcriptomic analysis of NAC-exposed planktonic cultures revealed that NAC could attenuate *P. aeruginosa* virulence, mainly by inducing a zinc starvation response, affecting anaerobic respiration and inhibiting flagellum-mediated motility (with the last two features confirmed experimentally). In this perspective, NAC, at the high concentrations achievable by inhalation, might have beneficial effects in the very first steps of lung infection, possibly preventing biofilm formation and the establishment of a chronic colonization, which should be further investigated.

**MATERIALS AND METHODS**

**Bacterial strains.** Seventeen strains were investigated, including 15 clinical isolates from CF patients, an MDR clinical isolate from a respiratory tract infection (RTI) from an intensive care unit (ICU), and the reference strain, *P. aeruginosa* PAO1 (Table 1). Identification was performed by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) (Bruker, Shimadzu). Antimicrobial susceptibility was determined using the reference broth microdilution method (38). Whole-genome sequencing of clinical isolates was performed with the Illumina (San Diego, CA, USA) MiSeq platform, using a 2 x 150-bp paired-end approach. Raw reads were assembled using SPAdes (39), and draft genomes were used to determine multilocus sequence types (MLSTs) and O types at the Oxford PubMLST site (https://pubmlst.org/) (40) and at the

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**FIG 8** NAC-mediated inhibition of *P. aeruginosa* PAO1 and Z154 swimming motility. Assays were performed in at least three independent experiments (with three replicates per condition per experiment), and representative data are shown.

**FIG 9** NAC-mediated inhibition of *P. aeruginosa* PAO1 swarming motility. Assays were performed in at least three independent experiments (with three replicates per condition per experiment), and representative data are shown.
Center for Genomic Epidemiology site (https://cge.food.dtu.dk/services/PAst/) (41), respectively. The complete genome of \( P. \) aeruginosa Z154 was obtained by combinatorial assembly from Illumina with those obtained using the Oxford Nanopore Technologies (Oxford, United Kingdom) MinION platform, and de novo assembly was generated using Unicycler v0.4.4 as previously described (42).

**Preparation of culture media.** NAC stock solutions (100 g/L) were prepared immediately before use. NAC powder (Zambon, Bresso, Italy) was dissolved in sterile distilled water, the pH was adjusted to 6.5 to 6.8 with NaOH at 10 M, and the solution was filtered through a 0.22-μm-pore membrane filter. All experiments were performed in cation-adjusted Mueller-Hinton broth (CAMHB) (Becton Dickinson, Milan, Italy), unless otherwise specified, starting from an appropriately concentrated medium to avoid broth dilution when NAC solution was used. The artificial sputum medium (ASM) was also used in selected experiments and was prepared as previously described by Kirchner et al. (43).

**In vitro biofilm susceptibility testing.** Biofilm susceptibility testing was first performed using the Nunc-TSP lid system (Thermo Fisher Scientific, Waltham, MA, USA), as described previously (44). Briefly, biofilms were grown for 24 h in CAMHB at 35°C under static conditions. Preformed biofilms were then exposed to NAC at 8,000 mg/L and colistin (colistin sulfate; Applichem, Darmstadt, Germany) at 2 to 32 mg/L, alone and in combination. The colistin concentration was selected according to preliminary results of antibiofilm susceptibility testing and the colistin MIC for each strain. After 24 h of exposure (i.e., 35°C, static conditions), biofilms were washed twice with 200 μL of phosphate-buffered saline (PBS) (Sigma-Aldrich, Milan, Italy) to remove loosely adherent bacteria, and sessile cells were removed from pegs by sonicating for 30 min (Elma Transsonic T 460; Elma, Singen, Germany) in 200 μL of tryptic soy broth (TSB) (Oxoid, Milan, Italy) supplemented with 1% Tween 20 (Sigma-Aldrich) (i.e., the recovery medium). The median number of CFU per peg was then determined by plating 10 μL of appropriate dilutions of the recovery medium onto tryptic soy agar (TSA) (Oxoid) and incubating for 24 h at 35°C (detection limit, 20 CFU/peg). The colony count was also double-checked after 48 h of incubation.

The potential antibiofilm synergism of NAC-colistin combinations was further investigated using an in vitro ASM biofilm model (43) in order to mimic \( P. \) aeruginosa biofilm conditions within the CF mucus. The study was carried out with two selected CF strains (\( P. \) aeruginosa Z154 and Z34), exhibiting different features (i.e., mucoid/nonmucoid phenotype, antimicrobial susceptibility pattern, MLST, and O type) (Table 1). In brief, biofilms were grown in 2 mL ASM in 24-well plates (Sarstedt, Nümbrecht, Germany), for 72 h at 35°C under static conditions. Preformed biofilms were then exposed to NAC at 8,000 mg/L and colistin at 64 mg/L, alone and in combination. Preliminary experiments carried out with lower colistin concentrations (i.e., 2 to 32 mg/L) did not show evident synergistic antibiofilm activity, while higher colistin concentrations (i.e., >64 mg/L) led to eradication of the biofilm cultures even in the absence of NAC (data not shown). After 24 h of exposure (i.e., 35°C, static conditions), bacterial biofilms were disrupted by 30 min of sonication following manual pipetting, and the median number of CFU per milliliter was determined following the same protocol described for the Nunc-TSP lid assay.

Data from both biofilm models were obtained in at least three independent experiments, with at least 12 replicates per condition per experiment.

**RNA-seq and transcriptomic analysis.** \( P. \) aeruginosa Z154 (i.e., colistin-susceptible CF strain, mucoid, MDR, ST412, O6) (Table 1) was selected for studies aimed at investigating the transcriptomic response of \( P. \) aeruginosa to NAC exposure. A CF strain, rather than a reference strain (such as \( P. \) aeruginosa PAO1), was selected for this analysis because of the known adaptive diversification of \( P. \) aeruginosa into “specialized” types during chronic/recurrent infections in CF patients (33). Because these represented the first data on the transcriptomic response of \( P. \) aeruginosa to NAC exposure and considering the complex and still only unknown effects of NAC on microbial physiology, we decided to perform the experiments with planktonic cultures, which represent a more homogeneous and better standardized model for transcriptomic studies.

Overnight cultures in CAMHB were diluted at 1:50 in the same medium and incubated at 35°C with agitation to achieve an optical density at 600 nm (OD600) of 1.0. The cells were then exposed to NAC at 8,000 mg/L for 30 min at 35°C under static conditions. Cultures treated in the same way but not exposed to NAC represented the control. Total RNA extraction was performed using the SV total RNA isolation system (Promega, Madison, WI, USA) following the manufacturer's instructions. RNA depletion, cDNA library construction, and Illumina HiSeq 4000 platform-based transcriptome sequencing (RNA-seq) were performed by Eurofins Genomics Europe Sequencing (Constance, Germany). The transcriptome libraries were single-end sequenced with 50-bp reads for a total of 10 million reads per sample. Bioinformatic analysis was performed using the SeqMan NGen v17.3 software tool (DNASTAR Lasergene, Madison, WI, USA), with default parameters. Reads were aligned using \( P. \) aeruginosa Z154 complete genome \( (n = 6,344 \) coding DNA sequences \( \text{CDSs} \) as a reference. Differentially expressed genes \( (\text{DEGs}) \) of the NAC-exposed cultures compared to the control were analyzed considering false-discovery rate (FDR) adjusted \( P \) values of <0.05 from DeSeq2. DEGs with a 99% confidence interval \( (\text{CI}) \) were discussed.

Results were obtained from two independent experiments. In order to favor comparison with data present in the literature, genes without a univocal name have been indicated as \( P. \) aeruginosa PAO1 locus tags throughout the text and reported in Table 2 also as \( P. \) aeruginosa UCBPP-PA14 locus tags.

**\( \text{NO}_2^- \) and \( \text{NO}_3^- \) quantification.** NAC-mediated inhibition of the denitrification pathway was investigated by measuring the concentration of \( \text{NO}_2^- \) and \( \text{NO}_3^- \) in anaerobic cultures of \( P. \) aeruginosa Z154 (i.e., the strain used for transcriptomic analysis). For this purpose, the Griess nitrite/nitrate colorimetric assay (Cayman Chemicals, Ann Arbor, MI, USA) was used according to the manufacturer’s recommendations and as previously described, with some modification (33). CAMHB was supplemented with 10 mM NaNO2 or KNO2 and allowed to equilibrate for 3 days at 35°C in an anaerobic atmosphere by using the AnaeroGen kit (Oxoid). Overnight cultures were then diluted in 20 mL of each anoxic culture medium to reach a concentration of 10^5 CFU/mL and challenged with NAC at 8,000 mg/L. At times 0, 24, and 48 h of incubation under
anoxic conditions at 35°C, supernatants were harvested and subjected to Griess colorimetric reaction in order to detect NO\textsubscript{3}\textsuperscript{-} and NO\textsubscript{2}\textsuperscript{-} levels. NAC-free cultures represented the control. Experiments were carried out in triplicate with three replicates per time point per condition.

**Time-kill assays.** Time-kill assays were performed according to CLSI guidelines (45) with the colistin-susceptible strain \textit{P. aeruginosa} Z154 (i.e., the strain used for transcriptomic analysis). Colistin at 0.25 mg/L was tested alone and in combination with NAC at 8,000 mg/L under both aerobic and anaerobic conditions. We decided to use this colistin concentration since a higher concentration led to eradication of the planktonic cultures (data not shown). The medium (CAMHB) used to obtain anoxic cultures was placed under an anaerobic atmosphere by using the AnaeroGen kit (Oxoid) for 3 days prior to use and during the whole experiment. The killing curves were carried out in borosilicate glass bottles with a final volume of 20 mL of CAMHB. At 0, 2, 4, 8, and 24 h of exposure, CFU per milliliter were determined by blating 60 \muL of appropriate dilutions of each condition onto TSA and incubating for 24 h at 35°C (detection limit, 17 CFU/mL). Data were obtained from at least four independent experiments with two replicates per condition per experiment.

**Motility tests.** NAC-induced inhibition of flagellum-mediated motility (i.e., both swimming and swarming motility) was investigated with the reference strain \textit{P. aeruginosa} PAO1, which has been used for similar motility experiments in several previous studies (46), and \textit{P. aeruginosa} Z154 (i.e., the strain used for transcriptomic analysis). \textit{P. aeruginosa} Z154 was not capable of swarming motility under our laboratory conditions (perhaps due to the known reduction of flagellar expression in mucoid CF-adapted strains) (47), so only the effect of NAC on swimming motility could be tested with this strain. Swim plates consisted of Luria-Bertani (LB) broth (Oxoid) containing 0.3% agar (46). Overnight cultures in CAMHB were diluted in an anaerobic atmosphere by using the AnaeroGen kit (Oxoid) for 3 days prior to use and during the whole experiment. The swimming plates were carried out in borosilicate glass bottles with a final volume of 20 mL of CAMHB. At 0, 2, 4, 8, and 24 h of exposure, CFU per milliliter were determined by blating 60 \muL of appropriate dilutions of each condition onto TSA and incubating for 24 h at 35°C (detection limit, 17 CFU/mL). Data were obtained from at least four independent experiments with two replicates per condition per experiment.

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\textit{P. aeruginosa} strains Z154 and Z152 were kindly provided by Lisa Cariani, Cystic Fibrosis Microbiology Laboratory, IRCCS Fondazione Cà Granda, Ospedale Maggiore Policlinico, Milan, Italy.

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**Data availability.** The complete genome sequence of \textit{P. aeruginosa} Z154 was deposited in GenBank under accession no. CP069177. RNA-seq data were also deposited in the NCBI Gene Expression Omnibus (GEO) database under accession no. GSE190946.

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