Role of *Williamsia* and *Segniliparus* in human infections with the approach taxonomy, cultivation, and identification methods

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**Abstract**

The genera *Williamsia* and *Segniliparus* are of aerobic actinomycetes and at the time of writing, they have 12 and 2 species, respectively. These genera cause various infections in humans. In this review, we surveyed their taxonomy, isolation, identification, as well as their role to cause human infections.

**Keywords:** Actinomycete, Isolation, Taxonomy, *Segniliparus*, Williamsia

**Introduction**

Aerobic actinomycetes are the group of Gram-positive bacilli belonging to the phylum Actinobacteria. Some species that cause human infections in this group are situated in one of the four suborders, including Corynebacterineae, Micrococcineae, Streptomycineae and Streptosporangineae [1]. Kämpfer et al. and Butler et al. suggested that the genera of *Williamsia* [2] and *Segniliparus* that belong to the actinomycete family, [3] respectively, can cause human infections. They non-spore, non-motive aerobic organisms with short rods without branching that contain mycolic acid components in the cell wall structure [4]. DNA G+C content in the genera *Williamsia* and *Segniliparus* are 64–65% and 68–72% [4] respectively, and they are into the order Corynebacteriales (Tindall [5] proposed the name of *Corynebacteriales* to be replaced by *Mycobacteriales*) and suborder Corynebacterineae. The various genera include *Corynebacterium*, *Dietzia*, *Hoyosella*, *Gordonia*, *Lawsonella*, *Millisia*, *Mycocacterium*, *Mycobacteroides*, *Mycolicibacillus*, *Mycelicibacter*, *Mycolicibacterium*, *Nocardia*, *Rhodococcus*, *Skermania*, *Smaragdicoccus*, *Tomitella* and, *Tsukamurella* are located in this suborder (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Undef&id=85007&lvl=3&lin=f&keep=1&srchmode=1&unlock). To date, various infections cause by actinomycetes are on the rise. The most common genera that cause infections in this suborder include *Corynebacterium* (such as *Corynebacterium accolens* [6], *Corynebacterium afermentans* [6], *Corynebacterium amycolatum* [6], *Corynebacterium appendicis* [7], *Corynebacterium argentarotense* [7], *Corynebacterium aurimucosum* [6], *Corynebacterium coyleae* [7], *Corynebacterium diphertheriae* bv. *mitis* [6], *Corynebacterium durum* [7], *Corynebacterium freneyi* [7], *Corynebacterium glucuronolyticum* [6], *Corynebacterium hansenii* [7], *Corynebacterium imitans* [6], *Corynebacterium jeikeium* [6], *Corynebacterium kroppenstedtii* [8], *Corynebacterium lipophilloflavum* [7], *Corynebacterium macginleyi* [6], *Corynebacterium masiliense* [7], *Corynebacterium minutissimum* [6], *Corynebacterium mucificiens* [6], *Corynebacterium mycetoides* [7], *Corynebacterium pseudodiphtheriticum* [6], *Corynebacterium pylareense* [7], *Corynebacterium propinquum* [6], *Corynebacterium pyruviciproducens* [7], *Corynebacterium riegelii* [7], *Corynebacterium resistans* [7], *Corynebacterium simulans* [6], *Corynebacterium singular* [7], *Corynebacterium sputi* [7], *Corynebacterium*...
stationis [7], Corynebacterium striatum [6], Corynebacterium sundsvalense [7], Corynebacterium thomsonii [7], Corynebacterium timonense [7], Corynebacterium tuberculostearicum [6], Corynebacterium tuscaniense [7], Corynebacterium ureicelerivorans [6], Gordonia (such as Gordonia aichiensis [9], Gordonia amicalis [9], Gordonia araii [9], Gordonia bronchialis [9], Gordonia effuse [9], Gordonia ottidis [9], Gordonia polyisoprenivorans [9], Gordonia spuiti [9], Gordonia terrae [9], Gordonia westfalica [10]), Mycobacterium (such as Mycobacterium abscessus [11], Mycobacterium ahvazicum [12], Mycobacterium alsense [13], Mycobacterium alsiense [14], Mycobacterium arupense [15], Mycobacterium avium [11], Mycobacterium bactERICum [14], Mycobacterium barraSiae [14], Mycobacterium bouchedorHionene [14], Mycobacterium canetti [16], Mycobacterium celerflaVum [14], Mycobacterium chelonea [11], Mycobacterium chimaera [17], Mycobacterium conceptionense [18], Mycobacterium engbaekii [14], Mycobacterium europauem [14], Mycobacterium flavescens [19], Mycobacterium fortuitum [11], Mycobacterium fragilis [14], Mycobacterium franklinii [14], Mycobacterium fukienense [14], Mycobacterium gadium [19], Mycobacterium gordonae [11], Mycobacterium heckeshornense [20], Mycobacterium heraklonense [14], Mycobacterium immunogenum [21], Mycobacterium insubricum [14], Mycobacterium intracellular [11], Mycobacterium iranicum [14], Mycobacterium malmoense [22], Mycobacterium mucogenicum [11], Mycobacterium kansasi [11], Mycobacterium koreense [14], Mycobacterium kumamonense [14], Mycobacterium kyorinense [14], Mycobacterium lentiflavum [11], Mycobacterium lepromatosis [14], Mycobacterium latzerense [14], Mycobacterium longobardum [14], Mycobacterium mageritense [23], Mycobacterium manteni [14], Mycobacteriummarinum [24], Mycobacterium marseillense [14], Mycobacterium monacense [14], Mycobacterium novocaenstre [19], Mycobacterium noviomagense [14], Mycobacterium orygis [14], Mycobacterium paraffinicum [14], Mycobacterium paragordanae [14], Mycobacterium parakoreense [14], Mycobacterium paraseoulense [14], Mycobacterium paraterrae [14], Mycobacterium peregrinum [19], Mycobacterium porcinum [19], Mycobacterium riyadhense [14], Mycobacterium scrofulaceum [11], Mycobacterium semuense [14], Mycobacterium seoulense [14], Mycobacterium setense [14], Mycobacterium sherrisi [14], Mycobacterium shigaense [14], Mycobacterium shinjukuenese [14], Mycobacterium simiae [25], Mycobacterium simulans [14], Mycobacterium sinense [14], Mycobacterium thermoresistibile [18], Mycobacterium timonense [14], Mycobacterium tuberculosis [26], Mycobacterium ulcerans [27], Mycobacterium vulneris [14], Mycobacterium xenopi [11], Mycobacterium yongonense [14], Tsukamurella (such as Tsukamurella asaccharolytica [28], Tsukamurella conjunctivitis [28], Tsukamurella hongkongensis [29], Tsukamurella inchoensis [29], Tsukamurella paurometabola [29], Tsukamurella pseudospunae [29], Tsukamurella pulmonis [29], Tsukamurella serpentinis [29], Tsukamurella sinensis [29], Tsukamurella soli [29], Tsukamurella spuana [29], Tsukamurella spuiti [28], Tsukamurella strandjordae [29], Tsukamurella tyrosinosolvens [29]), Nocardia (such as Nocardia abscessus [30], Nocardia amaniensis [30], Nocardia amikacinintolerans [31], Nocardia araoensis [30], Nocardia arthritidis [30], Nocardia asiatica [30], Nocardia asteroide [30], Nocardia barduii [32], Nocardia beijingensis [30], Nocardia blacklockiae [33], Nocardia boirouni [30], Nocardia brasiliensis [30], Nocardia caviae [30], Nocardia carnea [34], Nocardia cerradoensis [30], Nocardia colli [35], Nocardia concava [30], Nocardia cроссostreae [30], Nocardia cyriacigeorgica [30], Nocardia exalbida [30], Nocardia farcinica [30], Nocardia gipuzkoensis [32], Nocardia harenae [30], Nocardia higoensis [30], Nocardia ignorata [36], Nocardia kruzezakae [30], Nocardia mexicana [30], Nocardia neocaldoniensis [30], Nocardia nova [30], Nocardia otitidiscaviarum [30], Nocardia puvivorans [30], Nocardia pseudobrasiliensis [30], Nocardia puris [30], Nocardia takedensis [30], Nocardia thailandica [30], Nocardia transvalensis [30], Nocardia veterana [30], Nocardia wallacei [37], Nocardia yamashashiensis [30]) and, Rhodococcus (such as Rhodococcus equi (renamed to prescottiella equi) [38], Rhodococcus erythropolis [38], Rhodococcus ruber [38], Rhodococcus gordoniae [38], Rhodococcus facsians [38]). This study was performed because of the lack of attention and awareness of physicians to infections caused by these bacteria and to inform medical laboratory personnel about the methods of isolation and detection of these bacteria at the genus and species level. Our literature review focused on the human infections caused by Williamsia andSegnilparus considering taxonomy, cultivation, and identification methods through searching four databases, including Google Scholar, PubMed, Scopus, and Web of Science up to Oct 28, 2020, for all articles in English language, such as case reports, original articles, review article and books were 7, 17, 2, and 3 articles respectively.

Cell wall structure in Williamsia

The genera Williamsia and Segnilparus has a wall chemo type IV [4, 39]. In the cell wall, Williamsia contains meso-2,6-diaminohexanedioate(C₆H₁₂N₂O₄), dihydrogenated menaquinone with nine isoprene units (Williamsia deligens has dihydrogenated menaquinone with eight isoprene units [40]), diphosphatidyglycerol, tuberculostearic acids, phosphatidylethanol, phosphatidylglycerol, N-glycolyl muramic acid, phosphatidylinositol
and, mycolic acids [4]. Muramic acid is glycosylated in the genera of Tsukamurella, Tomitella, Smaragdicoccus, Skermania, Rhodococcus, Nocardia, Mycobacterium, Millisia, and Gordonia, but it is acetylated in the Dietzia and Corynebacterium [4]. The fatty acids of Williamsia are hexadecenoic acid (C16:1-trans) oleic acid (C18:1), palmitic acid (C16:0), and turbuclustearic acid (10-methyl octadecanoate) [4]. In the Williamsia, some carbons in chain mycolic acids are C50–C56 [41].

Cell wall structure in Segniliparus
The cell wall of Segniliparus contains meso-diaminopimelic acid, mycolic acids and, tuberculo-fatty acid [3]. The fatty acids of Segniliparus are C10:0, C14:0, C16:0, and turbuclustearic acid [3]. In the Segniliparus, some carbons in chain mycolic acids are C60–C100 [42], but in the other genera such as Nocardia, Skermania, Gordonia, Tsukamurella, Mycobacterium, Millisia, Rhodococcus, Dietzia, Hoyosella, and Corynebacterium they are C46–C60, C58–C64, C46–C66, C64–C78, C60–C90, C44–C52, C30–C54, C34–C38, C30–C35 and, C22–C36 [41] respectively.

Isolation methods for Williamsia spp.
Collection and transportation of clinical specimens to the medical laboratory are two important principles in the isolation of aerobic actinomycetes from the infections [1]. At the time of writing, the specific media have not been described for the isolation of Williamsia from human clinical samples. In literature, various media have been used for Williamsia isolation from various sources; however, those associated with good growth or appropriate for morphological examination are Columbia agar supplemented with 5% sheep blood agar and brain heart infusion (BHI) agar [40], M3 agar supplemented with cycloheximide and nystatin [44], glucose/yeast extract agar (GYEA) plates [44, 45], raffinose–histidine agar plate supplemented with cycloheximide and nystatin [45], tryptic soy agar (trypthicase soy agar/tryptone soy agar) [2, 46–48], starch-casein agar supplemented with cycloheximide [47], nystatin and rifampicin and ISP media 2–7 [47], modified Bennett’s agar [47], glucose-yeast extract malt extract agar [47], nutrient agar [47, 49, 50], Gauze’s medium with cycloheximide, nalidixic acid, novobiocin, and nystatin [51], M125 medium [49], tap water agar and ISP medium 2 [48], Reasoner’s 2A agar (R2A) [2], GC agar [52], serum broth [52], and M1 agar plate [53].

Isolation methods for Segniliparus spp.
For the genus Segniliparus, the use of Middlebrook 7H10 and 7H11 media [3], Lowenstein–Jensen (LJ) medium [54], LJ with 5% sodium chloride [54] and American Trudeau Society (ATS) media [54] have been suggested for isolation, good growth, and examination of morphological characteristics. Also, Segniliparus rugosus can grow on MacConkey agar [3] and it has been reported that S. rugosus is resistant to decontamination methods such as NaOH and N-acetyl-l-cysteine in clinical specimens [55].

Phenotypic identification of Williamsia
Phenotypic characterizations are the first step for these bacteria identification at the genus and species levels. In the Williamsia there is 12 species names validly published includes Williamsia aurantiacus [53], W. deligens [40], Williamsia faeni [51], Williamsia herbipolensis [50], Williamsia limnetica [47], Williamsia maris [44], Williamsia marianensis [45], Williamsia muralis [2], Williamsia phyllosphaerae [49], Williamsia serinedens [43], Williamsia spongiae [46], and Williamsia sterculiae [48]. The species of this genus are distributed in different environments; however, they have also been isolated from clinical specimens [40]. Various phenotypic tests are properties of colonial morphology and pigment production (pigment colors in Williamsia spp. are yellow to orange or red [1]), producing aerial hyphae (this phenotypic characterization is seen in Williamsia, Skermania, Nocardia and, Millisia [4]), Gram stain (the genus Williamsia is Gram-positive), acid-fast stain (the genus Williamsia is not acid-fast [56]), hydrolysis of amino acids, acid production of carbohydrates, high-performance liquid chromatography (HPLC), gas–liquid chromatography (GLC), thin-layer chromatography (TLC) procedures, and enzymes production [3, 4, 39, 56]. Some of the phenotypic characterization of the Williamsia spp. are shown in Table 1. Conventional phenotypic methods are unreliable and insufficient for differentiation of Williamsia and Segniliparus of related aerobic actinomycetes; therefore, molecular techniques have been used for accurate identification at the genus and species level. The temperature range for the growth for Williamsia spp. including W. limnetica, W. sterculiae, W. maris, W. muralis is 10 to 37 °C [2, 44, 47, 48], for W. aurantiacus and W. spongiae is 10 to 45 °C [46, 53], for W. phyllosphaerae and W. herbitopolensis is 25 to 30 °C [49, 50], for W. deligens is 37 °C [40], for W. serinedens is 22 to 30 °C [43], for W. marianensis is 4 to 30 °C [45], and for W. faeni is 10 to 30 °C [51]. Also, the pH range for the growth is between 4.0 and 10.0 for W. aurantiacus and W. spongiae [46, 53] and 5.0–8.0 for W. sterculiae [48].

Phenotypic identification of Segniliparus
Two species of Segniliparus rotundus and S. rugosus belong to the Segniliparus genus [3]. Its species are distributed in different environments; however, they have also been isolated from clinical specimens [57]. Pigment
| Name of bacteria | Source isolation/year | Utilization of | Production of urease | Hydrolysis of gelatin | Hydrolysis of casein | Hydrolysis of hypoxanthine | Hydrolysis of tyrosine | References |
|------------------|-----------------------|---------------|----------------------|----------------------|---------------------|--------------------------|-----------------------|------------|
| W. aurantiaca    | Marine sponge/2019    | +w            | +w                   | +                    | +                   |                          |                       |            |
| W. deligens      | Human blood/2006      | +             | +                    | +                    | +                   |                          |                       |            |
| W. faeni         | Hay meadow/2010       | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. herbitoporus  | Phyllosphere of Arabidopsis thaliana/2016 | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. limnetica     | Sediment/2012         | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. manis         | Sediment/2004         | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. muralis       | Indoor building materiais/1999 | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. phyllosphaerae| The leaf surface of Trifolium repens/2011 | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. secedens      | Oil-contaminated soil/2007 | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. sponglae      | Marine sponge/2017    | +             | +                    | +                    | +                   | +                       | +                     |            |
| W. sterculiae    | Stems of medicinal plants/2013 | +             | +                    | +                    | +                   | +                       | +                     |            |
| S. rugosus       | Sputum/2005           | +/-           | -                    | +/−                  | -                   |                          |                       |            |
| S. rotundus      | Sputum/2005           | +/-           | -                    | +/−                  | -                   |                          |                       |            |

Table 1: Some of the phenotypic characterization of the *Williamsia* and *Segniliparus* spp.
| Name of bacteria | Source isolation/year | Utilization of l-Rhamnose | l-Sorbose | l-Arabinol | d-Galactose | d-Raffinose | d-Ribose | l-Salicin | Production of urease | Hydrolysis of gelatin | Hydrolysis of casein | Hydrolysis of hypoxanthine | Hydrolysis of tyrosine | References |
|------------------|----------------------|---------------------------|----------|-----------|------------|------------|----------|----------|---------------------|---------------------|------------------|------------------------|------------------------|-----------|
| W. marianensis   | Sediment/2008        | +                         | −         | −         | −          | −          | +        | −        | −                   | −                   | +                | −                      | −                      | [45]       |
| W. maris         | Sediment/2004        | +                         | +         | −         | −          | −          | −        | −        | +                   | +                   | −                | −                      | −                      | [44]       |
| W. muralis       | Indoor building mate- | +                         |          |           |            |            |          |          | −                   | −                   | −                | −                      | −                      | [2]        |
| W. phylo-        | The leaf surface of   | −                         | −         | −         | −          | −          |          |          | −                   | −                   | −                | −                      | −                      | [49]       |
| sphaerae         | Trifolium repens/2011|                          |          |           |            |            |          |          | −                   | −                   | −                | −                      | −                      |           |
| W. serinedens    | Oil-contaminated soil/2007 | −              |            |          |            |            |          |          | −                   | −                   | −                | −                      | −                      | [43]       |
| W. spongiae      | Marine sponge/2017   | −                         | −         | −         | +          | −          |          |          | −                   | −                   | +                | +                      | −                      | [46]       |
| W. sterculiae    | Stems of medicinal plants/2013 | +                  | +         |          |            |            |          |          | −                   | −                   | −                | −                      | −                      | [48]       |
| S. rugosus       | Sputum/2005          |                           |           |           |            |            |          |          | −                   | −                   | −                | −                      | −                      |           |
| S. rotundus      | Sputum/2005          |                           |           |           |            |            |          |          | −                   | −                   | −                | −                      | −                      |           |
colors in *Segniliparus* spp. is white to beige [3]. An aerial hyphae are not seen in the *Segniliparus* [4]; and the genus is acid-fast [56]. Some of the phenotypic characterization of the *Segniliparus* spp. are shown in Table 1. The temperature range for the growth in *Segniliparus* spp. are as follows: *S. rotundus*: 28 to 37 °C [3] and *S. rugosus*: 22 to 42 °C [3]. Researchers, medical laboratory personnel, and clinicians should note that in pulmonary specimens, especially in cystic fibrosis patients, the genus *Segniliparus* is similar to the genus *Mycobacterium* in acid-fast staining [54].

**Molecular identification of the Williamsia**
The most common molecular method for *Williamsia* accurate identification and assessment of taxonomic characteristics is sequence-based identification. 16S rRNA gene sequencing is an effective standard method for accurate identification of the novel bacteria and emerging pathogens at the genus and species levels [58]. Primers to amplify 16S rRNA gene for *Williamsia* identification include 27F (5′-AGAGTTTGATCCTTGCTCAG-3′)/1492R (5′-AAGCTTGTGTTAGCTGACT-3′) and 27F (5′-GAGTATCTGCTGCTCAG-3′)/1525R (5′-GAGGAGGTGATCCAGC-3′) [40, 44]. Montoya-Porras et al. [59] identified the genus *Williamsia* with 454 pyrosequencing for the variable region of the 16S rRNA gene. The phylogenetic tree of the 16S rRNA gene for *Williamsia* standard species is shown in Fig. 1. The gold standard method to discern bacterial species is DNA–DNA hybridization (DDH) [30]; however, this method is not used in clinical laboratories for bacterial identification. Another molecular method is the whole-genome sequencing (WGS), which has been deposited for five *Williamsia* species in the National Center for Biotechnology Information (NCBI). Data are provided in Additional file 1.

**Molecular identification of the Segniliparus**
16S rRNA gene primers, such as 5′-GAGAGTTTG ATCTCTGCTCAG-3′/5′-AAGGAGGTGATCCAG CCGCA-3′ [3]; 8FPL (5′-AGTTTGATCCTTGCTCAG -3′)/806R (5′-GGACTACGAGGTATCTAAT-3′), and 515FPL (5′-TGCCACGACCAGCCTGATAA-3′)/13B (5′- AGGCCGGAAACGTATCCAC-3′) have been used for *Segniliparus* identification [60]. The phylogenetic tree of the 16S rRNA gene for *Segniliparus* standard species is shown in Fig. 1. Butler et al. [3] reported that three of the four isolates of *Segniliparus* were not amplified for the 65 kDa heat-shock protein (*hsp65*) gene with TB11 (5′-ACCAACAGATGGTGTTGATCAT-3′) and TB12 (5′-CTTGGCAACCAGCATACCT-3′) primers. Also, the cholesterol oxidase gene (*choE*) gene (this gene is a virulence factor gene in *Rhodococcus equi*) was not amplified for *Segniliparus* [3]. Koh et al. [55] used PCR-restriction fragment length polymorphism analysis (PRA) of the *hsp65* (527-bp) [F: 5′-GAGGATGTCATCACGCTGCAGG-3′/R: 5′-GGCCGATGGCGTGGAGATCC-3′] and *rpoB* (360-bp) [F: 5′-TCAAGGAGAGGCGCTACGC-A-3′/R: 5′-GGAATGTGATGACAGGCTGC-3′] genes for *Segniliparus* spp. identification. WGS of two *Segniliparus* isolates has been deposited in the National Center for Biotechnology Information (NCBI). Data are provided in Additional file 1.

![Fig. 1](image-url)

*Fig. 1* The 16S rRNA gene-based phylogenetic tree of standard *Williamsia* and *Segniliparus* spp. with using the molecular evolutionary genetics analysis (MEGA) 5.0 software [66] which computed by the neighbor joining (NJ) analyses and kimura 2-parameter (K2P) model. The sequences were downloaded from NCBI. W: *Williamsia*; N: *Nocardia*, S: *Segniliparus*.
Pathogenesis in Williamsia and Segniliparus

Our knowledge about pathogenesis and virulence factors in two genera is limited. Cell wall components, such as mycolic acid, phagolysosome inhibition, immune response promotes, and the production of enzymes, such as catalase, may play a role in their pathogenesis.

Clinical disease, antiobiem and treatment associated with Williamsia

Physicians need to pay attention to these symptoms such as bilateral alveolar infiltrates [61], fever [62], having an underlying disease such as diabetes mellitus for detection of this rare infection [52]. Infections in humans caused by Williamsia have been reported. Infection occurs as a result of exposure to the environment; however, there is no evidence of an environmental source for Williamsia and Segniliparus infections. For antimicrobial susceptibility testing (AST), breakpoints have not been established for these genera, and researchers use recommended AST (the gold standard for antibiotic micro broth dilution) for Nocardia and related aerobic actinomycetes by the Clinical and Laboratory Standards Institute (CLSI) [63]. Tomas et al. [61] first reported W. muralis as the cause of lung infection in an old woman. In their study, this bacterium was isolated from a brush sample and results of AST showed that this bacterium was susceptible to amoxicillin-clavulinate, cefalosporin (cefotaxime), carabpenem (imipenem), Quinolone (ciprofoxacin), aminoglycoside (tobramycin, gentamicin), sulfonamide (cotrimoxazole) and resistant to beta-lactam (ampicillin) and macrolide (erythromycin) family. In another study by Yassin et al. [40] reported W. deligens of human blood in 2006. Also, W. serinedens has been isolated of perinatal sepsis from a pregnant woman in 2010 and this bacterium was susceptible to amikacin, ampicillin, doxycycline, imipenem, linezolid, meropenem, penicillin G, tobramycin, vancomycin and was resistant to oxacillin and trimethoprim-sulfamethoxazole with E-test method [62]. The case reports published regarding Williamsia spp. are provided in Table 2.

### Table 2 Case reports published of Williamsia spp. in literature

| Age/sex/country | Underlying disease | Type of infection | Isolated from | Name of organism | Outcome | References |
|----------------|--------------------|-------------------|---------------|------------------|---------|------------|
| 66/M/Australia | Diabetic           | Endophthalmitis   | Vitreous fluid | W. muralis       | Cure    | [52]       |
| 80/F/Spain     | Allergy to penicillin and high blood pressure | Lung infection | Brush | W. muralis | Died    | [61]       |
| 31/F/Germany   | Pregnant           | Perinatal sepsis  | Blood         | W. serinedens    | Cure    | [62]       |

W. deligens isolated from blood [40] but case history is not available

### Table 3 Case reports published of Segniliparus spp. in literature

| Age/sex/country | Underlying disease | Type of infection | Isolated from | Name of organism | Outcome | References |
|----------------|--------------------|-------------------|---------------|------------------|---------|------------|
| /M/USA         | Cystic fibrosis    | Lung infection    | Sputum        | S. rugosus       | Cure    | [64]       |
| /M/USA         | Cystic fibrosis    | Lung infection    | Sputum        | S. rugosus       | Cure    | [64]       |
| 28/M/USA       | Cystic fibrosis    | Lung infection    | BAL           | S. rugosus       | Cure    | [64]       |
| Teenager/F/Australia | Cystic fibrosis | Lung infection | Sputum | S. rugosus | Cure    | [54]       |
| 43/F/South Korea | Immunocompetent    | Lung infection    | Sputum        | S. rugosus       | Cure    | [55]       |
| 47/F/Korea     | Immunocompetent    | Lung infection    | Sputum        | S. rugosus       | Cure    | [60]       |

Segniliparus rotundus and Segniliparus rugosus isolated from sputum [3] but case history is not available

### Clinical disease, antiobiem and treatment associated with Segniliparus

Physicians should pay more attention to symptoms such as chronic cough and sputum more than 3 months, fever, multiple small nodules in lung [55, 60] and radiologic finding similar to other genera in actinomycete family such as M. tuberculosis, non-tuberculous mycobacteria (NTM), and Nocardia for detection of this rare infection. Several studies have reported infections in humans caused by Segniliparus. The first report of the Segniliparus isolation from the clinical sample was published in 2005 by Butler et al. They isolated S. rugosus and S. rotundus from sputum and was AST performed using micro broth dilution. The results of AST showed that S. rotundus was susceptible to amikacin, cefoxitin, clarithromycin, ciprofloxacin, doxycycline, imipenem, sulfamethoxazole, and S. rugosus was susceptible to amikacin and sulfamethoxazole and resistant to clarithromycin, doxycycline, and tobramycin [3]. Butler et al. [64] isolated S. rugosus from 3 cystic fibrosis patients in 2007. Moreover, a study by Hansen et al. [54] isolated S. rugosus from sputum in a female with cystic fibrosis, and AST using micro
broth dilution showed that this isolate was susceptible to ciprofloxacin, gatifloxacin, imipenem and resistant to amikacin, cefoxitin, ceftriaxone, tobramycin. Koh et al. [55] isolated S. rotundus from sputum in 2011 in a patient treated with clarithromycin and ciprofloxacin. In another study, S. rugosus was isolated from sputum in 2014 [60]. S. rugosus possibly is an emerging pathogen in cystic fibrosis patients. Antibiotic resistance genes have not been reported in the genera William sia and Segniliparus [65]. The case reports published on Segniliparus spp. are provided in Table 3. On the basis of the clinical reports, the pulmonary infection of Segniliparus spp. is associated with chronic cough, fever and hypoventilation, as well as the presence of multiple small nodules, with symptoms of acid-fast bacilli in sputum and radiological results similar to M. tuberculosis, NTM, Nocardia and so on. Therefore, pulmonary infection should be identified in microbiology laboratories.

Conclusion
In this review, we surveyed taxonomy and the role of the genera Williamsia and Segniliparus in human infections. The identification of pathogenic factors in these bacteria requires more investigations. A few studies have been conducted on Williams and Segniliparus infections because of the lack of attention and insufficient experience in medical laboratory personnel as well as the lack of optimization of the phenotypic and molecular methods to identify these bacteria in hospitals. The use of novel molecular methods is necessary for accurate identification of Williamsia and Segniliparus species.

Supplementary Information
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Additional file 1. Whole genome sequence data of Williamsia and Segniliparus spp.

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Authors’ contributions
MFB participated in the design and drafting of the manuscript. The author read and approved the final manuscript.

Ethics approval and consent to participate
This research does not contain any human or animal participants performed by any of the authors.

Competing interests
The authors declare that they have no competing interests.

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