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| **Phylum** | **Class** | **Order** | **Family** | **Viral Infections** | **Neurologic Diseases** | **COVID-19 Drugs** |
| **SARS-CoV-2** | **Influenza** | ***Others*** | **Alzheimer’s disease** | **Parkinson’s disease** | ***Others*** |
| **Actinobacteria** | **Actinobacteria** | **Actinomycetales** | **Corynebacteriaceae** | * In a study by Zuo et al. [1], a correlation between baseline abundance of *Coprobacills*, *Clostridium ramosum*, and *Clostridium hathewayi* and **COVID-19** severity was observed.
 |  |  | * Actinobacteria levels was increased in **AD** patients [2].
* Actinobacteria was the most abundant phylum in postmortem **AD** brain samples [3].
 | * *Corynebacteriaceae* was increased in **PD** patients [4].
 |  |  |
| **Bifidobacteriales** | **Bifidobacteriaceae** | * In a study by Yeoh et al. [5], a decreased *Bifidobacterium adolescentis* in gut microbiota of **COVID-19** patientswas reported.
 | * Senico et al. reported [6] a decreased abundance of *Bifidobacteriaceae* family in fecal samples of **H3N2** infected mice.
* Zhang et al. [7] have revealed a significantly increased *Bifidobacterium pseudolongum* and *Bifidobacterium animalis* within **H7N9** survived mice.
 |  | * *Bifidobacterium* decreased levels was observed in **AD** participants [8].
 | * Bifidobacteriaceae was significantly increased in **PD** patients [9-12].
 | * *Bifidobacterium* level was decreased in **GBS** patients [13].
 | * Mengchen Guo et al. [14] found that in SLE patients without **Glucocorticoids** (SLE-G), Bifidobacterium level was lower in comparison to SLE patients receiving Glucocorticoid (SLE+G).
* Shaodong Wei et al. [15]have observed that Bifidobacterium abundance have been decreased during the Long-term (13–39 months after the use of **azithromycin**.
* Fiona Fouhy et al. have revealed that **gentamycin and ampicillin** reduce the proportion of Actinobacteria [16].
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| **Coriobacteriia** | **Coriobacteriales** | **Coriobacteriaceae** | * In a study by Zuo et al. [17], an increased abundance of *Collinsella aerofaciens* and *Collinsella tanakaei* in the fecalsamples **COVID-19** patients with high SARS-CoV-2 infectivity was reported.
 | * Sencio et al. [6] reported a decreased abundance of *Coriobacteriaceae* family in fecal samples of **H3N2** infected mice.
 | * Corrêa et al. [18] revealed that **Zika virus (ZIKV)** causes an increase in *Coriobacteriaceae* abundance in gut microbiota.
 | * Coriobacteriaceae was increased after 3, 6 and 8 months in **APP/PS1** mice [19].
 | * Coriobacteriaceae was increased in **PD** patients [10, 20].
 |  | * Rui Li et al. have found that **florfenicol** has decreased Gordonibacter [21].
 |
| ***Others*** | * Gu et al. [22] reported a Significant increase in *Actinomyces* relative abundance in **COVID-19**.
 |  |  |  | * Actinomycetaciaceae. *Actinomycetales* was increased in **PD** patients [23].
 |  |  |
| **Firmicutes** | **Clostridia** | **Clostridiales** | **Clostridiaceae** | * In a study by Zuo et al. [1], a correlation between *Clostridium ramosum* and *Clostridium hathewayi* abundance and **COVID-19** severity was observed.
 |  | * Corrêa et al. [18] revealed that **Zika virus (ZIKV)** causes an increase in *Clostridiaceae* abundance in gut microbiota.
 | * There is significant reductions of Firmicutes specially Clostridiaceae in APP/PS1 mouse models of **AD** and **AD** patients [8, 24-26].
 | * Non-significant reduction in Clostridia was associated with severity of PD [27].
* Clostridiaceae significantly increased in PD patients [28-30].
 |  | * Emmanouil Angelakis et al. have demonstrated that **doxycycline and hydroxychloroquine** can decrease the abundance of Bacteroidetes [31].
 |
| **Lachnospiraceae** | * In a study by Yeoh et al. [5], a *Eubacterium rectale* was decreased in gut microbiota of **COVID-19** patients.
* In a study by Zuo et al. [17], higher abundance of *Lachnospiraceae* bacterium 1\_1\_57FAA in fecal samples with none to low **SARS-CoV-2** infectivity was observed.
* Gou et al. [32] reported a negative correlation between Clostridia and inflammatory markers in **COVID-19** patients.
 | * In a study by Groves et al. [33], a significantly decreased *Lachnospiraceae* relative abundance in mice was reported.
 | * In a study by Groves et al. [33], significantly decreased *Lachnospiraceae* relative abundance in **RSV**-infected mice was reported [33]
 | * Lanchnospiraceae was decreased in **AD** patients [2, 24]
 | * Lachnospiraceae was significantly reduced in **PD** patients [9, 10, 12, 20, 30].
 | * The depletion of *Lachnospiraceae* occurred in **MS** and **ALS** patients [34, 35].
 | * In a study by Haoqing Shao et al. [36] they have provided a diarrhea model which was induced by cefradine and gentamycin to study the microbiota features in intestinal lumen of the mice with **Antibiotic-associated diarrhea (AAD)**, the 20 top genus with high abundance were achieved. It was 5.46% for Blautia.
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| **Ruminococcaceae** | * Zuo et al. [1] and Yeoh et al. [5], reported an inverse correlation between *Faecalibacterium prausnitzii* abundance and **COVID-19** severity.
* In a study by Yeoh et al. [5], enrichment of *Ruminococcus gnavus* and *Ruminococcus* *torques* in gut microbiota of **COVID-19** patients was observed [5].
* Gou et al. [32] identified *Ruminococcus gnavu* in **COVID-19** patients and its positive correlation with inflammatory markers [32]
* Sokol et al. [37] reported an increase in relative abundance of some genera of the *Ruminococcaceae* family (*Firmicutes*) in gut microbiota of **COVID-19** patients compared to controls.
 | * In a study by Yitbarek et al. [38], an increased *Ruminococcus* abundance in fecal microbiota of **H9N2** infected chickens was reported.
* Al Khatib et al. [39] reported a decrease in relative abundance of *Faecalibacterium prausnitzii* in **influenza (A or B)** infected patients compared to controls.
 |  | * The abundance of *Ruminococcaceae* was increased in **AD** patients [2, 24].
 | * The abundance of *Ruminococcaceae* was significantly increased in **PD** patients [11, 28, 40].
 | * The depletion of *Ruminococcaceae* occurred in **MS** patients [34].
 | * In a study by Haoqing Shao et al. [36] they have provided a diarrhea model which was induced by cefradine and gentamycin to study the microbiota features in intestinal lumen of the mice with **Antibiotic-associated diarrhea (AAD)**,the 20 top genus with high abundance were achieved. It was 5.37% for Ruminococcus.
* Jia Yin et al. have stated that **β-lactams (Ceftriaxone Sodium, Cefoperazone/Sulbactam and meropenem**) inhibited Papillibacter [41].
 |
| **Negativicutes** | **Veillonellales** | **Veillonellaceae** | * Gu et al. [22] reported a significant increase in *Veillonella* relative abundance in **COVID-19**.
 |  |  | * The abundance of *Veillonellaceae* was significantly decreased in **AD** patients [2].
 | * *Veillonellaceae was increased* in **PD** patients [42, 43].
 |  |  |
| **Bacilli** | **Lactobacillales** | **Lactobacillaceae** |  | * In a study by Groves et al. [33], a significantly decreased *Lactobacillaceae* relative abundance in a **H1N1** infected mice was reported.
* In a study by Yitbarek et al. [38], an increased *Isobaculum* abundance in fecal microbiota of **H9N2** infected chickens was observed.
 | * In a study by Groves et al. [33], a significantly decreased *Lactobacillaceae* relative abundance in **RSV**-infected mice was observed [33]
 | * The relative abundance of *Bacilli* wasincreased in **AD** patients [2].
 | * Lactobacillaceae was significantly increased in **PD** patients [9-11, 28, 40, 44, 45].
 |  | * Rui Li et al. have found that **azithromycin** has decreased Lactobacillus [21].
* In a study by Haoqing Shao et al. [36] they have provided a diarrhea model which was induced by cefradine and gentamycin to study the microbiota features in intestinal lumen of the mice with **Antibiotic-associated diarrhea (AAD)**, the 20 top genus with high abundance were achieved. It was 23.21% for Lactobacillus.
* Han-Ki Park et al.[46] have demonstrated that following the administration of **azithromycin**, Lactobacillus has been disappeared in control group.
* Mengchen Guo et al. [14] found that in SLE patients without **Glucocorticoids** (SLE-G), Streptococcus level was lower in comparison to SLE patients receiving Glucocorticoid (SLE+G).
* Emmanouil Angelakis et al. have demonstrated that **doxycycline and hydroxychloroquine** can decrease the abundance of Lactobacillus [31].
* Fiona Fouhy et al. have revealed that **gentamycin and ampicillin** reduce the proportion of Lactobacillus [16].
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| **Enterococcaceae** |  |  |  | * The relative abundance of *Enterococcaceae* was increased **AD** patients [2].
 | * *Enterococcaceae* is significantly increased PD patients [10, 20, 47].
 | * The enrichment of pro-inflammatory *Enterobacteriaceae* family have been reported in **MS** patients [34, 48].
 | * Jia Yin et al. have shown that **Meropenem and Azithromycin** induced the growth of Enterococcus[41].
* In a study by Haoqing Shao et al. [36] they have provided a diarrhea model which was induced by cefradine and gentamycin to study the microbiota features in intestinal lumen of the mice with **Antibiotic-associated diarrhea (AAD)**, the 20 top genus with high abundance were achieved. It was for 5.97% Enterooccus.
* Mengchen Guo et al. [14] found that in SLE patients without **Glucocorticoids** (SLE-G), Enterobacteriales level was lower in comparison to SLE patients receiving Glucocorticoid (SLE+G).
 |
| **Bacillales** | **Staphylocaccacea** |  |  |  | * *Staphylococcaceae* was more prominent in **AD** than in controls [49].
 | * *staphylococci* was increased in **PD** patients [50]
* Staphylococcaceae was decreased in **PD** patients [4].
 |  |  |
| ***Others*** | * Zuo et al. [1] reported a correlation

between Coprobacillus abundance and **COVID-19** severity. * Gu et al. [22] reported a significant

increase in *Streptococcus* relative abundance in **COVID-19**.* In a study by Zuo et al. [17], an

increased abundance of *Streptococcus infantis* in the fecal Samples of **COVID-19** patients with high SARS-CoV-2 infectivity was reported. | * Gu et al. [22] reported an increased abundance *of Finegoldia and*

*Peptoniphilus* in **H1N1** and **H7N9** Patients. |  | * *Gemellaceae* family and *Blautia*, *Phascolarctobacterium*, and *Gemella* genera were more abundant in **AD** participants [8].
 |  |  | * In a study by Haoqing Shao et al.[36] they have provided a diarrhea model which was induced by cefradine and gentamycin to study the microbiota features in intestinal lumen of the mice with **Antibiotic-associated diarrhea (AAD)**, the 20 top genus with high abundance were achieved. It was 5.24% for Bacillus.
* In a study by Haoqing Shao et al.[36] they have provided a diarrhea model which was induced by cefradine and gentamycin to study the microbiota features in intestinal lumen of the mice with **Antibiotic-associated diarrhea (AAD)**, the 20 top genus with high abundance were achieved. It was 4.62% for Eubacterium.
 |
| **Bacteroidetes** | **Sphingobacteriia** | **Sphingobacteriales** | **Sphingobacteriaceae** |  |  |  | * Within Bacteroidetes, *Bacteroidaceae* and *Rikenellaceae* at the family level, and *Bacteroides* and *Alistipes* at the genus level were more abundant in **AD** patients [8].
 | * *Sphingobacteriacea*e was significantly reduced in **PD** patients [12].
 |  | * Xiaoxian Xie et al. [51] have found that **crocin-I** at a dose of 40 mg kg−1 can maintain normal abundances of Bacteroidetes.
* Yakun Sun et al.[52] found out that Bacteroidetes was increased in mice treated with **Gentamicin**.
* Mengchen Guo et al. [14] found that in SLE patients without **Glucocorticoids** (SLE-G), Bacteroidetes level was increased, but the ratio of Firmicutes/Bacteroidetes has been decreased in comparison to SLE patients receiving Glucocorticoid (SLE+G).
* Zhi-Yuan Pan et al. [53] have shown that **Hydroxychloroquine (HCQ)** has raised the abundance of phylum Bacteroidetes.
 |
| **Bacteroidia** | **Bacteroidales** | **Bacteroidacea** | * Zuo et al. [1] reported an inverse correlation between *Bacteroides dorei, Bacteroides thetaiotaomicron, Bacteroides massiliensis, and Bacteroides ovatus* abundance and SARS-CoV-2 load in fecal samples of patients.
* In a study by Yeoh et al. [5], enrichment of *Bacteroides dorei* in gut microbiota of **COVID-19** patients was observed.
* In a study by Zuo et al. [17], a higher abundance of *Bacteroides stercoriin* in fecal samples with none to low **SARS-CoV-2** infectivity was reported.
 | * In a study by Groves et al. [33], a significantly increased *Bacteroidaceae* relative abundance in **H1N1** infected mice was observed.
* Al Khatib et al. [39] reported a higher *Bacteroides fragilis* abundance in fecal samples of **influenza A and B** shedders than non-shedders.
 | * In a study by Groves et al. [33], a significantly increased *Bacteroidaceae* relative abundance in RSV-infected mice was reported.
 | * Increased *Bacteroidaceae* was observed in **AD** patients [8].
* Zhuang, Z.-Q., et al showed that *Bacteroidia* decreased significantly in the **AD** group [2].
 | * Non-significant reduction in Bacteroidia was seen in **PD** patients [27].
* Significant reduction in Bacteroidacea was seen in **PD** [44].
 |  | * Emmanouil Angelakis et al. have demonstrated that **doxycycline and hydroxychloroquine** can decrease the abundance of Bacteroidetes [31]
 |
| **Tannerellaceae** | * In a study by Zuo et al. [17], a higher abundance of *Parabacteroides merdae* in fecal samples of patients with none to low **SARS-CoV-2** infectivity was reported [17]
 |  |  |  |  |  |  |
| **Rikenellacea** | * In a study by Zuo et al. [17], a higher abundance of and *Alistipes onderdonkii* in fecal samples of patients with none to low **SARS-CoV-2** infectivity was observed.
 |  |  | * Rikenellaceae was increased in **AD** patients [8].
 | * *Rikenellaceae* was decreased in **PD** patients [12, 40, 42].
 |  | * Rui Li et al. have found that **florfenicol and azithromycin** have decreased Alistipes [21].
* Jia Yin et al. have stated that **β-lactams (Ceftriaxone Sodium, Cefoperazone/Sulbactam and meropenem)** inhibited Alistipes [41].
* Rui Li et al. have found that **florfenicol and azithromycin** have decreased Rikenella [21].
 |
| **Prevotellaceae** | association between increase in *Prevotella* in gut microbiota and COVID-19 poor prognosis and higher infectivity  | * Gu et al. [22] reported an increased abundance of *Prevotella* in **H1N1** and **H7N9** patients.
* Al Khatib et al. [39] reported an increase in relative abundance of *Prevotella copri* in **influenza (A or B)** infected patients compared to controls.
 |  | * Prevotellaceae was more abundant in APP/PS1 mice models of **AD** [54, 55].
 | * Prevotellaceae was significantly reduced in **PD** patients [11, 20, 40, 56].
 |  | * Jia Yin et al. have stated that **β-lactams (Ceftriaxone Sodium, Cefoperazone/Sulbactam and meropenem)** inhibited Prevotella [41].
 |
| ***Others*** |  |  |  |  |  |  |  |
| **Proteobacteria** | **Gamma proteobacteria** | **Enterobacterales** | **Enterobacteriacea** |  | * Gu et al. [22] reported a higher abundance of *Escherichia-Shigella* among **H1N1** patients compared to controls and COVID-19 patients.
 |  | * The abundance of *Enterobacteriacea* was increased in **AD** patients [25].
 | * The higher mean abundance of Gammaproteobacteria was seen in mild and severe **PD** patients [27].
 |  | * Jia Yin et al. have stated that **Vancomycin** has induced the growth of Escherichia [41].
* Edward P. K. Parker et al. [57] evaluated the gut microbiota in the 6–11 month-old infants in India , receiving a 3-day period of placebo or **azithromycin** in a randomized trial which was of oral poliovirus vaccine. A remarkable decrease in the abundance of Proteobacteria in the azithromycin was seen in comparison to placebo group.
* Xiaoxian Xie et al. [51] have found that **crocin-I** at a dose of 40 mg kg−1 can maintain normal abundances of Proteobacteria.
* Yakun Sun et al.[52] found out that Proteobacteria was increased in mice treated with **Gentamicin**.
 |
| **Delta proteobacteria** | **Dasulfovibrionales** | **Dasulfovibrionaceae** |  |  |  | * Desulfovibrionaceae increased significantly in APP/PS1 mice models of **AD** [19].
 | * Desulfovibrionaceae was increased in **PD** patients [12, 20].
 | * Significant enrichment in relative abundance of members of *Desulfovibrionaceae* was observed in**MS** patients [34].
 | * Mengchen Guo et al. [14] found that in SLE patients without **Glucocorticoids** (SLE-G), Bilophila level was increased in comparison to SLE patients receiving Glucocorticoid (SLE+G).
* Rui Li et al. have found that **florfenicol and azithromycin** have decreased Desulfovibrio [21].
 |
| **Epsilon proteobacteria** | **Campylobacterales** | **Helicobacteriaceae** |  |  |  | * Helicobacteraceae increased significantly in APP/PS1 mice models of **AD** [19].
 | * *Helicobacter pylori* is a triggering factor in **PD** pathogenesis [58].
 |  | * Armin Hinterwirth et al. have recognized that Campylobacter ureolyticus, Campylobacter jejuni, and Campylobacter hominis had been decreased in the children who were treated with **azithromycin** [59].
 |
| ***Others*** | * In a study by Zuo et al. [17], an increased abundance of *Morganella morganii* in fecal samples of **COVID-19** patients with high SARS-CoV-2 infectivity was reported.
* Sokol et al. [37] reported an increase in relative abundance of *Acinetobacter (Proteobacteria*) in fecal samples of **COVID-19** patients.
 | * In a study by Yitbarek et al. [38], an increased *Proteobacteria* abundance in fecal microbiota of **H9N2** infected chickens was observed.
 |  | * Proteobacteria was positively correlated with the ratio of Aβ1-42/Aβ1-40 in **AD** [25, 60].
* The *Bilophila* genus was more abundant in **AD** participants [8].
 |  | * *Campylobacter jejuni* is associated with **GBS** and also **anxiety-like behavior** [61, 62].
 | * Rui Li et al. have found that **florfenicol and azithromycin** have decreased Parasutterella [21].
* Fiona Fouhy et al. [16] have revealed that **gentamycin and ampicillin** reduce the proportion of Proteobacteria.
* In a study by Haoqing Shao et al. [36] they have provided a diarrhea model which was induced by **cefradine and gentamycin** to study the microbiota features in intestinal lumen of the mice with Antibiotic-associated diarrhea (AAD), the 20 top genus with high abundance were achieved. It was 2.09% for Pseudomonas.
 |
| **Fusobacteria** | **Fusobacteriia** | **Fusobacteriales** | **Fusobacteriaceae** |  |  |  | * *Fusobacteriaceae* was decreased in **AD** patients [55].
 | * Fusobacteriaceae was increased in **PD** patients [4].
 |  |  |
| ***Others*** |  |  |  |  |  |  |  |
| **Verrumicrobia** | **Verrumicrobiae** | **Verrumicrobiales** | **Akkermansiaceae** |  | * Senico et al. reported [6] an increased abundance of *Verrucomicrobia* in fecal samples of **H3N2** infected mice.
 |  | * The abundance of *Verrucomicrobia*is declined in APPPS1 mice model of **AD** [26].
* Others studies have shown that Verrucomicrobiais and Verrucomicrobiaceae increased significantly in APP/PS1 mice models of **AD** [54, 63].
* *Akkermansia*  abundance was decreased in APP/PS1 mice models of **AD** [64].
 | * Elevated levels of Verrucomicrobiae was seen in both mild and severe **PD** patients [9, 10, 27, 28, 30, 40, 43].
* The abundance of *A. muciniphila* was 80% higher in **PD** patients [28].
 | * Verrucomicrobia was increased in **MS** patients [65].
 | * Edward P. K. Parker et al. [57] evaluated the gut microbiota in the 6–11 month-old infants in India, receiving a 3-day period of placebo or **azithromycin** in a randomized trial which was of oral poliovirus vaccine. A remarkable decrease in the abundance of Verrucomicrobia in the azithromycin was seen in comparison to placebo group.
* Jonathan D Schepper et al. [66] observe that **GC-Tx** reduced levels of Verrucomicrobials and Bacterials.
 |
| ***Others*** |  |  |  |  |  |  |  |
| ***Other Microorganisms*** | * In a study by Yeoh et al. [5], a significant increase in Rothia relative abundance in **COVID-19** patients was reported.
 | * Senico et al. reported [6] an increased abundance of Cyanobacteria in fecal samples of **H3N2** infected mice.
* In a study by Yitbarek et al. [38], an iIncreased *Pseudoflavonifractor, Vampirovibrio* abundance in fecal microbiota of **H9N2** infected chickens was observed.
 | * Corrêa et al. [18] revealed that **Zika virus (ZIKV)** causes an increase in *Deferribacteraceae* abundance in gut microbiota.
 |  |  |  |  |
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