

REVIEW ARTICLE

Drug–gut microbiota interactions:
implications for neuropharmacology

Correspondence Gerard Clarke, APC Microbiome Ireland, University College Cork, Cork, Ireland. E-mail: g.clarke@ucc.ie

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Jacinta Walsh^{1,4}, Brendan T Griffin^{2,4}, Gerard Clarke^{3,4} and Niall P Hyland^{1,4,5} 

¹Department of Pharmacology and Therapeutics, University College Cork, Cork, Ireland, ²School of Pharmacy, University College Cork, Cork, Ireland, ³Department of Psychiatry and Neurobehavioural Science, University College Cork, Cork, Ireland, ⁴APC Microbiome Ireland, University College Cork, Cork, Ireland, and ⁵Department of Physiology, University College Cork, Cork, Ireland

The fate and activity of drugs are frequently dictated not only by the host *per se* but also by the microorganisms present in the gastrointestinal tract. The gut microbiome is known to, both directly and indirectly, affect drug metabolism. More evidence now hints at the effects that drugs can have on the function and composition of the gut microbiome. Both microbiota-mediated alterations in drug metabolism and drug-mediated alterations in the gut microbiome can have beneficial or detrimental effects on the host. Greater insights into the mechanisms driving these reciprocal drug–gut microbiota interactions are needed to guide the development of microbiome-targeted dietary or pharmacological interventions, which may have the potential to enhance drug efficacy or reduce drug side effects. In this review, we explore the relationship between drugs and the gut microbiome, with a specific focus on potential mechanisms underpinning the drug-mediated alterations on the gut microbiome and the potential implications for psychoactive drugs.

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Abbreviations

B-GOS, Bimuno™ galacto-oligosaccharides; CDI, *Clostridium difficile* infection; CYP, cytochrome P450; FMT, fecal microbiota transplantation; GF, germ-free; GI, gastrointestinal; HFD, high-fat diet; MAOI, MAO inhibitor; MDD, major depressive disorder; NSAID, non-steroidal anti-inflammatory drug; PEG, polyethylene glycol; PKPD, pharmacokinetics/pharmacodynamics; PPI, proton pump inhibitor; SCFA, short chain fatty acids; SSRI, selective serotonin reuptake inhibitor; TCA, tricyclic antidepressant

Introduction

Although not prominently featured in the classical teaching of pharmacokinetics and pharmacodynamics (PKPD), the fate and activity of drugs are frequently decided not only by the host *per se* but also by the collection of microorganisms present in the gastrointestinal (GI) tract. These microorganisms represent the gut microbiota, the trillions of microbes with more than 700–1000 different bacterial species which reside in the gut (Qin *et al.*, 2010). The terms microbiota and microbiome are often used interchangeably in the literature but can be differentiated based on their more recent definitions. The term ‘microbiota’ refers to the collection of microorganisms, whereas the term ‘microbiome’ refers to the collective genomes of these microorganisms (Jandhyala *et al.*, 2015; Marchesi *et al.*, 2016). It is estimated that 10 different phyla are thought to contribute to the functional role of the gut microbiome; Firmicutes and Bacteroidetes are the most dominant phyla. Indeed, the ratio of Firmicutes to Bacteroidetes (F/B ratio) is often used as a surrogate indicator of bacterial shifts, although it may be an overly simplistic descriptor of variations in human gut microbiota composition (Mariat *et al.*, 2009). Many factors have been identified that influence the biogeography and composition (both abundance and diversity) of bacteria along the GI tract including pH variation, diet, mucus, host immunity and environmental factors (Thursby and Juge, 2017). For example, the acidic environment of the stomach has a sparse microbiota (10^1 bacteria/g) compared to the estimated 10^3 bacteria/g found in the less acidic small intestine, which is the main site of drug absorption. The neutral pH or weakly basic environment found in the large intestine is the most densely colonized area of the GI tract, with an estimated 10^{12} bacteria/g (O’Hara and Shanahan, 2006).

The gut microbiome is implicated in the maturation of the immune system, nutrient absorption, energy homeostasis and protection against pathogens (Antunes *et al.*, 2011; Jandhyala *et al.*, 2015). It also plays a significant role in health, both in homeostasis and, likely, in the pathogenesis as well as treatment of disease. The initial composition and assembly of the gut microbiome are considered unique among individuals, and research has identified many factors which affect its composition including age, ethnicity, gender, environmental factors, diet and lifestyle (Quigley, 2017). For example, the composition of the gut microbiota in the newborn is dictated by the method of delivery, gestational age, infant antibiotic exposure and method of feeding (formula vs. breastfeeding) (Penders *et al.*, 2006; Salazar *et al.*, 2014). Though considered highly stable and resilient to change during adulthood, instability and variability in the gut microbiome become more prevalent during disease and at the extremes of life (e.g. early infancy and senescence) (Salazar *et al.*, 2014). The young and the old are also considered to be the most vulnerable patient groups regarding the occurrence of adverse drug reactions and display the most variation in drug pharmacokinetic responses (Turnheim 2003).

The implication of the gut microbiome in drug metabolism is gaining more traction and has led to the emergence of a new term, pharmacomicrobiomics (Rizkallah *et al.*, 2010). Pharmacomicrobiomics investigates the effect of

variations of the gut microbiome on drugs, through the lens of PKPD. In this review, we explore the relationship between drugs and the gut microbiota, with a specific focus on the potential mechanisms underpinning the drug-mediated alterations on the gut microbiota and the potential implications for the PKPD profile of drugs. With the increasing development of extended-release drug formulations, especially in the field of neuropharmacology, which may increase the proportions of the drug reaching the bacterially dense large intestine, a higher number of psychoactive drugs, which are subject to microbiota-mediated degradation, may be identified. While the gut microbiome may affect all classes of drugs, the purpose of this review is to focus specifically on psychoactive drugs given that most of these drugs display high lipophilicity to ensure CNS penetration (Alavijeh *et al.*, 2005). In general, highly lipophilic drugs are at greater risk of poor drug absorption from the intestine; hence, any microbial-mediated changes in intestinal absorption or metabolism merit further consideration. Developing a greater understanding of these important, but underappreciated, drug-microbiota dynamics could help to identify drug–drug interactions and perhaps explain inter-individual variation in drug efficacy and adverse effects.

The effects of drug therapy on the gut microbiome

Drug effects on the gut microbiome

Recently, two large-scale human observational studies highlighted correlations between the gut microbiota and the intake of different classes of medication. Falony *et al.* (2016) compared the composition of the gut microbiota against the use of β -lactam antibiotics, nitrofurantoin, an osmotic laxative, biological agents (TNF- α inhibitor), disease modifying anti-rheumatic drugs (mesalazine and azathioprine), oestrogen and progesterone hormones, benzodiazepines (clonazepam), antidepressants (venlafaxine) and antihistamines. While 95% of samples had a similar core microbiome, medication exposure was identified as the factor causing greatest variability in the study cohort, with 63% of the detected covariate interactions driven by medication. A positive correlation, for example, was identified between the abundance of a species from the *Eggerthella* and *Coprabacillus* genera and medication use. In another metagenomic-based study, Zhernakova *et al.* (2016) identified extrinsic and intrinsic factors correlating with microbial shifts in a Dutch population study. Forty-four categories of drugs were tested in the analysis and antibiotics, gastric acid suppressants [proton pump inhibitors (PPIs)], lipid-lowering medication (3-hydroxy-3-methylglutaryl coenzyme reductase inhibitors or ‘statins’), anti-hyperglycaemic (metformin) and laxatives were found to have a distinct effect on the gut microbiome. PPIs were, for example, associated with profound changes in 33 bacterial pathways, and metformin use positively correlated with *Escherichia coli* abundance. While a wide range of medication has been identified to interact with the gut microbiota, certain drug classes, including antibiotics, anti-inflammatories, gastric acid suppressants, anti-hyperglycaemics and

psychotropics, have repeatedly been shown to have distinct gut microbiota signatures and will be discussed further in the review (see sections: Secondary effects of drugs on the gut microbiome and Effects of psychoactive drugs on the composition of the gut microbiota sections).

Combination of drugs and polypharmacy

The composition of the microbiota can vary depending on both the number and combination of medication ingested. A significant difference in microbiota composition was observed in patients taking a single drug on a long-term basis in comparison to non-drug taking patients (Rogers and Aronoff, 2016). Moreover, the combined use of non-steroidal anti-inflammatory drugs (NSAIDs) and PPIs differentially influenced the relative abundance of *Bacteroides* spp. and *Erysipelotrichaceae* spp., compared with NSAIDs alone. Similarly, *Bacteroides* spp. and a species belonging to the Ruminococcaceae family differentiated individuals who were concomitantly taking NSAIDs, antidepressants and laxatives from NSAID-only users. Therefore, the composition of the gut microbiota may depend on an individual's drug use. In this study, the diversity of the gut microbiota was not significantly influenced by the number of medications taken, even though it was significantly influenced by the specific type of medication ingested by study participants. Of note, the median number of medications taken by the community-dwelling subjects was 4, which falls below the threshold for polypharmacy. Once this threshold is reached (i.e. ≥ 5 concomitantly taken medications), an effect is frequently observed. A significant decrease in species richness, a measurement of the number of species present in an area and significant alterations in the relative abundance of 15 bacterial taxa have been reported in patients taking more than five concomitant medications (Ticinesi *et al.*, 2017). Specifically, the relative abundance of the *Helicobacter* genus was significantly associated with polypharmacy, and an inverse relationship between polypharmacy and the abundance of the Lachnospiraceae and Succinivibrionaceae families was also found. The co-administration of drugs may precipitate shifts in the composition of the microbiota to favour the abundance of microbial taxa that have metabolizing capacity for those drugs (Ticinesi *et al.*, 2017). Not only is it important, therefore, to evaluate specific microbiota alterations induced by a single drug but it is also imperative to account for differences when multiple drugs are co-administered. Further study of the effects of multiple co-administered drugs on the gut microbiota is very relevant due to the increasing prevalence of polypharmacy in the ageing population (Dagli and Sharma, 2014). In a European study across eight countries, the prevalence of polypharmacy in 4023 nursing home residents, the mean age of whom was 83.5 (SD 9.3) years, was found to be almost 50%, while excessive polypharmacy (defined as ≥ 10 medication) was evident in an additional 24.3% of residents, which serves to highlight the potential for drug-associated effects on the microbiota in a vulnerable population in which the gut microbiome is already compromised (Claesson *et al.*, 2012; Onder *et al.*, 2012).

Duration of drug treatment and recovery

In vitro evidence suggests that even a single dose of antibiotic or short-term antibiotic courses, albeit at high doses, can

significantly affect the microbiome (Maurice *et al.*, 2013). Specifically, eight different antibiotics altered the fecal microbiota after a 4 hour incubation, and a significantly increased proportion of cells associated with loss of membrane integrity and altered polarity was observed. Most antibiotic-induced alterations to the microbiome are reversed upon cessation of treatment. Some modifications can, however, persist after treatment (Jakobsson *et al.*, 2010). For example, the combined treatment with the antibiotics clarithromycin and metronidazole and a PPI, **omeprazole**, induced alterations to macrolide resistance gene, *ermB*, which persisted in patients for up to 4 years after treatment.

Additionally, the antipsychotic, **risperidone**, was associated with a reduction in the F/B ratio, which was evident at the 2–3 month follow-up of treatment, but a further reduction in Bacteroidetes, and increased weight gain, was observed after prolonged use (Bahr *et al.*, 2015a). The continued use of drugs may, therefore, strengthen microbiota alterations, which may be evident from initiation of treatment, but further comparisons between short-term and long-term users of medication are required.

Excipient effects

An excipient is a pharmacologically inert substance or non-active ingredient that is added to a formulation to stabilize the active substance or enhance the function of the dosage form (Debotton and Dahan, 2017). Most excipients are not absorbed from the gut lumen. Moreover, polysaccharide-based formulations are often utilized in the delivery of probiotics and colonic-targeted drug dosage forms, for example, targeted local delivery of the anti-inflammatory **sulfasalazine** (Kosaraju 2005; Prudhvira *et al.*, 2015). Recent research hints at the possibility that the excipients themselves might mediate microbiota changes, independent of changes induced by the drug. Recently, it was hypothesized that the presence of fermentable polysaccharides as drug formulation excipients may act as metabolic substrates for the gut microbiota, thereby promoting their growth (Ticinesi *et al.*, 2017). Additionally, polyethylene glycol (PEG), a polymer used in drug delivery, is linked to changes in GI transit time and changes in the gut microbiota (Kashyap *et al.*, 2013). Humanized mice [ex-germ-free (GF) mice colonized with human faecal microbiota] fed a standard diet supplemented with 15% PEG 3350 for 10 days, had significantly reduced abundance of the Peptococcaceae and Eubacteriaceae bacterial families and the Anaeroplasmataceae order. As the dosage used in this animal study was expressed as %w/w of the animal chow, it is, however, difficult to extrapolate this dose to that used in pharmaceutical formulations. PEGs are commonly included in dosage forms, with diverse excipient functions including as solubilizing agents, tablet binders, plasticizers in film coating, tablet lubricants and vehicles (D'souza and Shegokar, 2016). Additional studies are warranted to elucidate the potential effect of the different categories of PEG polymers used in drug formulations at pharmaceutically relevant concentrations. Excipient-induced changes in the composition or functionality of the microbiome could potentially complicate the interpretation of drug-microbiota-based observational studies, as it may be difficult to differentiate drug-induced changes from excipient-induced changes in the gut microbiome. More

research is needed to evaluate the independent effects of different formulation excipients, and the possible unintended consequences that their inclusion in drug formulations could have on the gut microbiome.

Gut microbiome drug–drug interactions

Drug-induced changes in the gut microbiome may alter the pharmacokinetics of concomitantly taken medication. An increased plasma level of the antiplatelet drug, **aspirin**, was observed in rats who were treated with a β -lactam antibiotic, ampicillin, 3 days previously (Kim *et al.*, 2016). This enhanced bioavailability was attributed to the antibiotic-induced suppression of the metabolic activity of the gut microbiome. Moreover, ampicillin treatment significantly prolonged bleeding time in aspirin-treated rats, suggesting antibiotic treatment may potentiate its anti-thrombotic effect. Similar microbiome-mediated drug interactions have been demonstrated for both the lipid-lowering drug, **lovas-tatin**, and the antihypertensive, **amlodipine** (Yoo *et al.*, 2014; Yoo *et al.*, 2016).

Gut microbiota–drug interactions

The gut microbiome can both directly metabolize drugs and indirectly influence host metabolizing capacity of

drugs (Haizer and Turnbaugh, 2013; Wilson and Nicholson, 2017). While many drugs undergo microbial biotransformation, the specific microorganisms involved are often unknown. In this review, we will mainly refer to bacterial drug-metabolizing enzymes, and the effects of the gut microbiome on the metabolism of drugs by the liver, as the primary focus of the review, is the reciprocal effect drugs can have on the gut microbiome, a relatively unexplored and unappreciated area in the literature. Microbial drug metabolism has been extensively reviewed recently (Koppel *et al.*, 2017; Wilson and Nicholson, 2017).

Drug metabolism by microbial enzymes

Microbial-derived drug-metabolizing enzymes have been implicated both in the activation and inactivation of drugs. For example, the activation of the prodrug sulfasalazine into its anti-inflammatory active moiety mesalazine (5-aminosalicylic acid or 5-ASA) is mediated by bacterial azoreductase (Peppercorn and Goldman, 1972). The direct metabolism of drugs by microbial-derived enzymes has been shown for a variety of different drugs, examples of which are detailed in Table 1. In contrast to the oxidation and conjugation reactions characteristic of hepatic metabolism, reduction and hydrolysis reactions dominate gut microbiota-mediated metabolic reactions (Haizer and Turnbaugh, 2013). β -Glucuronidase is among the most

Table 1

The metabolism of drugs by bacterial drug-metabolizing enzymes

Microbiota-derived enzyme	Hypothesized reaction mechanisms	Drug (or metabolite) substrate	References
β -Glucuronidase	Remove glucuronic acid moiety from hepatic phase 2 metabolites	Irinotecan (SN-38 glucuronide) NSAIDs, for example, indomethacin and diclofenac	Yamamoto <i>et al.</i> (2008) and Saitta <i>et al.</i> (2014)
Azoreductase	Reduction of azo or quinone bonds	Azo-containing drugs, for example, olsalazine (5-ASA prodrug) Nitrofurans antibiotics, for example, nitrofurazone and nitrofurantoin Ester-containing prodrugs	Ryan (2017)
Carboxylesterase	Hydrolyse ester, thioester, amide or carbamate containing drugs to corresponding free acids Hydrolyse esters to carboxylic acids	Aspirin, ester-containing prodrugs	Imai and Ohura (2010), Laizure <i>et al.</i> (2013) and Kim <i>et al.</i> (2016)
Nitroreductase	Reduction of nitro group	Metronidazole Benzodiazepines	Koch <i>et al.</i> (1979), Elmer and Rimmel (1984) and Takeno <i>et al.</i> (1990)
<i>N</i> -acetyltransferase	Transfer of acetyl group to nitrogen or oxygen atom of primary arylamines, hydrazines and <i>N</i> -hydroxylated metabolites	5-Aminosalicylic acid	van Hogezaand <i>et al.</i> (1992) and Deloménie <i>et al.</i> (2001)
β -Lyase	Cleavage of C–S bond in hepatic-production cysteine-S-conjugated metabolites	Cysteine-conjugated metabolites Bio-activation of sulfur and selenocysteine derivatives	Mikov (1994)
Sulfatases	Hydrolysis of sulfate esters utilizing formylglycine	Sulfate ester hepatic metabolites	Ulmer <i>et al.</i> (2014) and Koppel <i>et al.</i> (2017)

studied bacterial drug-metabolizing enzymes due to its role in the deconjugation of hepatically glucuronidated metabolites and the resultant enterohepatic recycling of drugs (Takasuna *et al.*, 1998; Klaassen and Cui, 2015). Multiple different bacterial genera, including *Clostridium*, *Streptococcus*, *Lactobacillus*, *Ruminococcus* and *Bifidobacterium*, express β -glucuronidase (Gloux *et al.*, 2011).

The development of a chemically guided functional strategy to identify, quantify and assign functionality of enzymes associated with the gut microbiome is among the recent advances in this area. This strategy led to the identification of trans-4-hydroxy-L-proline dehydratase as a microbial enzyme implicated in the metabolism of a non-proteinogenic amino acid, **trans-4-hydroxy-L-proline** (Levin *et al.*, 2017). Application of this strategy for the identification and characterization of microbial drug-metabolizing enzymes holds much potential and could uncover previously unknown metabolic activities of the gut microbiome.

Indirect effects of the gut microbiome on host drug metabolism

It was traditionally assumed that only drugs reaching the colon are subject to microbiota-associated alterations with relevance to drug PKPD. The concerted role of the gut bacteria and the liver in the enterohepatic recirculation of drugs is not a new concept (Takasuna *et al.*, 1998). However, more recently, it was highlighted that the gut microbiome could also influence hepatic function, which may, in turn, precipitate changes in patient response to drugs.

Microbial-derived metabolites can mimic and compete with drug intermediates of hepatic metabolic reactions and thereby interfere with host detoxification pathways. For example, P-cresol is a microbial metabolite of **tyrosine** or phenylalanine, which competes with **paracetamol** for the hepatic enzyme, sulfotransferase family 1A member 1 (SULT1A1) (Clayton *et al.*, 2009). This competition for SULT1A1 induces a shift in the metabolism of paracetamol towards alternative host metabolic reactions leading to increased production of the paracetamol metabolite, **N-acetyl-4-benzoquinone imine**, whose accumulation has been associated with hepatotoxicity (Mitchell *et al.*, 1973).

Moreover, the gut microbiome can alter the expression of hepatic enzymes or genes responsible for host metabolism. Claus *et al.* (2011) detected significantly reduced expression of hepatic cytochrome P450 (CYP) 2c29, CYP3a11 and CYP8b1 in GF mice in comparison to conventionally-raised control mice. Increased expression of hepatic drug-sensing transcription factors has also been observed in GF mice including the **aryl hydrocarbon receptor**, a regulator of downstream CYP enzyme expression (Selwyn *et al.*, 2015). However, the mechanisms responsible for the microbiome-induced changes in the expression of hepatic enzymes requires further exploration. The accumulation of **bilirubin**, bile acids and steroid hormones in GF mice has been suggested as a potential mechanism mediating the altered activation of the **constitutive androstane receptor**, a 'xenosensor' nuclear receptor, and further implicates an

indirect role for the microbiome in drug metabolism (Björkholm *et al.*, 2009).

Effect of diet-induced changes on the gut microbiome and drug pharmacokinetics

Diet is a factor that can shape the composition and function of the gut microbiome (Sandhu *et al.*, 2016; Shanahan *et al.*, 2017). It is plausible that in the future, dietary interventions may be utilized to augment drug efficacy or decrease toxicity. The amino acid **arginine** has been shown to inhibit the *Eggerthella lenta*-encoding *cgr* operon, previously identified as essential for the microbiota-mediated reduction of the cardiac glycoside, **digoxin** (Haider *et al.*, 2013). Following confirmation of high levels of *cgr* operon expression, *E. lenta* colonized GF mice were fed a high-protein diet, and significantly increased serum and urine levels of digoxin (following a single 0.2 mg·mL⁻¹ intra-gastric digoxin dose) were identified. Interestingly, high-protein diet conferred no effect on digoxin pharmacokinetics in GF mice colonized with a non-digoxin reducing strain, FAA1-3-56, ruling out any indirect effect of host diet. Increased dietary protein, leading to increased arginine, could thus constitute a potential dietary intervention to improve digoxin efficacy. Recent data have also elucidated the role of diet-induced changes in the gut microbiota on the oral bioavailability of the herbal supplement, berberine, used for the treatment of hyperlipidaemia and type 2 diabetes (Wang *et al.*, 2017). The bioavailability of berberine was significantly increased in high-fat diet (HFD)-fed hamsters in comparison to hamsters fed a normal diet. The HFD significantly induced bacterial nitroreductase activity in hamster feces. The authors also observed higher blood concentrations of berberine in individuals with a higher fecal nitroreductase activity, which further corroborated the findings in their animal model.

Effect of probiotics on drug pharmacokinetics

Microbiota-targeted interventions, including probiotics, prebiotics and antibiotics, may alter drug pharmacokinetics. There are no studies thus far, to our knowledge, exploring the effects of probiotics on psychoactive drug absorption and metabolism. The pharmacokinetics of an oral hypoglycaemic agent, gliclazide (administered as a single dose at 20 mg·kg⁻¹), was significantly altered in diabetic rats pretreated with a cocktail of three probiotics (*Lactobacillus acidophilus*, *Lactobacillus rhamnosus* and *Bifidobacterium lactis*) for 3 days (Al-Salami *et al.*, 2008). Similarly, probiotic treatment significantly altered the absorption of the anti-arrhythmic agent **amiodarone** (Matuskova *et al.*, 2014). In this study, the probiotic *E. coli* strain Nissile (EcN) 1917 was administered to rats for 7 days, prior to a single p.o. dose of amiodarone hydrochloride (50 mg·kg⁻¹). EcN significantly increased amiodarone bioavailability by 43% in comparison to saline-treated control rats. No significant effect was observed with the treatment of a non-probiotic *E. coli* strain, further indicating that the bacterial-mediated changes in drug pharmacokinetics may be strain specific.

Probiotics may also affect drug pharmacokinetics by modulating the composition or metabolic activity of the gut microbiota. Recent data showed probiotic treatment significantly increased the microbiota-mediated degradation of

the antipyretic and analgesic, paracetamol; an effect suggested to be mediated by probiotic-induced modulation of gut microbial enzyme activity (Kim *et al.*, 2018). In this study, the probiotic, *Lactobacillus reuteri*, significantly increased both sulfatase and arylsulfate transferase and significantly decreased β -glucuronidase activity during treatment, which are the bacterial enzymes involved in paracetamol metabolism. Following a 24 hour washout period after pretreatment with *L. reuteri*, a single dose of paracetamol [by i.v. (0.5 mg·kg⁻¹) or p.o. gavage (10 mg·kg⁻¹)] was administered to mice. *L. reuteri* significantly reduced the paracetamol plasma concentration to 68.4% in comparison to control mice. Similarly, administration of a probiotic cocktail consisting of *L. acidophilus*, *B. lactis* and *Streptococcus salivarius* to rats for 3 days significantly increased azoreductase activity in *ex vivo* colon contents (Lee *et al.*, 2012). The *ex vivo* incubation of sulfasalazine with colon contents significantly increased the metabolism of the drug. No clinical significance was observed, however, in the *in vivo* setting when a single dose of sulfasalazine (100 mg·kg⁻¹) was administered to rats following pretreatment with the probiotic cocktail for 3 days.

Drug–microbiome interactions

In this section, the mechanisms underpinning the drug-mediated changes to the composition and function of the gut microbiome will be explored.

Antibacterial effects of drugs on the gut microbiota

Direct disruption of the gut microbiota, through bacteriostatic or bactericidal activity, can alter the metabolic capability of the microbiota and have long-term effects on host functions and health. Such ‘antibiotic’-induced changes have been well studied. Antibiotic therapy in neonates can disrupt the bacterial colonization of the intestine and can have long-term health implications with links to the development of eczema, allergic rhinitis and inflammatory bowel disease in later life (Rodríguez *et al.*, 2015). Antimicrobial activity, linked to the depletion of ‘good’ commensal gut microbiota, provides an impetus for the overgrowth of hazardous commensal bacteria (Antunes *et al.*, 2011). For example, antibiotics can decrease host resistance to the growth of the opportunistic pathogen, *Clostridium difficile* (Theriot *et al.*, 2016).

Non-antibiotic drugs have also been shown to exert antimicrobial activity. *In vitro* studies have detected antimicrobial activity, against at least one bacterial strain, for a wide range of non-antibiotic drug classes including NSAIDs, mucolytic agents, bisphosphonates, PPIs, antihistamines, statins, cytostatic agents and psychotropics (Kruszewska *et al.*, 2000; Kruszewska *et al.*, 2002). Sulfasalazine and the bacterial metabolite, *N*-acetyl 5-ASA, inhibited the *in vitro* growth of fecal anaerobic strains including *C. difficile* (Sandberg-Gertzen *et al.*, 1985; Deloménie *et al.*, 2001). The anti-neoplastic drug, **5-fluorouracil** (5-FU), has also shown bactericidal effects against clinical isolates of *Staphylococcus aureus* even at lower absorption concentrations than would be expected after i.v. administration of 5-FU (Bodet *et al.*, 1985). Similarly, the anti-metabolite and antifolate drug, **methotrexate**, displayed

strong *in vitro* antibacterial activity only against *S. aureus* following a surveillance study of the drug against a variety of microbial strains including *E. coli*, *Pseudomonas aeruginosa* and *Candida albicans* (Kruszewska *et al.*, 2000). Non-antibiotic drugs, chiefly psychotropics, can also affect the gut microbiome by acting synergistically with a co-administered antibacterial or by modulating the activity or pathogenicity of microbes, which will be discussed later in the review (Effects of Psychoactive Drugs on the Composition of the Gut Microbiota section) (Martins *et al.*, 2008).

Recently, Maier *et al.* (2018) further elucidated the extensive effects of non-antibiotic drugs on the gut microbiota. The authors explored the antibacterial effects of 362 anti-infective and 835 host-targeted drugs (all drugs screened at 20 μ M; a concentration deemed representative of the predicted concentration of the drugs reaching the bacteria-dense ileum and colon) *in vitro* against 40 bacteria found to colonize the GI tract. About 24% of host-targeted drugs had antibacterial activity against at least one bacterial strain, with 40 drugs inhibiting the growth of up to 10 different bacteria. Antipsychotics, chemotherapeutic agents and antihypertensives were among the host-targeted drugs exhibiting the greatest antibacterial activity. Certain bacteria, previously identified as being highly abundant in healthy individuals such as *Prevotella copri* and *Eubacterium rectale*, were found to be most susceptible to the host-targeted drugs. Using available data from previously published metagenomic-based human studies, the authors validated the antibacterial effects of the drugs identified in their high-throughput drug screens and suggested that the use of some host-targeted drugs may increase patient susceptibility to antibiotic resistance. This study reaffirms the importance of accounting for drug-induced changes in the gut microbiota as a potential confounder in assessing compositional changes in microbiota-related studies.

Secondary effects of drugs on the gut microbiome

Drugs can directly alter the GI tract environment (e.g. pH and transit time), mucosa integrity, host and bacterial metabolic activity and the production of microbial metabolites. These drug-induced changes could, in turn, have secondary effects on the microbiome with the potential to cause drug–drug interactions.

As the gradient of pH along the GI tract is known to influence bacterial abundance and diversity, drug-induced changes in gastric and intestinal pH may shape the gut microbiome (Walker *et al.*, 2005; Krajmalnik-Brown *et al.*, 2012). Imhann *et al.* (2017) reported changes in 20% of bacterial taxa and a significant decrease in alpha diversity in PPI users (211 participants) compared with non-users (1604 participants). Alpha diversity refers to the within habitat or sample diversity (a single sample value for average species diversity at an individual site). It usually includes species richness but also accounts for the abundance of the species present in the sample (Gotelli and Colwell, 2001). A PPI-mediated increase in the pH of the stomach and upper small intestine precipitated the growth of specific taxa (*Enterococcaceae* and *Streptococcaceae*) and increased the susceptibility of enteric mucosa to NSAID-induced damage

(Freedberg *et al.*, 2015). Increased abundance of gastric and fecal *Streptococcus* in PPI users has been linked to the suppression of gastric acid production and associated with increased risk of *C. difficile* infection (CDI). Moreover, PPI use has also been linked to increases in expression of bacterial invasion genes, which may also mediate the predisposition to CDI in PPI users (Freedberg *et al.*, 2015).

Additionally, GI transit time can dictate the length of exposure of the microbiota to the gut environment. The anti-diarrhoeal, **loperamide**, administered to humanized GF mice in drinking water (0.1%) for 10 days significantly increased GI transit time and altered the composition of the distal gut microbiota with an increased F/B ratio and a significant reduction in abundance of the Lachnospiraceae family (Kashyap *et al.*, 2013). These changes were reversible upon cessation of loperamide administration and normalized gut transit time.

Drugs may also challenge both the integrity and permeability of the intestinal mucosa. The anti-hyperglycaemic drug, metformin, has been linked with mucosal modifications that influenced the bacterial growth of *Akkermansia* spp. (Forslund *et al.*, 2015). An enrichment of virulence factors and gas metabolism genes, mediated by the associated increase in *Escherichia*, are thought to contribute to the GI disturbances, bloating and increased flatulence, associated with metformin use.

The liver is continually exposed to gut microbiota-derived metabolites, including secondary bile acids and short chain fatty acids (SCFAs), as it receives an estimated 70% of its blood supply from the intestine (Marchesi *et al.*, 2016). Recent data showed bile acids were involved in the solubilization and absorption of lipophilic drugs (Enright *et al.*, 2017). Drug treatment can, however, alter the gut microbiota production of bile salts, which may subsequently affect the absorption and metabolism of co-administered medication. Cefoperazone, vancomycin and clindamycin were identified as antibiotics associated with changes in the gut microbiota composition and caused decreased levels of secondary bile acids precipitating the growth and spore germination of *C. difficile* (Theriot *et al.*, 2016). Studies have found a correlation between the reduced levels of SCFAs in the proximal to distal colon with the corresponding increase in pH from the caecum to rectum (den Besten *et al.*, 2013). Drug-induced changes in the production of SCFAs could thus indirectly alter GI pH, which as mentioned previously may precipitate changes in the microbiome. For example, increased levels of SCFAs were linked with metformin, which could instigate the microbiota modifications associated with this drug (Zhernakova *et al.*, 2016).

Secondary effects of drugs on the gut microbiome could also arise from drug-induced modification of genes or enzymes involved in drug metabolism or drug transport. Metabolomic studies have been employed to investigate the effects of antibiotics on the gut microbiome before and after treatment (Antunes *et al.*, 2011). High-dose treatment of mice with an aminoglycoside antibiotic (20 mg streptomycin via p.o. gavage) altered 87% of all detected intestinal metabolite features and affected many host metabolic pathways involving the metabolism of bile acids, sugars, amino acids and fatty acids with the most significant effect on the steroidal metabolic pathway. Additionally, a marginally increased level of

CYP-metabolizing enzymes was observed after antibiotic treatment. Meta-transcriptomic approaches have also been employed to analyse gut microbiome samples exposed to various drugs and have identified many candidate genes for their microbial metabolism (Maurice *et al.*, 2013). This *ex vivo* study investigated the effects of short-term exposure of human faeces to various non-antibiotic drugs (10 mg·mL⁻¹ concentration used for all the following drugs) including cardiac glycosides (digoxin and **digitoxin**), an anthelmintic (**levamisole**), gastric acid suppressant (**nizatidine**), an analgesic (**phenacetin**) and sulfasalazine. Even though these drugs did not directly alter microbial physiology (i.e. membrane integrity and polarity), even at very high concentrations, they all significantly changed the expression of microbial genes linked to drug import and metabolism. For example, sulfasalazine induced the expression of thioredoxins and nitrate reductases, while nizatidine, subject to bacterially mediated N-oxide bond cleavage, up-regulated the expression of drug enzymes and transporters acting on nitrogen bonds (Maurice *et al.*, 2013). This finding supports the earlier hypothesis that drugs may shift the microbiota to favour the abundance of taxa involved in its metabolism. Furthermore, this altered metabolic capacity of the microbiota could consequently affect not only the pharmacokinetics of subsequent doses of the drug itself (a phenomenon referred to as autoinduction) but also the pharmacokinetics of co-administered medication that are substrates of the same metabolic pathway or transporter.

Implications of the drug–gut microbiome relationship for neuropharmacology

Effect of antibiotics on inflammation and brain–gut axis

Recent studies have explored the effects of antibiotics on the inflammasome-gut microbiota regulation of brain function and behaviour. Wong *et al.* (2016) investigated whether the caspase-1 antagonist and tetracycline antibiotic, minocycline, has a protective effect on the stress response by modulating the microbiota–gut–brain axis. Minocycline treatment (5 mg·kg⁻¹ via i.p. injection for 21 days) increased the abundance of *Akkermansia* spp., which is consistent with attenuation of inflammation and ameliorated the stress-induced depressive-like behaviour in wild-type mice. This suggests that the behavioural effects of minocycline may be mediated via the microbiota and not just via its effects on the activation of CNS microglia (Inta *et al.*, 2017).

Psychoactive drugs and the gut–brain axis: effects on intestinal barrier function

Several psychoactive drugs have marked effects on the intestinal barrier (e.g. permeability and mucus secretion) and alter GI transit. Serotonergic psychoactive drugs have been utilized as a treatment in functional GI diseases; the selective serotonin reuptake inhibitor (SSRI), **paroxetine**, increases the motility rate of the small intestine, while tricyclic antidepressants (TCAs) are known to delay gastric emptying (Grover and Camilleri, 2013). Concurrently, the gut microbiota

modulates intestinal permeability with consequential effects on the absorption and metabolism of psychoactive drugs. Maintenance of intestinal mucosal integrity is important for appropriate absorption of psychoactive drugs in the small intestine. The gut microbiota challenges the intestinal barrier function via induced alterations in intestinal pH and effects on intestinal epithelial integrity (Cani *et al.*, 2008; Carvalho *et al.*, 2012). The presence of the bacterium *Helicobacter pylori* decreases the absorption of the anti-Parkinson's drug and dopamine precursor, **levodopa**. It was hypothesized that *H. pylori* might alter gastric motility, disrupt the duodenal mucosa or produce ROS, which may inactivate levodopa (Hamlet *et al.*, 1999; Miyaji *et al.*, 1999). More recently, eradication of *H. pylori* has been shown to significantly improve clinical symptoms of patients with Parkinson's disease and improve levodopa efficacy (Hashim *et al.*, 2014). Additionally, several neuropsychiatric disorders have been associated with a dysfunctional intestinal barrier; acute stress is associated with expression of the tight junction proteins, zonula occludens-1 and occludin, in the duodenal mucosa of rats subjected to water immersion restraint stress (Lee *et al.*, 2013). Moreover, **corticotrophin-releasing hormone receptors** mediate the colonic barrier dysfunction observed in response to maternal separation-induced mild stress (Söderholm *et al.*, 2002). Hence, both the gut microbiota and psychiatric disorders modulate intestinal permeability and barrier function, which in turn may precipitate changes in the absorption of psychoactive drugs (Kelly *et al.*, 2015).

Effects of CNS-related disorders on the composition of the gut microbiota

In addition to drug-induced changes in the gut microbiome, alterations in the composition of the gut microbiota have also been associated with neurological dysfunction and psychiatric disorders (Cenit *et al.*, 2017). Kelly *et al.* (2016) observed decreased richness and diversity of the gut microbiota in depressed patients, and numerous studies have identified an altered microbiota composition in children with autism

spectrum disorder; increased abundance of *Lactobacillus* and *Desulfovibrio* spp. has correlated with autism severity (Finegold, 2011; Tomova *et al.*, 2015). The gut microbiota has also been identified as a potential regulator of other neuropsychiatric disorders, for example, schizophrenia (Dinan *et al.*, 2014; Shen *et al.*, 2018). It is yet to be established whether these disease-associated changes to the gut microbiota are involved in the initiation of disease pathogenesis (altered microbiota state precipitating changes in brain development or function) or occur because of the disease (i.e. whether changes in gut microbiota arise following alterations in brain development or function). Alternatively, the microbiota changes could also occur as a result of dietary patterns or medication (Mayer *et al.*, 2015). As both the CNS-related disease itself and the pharmacological treatment of the disease can alter the composition of the microbiota, it is thus essential to account for independent effects of the disease or drug treatment in both animal and human studies.

Microbial metabolism of psychoactive drugs

Few studies have offered mechanistic insight into the microbiota-mediated metabolism of psychoactive drugs; however, those that have are summarized in Table 2. In most cases, the specific microbial species, or microbial-derived enzymes, responsible for the metabolism of psychoactive drugs by the gut microbiome are unknown.

There is evidence to suggest that benzodiazepines are subject to microbiota-mediated drug metabolism. Older studies have demonstrated the microbiota-mediated nitroreduction of the hypnotics, **clonazepam** and nitrazepam, to their corresponding 7-amino metabolite derivatives. Elmer and Rimmel (1984) administered radiolabelled clonazepam and quantified the production of the nitro-reduced clonazepam metabolites in GF rats before and after colonization with faecal microbiota. The production of these metabolites increased significantly from 15% in GF mice to 77% after microbial colonization. Similarly, the reduction of the hypnotic, nitrazepam, to 7-aminonitrazepam and

Table 2

Psychoactive drugs are subject to direct metabolism by the gut microbiota

Drug	Drug class	Nature of study; animal species/human	Suggested implicated microbial species	Microbial-mediated mechanism	References
Risperidone	Anti-psychotic	<i>In vivo</i> ; rats and dogs	Unknown	Isoxazole scission of benzisoxazole ring system	Meuldermans <i>et al.</i> (1994)
Nitrazepam and clonazepam	Hypnotic	<i>In vivo</i> ; rats	Unknown	Nitroreductase-mediated reduction	Takeno <i>et al.</i> (1990)
Methamphetamine	Psychostimulant	<i>In vitro</i>	Lactobacilli, Enterococci and Clostridia	<i>N</i> -demethylation	Caldwell and Hawksworth (1973)
Levodopa	Dopamine precursor	<i>In vivo</i> ; rats	Unknown	Decarboxylation and <i>p</i> -dehydroxylation-mediated conversion to <i>m</i> -tyramine and subsequent oxidation to <i>m</i> -hydroxyphenylacetic acid	Goldin <i>et al.</i> (1973)

7-acetylamino nitrazepam was shown to be mediated by several anaerobic bacteria isolated from human gut isolates including species from the *Clostridium*, *Bacteroides* and *Eubacterium* genera. The authors identified the bacterium, *Clostridium leptum*, as having highly specific nitroreductase activity (Rafii *et al.*, 1997). A previous study highlighted antibiotics can deplete the activity of this microbial enzyme (Takeno and Sakai, 1991). The production of nitro-reduced nitrazepam metabolites in pregnant rats, following a p.o. dose of nitrazepam 300 mg·kg⁻¹, was quantified before and after antibiotic treatment, which was given to diminish nitroreductase enzymatic activity. The levels of 7-aminonitrazepam and 7-acetylamino nitrazepam decreased from 30% pretreatment to 2% after antibiotic treatment.

Effects of psychoactive drugs on the composition of the gut microbiota

Antidepressants and antipsychotics are associated with distinct gut microbiota signatures. Gastric acid suppressants, antipsychotics and antidepressants have repeatedly been confirmed as the three non-antibiotic drug classes most associated with the abundance of single taxa. Antipsychotics, for example, were associated with the abundance of *Prevotella*, an unclassified member of the Desulfovibrionaceae family and *Vitvallis* genus in an observation-based study in an elderly (≥65 years) hospitalized cohort (Ticinesi *et al.*, 2017). On the other hand, antidepressant use in this cohort significantly correlated with the increased abundance of five specific bacterial taxa belonging to the *Helicobacter*, *Asteroleplasma* and *Marinilactibacillus* genera and unclassified members of both the Bacillus class and Succinivibrionaceae family. In an observation-based study in community-dwelling patients (mean age 52 years), the SSRI antidepressant, **citalopram**, was associated with a significantly increased relative abundance of the Enterobacteriaceae family in comparison to patients not taking any medication (Rogers and Aronoff, 2016). The specific use of the antipsychotics, **olanzapine** and **risperidone**, causes a shift in the gut microbiota composition to a state previously shown to be associated with obesity in both rat and human [12.2 (SD 2.5) years] *in vivo* studies (Davey *et al.*, 2012; Bahr *et al.*, 2015a). Chronic olanzapine treatment of rats (2–4 mg·kg⁻¹·day⁻¹) and mice (50 mg·kg⁻¹ HFD) was associated with an increase in Firmicutes, a decrease in Bacteroidetes and an overall reduction in biodiversity (Davey *et al.*, 2012; Morgan *et al.*, 2014). Similarly, chronic risperidone treatment (approximately 80 µg risperidone per day for 58 days) resulted in a 22.4% decrease in Bacteroidetes and a reciprocal 32.6% increase in Firmicutes in the risperidone-treated mice relative to control mice (Bahr *et al.*, 2015b).

The mechanisms underpinning these changes in bacterial abundance or diversity induced by psychoactive drugs are not fully understood, but both these drug classes have shown *in vitro* antimicrobial activity. There is preliminary evidence to suggest that olanzapine has antimicrobial activity. Morgan *et al.* (2014) found olanzapine inhibited the *in vitro* growth of two commensal strains, *E. coli* and *Enterococcus faecalis*. The dose investigated, however, was above the recommended dosage range of 5–20 mg·day⁻¹, and therefore, whether clinically relevant doses of olanzapine would still possess

antimicrobial activity remains to be tested. Similarly, the phenothiazine group of antipsychotics exerted antimicrobial effects at higher than clinically relevant drug doses (Amaral *et al.*, 2004). The phenothiazine antipsychotic, **chlorpromazine**, was the first psychoactive drug associated with antibacterial properties. *S. aureus*, *Mycobacterium* and some gram-negative rods such as *Shigella* spp. have been identified as the bacteria most susceptible to the antibacterial activity of phenothiazine antipsychotics (Amaral *et al.*, 2004). Evidence suggests phenothiazine antipsychotics may mediate their effects on microbial growth through the alteration of bacterial morphology (phenothiazines cause filamentation of *E. coli*) or inhibition of bacterial adherence to epithelial cells (phenothiazines reduce *E. coli* adherence to urinary epithelium) (Amaral *et al.*, 2004).

Similarly, antidepressant-induced changes in gut microbiota may be mediated by direct antimicrobial activity. SSRIs (including paroxetine, **sertraline** and **fluoxetine**) are associated with a broad-spectrum of antibacterial activity, including activity against strains of *Staphylococcus*, *Enterococcus*, *Clostridium*, *Pseudomonas* and *Citrobacter* (Munoz-Bellido *et al.*, 2000). Sertraline can also influence microbial growth by acting synergistically with other antibiotics. Sertraline increased the efficacy of co-administered tetracycline and fluoroquinolone antibiotics against, a pathogenic strain associated with urinary tract infections, *Corynebacterium urealyticum* (Munoz-Bellido *et al.*, 1996). The inhibition of efflux pumps in bacterial cells by sertraline is hypothesized as one causative mechanism. SSRIs may also interfere with the biosynthesis of the slime layer on bacteria (Munoz-Bellido *et al.*, 2000); the disruption of the slime layer may also act to increase bacterial susceptibility to co-administered antibiotics. Apart from SSRIs, other antidepressants have antimicrobial effects, including MAO inhibitors (MAOIs) and TCAs. The inhibition of cell wall synthesis and anti-plasmid activity has been proposed as mechanisms underlying the antimicrobial activity of the MAOI, iproniazid and the TCA drug class respectively (Molnar, 1988; Macedo *et al.*, 2017).

Psychotropic drugs can also modulate the activity and pathogenicity of microbes, which can precipitate changes in the gut microbiome. Sertraline can alter the *in vitro* pathogenicity of fungi, for example, by significantly affecting the virulence properties associated with *Candida* including decreased hyphal elongation and reduced secretion of aspartyl proteinases, thereby preventing fungal adherence and tissue invasion of *Candida* spp. (Lass-Flörl *et al.*, 2003).

The effects of psychoactive drug–microbiota interactions: implications for drug response and toxicity

The growing evidence of the complex relationship between drugs and the gut microbiome, illustrated in Figure 1, underscores the importance of considering the gut microbiota as an additional factor contributing to the inter-individual variation observed in drug metabolism and response.

The interaction of psychoactive drugs with the gut microbiota has implications for drug absorption and bioavailability. As mentioned previously, levodopa is one of the most studied psychoactive drugs that interact with the gut microbiome. Research illustrating the metabolism of this

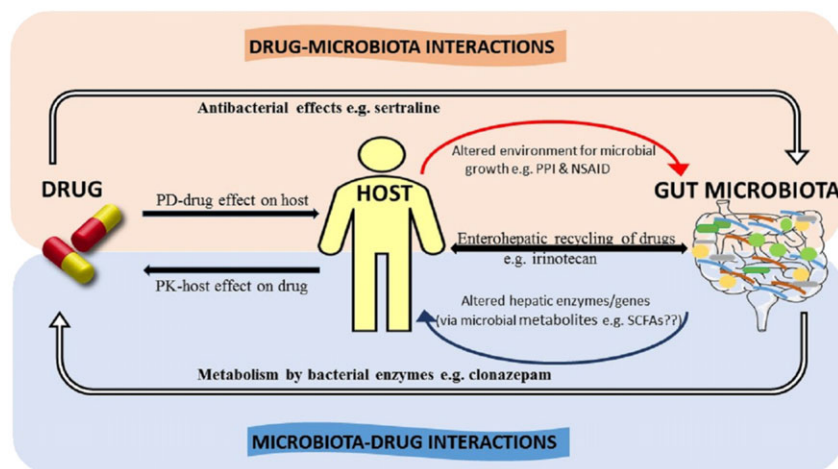


Figure 1

The complex interplay between drugs and the gut microbiota. The reciprocal relationship between drugs and the gut microbiome is composed of both microbiota-mediated alterations to drug pharmacokinetics and drug-mediated alterations to the function and composition of the gut microbiome. These interactions can occur by both direct (illustrated by solid white arrows with black outline) and indirect or secondary (illustrated by curved line arrows) mechanisms. 'Microbiota–Drug Interactions': the microbiota can directly metabolize drugs through bacterial-derived enzymes (e.g. nitroreductase-mediated metabolism of clonazepam) but can also indirectly affect drug metabolism through the alteration of the hosts capacity to metabolize drugs (curved-up line arrow), potentially altering drug PK profile. Microbial-derived metabolites (e.g. SCFAs and secondary bile acids) may be potential mediators of this effect. The interactions between the host and gut microbiome are responsible for the enterohepatic recirculation of drugs. For example, the hepatic-glucuronidated irinotecan metabolite is deconjugated by β -glucuronidase enzymes expressed by the gut microbiota. 'Drug–Microbiota Interactions': the mechanisms underpinning the drug-mediated changes to the function and composition the gut microbiome are yet to be fully elucidated. Drugs can have antibacterial properties that directly affect the composition of the gut microbiota (e.g. sertraline). Drugs can also alter the physiological properties or functions of host organs (i.e. PD effect) (e.g. PPI-mediated alterations to gastric acid production and pH, NSAID-induced changes to mucosal integrity), which may, in turn, precipitate secondary effects on the composition of the gut microbiota (illustrated by the curved-down line arrow).

drug by the gut microbiota-mediated dehydroxylation dates back to the 1970s (Goldin *et al.*, 1973). Follow-on studies found decreased plasma levels of the drug with the presence of *H. pylori*, attributed to levodopa-mediated interaction with the bacterial surface adhesions (Niehues and Hensel, 2009).

Antidepressants are associated with considerable inter-individual variation in drug response and a lack of efficacy; it is estimated that antidepressants are only 20–30% more effective than placebo (Arroll *et al.*, 2005). Pharmacogenetics, although still in its relative infancy, has thus far proven unsuccessful in identifying and optimizing factors that may hinder antidepressant efficacy. The pathophysiology of major depression disorder (MDD) has, however, been linked to alterations in the gut microbiota composition. MDD is associated with increased levels of Bacteroidetes and Enterobacteriaceae and decreased levels of Firmicutes. This altered microbiota state has been linked to increased gut permeability, a factor that can dictate intestinal drug transport and absorption (Jiang *et al.*, 2015). Continued metabolomic and metagenomic analysis of the microbiome and further pharmacomicrobiomic based-studies may thus offer some additional insight.

The gut microbiota has also been implicated in the propagation of the side effects and toxicity of psychoactive drugs. With patient adherence to psychotropic therapy estimated to be only 30%, poor compliance has been linked to the unfavourable side-effect profile associated with these drugs (Weich *et al.*, 2007). As previously highlighted, antibiotic treatment of rats attenuated both the microbial

metabolism and the teratogenicity-associated adverse effect of nitrazepam and its metabolites (Elmer and Rimmel, 1984). More recently, antipsychotic-induced metabolic dysfunction has been linked to shifts in the composition of the gut microbiota. The role of the gut microbiome in the development of olanzapine-induced weight gain was elucidated when olanzapine-treated GF mice did not gain weight but did so upon colonization with caecal microbiota (Morgan *et al.*, 2014). Furthermore, an antibiotic cocktail co-administered with olanzapine, to chemically deplete the gut microbiota, attenuated the metabolic side effects associated with the drug treatment alone in rats; increased weight gain, increased uterine fat deposition and increased plasma free fatty acid levels were side effects attenuated in microbiota-depleted rats (Davey *et al.*, 2013).

A recent follow-on study by Kao *et al.* (2018) investigated whether treatment with a prebiotic, Bimuno™ galacto-oligosaccharides (B-GOS), modified the olanzapine-induced weight gain. Female rats were treated with B-GOS (0.5 g·kg⁻¹·day⁻¹) for 21 days, in conjunction with administration of olanzapine (10 mg·kg⁻¹ once daily via i.p. injection) or saline on days 8–21. B-GOS treatment significantly attenuated the drug-induced weight gain without altering the antagonism of central serotonergic receptors necessary for drug efficacy. B-GOS treatment alone altered the microbiota composition; differences in the abundance of *Bifidobacterium* spp. and Firmicutes spp. were evident in B-GOS-only-treated rats in comparison to both water-only and B-GOS-olanzapine-treated rats. Contrary to the

previous findings by Davey *et al.* (2013) and Morgan *et al.* (2014) discussed above, administration of olanzapine, however, did not significantly alter the composition of the faecal microbiota, although different dosage regimens were employed in the respective studies. Furthermore, the authors deduced, contrary to their hypothesis, that elevated levels of the SCFA, acetate, may mediate the olanzapine-induced weight gain. Considering the risks associated with antibiotic resistance, prebiotic treatment may constitute a more suitable adjunctive therapy in comparison to long-term antibiotic use to improve patient tolerance to olanzapine.

Both olanzapine-induced and risperidone-induced weight gain correlated with an altered composition of gut microbiota (Davey *et al.*, 2012; Bahr *et al.*, 2015b). Suppressed energy expenditure, induced by the gut microbiota, was found to cause the observed weight gain in risperidone-treated mice. Furthermore, fecal microbiota transplantation (FMT) from risperidone-treated mice to treatment-naïve mice induced weight gain and suppressed energy expenditure in the FMT-recipient mice (Bahr *et al.*, 2015b). On the premise that some antidepressants (e.g. SSRIs and TCAs) are associated with similar effects to these antipsychotics, that is, changes in the gut microbiota and drug-induced weight gain, it may be timely to extend these studies to antidepressants.

Conclusion and future directions

Research has identified many clinically relevant drugs, including psychotropics, which are metabolized by the microbiome, often via as yet unknown mechanisms. There remains a need to establish the microorganism responsible for metabolism and identify the molecular mechanisms involved. While medication use can precipitate changes in the abundance and diversity of a wide array of different bacterial phyla, the resultant effects of these compositional changes on drug response and patient outcomes requires further study. Matching specific microbial genes or enzymes, which may dictate drug response, to specific bacterial phyla could lead to greater understanding of the consequences of disturbances in the microbiome on patient outcomes and provide additional impetus to explore the contribution of these important, but underappreciated, drug-microbiome interactions to the inter-individual variability observed in drug response.

Nomenclature of targets and ligands

Key protein targets and ligands in this article are hyperlinked to corresponding entries in <http://www.guidetopharmacology.org>, the common portal for data from the IUPHAR/BPS Guide to PHARMACOLOGY (Harding *et al.*, 2018), and are permanently archived in the Concise Guide to PHARMACOLOGY 2017/18 (Alexander *et al.*, 2017a,b).

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Conflict of interest

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