Distinct Actions of the Fermented Beverage Kefir on Host Behaviour, Immunity and Microbiome Gut-Brain Modules in the Mouse

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Abstract

Background Mounting evidence suggests a role for the gut microbiota in modulating brain physiology and behaviour through bi-directional communication along the gut-brain axis. As such, the gut microbiota represents a potential therapeutic target for influencing centrally-mediated events and host behaviour. It is thus notable that the fermented milk beverage kefir has recently been shown to modulate the composition of the gut microbiota in mice. It is unclear whether kefirs have differential effects on microbiota-gut-brain axis and whether they can modulate host behaviour per se.

Methods To address this, two distinct kefirs (Fr1 and UK4) or unfermented milk control were administered to mice that underwent a battery of tests to characterise their behavioural phenotype. In addition, shotgun metagenomic sequencing of ileal, cecal and faecal matter was performed, as was faecal metabolome analysis. Finally, systemic immunity measures and gut serotonin levels were assessed. Statistical analysis was performed by ANOVA followed by Dunnett's post hoc test or Kruskal-Wallis test followed by Mann-Whitney U test.

Results Fr1 ameliorated the stress-induced decrease in serotonergic signalling in the colon and reward-seeking behaviour in the saccharin preference test. On the other hand, UK4 decreased repetitive behaviour and ameliorated stress-induced deficits in reward-seeking behaviour. Furthermore, UK4 impaired long-term spatial learning, yet increased fear-dependent contextual memory. In the peripheral immune system, UK4 increased the prevalence of Treg cells and interleukin 10 levels, whereas Fr1 ameliorated the milk gavage stress-induced elevation in neutrophil levels and CXCL1 levels. Analysis of the gut microbiota revealed that both kefirs significantly changed the composition and functional capacity of the host microbiota, where specific bacterial species were changed in a kefir-dependent manner. Furthermore, both kefirs increased the capacity of the gut microbiota to produce GABA, which was linked to an increased prevalence in Lactobacillus reuteri.

Conclusions Altogether, these data show that kefir can signal through the microbiota-gut-immune-brain axis and modulate host behaviour. In addition, different kefirs may direct the microbiota toward distinct immunological and behavioural modulatory effects. These results indicate that kefir can positively modulate the microbiota-gut-brain axis and support the broadening of the definition of psychobiotic to include fermented foods such as kefir.

Introduction

Mounting evidence suggests that the gastrointestinal microbiota influences host behaviour via bi-directional communication through what has been coined the microbiota-gut-brain axis (Rhee et al. 2009, Collins et al. 2012, Cryan et al. 2012, Mayer et al. 2014, Foster et al. 2017, Cryan et al. 2019, Sherwin et al. 2019). Various nutritional interventions have already been demonstrated to influence this axis, with host-indigestible dietary fibres (prebiotics) and live bacterial strains that confer health benefits (probiotics) receiving particular attention (Kao et al. 2016, Cryan et al. 2019, long-Smith et al. 2019). Such interventions that modulate mood through manipulation of the microbiota have been coined psychobiotics (Dinan et al. 2013). It is becoming apparent that fermented foods may also confer beneficial effects on aspects of mood, as fermented food intake is associated with decreased social anxiety (Hilimire et al. 2015) and gestational depression in humans (Miyake et al. 2014). In addition, a fermented milk product, which was produced using known probiotics, has been demonstrated to modulate brain activity in healthy women (Tillisch et al. 2013). Such findings merit an investigation into the mechanisms by which different fermented foods might affect the microbiota-gut-brain axis.

One such fermented foods are kefir, a traditional fermented milk beverage originating from the Caucasus mountains that is produced by adding a kefir grain to milk. These grains consist of exopolysaccharide matrices harbouring symbiotic microbial communities, including bacteria and yeasts, which together are responsible for fermentation (Bourrie et al. 2016). Notably, the word kefir is derived from the Turkish keyif, which translates as “good feeling”. Indeed, numerous health benefits have been ascribed to kefir (Rosa et al. 2017, Slattery et al. 2019), such as anti-inflammatory effects in animal models (Rodrigues et al. 2005, Liu et al. 2006, Lee et al. 2007), reduced obesity symptomatology high fat diet-induced obese mice (Kim et al. 2017, Bourrie et al. 2018, Gao et al. 2019), and reduced hypertension in spontaneously hypertensive rats (Silva-Cutini et al. 2019). Furthermore, kefir administration has been shown to reduce physical fatigue and improve exercise performance in mice (Hsu et al. 2018). A recent randomized, controlled trial has even shown that kefir can reduce bloating and improve mood in patients with inflammatory bowel disease (Yilmaz et al. 2019). Finally, kefir has been shown to modulate the composition of the gastrointestinal microbiota in rodents (Kim et al. 2017, Bourrie et al. 2018, Hsu et al. 2018, Gao et al. 2019). Overall, current evidence indicates that the traditionally fermented milk drink kefir merits investigation to determine its ability to modulate the microbiota-gut-brain axis and affect the mood of the host. It is not clear if different kefir's exert differential influence across the microbiota-gut-brain axis. As such, we aimed to investigate if two different kefirs could affect the microbiota of ileal, cecal and faecal contents, the faecal metabolome, gastrointestinal function, host adaptive and innate immunity, and behaviour in mice.

Results

Kefir microbiota was relatively stable over time

The milk kefir used in this study was generated in a manner to represent traditional kefir production (i.e., repeated fermentation of milk by a kefir grain). Considering that kefir contains a complex microbiota community composed of a variety of strains (Bourrie et al. 2016), we aimed to determine if this community remained stable over time. Shotgun metagenomics was used to determine the species-level composition of the two kefirs, Fr1 and UK4, at 6 time-points at intervals of 2 weeks throughout the experiment. Overall, the populations were generally temporally stable, with both kefirs being dominated by *Lactococcus lactis,* while also consistently containing *Lactobacillus kefiranofaciens* (**Figure S4**). Several other species were identified at specific time-points at >1% relative abundance in both kefirs, such as *Bifidobacterium breve* and *Pseudomonas* species.

The fermented milk drink kefir is well-tolerated

Kefir administration did not affect body weight, body composition, food intake and drinking water intake (**Figure S5**). In addition, no differences were found in basal body temperature, as detected in the stress-induced hyperthermia test, as well as the locomotor activity assessed in the open field test (**Figure S5**). Overall, this indicates that the fermented milk drink kefir was well-tolerated by mice.

Kefir did not affect gastrointestinal motility

Assessment of gastrointestinal motility by carmine red administration showed that kefir did not induce any changes in gastrointestinal propulsion (**Figure S6**). In line with these findings was the absence of differences in faecal pellet weight and faecal water content (**Figure S6**). Finally, no differences in cecum weight and colon length were detected at the end of the study (**Figure S6**). Overall, these data indicate that changes in the gut microbiota are likely independent of host gastrointestinal motility.

Kefir modulates repetitive behaviour and reward-seeking behaviour

In the marble burying test, we found that administration of UK4 decreased the number of marbles buried indicative of reduced anxiety ($F(2,35) = 5.464$, $p = 0.009$) (**Figure 1A**). No changes were observed in other tests assessing anxiety-like behaviours such as the elevated plus maze, open field test and stress-induced hyperthermia test (**Figure S7**), as well as depressive-like behaviour in the forced swim test and tail-suspension test (**Figure S7)**. It is interesting to note that the repeated stress of milk gavage increased the corticosterone response to an acute stressor, which remained unaffected by kefir (**Figure S7**)

In the female urine sniffing test of reward-seeking, mice receiving milk spent less time interacting with the cotton bulb containing water compared to undisturbed mice ($^2(1) = 6.367$, $p = 0.012$), which was ameliorated by both Fr1 and UK4 ($^2(2) = 13.238$, $p < 0.001$) (**Figure 1B**). In addition, mice receiving UK4 spent more time interacting with the cotton bulb containing the urine from a female mouse in esterus ($^2(2) = 6.280$, $p = 0.043$) (**Figure 1B**), even though no differences were observed in the preference index (**Figure 1C**). Finally, Fr1 administration increased saccharin preference in the saccharin preference test ($^2(2) = 12.826$, $p = 0.002$), which is often used as a measure of reward-seeking behaviour (**Figure 1D, E**).

*__Figure 1. Kefir modulates repetitive behaviour and reward-seeking behaviour.__ Repetitive/anxiety-like behaviour was assessed using the marble burying test (A). Anhedonia and reward-seeking behaviours were investigated using the female urine sniffing test (B, C) and saccharin preference test (D, E). The marble burying test was normally distributed and analysed using a one-way ANOVA, followed by a Dunnett's post hoc test. The female urine sniffing test and saccharin preference test were non-normally distributed and analysed using the Kruskal-Wallis test, followed by the Mann-Whitney test. Significant differences are depicted as: *p < 0.05, **p < 0.01 and ***p < 0.001; Milk control compared to Kefir supplementation, $^{\$}p < 0.05$; Undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 11-12). Dots on each graph represent individual animals.*

Kefir does not affect sociability

All groups exhibited normal social preference and recognition in the 3-chamber social interaction test, indicating that kefir did not affect sociability (**Figure S8**).

Kefir – UK4 modulates contextual learning and memory

No differences were observed in the fear conditioning test in phase 1 – acquisition, as determined by the time mice spent frozen during the presentation of the cue, as well as in-between the cues (**Figure 2A, B**). In addition, no differences were seen during phase 2, when cued-dependent fear memory was assessed (**Figure 2C**). However, mice receiving UK4 showed a trend towards increased freezing behaviour in phase 3 – contextual memory (F(2,34) = 3.181, p = 0.055) (**Figure 2D**). Conversely, mice receiving UK4 made more errors in the reverse learning phase of the appetitive Y-maze as seen by the percentage correct choices (treatment effect: F(2,33) = 3.870, p = 0.031) (**Figure 2E**), and the amount of entries mice needed to reach the food reward (treatment effect: F(2,33) = 3.387, p = 0.046) (**Figure 2F**). It is interesting to note, however, that a similar difference was found on day 10 in the percentage correct choices made between the undisturbed control and Milk control group (*t*(22) = -2.303, p = 0.031), where the mice receiving milk control performed superior (**Figure 2F**).

*__Figure 2. UK4 enhances fear-dependent contextual memory yet decreases long-term spatial learning.__ Fear-dependent memory and learning were assessed using fear conditioning. At phase 1 – Acquisition, mice were presented with a tone, followed by a foot shock. Cue-associative learning was assessed by measuring freezing behaviour during the presentation of the tone (A), whereas context-associative learning was determined in-between tones (B). At phase 2 – Cued memory, mice received 40 presentations of the same cue (the first 10 are shown), without foot shock, in a different context, in which fear-dependent cued memory was assessed (C). At phase 3 – Contextual memory, mice were exposed to the same context as day one for 5 minutes and contextual memory was assessed (D). Long-term spatial learning was assessed in the appetitive Y-maze, as determined by the percentage of times the mice made the correct choice as the first choice for reaching the goal (food reward) (E), as well as the number of average entries it took the mice to reach the goal (F). All data were normally distributed and analysed using a repeated measures ANOVA or one-way ANOVA, followed by a Dunnett's post hoc test. Significant differences are depicted as: *p < 0.05; Milk control compared to Kefir supplementation, $^{\$}p < 0.05$; undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 10-12). Dots on each graph represent individual animals.*

Kefirs differentially impact the peripheral immune system

Interestingly, we observed an increase in circulating LY6C^{high} monocytes in mice receiving milk, compared to undisturbed mice, indicating an activation of the innate immune system (Gururajan et al. 2019, van de Wouw et al. 2019). Furthermore, there were increased levels of various inflammatory cytokines in the peripheral circulation (**Figure S9**). In line with this finding, was an increase in neutrophil levels induced by milk administration (*t*(22) = −3.583, p = 0.002) (**Figure 3A**). Interestingly, neutrophil levels were ameliorate by Fr1 administration (F(2,34) = 5.412, p = 0.009) (**Figure 3A)**. Similarly, Fr1 ameliorated the increased CXCL1 levels observed in mice chronically stressed by milk gavage (*t*(21) = −2.589, p = 0.017; F(2,32) = 7.006, p = 0.003) (**Figure 3B**), which is one of the major chemoattractants for neutrophils (Silva et al. 2017).

UK4 increased the prevalence of T regulatory cells (Treg) cells in mesenteric lymph nodes (MLNs) ($F(2,34) = 8.709$, $p < 0.001$) (**Figure 3C**), an anti-inflammatory T helper cell subset known to be induced by gut microbial metabolites (Tanoue et al. 2016). Interestingly, these cells did not express the Helios transcription factor ($F(2,34) = 7.548$, $p = 0.002$) (**Figure 3D**). This indicated that they were induced in the periphery (pTreg) rather than in the thymus (Shevach et al. 2014), suggesting that gut microbial-derived metabolites could have driven this increase in Treg cells. We subsequently investigated the prevalence of MLN CD103+ dendritic cells, which are known to induce Treg cell differentiation (Tan et al. 2016), but found no corresponding differences (**Figure S10**). The effects of UK4 also reached the peripheral circulation, where there was an increased prevalence of Treg cells ($F(2,31) = 3.420$, $p = 0.046$) (**Figure 3E**). Similarly, we observed increased plasma IL-10 levels ($F(2,32) = 6.205$, $p = 0.006$) (**Figure 3F**), one of the primary cytokines secreted by Treg cells (Sabat et al. 2010).

Figure 3. UK4 increases Treg cells levels, while Fr1 decreases neutrophil levels. *T regulatory cells (CD4+, CD25+, FoxP3+) were assessed in mesenteric lymph nodes (MLNs) (A) and were subsequently analysed for Helios expression (B), to investigate their origin as Helios+ cells exclusively originate in the thymus. Blood was also assessed for Treg cell levels (C), and plasma interleukin 10 (IL-10) levels (D). Similarly, neutrophils (CD11b+, LY6C^{mid}, SSC^{high} and CXCL1 levels were also investigated in peripheral blood (E, F). All data were normally distributed and analysed using a one-way ANOVA, followed by a Dunnett's post hoc test. Significant differences are depicted as: *$p < 0.05$, **$p < 0.01$; Milk control compared to Kefir supplementation, $^{\$}p < 0.05$ and $^{\$\$}p < 0.01$; Undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 11-12). Dots on each graph represent individual animals.*

Kefir – Fr1 selectively increases colonic serotonergic activity

Serotonergic signaling is well-known to play a key-role in microbiota-host cross-talk (Sudo et al. 2004, O'Mahony et al. 2015), which is why we quantified gut serotonin (5-HT) levels. We found that mice receiving milk showed decreased ileal 5-HT levels compared to undisturbed mice ($t(21) = 2.650$, $p = 0.015$) (**Figure 4B**). This resulted in an increased 5HIAA/5-HT ratio ($t(22) = 2.650$, $p < 0.001$) (**Figure 4C**), indicating an increased serotonin turnover and serotonergic activity. The opposite was observed in the colon, where the milk induced a trend towards increased 5-HT levels ($t(22) = -1.937$, $p = 0.066$) (**Figure 4E**), whilst decreasing the 5HIAA/5-HT ratio ($t(22) = 2.907$, $p = 0.008$) (**Figure 4F**). Interestingly, this phenotype in the colon, but not ileum, was ameliorated by Fr1 (for 5-HT; $F(2,35) = 6.387$, $p = 0.005$, for 5HIAA/5-HT ratio; $F(2,35) = 9.026$, $p < 0.001$) (**Figure 4E, F**).

Figure 4. Fr1 modulates serotonergic signaling in the colon, but not ileum. *Ileal (A-C) and colonic (D-F) tissues were quantified for 5HIAA and serotonin (5-HT) levels using HPLC. The 5HIAA/5-HT ratio was subsequently calculated. All data was normally distributed and analysed using a one-way ANOVA, followed by a Dunnett's post hoc test. Significant differences are depicted as: **$p < 0.01$; Milk control compared to Kefir supplementation, $^{\$}p < 0.05$, $^{\$\$}p < 0.01$ and $^{\$\$\$}p < 0.001$; Undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 11-12). Dots on each graph represent individual animals.*

Both kefirs affect gut microbiota composition, at both the species- and strain-levels

We subsequently investigated if kefir administration could affect the composition of the ileal, cecal and faecal microbiota. Alpha diversity (Shannon) was not significantly altered by kefir Fr1 administration (Fr1; Ileum: $p = 0.11$; Cecum: $p = 0.19$; Faeces: $p = 0.16$), whereas kefir UK4 increased alpha diversity in the cecum ($p = 0.017$), but not ileum and faeces ($p = 0.44$; $p = 0.24$) (**Figure 5A**). Analysis of beta diversity revealed a trend towards significant separation induced by the administration of Fr1 (Ileum: $p = 0.088$, $R^2 = 0.111$; Cecum: $p = 0.087$, $R^2 = 0.087$; Faeces: $p = 0.077$, $R^2 = 0.114$) and UK4 (Ileum: $p = 0.058$, $R^2 = 0.092$; Cecum: $p = 0.1$, $R^2 = 0.092$; Faeces: $p = 0.073$, $R^2 = 0.09$) (**Figure 5A**). It is notable that, the kefir treatment overall did influence beta diversity (p-value ranged from $0.05 < p \leq 0.10$ for all regions). Notably, no significant differences were found between the administration of

Fr1 and UK4 in alpha diversity (Ileum: $p = 0.37$; Cecum: $p = 0.34$; Faeces: $p = 0.8$) and beta diversity (Ileum: $p = 0.316$, $R^2 = 0.05$; Cecum: $p = 0.14$, $R^2 = 0.07$; Faeces: $p = 0.2$, $R^2 = 0.062$).

Figure 5. Kefir modulates the composition of the gastrointestinal microbiota. *Alpha diversity (Shannon) of the ileal, cecal and faecal microbiota was compared between mice receiving kefir (Fr1 or UK4) and mice receiving milk control using violin plots (A). Beta diversity was assessed by PERMANOVA to investigate the dissimilarity in the gut microbial composition, which were depicted using MDS plots. Dots represent individual animals (n = 12) (B). Differentially abundant taxa were determined using LEfSe (C).*

A total of 15 bacterial species were identified as being differentially abundant between at least one pair of groups in at least one region of the gut (**Figure 5C**). Both kefirs increase the abundance in or more region in the gut of *Lactobacillus reuteri* (Fr1, cecum: LDA=4.36, UK4, cecum: LDA=4.02, UK4, faeces: LDA=4.07), *Eubacterium plexicaudatum* (Fr1, faeces: LDA=3.77, UK4, cecum: LDA=4.22, UK4, faeces: LDA=3.67), *Bifidobacterium pseudolongum* (Fr1, ileum: LDA=4.93, UK4, cecum: LDA=4.7). Both kefirs induced a decrease in the prevalence of *Lachnospiraceae bacterium* 3_1_46FAA (Fr1, cecum: LDA=4.25, UK4: cecum: LDA=4.28), *Propionibacterium acnes* (Fr1, faeces: LDA=3.25, UK4, faeces, LDA=4.04), and *Bacillus amyloliquefaciens* (Fr1, faeces: LDA=3.04, UK4, faeces: LDA=3.58). Only Fr1 increased the prevalence of *Parabacteroides goldsteinii* (cecum: LDA=3.99), *Bacteroides intestinalis* (faeces: LDA=3.49), *Anaerotruncus* unclassified (faeces: LDA=3.75), and *Parabacteroides goldsteinii* (faeces: LDA=4.02). Conversely, only UK4 increased the prevalence of *Alistipes* unclassified (cecum: LDA=4.45) and decreased *Candidatus* Arthromitus unclassified (ileum: LDA=4.45).

We subsequently correlated significantly altered behavioural and immunological parameters with bacterial species present throughout the gastrointestinal microbiota (**Figure 6**). Most notable was the correlation between ileal *C. Arthromitus* unclassified abundances and circulating Treg cell levels ($p = 0.004$, $R = -0.49$), and ileal *B. pseudolongum* abundances and circulating neutrophil levels ($p = 0.001$, $R = -0.52$).

Figure 6. Bacterial species in the gastrointestinal microbiota correlate with changes in host immunity and measures of gut serotonin. *The prevalence of bacterial species in the ileum, cecum and faeces were correlated with significantly altered changes in host behaviour and immunity using HAllA.*

PanPhlAn was used alongside StrainPhlAn to characterise differentially abundant species to the strain-level. Both tools indicated that the detected *B. pseudolongum* strain was closely related to *B. pseudolongum* UMB-MBP-01 (**Figure S11**). Similarly, PanPhlAn indicated that the detected *L. reuteri* strain was closely related to *L. reuteri* TD1. No other differentially abundant species could be characterised to the strain-level. Finally, neither PanPhlAn nor StrainPhlAn identified any kefir-derived strains in the gut microbiota of mice receiving kefir, establishing that the microbiota of the administered kefir did not colonise to high levels.

Kefir induces shifts in the functional potential of the gut microbiome

We subsequently investigated if kefir administration could affect the functional potential of the microbiome in mice. Fr1 induced a significant functional separation in the microbiome in the ileum ($p = 0.052$, $R^2 = 0.099$) and the cecum ($p = 0.019$, $R^2 = 0.079$), but not in the faeces ($p = 0.108$, $R^2 = 0.068$) (**Figure 7A**). Similarly, UK4 induced a significant functional separation in the cecum ($p = 0.018$, $R^2 = 0.092$) and the faeces ($p = 0.010$, $R^2 = 0.09$), but not in the ileum ($p = 0.212$, $R^2 = 0.092$) (**Figure 7A**). No significant functional separations were identified between any other pair of groups in any other regions. The faecal metabolome was assessed using GC-MS from a subset of animals from each group (n = 6) to validate any changes observed in the predicted functional potential of the gut microbiome (**sTable 3**). Analysis of the beta diversity of the faecal metabolome revealed a predominant effect of kefir Fr1 on the measured metabolites ($p = 0.045$, $R^2 = 0.196$). Notably, no significant differences in the concentrations of any compound between any pair of groups were identified following p-value adjustment, which included short-chain fatty acid (SCFA) levels (**Figure S12**).

Figure 7. Kefir modulates the functional capacity of the gastrointestinal microbiota. Beta diversity was assessed by PERMANOVA to investigate the dissimilarity in the functional capacity of the gut microbiota, which were depicted using MDS plots Dots represent individual animals (n = 12) (A). Differential abundances were assessed of enzyme categories (EC) and depicted as violin plots (B). Gut-brain modules (GBMs) were additionally assessed for their differential abundance (C).

A total of 59 level-4 enzyme commission (EC) categories were differentially abundant between at least one pair of groups in at least one region of the gut. Notably, there were significant differences in several EC categories involved in the production of neuroactives (Figure 6B). Specifically, ileal glutamine–fructose-6-phosphate transaminase (isomerising) (EC 2.6.1.16) levels, which produces glutamate, was elevated by the administration of both Fr1 (p = 0.002) and UK4 (p = 0.021). In addition, glutamate–ammonia ligase (EC 6.3.1.2), which produces glutamine, was higher in the ileum of mice receiving Fr1 (p = 0.024). UK4 increased the prevalence of predicted cecal and faecal glutamate–cysteine ligase (EC 6.3.2.2) levels (p = 0.038; p = 0.011 respectively), while cecal tryptophan synthase (EC 4.2.1.20) was decreased (p = 0.028).

Kefir increases the prevalence of a *Lactobacillus reuteri* strain with the potential to produce GABA

Subsequently, changes in the microbiome were explored in the context of the gut-brain axis by examining the abundances of gut-brain modules (GBMs) (**Figure 7C**), which are groups of KEGG Orthogroups (KOs) that are associated with the production of neuroactive compounds (Valles-Colomer et al. 2019). In mice receiving Fr1, cecal “p-Cresol biosynthesis” was decreased, while “Quinolinic acid synthesis” was decreased in the faeces (LDA=4.43) compared to milk control. In mice receiving UK4, there was an increase in ileal "Inositol synthesis" (LDA=4.77) and "GABA degradation" (LDA=4.70). Finally, the GBM "GABA synthesis III" was significantly higher in mice receiving either kefir (Fr1: (LDA=4.39; UK4: LDA=4.21) in the faeces. These increases in "GABA synthesis III" were attributed to *L. reuteri*, which showed a significantly higher prevalence of this GBM compared to milk controls (Fr1: LDA=4.20, UK4: LDA=4.11). Similarly, the GBM "S-Adenosylmethionine synthesis" from *P. goldsteinii* was significantly higher in the faeces of mice receiving Fr1 (LDA=4.21) and UK4 (LDA=4.08). It is also interesting to note that the GBM "GABA degradation" from *L.* reuteri was significantly higher in the ileum of mice receiving UK4 (LDA=4.16). While "Glutamate synthesis I" from *B. pseudolongum* was higher in the faeces of Fr1 mice (LDA=4.64).

To corroborate the results from HUMAnN2, PanPhlAn gene-family matrices were examined to identify genes associated with the production of neurotransmitters in the detected strains. The detected *B. pseudolongum* strain encoded two enzymes involved in the production of glutamate: glutamate synthase and glutamine–fructose-6-phosphate transaminase (isomerising). Furthermore, this strain also encoded a glutamate/GABA antiporter, which may be involved in exporting glutamate from the cell. Similarly, the detected *L. reuteri* strain was also found to encode two enzymes associated with the production of glutamate from glutamine: glutaminase and glutamine–fructose-6-phosphate transaminase (isomerising). Importantly, this strain encoded glutamate decarboxylase, which produces GABA by the decarboxylation of glutamate, along with a glutamate/GABA antiporter.

In line with the predicted capacity of *L. reuteri* to produce GABA, we observed a negative correlation between *L. reuteri* and faecal levels of 2-oxoglutarate (R=-0.474, p=0.047) and glutamate (R=-0.420, p=0.083), as detected by GC-MS (**Figure 8A**). Furthermore, there was a trend towards a positive correlation between *L. reuteri* and succinate levels (R=0.60, p=0.100) (**Figure 8A**). It is therefore interesting to note that faecal succinate levels were increased in mice receiving kefir (Fr1: unadjusted p = 0.037; UK4: unadjusted p = 0.030). The pattern of correlation suggests that *L. reuteri* was potentially converting 2-oxoglutarate to glutamate, which was subsequently converted into GABA, resulting in the production of succinate as a by-product. Subsequently, we employed metabolic modelling using FVA of *L. reuteri* to explore this hypothesis in depth. The results indicated that *L. reuteri* had the ability to consume 2-oxoglutarate and glutamate, while it also could secrete GABA and succinate (**Figure 8B**).

Figure 8. The kefir-induced increased Lactobacillus reuteri strain has the potential to produce GABA. Spearman rank correlations between Lactobacillus reuteri abundances and levels of faecal 2-oxoglutarate, glutamate and succinate were performed (A). Faecal metabolite levels were quantified using chromatography–mass spectrometry (GC-MS). Flux Variability Analysis was used to assess whether L. reuteri can influence 2-oxoglutarate, glutamate and succinate levels (B).

Discussion

In the present study, we demonstrate that two different traditionally fermented kefirs differentially affect host behaviour and immunity. For instance, Kefir Fr1 increased reward-seeking behaviour and ameliorated stress-induced increases in circulating neutrophil and CXCL1 levels. Furthermore, UK4 decreased repetitive behaviour, increased circulating Treg cells and IL-10 levels, and ameliorated deficits in reward-seeking behaviour induced by chronic oral gavage stress. In addition, UK4 also impaired long-term spatial learning, yet increased fear-dependent contextual memory. Interestingly, both kefirs modulated the composition and functional capacity of the microbiota, which was associated with an increased capacity to produce GABA. This function was linked to an increased prevalence of L. reuteri.

We observed some changes in the gut microbiota that were specific to kefir Fr1, such as an increase in P. goldsteinii, B. intestinalis, Anaerotruncus unclassified and P. goldsteinii. Analysis of GBMs revealed that Fr1 decreased the GBM “p-Cresol biosynthesis” and “Inositol synthesis”, while UK4 increased “Inositol synthesis”. Interestingly, the increase in P. goldsteinii abundances were linked to an increased in the GBM "S-Adenosylmethionine synthesis". S-Adenosylmethionine supplementation has been studied in numerous randomized, controlled trials involving depressed adults (Joffe et al. 2010, Sharma et al. 2017). It is therefore interesting to note that one of the key features of depression is decreased reward-seeking behaviour (i.e. anhedonia) and that Fr1 increased reward-seeking behaviour in the saccharin preference test. As such, the increase in predicted S-Adenosylmethionine synthesis could indicate increased levels of S-Adenosylmethionine, which in turn might have contributed to the Fr1-induced increase in reward-seeking behaviour. Our results also reveal that Fr1 ameliorated stress-induced deficits in colonic serotonergic signalling, as well as increases in circulating neutrophil and CXCL1 levels. It is interesting to note that p-Cresol, of which the predicted biosynthesis was decreased by Fr1, alters neutrophil function in dogs (Bosco et al. 2016). Furthermore, Fr1 increased B. pseudolongum abundances in the ileum, whereas UK4 increased B. pseudolongum abundances in the cecum. In tandem, ileal B. pseudolongum abundances correlated with circulating neutrophil levels, indicating that B. pseudolongum abundances in the ileum specifically, might contribute to the decrease in neutrophil levels observed in mice receiving Fr1.

Some of the other changes in the composition of the microbiota were specific to UK4, such as an increased prevalence of Alistipes unclassified and decreased C. Arthromitus unclassified. In tandem, UK4 decreased repetitive behaviour, and increased reward-seeking behaviour in the female urine sniffing test, also often used as a measure of depression-related anhedonia. UK4 also impaired long-term spatial learning, yet increased fear-dependent contextual memory, indicating that not all behavioural effects induced by kefir are positive. Finally, UK4 increased circulating Treg cells and IL-10 levels. In tandem, ileal C. Arthromitus unclassified abundances correlated with circulating Treg cell levels, indicating that this bacterial species is likely contributing to the increase in Treg cell levels induced by UK4. It is also interesting to note that supplementation of L. kefiri CIDCA 8348 results in increased gene expression of IL-10 in the ileum and MLNs in mice (Carasi et al. 2015). In addition, it is interesting to note that specific bacterial species that were increased by kefir administration, such as B. pseudolongum and L. reuteri, have previously been associated with increased levels of the anti-inflammatory cytokine IL-10 in mice and Treg cells in mice and humans, respectively (Sasajima et al. 2009, Mu et al. 2018).

Analysis of the gut microbiota revealed that UK4 increased alpha diversity in the cecum, but no other changes in alpha diversity were observed in any other region or comparison. Analysis of beta diversity revealed a trend towards significant separation induced by both Fr1 and UK4, which resulted in a significant separation induced by kefir overall. Changes in the overall composition of the gut microbiota induced by kefir, or kefir-associated bacterial strains have been reported previously (Carasi et al. 2015, Kim et al. 2017, Hsu et al. 2018, Gao et al. 2019, Yilmaz et al. 2019). Interestingly, none of the bacterial strains present in the kefir microbiota was detected in the gut microbiota of mice receiving kefir, indicating that the kefir microbiota did not colonise to high levels. This has parallels with the fact that probiotics most frequently do not colonise the gut (Derrien et al. 2015). Our analysis additionally revealed that both kefirs increased the prevalence of L. reuteri, E. plexicaudatum, B. pseudolongum, while decreasing of L. bacterium 3_1_46FAA, P. acnes, and B. amyloliquefaciens. Notably, L. reuteri is a bacterial strain that has been ascribed numerous beneficial effects on host immunity and metabolism (Mobini et al. 2017, Mu et al. 2018). It is also interesting to note that previous reports have also demonstrated an increased prevalence of Lactobacillus species in response to kefir supplementation (Kim et al. 2017), as well as L. kefiri CIDCA 8348 administration, a species frequently found in kefir (Carasi et al. 2015).

Our data also reveals that both kefirs significantly modulated the functional capacity of the gut microbiota and altered the levels of GBMs, which was related to the prevalence of specific bacterial strains. Importantly, kefir-induced increases in L. reuteri levels were linked to an increased capacity to produce GABA. Indeed, Lactobacillus strains have previously been reported to produce GABA (Bienenstock et al. 2010, Barrett et al. 2012, Lin 2013). Our data additionally reveals that L. reuteri encodes enzymes and antiporters associated with GABA production. Furthermore, levels of faecal metabolites associated with GABA synthesis (i.e. 2-oxoglutarate, glutamate and succinate) correlate with L. reuteri abundances. GABA is the primary inhibitory neurotransmitter in the brain and central GABA levels have been linked to anxiety and depression (Bienenstock et al. 2010), indicating that enhancing GABA production in the gut might be associated with affect anxiety- and depressive-like behaviour. Indeed, two GABA-producing Lactobacillus strains have recently been shown to reduce depressive-like behaviour in high fat diet-induced obese mice (Patterson et al. 2019). Various Lactobacillus strains, or Lactobacillus-containing supplements, have been shown to reduce depressive-like behaviour in rodents (Bravo et al. 2011, Liang et al. 2015, Abildgaard et al. 2017, Liang et al. 2017, Dhaliwal et al. 2018) and improve measures of depression in humans (Steenbergen et al. 2015, Akkasheh et al. 2016, Bagga et al. 2018, Kazemi et al. 2019). Furthermore, abundances of faecal GABA-producers, such as Bacteroides, correlate negatively with brain signatures associated with depression (Strandwitz et al. 2019). It is therefore interesting to note that one of the key features of depression is decreased reward-seeking behaviour (i.e. anhedonia) and that both kefirs increased reward-seeking behaviour.

Conclusion

These data demonstrate that kefir can modulate the microbiota-gut-brain axis in mice, supporting the recent broadening of the definition of psychobiotics to include fermented foods, such as the fermented milk drink kefir (Sarkar et al. 2016). In addition, both kefirs differentially affected repetitive behaviour and reward-associated behaviour. In line with these findings, kefirs differentially impacted systemic immunity and colonic serotonergic signalling. Furthermore, kefir influenced specific gut microbial functional capacities, including the biosynthesis of various neuroactives such as GABA. These changes in the gut microbiota function and peripheral immunity might contribute to the kefir-induced behavioural phenotype, even though more research is warranted to validate whether these specific microbiota-gut-brain axis pathways are involved at all. Moreover, studies on the validation of kefir as a dietary intervention to improve mood in humans is now warranted.

Methodology

Animals

This study used male C57BL/6j mice (8 weeks of age on arrival; Envigo, UK; n = 12/group, n = 48 in total). Treatment groups were divided into 1) (cow's) Milk control, 2) Kefir gavage – Fr1, 3) Kefir gavage UK4, 4) Undisturbed control. The last group was added to control for the fact that chronic oral gavage or milk administration is a stressor and could affect behaviour or physiology (Walker et al. 2012). Experiments were conducted in accordance with the European Directive 86/609/EEC and the Recommendation 2007/526/65/EC and approved by the Animal Experimentation Ethics Committee of University College Cork. All efforts were made to reduce the number of animals used and to minimise the suffering of these animals. See the supplementary methods for more information.

Experimental timeline and behavioural testing

Animals were habituated for one week prior to the onset of daily kefir administration by oral gavage. After three weeks of treatment, animals were assessed for various their behavioural phenotype using various tests, which were formed in order of least stressful to most stressful to reduce the likelihood of prior behavioural tests influencing subsequent ones (**Figure S1**). In addition, there was a minimum of 36-hours between tests. The behavioural assessment consisted of a battery of tests investigating sociability, anxiety- and depressive-like behaviours, stress-responsiveness and cognition. The order of testing was as follows: 1) Marble burying test, 2) 3-Chamber social interaction test, 3) Elevated plus maze, 4) Open field test, 5) Tail-suspension test, 6) Saccharin preference test, 7) Female urine sniffing test, 8) Stress-induced hyperthermia test, 9) Intestinal motility test, 10)

Assessment of faecal water content and weight, 11) Appetitive Y-maze, 12) Fear conditioning, 13) Forced swim test. At the end of the study, body composition (i.e., percentage lean, fat and fluid mass) was assessed (Minispec mq 7.5), after which animals were immediately sacrificed by decapitation.

Kefir culturing and administration

Kefir grains were cultured in whole full fat cow's milk (2% w/v) at 25 °C and milk were renewed every 24 hours using a sterile Buchner funnel and sterile Duran bottle, as previously described (Dobson et al. 2011, Walsh et al. 2016).

Marble burying test

Mice were tested for repetitive and anxiety-like behaviour with the marble burying test, which was conducted as previously described (Burokas et al. 2017). See the supplementary methods for more information.

3-Chamber social interaction test

The three-chamber sociability test was used to assess social preference and recognition and was conducted as previously described (Desbonnet et al. 2014). See the supplementary methods for more information.

Elevated plus maze

The elevated plus maze test was used to assess anxiety-like behaviour and was conducted as previously described (Burokas et al. 2017). See the supplementary methods for more information.

Open field test

Mice were assessed for locomotor activity and response to a novel environment in the open field test, which was conducted as previously described (Burokas et al. 2017). See the supplementary methods for more information.

Tail-suspension test

The tail-suspension test was used to assess depressive-like behaviour and was conducted as previously described (Burokas et al. 2017). See the supplementary methods for more information.

Saccharin preference test

Mice were assessed for reward-seeking behaviour using the saccharin preference test as previously conducted (O'Leary et al. 2014). See the supplementary methods for more information.

Female urine sniffing test

Mice were assessed for hedonic and reward-seeking behaviour in the female urine sniffing test, which was performed as previously described (Finger et al. 2011). See the supplementary methods for more information.

Stress-induced hyperthermia test

The stress-induced hyperthermia test was used to assess stress-responsiveness, which was conducted as previously described (Burokas et al. 2017). See the supplementary methods for more information.

Intestinal motility assay

Gastrointestinal motility was assessed as previously described (Golubeva et al. 2017). See the supplementary methods for more information.

Assessment of faecal water content and weight

Mice were single-housed for one hour during which faecal pellets were collected (± 9 per animal). Pellets were subsequently weighed, dried at 50 °C for 24 hours and weighed again. The average weight per pellet and percentage of faecal water content was calculated.

Appetitive Y-maze

The appetitive Y-maze was used to assess long-term spatial learning and was performed as previously described (Finger et al. 2010). The test consisted of two phases; the initial learning phase, where the first association between the location of the food reward and spatial reference cues were formed, and the reversal learning phase, where the location of the food reward was altered in reference to the spatial reference cues, in which the relearning of a context was measured. See the supplementary methods and (**Figure S2**) and for more information.

Fear conditioning

Fear conditioning was used to assess amygdala-dependent learning memory and was conducted as previously described (Izquierdo et al. 2006). The test consisted of 3 days/phases; 1) Training, 2) Assessment of cued memory, 3) Assessment of contextual memory, each of which was carried on successive days with a 24-hour interval. See the supplementary methods for more information

Forced swim test

The forced swim test was used to assess depressive-like behaviour and was conducted as previously described (Cryan et al. 2004). See the supplementary methods for more information.

Repeated plasma sampling for corticosterone quantification

Plasma from each animal was sampled by tail-tip five minutes before the forced swim test, and repeatedly after the test in 30-min intervals up to 120 minutes. Plasma was collected and stored at −80 °C for later corticosterone quantification. See the supplementary methods for more information.

Tissue collection

Collection of faecal samples for metabolomics was done one week prior to euthanasia. Animals were sacrificed by decapitation in a random fashion regarding test groups between 9.00 a.m. and 2.00 p.m. Trunk blood was collected in 3 mL EDTA-containing tubes (Greiner bio-one, 454086) and 100 µl was put in a separate Eppendorf for flow cytometry. Both tubes were centrifuged for 10 min at 3,500 g at 4°C, after which plasma was collected and stored at −80 °C for cytokine quantification. The remaining cell pellet of the Eppendorf containing 100 µl blood was stored on ice and subsequently used for flow cytometry. Mesenteric lymph nodes (MLNs) were extracted and stored in RPMI-1640 medium with L-glutamine and sodium bicarbonate (R8758, Sigma), supplemented with 10% FBS (F7524l, Sigma) and 1% Pen/strep (P4333, Sigma) on ice for flow cytometry. The faecal pellets, cecum, and contents of the distal part of the ileum (2 cm) were collected, snap-frozen on dry ice and stored at −80 °C for shotgun sequencing. See the supplementary methods for more information.

Flow cytometry

Blood and MLNs collected when animals were sacrificed were processed on the same day for flow cytometry, as previously described (Boehme et al. 2019, van de Wouw et al. 2019). See the supplementary methods and (**Figure S3**) for more information.

Plasma corticosterone and cytokine assessment

Corticosterone quantification of plasma samples (20 µl) obtained in the forced swim test was performed using a corticosterone ELISA (Enzo Life Sciences, ADI-901-097). Plasma cytokine quantifications were performed using the Proinflammatory panel 1 (mouse) kit (MSD, K15048G). See the supplementary methods for more information.

High-performance liquid chromatography

5-hydroxytryptamine (5-HT) and 5-hydroxyindoleacetic acid (5-HIAA) concentrations were determined using HPLC based on a methodology previously described (Clarke et al. 2013). See the supplementary methods for more information.

DNA extractions and sequencing

For analysis of the kefir microbiome, DNA was extracted from the fermented milk using the PowerSoil DNA Isolation Kit, as described previously (Walsh et al. 2016). For analysis of the murine gut microbiome, DNA was extracted from the total ileal contents, cecal contents and faecal pellets using the QIAamp PowerFaecal DNA Kit. Whole-metagenome shotgun libraries were prepared using the Nextera XT kit in accordance with the Nextera XT DNA Library Preparation Guide from Illumina, with the exception that tagmentation time was increased to 7 minutes. Kefir libraries were sequenced on the Illumina MiSeq sequencing platform with a 2 x 300 cycle v3 kit. Gut libraries were sequenced on the Illumina NextSeq 500 with a NextSeq 500/550 High Output Reagent Kit v2 (300 cycles). All sequencing was performed at the Teagasc sequencing facility in accordance with standard Illumina protocols.

Faecal metabolomics

The faecal metabolome was analysed by chromatography–mass spectrometry (GC-MS) by MS-Omics, Copenhagen. Samples were derivatized using methyl chloroformate. For SCFA quantification, samples were acidified with hydrochloric acid.

Bioinformatics

Murine reads were removed from the raw sequencing files using the NCBI Best Match Tagger (BMTagger) (ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/), and fastq files were converted to unaligned bam files using SAMtools (Li et al. 2009). Duplicate reads were subsequently removed using Picard Tools (https://github.com/broadinstitute/picard). Next, low-quality reads were removed using the trimBWAstyle.usingBam.pl script from the Bioinformatics Core at UC Davis Genome Center (https://github.com/genome/genome/blob/master/lib/perl/Genome/Site/TGI/Hmp/HmpSraProcess/trimBWAstyle.usingBam.pl). Specifically, MiSeq reads were filtered to 200 bp, while NextSeq were filtered to 105 bp. All reads with a quality score less than Q30 were discarded. The resulting fastq files were then converted to fasta files using the fq2fa option from IDBA-UD (Peng et al. 2012).

Compositional analysis was performed using MetaPhlAn2 (Truong et al. 2015). Strain-level metagenomic analysis was performed using StrainPhlAn (Truong et al. 2017) and PanPhlAn (Scholz et al. 2016) StrainPhlAn outputs were visualised using GraPhlAn (Asnicar et al. 2015). Custom PanPhlAn databases were constructed from complete genome assemblies which were annotated using Prokka (Seemann 2014). See **Table S1** for the list of reference genomes used in this study. Functional analysis was performed with HUMAnN2 (Abubucker et al. 2012), using the –bypass-translated-search option, and PanPhlAn. HUMAnN2 gene families were mapped to level-4 enzyme commission (EC) categories using HUMAnN2 utility mapping files. Sequence data have been deposited in the European Nucleotide Archive (ENA). Correlations between gut microbial species and significantly altered behavioural and immunological parameters were investigated using HAllA (https://bitbucket.org/biobakery/halla/wiki/Home).

Analysis of gut-brain modules (GBMs) was performed as previously described (Valles-Colomer et al. 2019). Briefly, the UniRef gene families that were detected by HUMAnN2 were mapped to KEGG Orthogroups (KOs) using the humann2_regroup_table function, and the abundances of KOs were normalised using the humann2_renorm_table function. Next, these KOs were further mapped to GBMs using Omixer-RPM.

Metagenome co-assembly was performed using MEGAHIT (Li et al. 2015). MetaBAT 2 (Kang et al. 2015) was used to recover genomes from the metagenome. CheckM (Parks et al. 2015) was used to assess the quality of the MAGs. The *Lactobacillus reuteri* genome was identified using PhyloPhlAn (Segata et al. 2013). Prokka was used to annotate the genome and CarveMe (Machado et al. 2018) was used to construct a metabolic model. COBRApy (Ebrahim et al. 2013) was used to perform flux variability analysis (FVA), with an objective of 95% biomass, of this model.

Raw microbiota reads have been deposited to the European Nucleotide Archive under the project accession number PRJEB35751.

Statistical analysis

All behavioural and physiological data were assessed for normality using the Shapiro-Wilk test and Levene's test for equality of variances. The effect of kefir was determined by a one-way ANOVA, followed by Dunnett's post hoc test whenever data were normally distributed. If data were non-parametrically distributed, then a Kruskal-Wallis test followed by a Mann-Whitney U test was used. Undisturbed control and milk control datasets were assessed for statistical significance using an unpaired Student's t-test or a Mann-Whitney U test to investigate the impact of milk gavage. Bodyweight, fear conditioning and appetitive Y-maze data were assessed using repeated-measures ANOVA, followed by a Dunnett's post hoc test. The presence of social preference and recognition in the 3-chamber sociability test was assessed using a paired Student's t-test. Parametric data are depicted as bar graphs with points as individual data points and expressed as mean ± SEM. Non-parametric data is depicted as a box with whiskers plot. Statistical analysis was performed using SPSS software version 24 (IBM Corp). A p-value < 0.05 was deemed significant

Statistical analysis for bioinformatics data was performed using the R package vegan for alpha diversity analysis and principal component analysis (Oksanen et al. 2007). The Wilcoxon rank-sum test was used to measure statistical differences in alpha diversity between groups. The adonis function from vegan was used for PERMANOVA. The linear discriminant analysis (LDA) effect size (LEfSe) method (Segata et al. 2011) was used to investigate if any taxa or HUMAnN2 pathways were differentially abundant between groups. Data were visualised using hclust2 (https://bitbucket.org/nsegata/hclust2), GraPhlAn, and the R package ggplot2 (Wickham 2016).

Abbreviations

Treg: T regulatory cell

MLN: Mesenteric lymph node

pTreg: Peripheral-derived T regulatory cells

5-HT: Serotonin

5HIAA: 5-hydroxyindoleacetic acid

SCFA: Short-chain fatty acid

GC-MS: Chromatography–mass spectrometry

EC: Enzyme commission

GBM: Gut-brain modules

KO: KEGG Orthogroup

GABA: Gamma aminobutyric acid

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and materials

Raw microbiota reads have been deposited to the European Nucleotide Archive under the project accession number PRJEB35751.

Competing Interests

J.F.C and T.G.D have research support from Mead Johnson, Cremo, 4D Pharma, Dupont, and Nutricia. P.D.C has research support from PepsiCo and Danone. J.F.C, T.G.D and P.D.C. have spoken at meetings sponsored by food and pharmaceutical companies. All other authors report no potential conflicts of interest.

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Author Contributions

M.vd.W. performed the *in vivo* study, behavioural analysis, flow cytometry and ELISAs. A.M.W. performed DNA extractions, sequencing and bioinformatics. F.C. assisted with bioinformatics. L.v.L. assisted with the *in vivo* study and the behavioural analysis. J.M.L performed the HPLC analysis. M.B. assisted with flow cytometry. G.C., T.G.D., P.D.C, and J.F.C contributed to the experimental design and drafting and critical revision of the manuscript.

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Figures

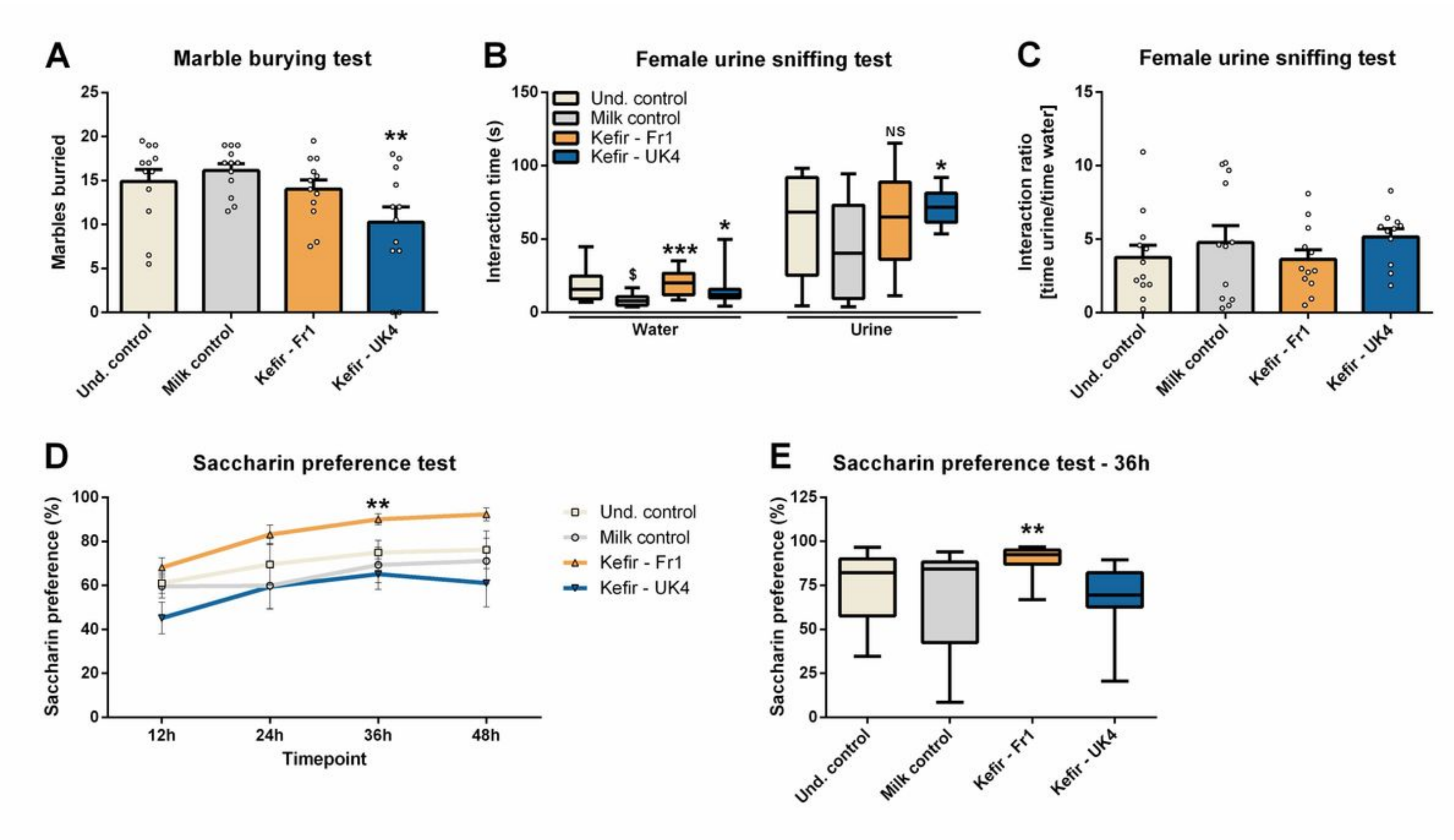

Figure 1

Kefir modulates repetitive behaviour and reward-seeking behaviour. Repetitive/anxiety-like behaviour was assessed using the marble burying test (A). Anhedonia and reward-seeking behaviours were investigated using the female urine sniffing test (B, C) and saccharin preference test (D, E). The marble burying test was normally distributed and analysed using a one-way ANOVA, followed by a Dunnett's post hoc test. The female urine sniffing test and saccharin preference test were non-normally distributed and analysed using the Kruskal-Wallis test, followed by the Mann-Whitney test. Significant differences are depicted as: *p < 0.05, **p < 0.01 and ***p < 0.001; Milk control compared to Kefir supplementation, $p < 0.05; Undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 11-12). Dots on each graph represent individual animals.

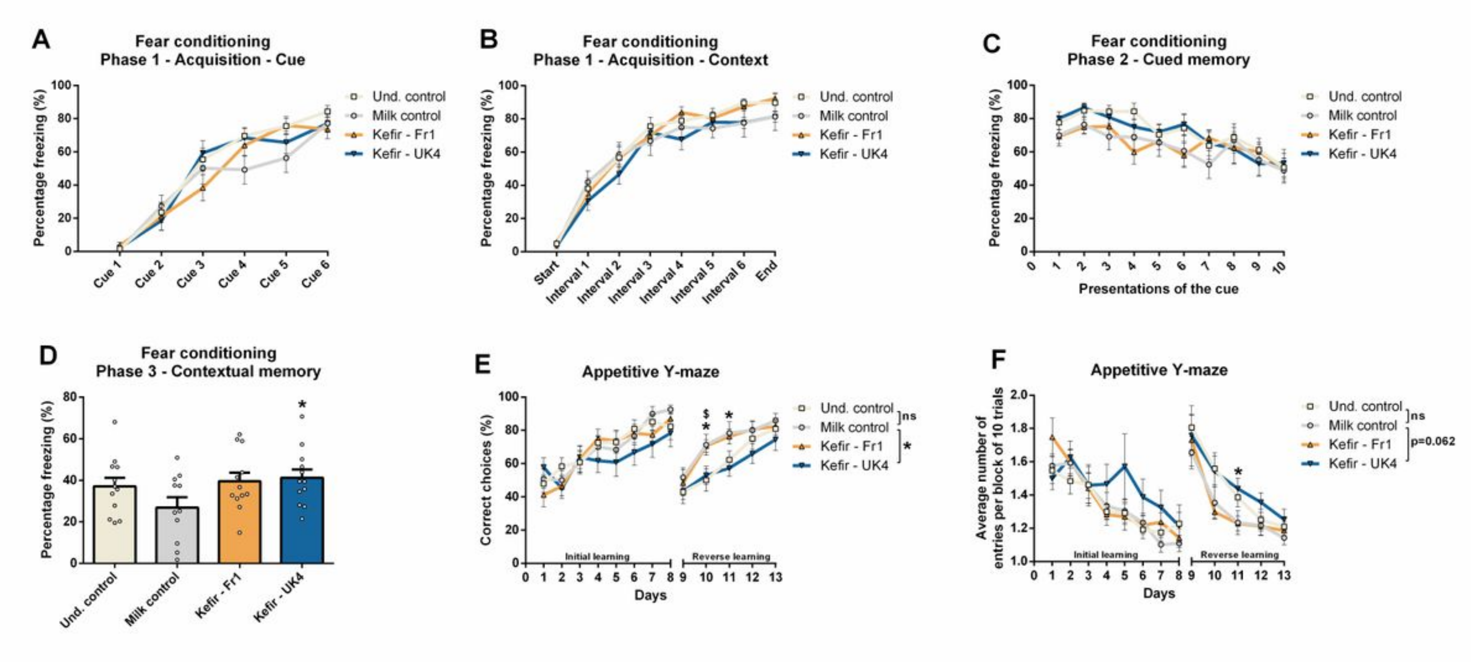

Figure 2

UK4 enhances fear-dependent contextual memory yet decreases long-term spatial learning. Fear-dependent memory and learning were assessed using fear conditioning. At phase 1 – Acquisition, mice were presented with a tone, followed by a foot shock. Cue-associative learning was assessed by measuring freezing behaviour during the presentation of the tone (A), whereas context-associative learning was determined in-between tones (B). At phase 2 – Cued memory, mice received 40 presentations of the same cue (the first 10 are shown), without foot shock, in a different context, in which fear-dependent cued memory was assessed (C). At phase 3 – Contextual memory, mice were exposed to the same context as day one for 5 minutes and contextual memory was assessed (D). Long-term spatial learning was assessed in the appetitive Y-maze, as determined by the percentage of times the mice made the correct choice as the first choice for reaching the goal (food reward) (E), as well as the number of average entries it took the mice to reach the goal (F). All data were normally distributed and analysed using a repeated measures ANOVA or one-way ANOVA, followed by a Dunnett's post hoc test. Significant differences are depicted as: *p < 0.05; Milk control compared to Kefir supplementation, $p < 0.05; undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 10-12). Dots on each graph represent individual animals.

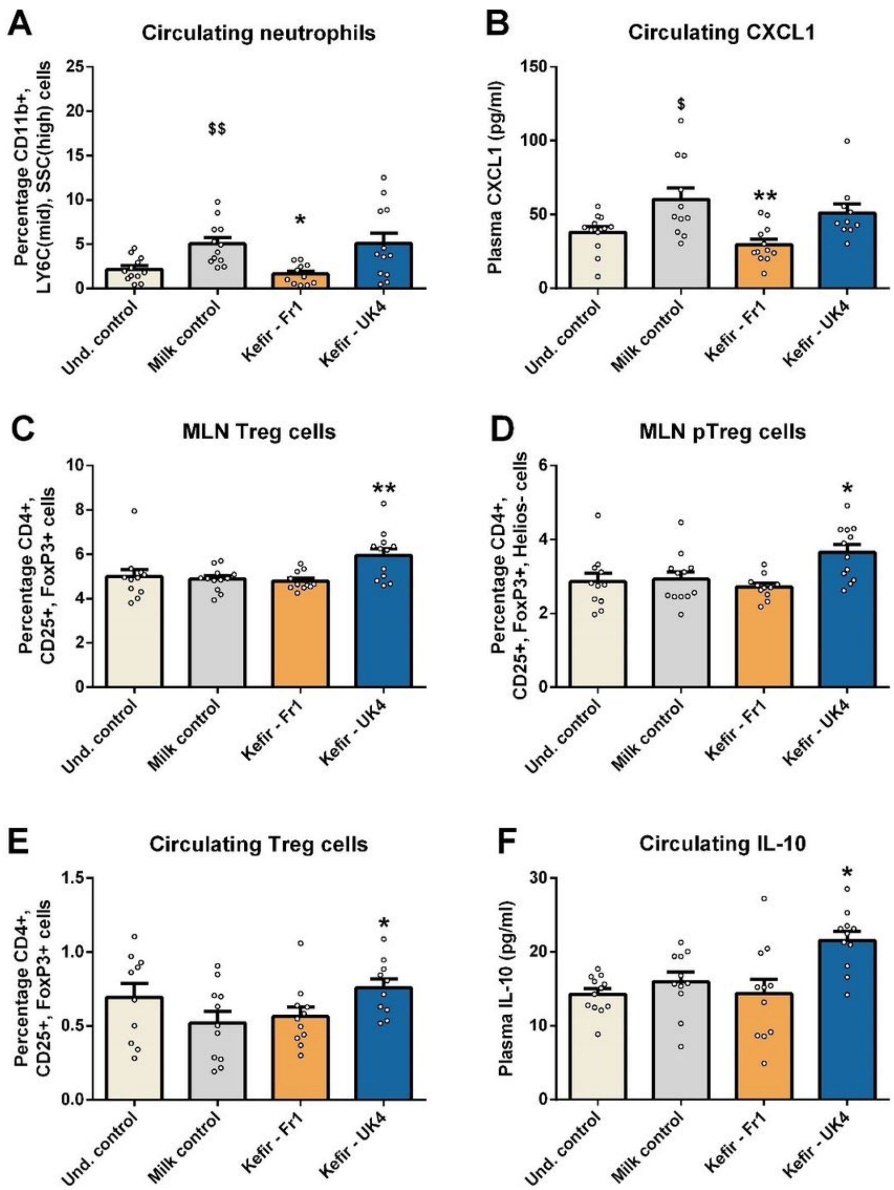

Figure 3

UK4 increases Treg cells levels, while Fr1 decreases neutrophil levels. T regulatory cells (CD4+, CD25+, FoxP3+) were assessed in mesenteric lymph nodes (MLNs) (A) and were subsequently analysed for Helios expression (B), to investigate their origin as Helios+ cells exclusively originate in the thymus. Blood was also assessed for Treg cell levels (C), and plasma interleukin 10 (IL-10) levels (D). Similarly, neutrophils (CD11b+, LY6Cmid, SSChigh and CXCL1 levels were also investigated in peripheral blood (E, F). All data were normally distributed and analysed using a one-way ANOVA, followed by a Dunnett's post hoc test. Significant differences are depicted as: *$p < 0.05$, **$p < 0.01$; Milk control compared to Kefir supplementation, \$$p < 0.05$ and \$\$$p < 0.01$; Undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 11-12). Dots on each graph represent individual animals.

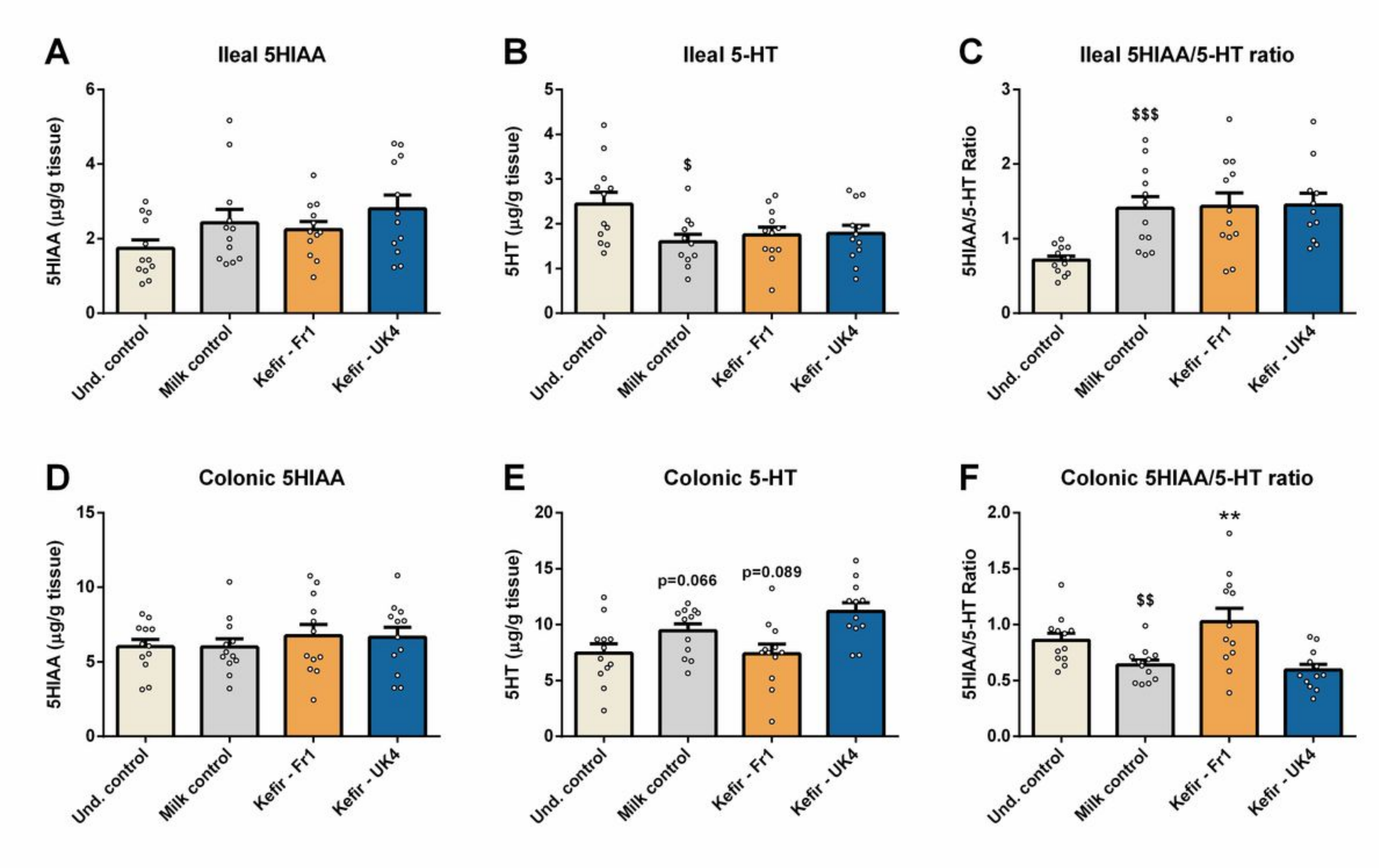

Figure 4

Fr1 modulates serotonergic signaling in the colon, but not ileum. Ileal (A-C) and colonic (D-F) tissues were quantified for 5HIAA and serotonin (5-HT) levels using HPLC. The 5HIAA/5-HT ratio was subsequently calculated. All data was normally distributed and analysed using a one-way ANOVA, followed by a Dunnett's post hoc test. Significant differences are depicted as: **p < 0.01; Milk control compared to Kefir supplementation, $p < 0.05,

$$p < 0.01 and$$

$p < 0.001; Undisturbed control compared to Milk control. All data are expressed as mean ± SEM (n = 11-12). Dots on each graph represent individual animals.

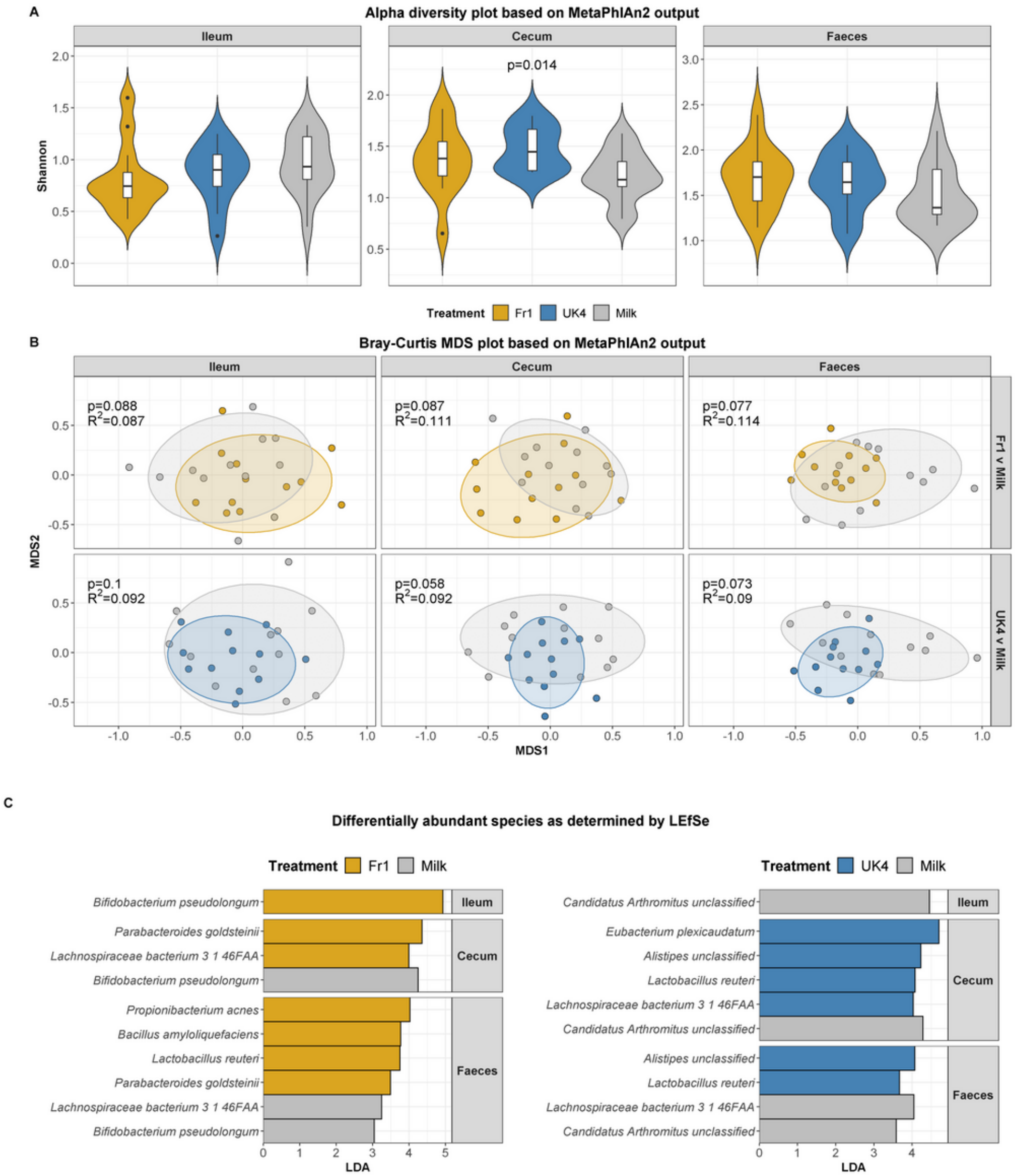

Figure 5

Kefir modulates the composition of the gastrointestinal microbiota. Alpha diversity (Shannon) of the ileal, cecal and faecal microbiota was compared between mice receiving kefir (Fr1 or UK4) and mice receiving milk control using violin plots (A). Beta diversity was assessed by PERMANOVA to investigate the dissimilarity in the gut microbial composition, which were depicted using MDS plots. Dots represent individual animals (n = 12) (B). Differentially abundant taxa were determined using LEfSe (C).

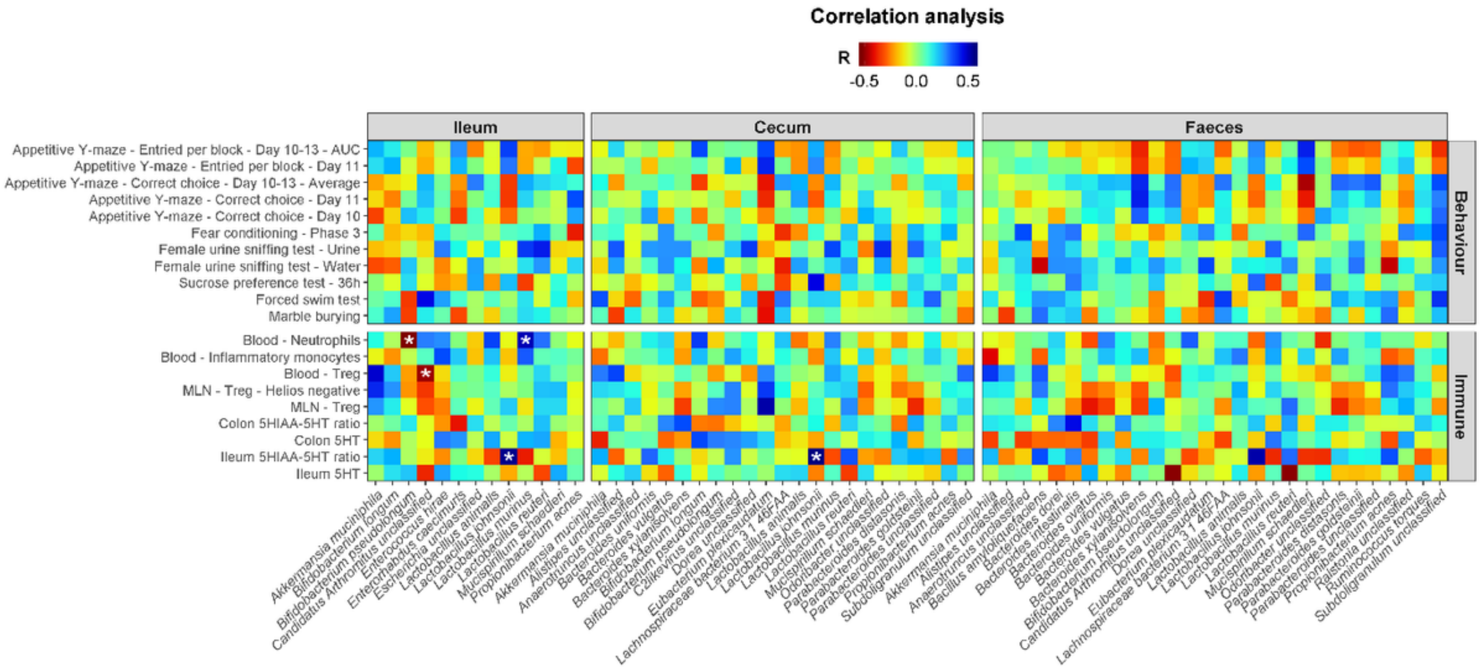

Figure 6

Bacterial species in the gastrointestinal microbiota correlate with changes in host immunity and measures of gut serotonin. The prevalence of bacterial species in the ileum, cecum and faeces were correlated with significantly altered changes in host behaviour and immunity using HAllA.

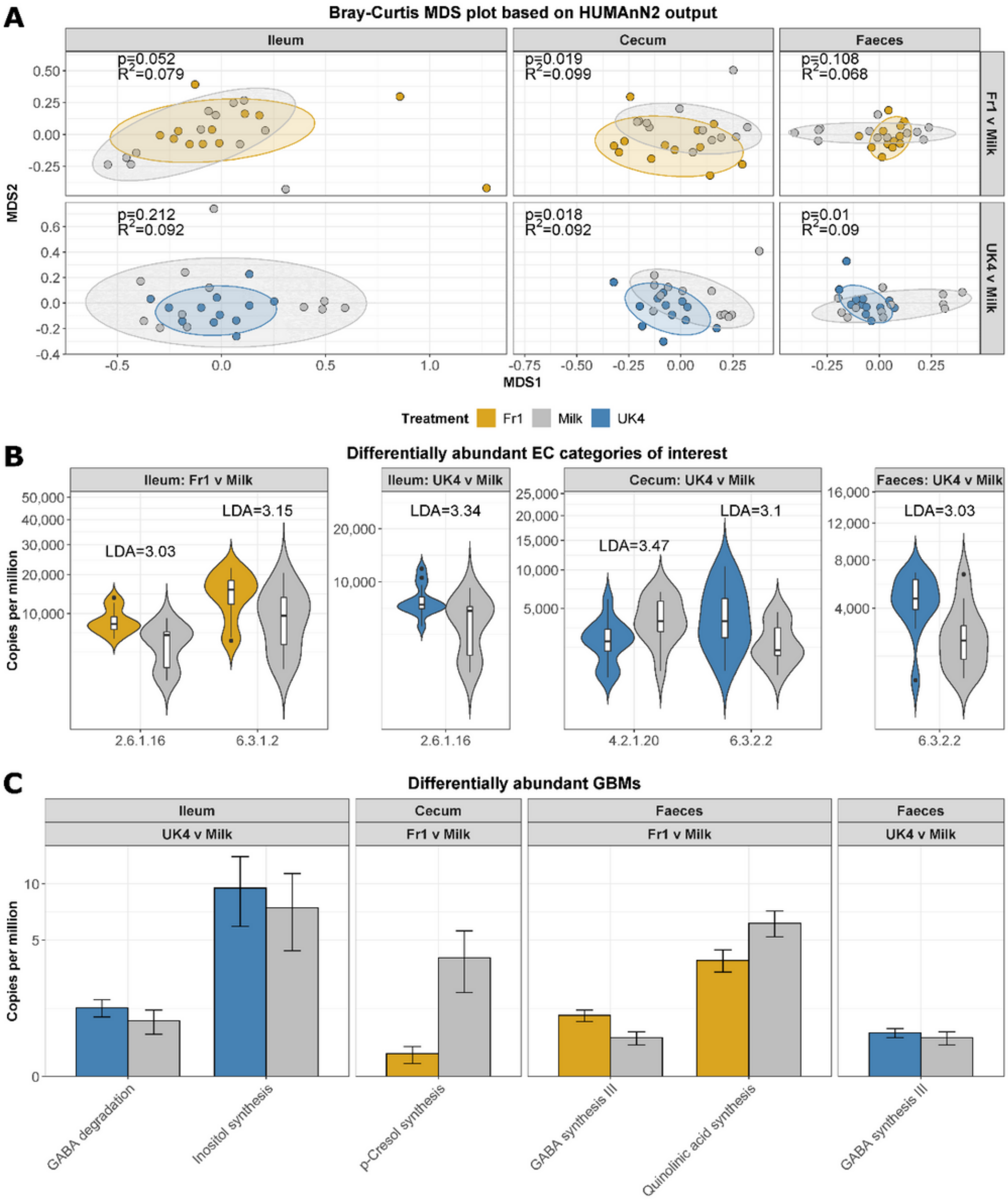

Figure 7

Kefir modulates the functional capacity of the gastrointestinal microbiota. Beta diversity was assessed by PERMANOVA to investigate the dissimilarity in the functional capacity of the gut microbiota, which were depicted using MDS plots Dots represent individual animals (n = 12) (A). Differential abundances were assessed of enzyme categories (EC) and depicted as violin plots (B). Gut-brain modules (GBMs) were additionally assessed for their differential abundance (C).

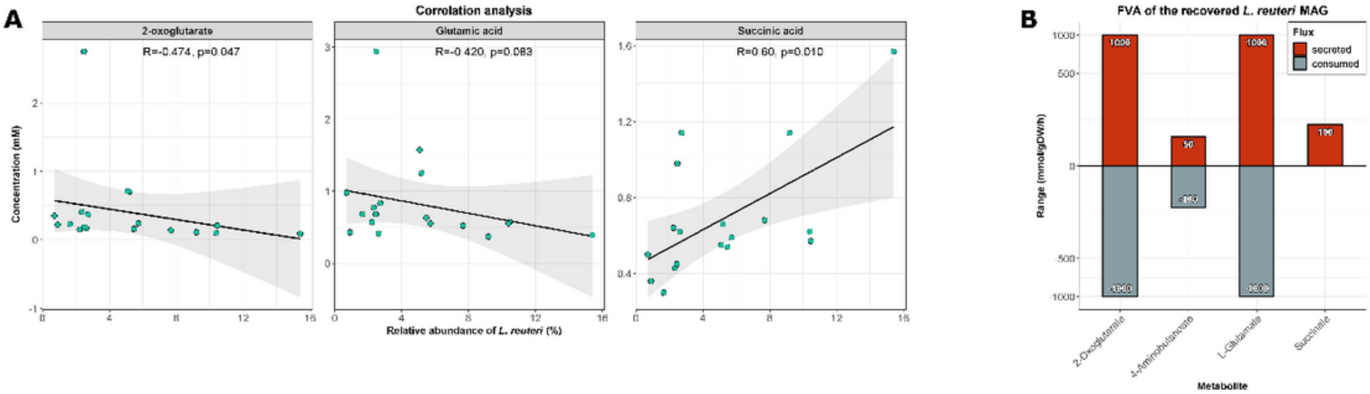

Figure 8

The kefir-induced increased Lactobacillus reuteri strain has the potential to produce GABA. Spearman rank correlations between Lactobacillus reuteri abundances and levels of faecal 2-oxoglutarate, glutamate and succinate were performed (A). Faecal metabolite levels were quantified using chromatography–mass spectrometry (GC-MS). Flux Variability Analysis was used to assess whether L. reuteri can influence 2-oxoglutarate, glutamate and succinate levels (B).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementsKefirMvdW.docx