Related mobile pathogenicity chromosomes in Fusarium oxysporum determine host range on cucurbits

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INTRODUCTION

Fusarium oxysporum (Fo) is a soilborne fungus and is very common worldwide (Di Pietro et al., 2003). Most Fo strains are not pathogenic and some are known to be beneficial to plants (Di Pietro et al., 2003; Bubici et al., 2019). However, as a species complex, Fo can cause severe disease on more than 100 plant species, including some economically important crops such as chickpea, tomato, banana, and cucurbits (Michielse and Rep, 2009). Individual strains of Fo can only infect one or a few related plant species (Kistler, 1997). Based on this...
host specificity, pathogenic Fo strains are classified into different forms \( \text{f} \). \( \text{sp} \). For example, Fo \( \text{f} \). \( \text{sp} \). \( \text{radicis-cucumerinum} \) (Forc) causes disease on the cucurbit species cucumber, melon, and watermelon, while Fo \( \text{f} \). \( \text{sp} \). \( \text{melonis} \) (Fom) can only cause disease on melon. The genetic basis underlying the difference in host range between Fom and Forc is still unknown.

To cause disease Fo first penetrates the root epidermis and then grows intercellularly or intracellularly in the root cortex. Eventually the fungus reaches the xylem vessels of the roots and then spreads to the main root and stem in susceptible plants (Michielse and Rep, 2009). In resistant plants, however, the fungus is mostly restricted to epidermal cells and the cortex (Upasani et al., 2016). Colonization patterns of compatible or incompatible interactions between Fo and its host plants has been investigated in several \( \text{f} \). \( \text{sp} \), including \( \text{f} \). \( \text{sp} \). \( \text{melonis} \) (Zvirin et al., 2010), \( \text{f} \). \( \text{sp} \). \( \text{ciceris} \) (Jimenez-Fernandez et al., 2013; Upasani et al., 2016), \( \text{f} \). \( \text{sp} \). \( \text{conglutinans} \) (Li et al., 2014), \( \text{f} \). \( \text{sp} \). \( \text{radicis-cucumerinum} \) (Cohen et al., 2015), \( \text{f} \). \( \text{sp} \). \( \text{phaseoli} \) (Niño-Sánchez et al., 2015; Garces-Fiallos et al., 2017), \( \text{f} \). \( \text{sp} \). \( \text{niveum} \) (Zhang et al., 2015), and \( \text{f} \). \( \text{sp} \). \( \text{psi} \) (Bani et al., 2018). However, to our knowledge, colonization differences between host and nonhost plants by Fo have not been studied so far.

To colonize plants, pathogens secrete a variety of molecules, including cell wall-degrading enzymes, secondary metabolites, and small proteins called effectors (Perez-Nadales et al., 2014). Effectors have been shown to contribute to the virulence of xylem-colonizing fungal pathogens including Fo (de Sain and Rep, 2015), Verticillium (de Jonge et al., 2012, 2013), Ceratocystis, and Ophiostoma (de Sain and Rep, 2015). For example, in Fo \( \text{f} \). \( \text{sp} \). \( \text{lycopersici} \) (Fol), \( \text{Six} \) (Secreted in xylem) \( \text{1} \) (Rep et al., 2004), \( \text{Six} \) \( \text{3} \) (Houterman et al., 2009), and \( \text{Six} \) \( \text{5} \) (Ma et al., 2015) have been shown to contribute to virulence. Some effectors also act as avirulence factors that can be recognized by host immune receptors (Rep et al., 2004; Houterman et al., 2008; 2009; de Jonge et al., 2012).

In filamentous plant pathogens, virulence genes are commonly located in distinct genomic regions (Croll and McDonald, 2012). These chromosomal regions or chromosomes are often rich in transposable elements (TEs) and undergo relatively fast evolution compared to the rest of the genome (Croll and McDonald, 2012). For example, in Fol all identified \( \text{Six} \) genes are located on one “pathogenicity” chromosome, which is essential for infection (Ma et al., 2010). TEs occupy at least 24% of this chromosome – twice as much as non-TE genes (Schmidt et al., 2013). In Forc, some \( \text{Six} \) homologs are present in a region of a horizontally transferrable pathogenicity chromosome that is exceptionally TE-rich (van Dam et al., 2017).

In several fungal plant pathogens, virulence genes or entire chromosomes can undergo horizontal transfer and thereby confer host-specific pathogenicity (Friesen et al., 2006; Akagi et al., 2009; Ma et al., 2010; Mehrabi et al., 2011). In Fo, mobile pathogenicity chromosomes have been identified for tomato-infecting and cucurbit-infecting strains (Ma et al., 2010; Vlaardingerbroek et al., 2016a; van Dam et al., 2017). In cucurbit-infecting Forc strains, the pathogenicity chromosome chr\( \text{RC} \) that determines root and shoot rot was identified recently and shown to be largely syntenic with a contig in the genome assembly of melon-infecting strain Fom001 (van Dam et al., 2017). We hypothesized that this contig in Fom001 determines virulence towards melon plants, and differences between chr\( \text{RC} \) and this contig determine differences in host range between Forc and Fom. Furthermore, we hypothesized that if this contig determines virulence towards melon, it is also present in Fom strains other than Fom001, hence we included Fom005 (vegetative compatibility group [VCG] 0134), which does not belong to the same clonal line as Fom001 (VCG 0136) (Schmidt et al., 2016; van Dam et al., 2017).

In this study, we set out to (a) investigate colonization of different cucurbit species by green fluorescent protein (GFP)-labelled Forc and GFP-labelled Fom strains, (b) identify pathogenicity chromosomes in two Fom strains, and (c) identify genomic regions or chromosomes that contribute to differences in host range between Fom and Forc.

2 | RESULTS

2.1 | Forc and Fom can colonize xylem vessels of cucumber, melon, and watermelon roots

Forc causes disease on multiple cucurbit plant species, while Fom only causes disease on melon plants (van Dam et al., 2016). We hypothesized that Forc strains fully colonize cucumber and watermelon plants, while colonization by Fom strains is restricted in cucumber and watermelon roots. Fungal biomass in cucumber and melon roots 1 week after inoculation with Forc016, Fom001 or Fom005 was quantified by quantitative PCR (qPCR). The phenotypes of respective cucumber and melon plants are shown in Figure S1. The identical single-copy gene \( \text{Six6} \) in Forc and Forc was selected to quantify fungal biomass, while the \( \alpha \)-tubulin gene of cucumber or melon was used for normalization to plant DNA. As expected, in the infected cucumber roots the biomass of Fom001 and Fom005 was about 20 times less than the biomass of Forc016 (Figure 1a). In the infected melon roots, no significant fungal biomass differences were observed between these three strains (Figure 1b). The biomass differences between Fom001 and Fom005 were very small (Figure 1), therefore only Fom005 and Forc016 were used in the remaining experiments described in this section.

To further assess potential differences in colonization of cucumber, melon, and watermelon roots by Forc and Fom, Forc016 and Fom005 transformants carrying GFP under a constitutive promoter (FEM1 promoter), which showed wild-type virulence on cucumber and melon, were selected to inoculate cucumber, melon, and watermelon seedlings on Petri dishes. Colonization of infected cucumber and melon roots was then observed microscopically at 6 days post-inoculation (dpi) and at 16 dpi. Both Forc016_GFP and Fom005_GFP reached xylem vessels of cucumber and melon roots at 6 dpi. However, further growth of Fom005_GFP hyphae into the hypocotyl of cucumber was not observed, and these plants still appeared healthy (data not shown).
To investigate colonization differences before 6 dpi in more detail, infected roots of cucumber, melon, and watermelon plants were observed microscopically at 1, 2, 3, 4, and 14 dpi using the same methods mentioned above. At 1 dpi both Forc016_GFP and Fom005_GFP spores had germinated and some hyphae were present intercellularly between epidermal cells of all infected plants, while the plants appeared to be healthy. At 2 dpi hyphae were present extensively in the root cortex of all infected plants. At this stage, while no colonization of the xylem was observed, root browning in all infected plants was apparent. During 3–4 dpi (Figure 2), xylem colonization for all infected roots was observed and all roots were dark brown. Disease progress was followed until 14 dpi, at which time Forc016_GFP-infected cucumber, melon, and watermelon plants all showed severe wilting, and root and stem rot (Figure S2).

FIGURE 1 Fom001 and Fom005 are restricted in cucumber roots. Fungal biomass of Fom001, Fom005, and Forc016 in cucumber and melon roots was quantified using quantitative PCR 1 week after infection. The single-copy gene SIX6 in Fusarium oxysporum f. sp. melonis (Fom) and F. oxysporum f. sp. radicis-cucumerinum (Forc) was used to quantify fungal DNA, while the α-tubulin gene of cucumber or melon was used for normalization to plant DNA. Five biological replicates and three technical replicates were used for each treatment. RQ, relative quantification of fungal biomass; the lowest sample was given a value of 1 and the rest were calculated relative to that value. The asterisks (***) indicate significantly less fungal biomass when compared with the biomass of Forc016 (one-way analysis of variance test, p < .0001). (a) In cucumber roots, the fungal biomass of Fom001 and Fom005 was about 20 times less than the biomass of Forc016. (b) In melon roots, no significant biomass differences were observed between these three strains.

FIGURE 2 Forc016 and Fom005 can colonize xylem vessels of cucumber, melon, and watermelon at 3–4 days post-inoculation (dpi). Six-day-old cucumber and 10-day-old melon and watermelon seedlings were treated with water (not shown), Forc016_GFP (10^7 spores/ml), and Fom005_GFP (10^7 spores/ml) in Petri dishes. At 3–4 dpi, xylem colonization of all plants by both Forc016_GFP and Fom005_GFP was observed. The white arrows indicate hyphae growing inside xylem vessels. The white bars are 200 μm in length.
Fom005\_GFP still appeared healthy with light brown roots (Figure S2). To assess whether Fom005\_GFP colonized the upper part of healthy-appearing cucumber and watermelon plants at 14 dpi, the presence of Fom005\_GFP hyphae at the hypocotyl level was assessed. No hyphae or spores were found at the hypocotyl level for both cucumber (Figure S3) and watermelon plants (data not shown).

Interestingly, at 3–4 dpi, we observed that cucumber roots started to produce new roots. This was not the case for melon and watermelon. At 14 dpi, Fom005\_GFP-infected cucumber plants still appeared healthy with a large number of newly produced, thick lateral roots (Figure S2), while Forc016\_GFP-infected cucumber plants had fewer and shorter newly produced lateral roots (Figure S2). In addition, Forc016\_GFP-infected cucumber showed severe root rot within 2 weeks. Fom005\_GFP-infected watermelon plants showed stress symptoms (leaves turning from shiny to dull) during 3–4 dpi but they were fully recovered at 14 dpi; production of new roots was not observed. In addition, watermelon had fewer roots than cucumber and melon, but watermelon roots were much thicker than cucumber and melon roots.

To conclude, like Forc, melon-infecting strains can enter the root xylem of cucumber and watermelon plants without reaching the stem in the hydroponic infection system employed.

2.2 Part of the genome of Fom001 and Fom005 is syntenic with the pathogenicity chromosome in Forc

Previously, a mobile pathogenicity chromosome, called chrRC, was identified in Forc016 (van Dam et al., 2017). Comparisons of chrRC to a high-quality assembly of Fom001 revealed that the genome of Fom001 contains two contigs, contig 127 and contig 13, that are largely syntenic with chrRC (van Dam et al., 2017) (Figure 3a). These two contigs have an overlap of around 10 kb but with some single nucleotide polymorphisms in the overlap region. If these two contigs constitute a pathogenicity chromosome in Fom (chrMLN), syntenic contigs were expected to be present in a genome assembly of Fom005. The genome of Fom005 was sequenced with single molecule real-time (SMRT) sequencing to achieve a high-quality genome assembly (Table S1). This assembly was compared to the putative pathogenicity chromosome contigs of Fom001 and the previously identified chrRC of Forc016. We found that in the genome assembly of Fom005, chrRC-syntenic contigs include contigs 16, 139, 129, 168, and 144 (Figure 3b). No end-overlap was found among these contigs. Interestingly, chrRC-syntenic regions in Fom001 and Fom005 are almost 100% identical (Figure 3c). Two single-copy candidate effector genes, SIX6 and SIX11, are located in the repeat-rich region of

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**Figure 3** chrRC syntenic regions are present in Fom001 and Fom005. (a) Contigs 13 and 127 of Fom001 are largely syntenic with Forc016 chrRC (nucmer alignment with manual adjustment). These syntenic regions are also present in Fom005 and include contigs 16, 139, 129, 168, and 144 (b). Contigs 13 and 127 of Fom001 are almost identical to contigs 16, 139, 129, 168, and 144 of Fom005 (c). Alignments are colour-coded according to their similarity.
Fom001 contig 127 and Fom005 contig 129. Both of these SIX gene homologs are identical to the SIX6 and SIX11 homologs present on chr\textsuperscript{RC}. We hypothesized that the chr\textsuperscript{RC}-syntenic contigs in Fom001 and Fom005 constitute a pathogenicity chromosome containing virulence genes for infection of melon.

### 2.3 Horizontal transfer of Fom chromosomes

If the putative pathogenicity chromosome (chr\textsuperscript{MLN}) that we identified in Fom001 and Fom005 is sufficient to enable melon infection, transfer of this chromosome into a nonpathogenic strain was expected to render the recipient strain pathogenic on melon. To test this, a hygromycin-resistance gene (HYG) as a marker was placed in the SIX6 locus to select for transfer of chr\textsuperscript{MLN} from Fom001 and Fom005 to a nonpathogenic strain. Two Fom001-derived strains (Fom001\textDeltaSIX6\#11 and Fom001\textDeltaSIX6\#34) and three Fom005-derived strains (Fom005\textDeltaSIX6\#1, Fom005\textDeltaSIX6\#17, and Fom005\textDeltaSIX6\#87) were obtained in which SIX6 was replaced with HYG. When melon plants were inoculated with these SIX6 deletion strains, no reduction of virulence was observed compared to the wild-type strains (Figure S4), indicating that SIX6 does not contribute to virulence of Fom under the tested conditions.

To test the transferability of HYG-labelled chr\textsuperscript{MLN} from Fom001 and/or Fom005, three potential hygromycin-resistant donor strains, Fom001\textDeltaSIX6\#11, Fom005\textDeltaSIX6\#1, and Fom005\textDeltaSIX6\#87, were co-incubated with the nonpathogenic strain Fo47 containing a randomly inserted zeocin-resistance marker (Vlaardingerbroek et al., 2016a). As positive control, Forc016\textDeltaSIX6\#46 was included as a donor strain (van Dam et al., 2017). Double drug-resistant colonies were found for all combinations (Table 1). Ten double drug-resistant colonies were recovered from co-incubating Fom001\textDeltaSIX6\#11 with Fo47, and two double drug-resistant colonies were found by co-incubating Fom005\textDeltaSIX6\#1 and Fom005\textDeltaSIX6\#87 with Fo47, respectively. For Forc016\textDeltaSIX6\#46, only one double drug-resistant colony was obtained. All double drug-resistant colonies were confirmed by PCR to have a Fo47-specific SCAR marker and to carry both HPH and BLE genes.

To assess horizontal chromosome transfer (HCT) and visualize the karyotypes of the putative HCT strains, Fom001\textHCT, HCT#3, #4, #5, Fom005\textHCT, #1, #2, and Forc016\textHCT, #1 (Table 1) were selected for contour-clamped homogeneous electric field (CHEF) electrophoresis analysis. All HCT strains showed the karyotype pattern of Fo47, with extra chromosomes visible in some strains (Figure 4). Surprisingly, two chromosomes were transferred from Fom005\textDeltaSIX6\#1 to Fo47 for both HCT strains tested. These two HCT strains may have originated from the same transfer event as they emerged on the same double-selective plate. For HCT strains Fom001\textHCT, #3, #4, and #5, no extra band was observed. In the case of Forc016\textHCT, chr\textsuperscript{RC} comigrated with the smallest chromosome of Fo47, which showed a band with double intensity on the gel, as was also observed in the previous study (van Dam et al., 2017).

To investigate which sequences of the Fom001 and Fom005 genomes had been transferred to Fo47, the genomes of three Fom001 HCT strains, Fom001\textHCT, #3, #4, #5, and three Fom005 HCT strains, Fom005\textHCT, #2, #3, #4 were sequenced. In addition, the genome of the recipient strain Fo47 was also sequenced with SMRT sequencing (Table S1) and used this assembly in downstream analyses. To identify which chromosomes were newly acquired during the transfer experiment, all reads that did not map to the genome of the recipient strain Fo47 were extracted, and these reads were mapped to the genome assembly of the donor strain Fom001 (Figure 5) or Fom005 (Figure 6). Figure 5a,b shows that, even though no extra band was observed on the CHEF gel, HCT strains Fom001\textHCT, #3 and #4 resulted from transfer of Fom001 contigs 124 (c.2.1 Mb), 3 (c.1.5 Mb), 34 (c.0.07 Mb), 13 (c.0.1 Mb), and 127 (c.1.7 Mb) to Fo47. The HCT strain Fom001\textHCT, #5 resulted from transfer of part of contig 124, part of contig 3, and the entire contigs 13, 34, and 127. It was shown earlier that the size of the SIX6-containing chromosome in Fom001 is around 2 Mb (van Dam et al., 2017). Therefore, contigs 127 and 13 most likely constitute chr\textsuperscript{MLN}, which is largely syntenic with chr\textsuperscript{RC}, while contig 124, contig 3, and contig 34 could form one chromosome or belong to different chromosomes. Part of the read densities of contig 127 were twice as high as those of the rest of the contig in all three HCT strains.

HCT strains Fom005\textHCT, #2, #3, and #4 all resulted from transfer of contigs 17 (1.6 Mb), 134 (c.0.2 Mb), 140 (c.0.2 Mb), 41 (c.0.1 Mb), 29 (c.0.1 Mb), 16 (c.0.1 Mb), 139 (c.0.6 Mb), 129 (c.0.7 Mb), 168 (c.0.4 Mb), 144 (c.0.1 Mb), and 142 (c.0.15 Mb) to Fo47 (Figure 6), contigs in bold [c.2 Mb] are syntenic with chr\textsuperscript{RC}). Read densities of contigs 16, 139, 129, 168, 144, and 142 were twice as high as those of contigs 17, 134, 140, 41, and 29 (Figure 6, contigs in bold are syntenic with chr\textsuperscript{RC}). Because two chromosomes, both of around 2 Mb in size, were observed to be transferred from Fom005 to Fo47.

<table>
<thead>
<tr>
<th>Donor strain</th>
<th>HCT strain</th>
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<tbody>
<tr>
<td>Fom001\textDeltaSIX6#11</td>
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<td>Fom001\textHCT#2</td>
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<td>Fom005\textDeltaSIX6#1</td>
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<td>Fom005\textDeltaSIX6#87</td>
<td>Fom005\textHCT#1</td>
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<tr>
<td>Fom016\textDeltaSIX6#46</td>
<td>Forc016\textHCT#1</td>
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Note. The recipient strain is Fo47 in all cases.
(Figure 4) and the contigs with higher read densities were syntenic to chr<sup>RC</sup> (Figure 3), we speculate that the contigs with higher read densities together form one transferred chromosome and the contigs with lower read densities form the other chromosome. In conclusion, all Fom001 and Fom005 HCT strains had gained extra sequences besides the chr<sup>RC</sup> syntenic regions. These extra sequences are not syntenic between the Fom001 and Fom005 HCT strains (Figure S5).

To determine whether core chromosomes may have been transferred to HCT strains (Vlaardingerbroek et al., 2016a), reads of the HCT strains were mapped directly to the SMRT assembly of the donor strains Fom001 or Fom005, and only those reads that mapped completely and without any mismatches were selected. In the case of transfer of core chromosomes, a high density of perfectly mapped reads was expected, even in the subtelomeric regions. However, this was not observed (Figure S6a–d) and thus we concluded that no core chromosomes had been transferred. This result was corroborated by the fact that the band pattern of the HCT strains on the CHEF gel was more similar to that of the recipient strain (Figure 4). In addition, no reads of the HCT strains mapped to part of contig 10 and the complete contig 22 in Fom001 (Figure S6a), indicating that these regions belong to the accessory (nonconserved) genome of Fom001 and were not transferred. Interestingly, a SIX11 homolog and a SIX13 homolog are located on this part of contig 10, while a SIX1 homolog is located on contig 22. Contigs 4 and 23 of Fom005 are also absent in Forc016 (Figure S6c), but no SIX gene homologs are present on these contigs. A SIX1 homolog, a SIX11 homolog, and a SIX13 homolog, which are located on contig 8 of Fom005, were also not transferred.

To check whether contigs 129, 139, 168, 144, 142, and 16 of Fom005 have duplicated in the HCT strains, or whether these apparently duplicated regions had been collapsed during assembly of the Fom005 genome, previously generated Fom005 reads (Schmidt et al., 2016) and HCT strains Fom005_HCT#2, #3, and #4 were mapped to the SMRT assembly of Fom005. If these large-scale duplicated regions had collapsed during assembly of Fom005, higher read densities of Fom005 in these regions were expected compared

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To check whether contigs 129, 139, 168, 144, 142, and 16 of Fom005 have duplicated in the HCT strains, or whether these apparently duplicated regions had been collapsed during assembly of the Fom005 genome, previously generated Fom005 reads (Schmidt et al., 2016) and HCT strains Fom005_HCT#2, #3, and #4 were mapped to the SMRT assembly of Fom005. If these large-scale duplicated regions had collapsed during assembly of Fom005, higher read densities of Fom005 in these regions were expected compared
to other regions. We did not observe this, however, and thus concluded that these regions had duplicated in the HCT strains derived from Fom005 (Figure S6e). Clear read density differences between HCT strains and the donor strain were observed (dark blue line) (Figure S6e), confirming that no core chromosomes had been transferred into Fom005 HCT strains.

2.4 | Horizontal transfer of Fom chromosomes can turn a nonpathogen into a strain that can infect melon, but not cucumber or watermelon

To test whether chromosomes transferred from Fom strains are sufficient for infecting melon, bioassays on susceptible melon plants were performed, comparing Fom001_HCT #3, #4, #5, Fom005_HCT #1, #2, #3, #4, and Forc016_HCT#1 to donor strains Fom001, Fom005, Forc016, and mock treatment. All donor strains and HCT strains caused disease on melon plants, but there were differences in the severity of disease symptoms observed (Figure 7a). The three Fom001_HCT strains caused only moderate disease symptoms on melon plants compared to their donor strain (Figure 7a). In contrast, melon plants infected with each of the four Fom005_HCT strains showed severe disease symptoms, comparable to infection with the respective donor strains. To conclude, the chromosomes transferred from Fom001 and Fom005 determine virulence on melon plants (Figure 8a,b).

We considered that the difference in host range between Fom and Forc could be caused by (a) avirulence genes present in Fom (but absent
in Forc) that are recognized by cucumber and watermelon and elicit an immune response, or (b) virulence genes on chrRC that are absent in Fom and that facilitate colonization and infection of cucumber and watermelon, or a combination of both (a) and (b). If the first hypothesis is true and the avirulence genes in Fom are present in nontransferred parts of the genomes, HCT strains of Fom should be able to cause disease on cucumber and watermelon plants. To test this, bioassays on cucumber and watermelon with Fom_HCT strains were performed. It turned out that none of the Fom_HCT strains could cause disease on cucumber or watermelon (Figure 7b,c). This excludes the possibility that avirulence genes are present in nontransferred parts of the Fom genomes. Among all transferred sequences of Fom001 and Fom005, only contigs 13 and 127 of Fom001 are syntenic with contigs 16, 139, 129, and 168 of Fom005 (Figure S5). Therefore, genes that determine virulence on melon plants are most likely located on these shared regions. These shared regions between Fom001 HCT strains and Fom005 HCT strains are largely syntenic with chrRC (Figure 3). However, around 300 kb of the repeat-rich region of chrRC is absent in shared regions of transferred sequences of Fom001 and Fom005 (Figure 3) (van Dam et al., 2017). This suggests that genes on the 300 kb region may determine virulence on melon and watermelon plants.

In conclusion, differences between transferred chromosomes of Fom001 or Fom005 and chrRC determine differences in host range between Fom and Forc (Figure 8).

**FIGURE 6** Normalized Illumina read mapping confirms horizontal chromosome transfer (HCT) from Fom005 to Fo47 and reveals duplications. Reads of HCT strains were first mapped to Fo47. Read-pairs that were not mapped to Fo47 were extracted and these unmapped reads were mapped to the single molecule real-time (SMRT) sequencing assembly of Fom005 (a). HCT strains Fom005_HCT#2 (grey line), #3 (purple line), and #4 (green line) all resulted from transfer of contigs 17 (1.6 Mb), 134 (c.0.2 Mb), 140 (c.0.2 Mb), 41 (c.0.1 Mb), 29 (c.0.1 Mb), 16 (c.0.1 Mb), 139 (c.0.6 Mb), 129 (c.0.7 Mb), 168 (c.0.4 Mb), 144 (c.0.1 Mb), and 142 (c.0.15 Mb) to Fo47. Read densities of contigs 16, 139, 129, 168, 144, and 142 were twice as high as those of contigs 17, 134, 140, 41, and 29 (b). Read densities were normalized by dividing by average read density.
3 | DISCUSSION

We have found that both Forc and Fom are able to colonize xylem vessels of cucumber, melon, and watermelon plants, but colonization of cucumber and watermelon by Fom is limited and restricted to the roots. In addition, transferred chromosomes of two Fom strains can turn a nonpathogenic Fo strain into a melon-infecting strain. Lastly, we demonstrate that differences between transferred chromosomes of Fom and chrRC determine differences in host range between Fom and Forc.

GFP-labelled cucurbit-infecting strain Forc016 and melon-infecting strain Fom005 were used to infect cucumber, melon, and watermelon and the colonization process was followed until 14 dpi. Even though Fom005_GFP did not cause disease symptoms on non-host cucumber and watermelon plants, it colonized root xylem vessels of all these plants by 3–4 dpi. Similarly, root xylem colonization
of resistant host plants by Fo was observed in different plant species, including melon (Zvirin et al., 2010), chickpea (Jimenez-Fernandez et al., 2013), and common bean (Garces-Fiallos et al., 2017). In most cases, however, colonization of xylem vessels of resistant plants by Fo was delayed compared to colonization of susceptible plants, and only the lower hypocotyl was colonized (Zvirin et al., 2010) or only root xylem vessels were colonized (Li et al., 2014). In other studies, colonization of xylem vessels of resistant plant roots by Fo was not observed (Cohen et al., 2015; Upasani et al., 2016). In the present study, colonization of the hypocotyl of cucumber and watermelon plants by Fom005_GFP was also not observed, suggesting strong defense responses of nonhosts cucumber and watermelon at the root-stem transition. Moreover, the biomass of Fom in cucumber roots was significantly less than of Forc (Figure 1), indicating that Fom005 growth was restricted in cucumber roots. Forc016_GFP-infected cucumber showed severe and fast root rot in 2 weeks, which possibly influenced the growth of new roots to compensate for the function of the original roots, resulting in completely destroyed roots and death of plants in less than 2 weeks.

Xylem colonization does not necessarily cause external disease symptoms. This raises the question of what allows plants to stay “symptom-free” on pathogen colonization. Our data suggest that fast-growing new roots (cucumber) may act as a strategy to compensate for the loss of function of infected roots. This may buy plants some time to employ other strategies to counteract infection more directly.

Effectors have been shown to contribute to virulence in various xylem-colonizing fungi (de Sain and Rep, 2015). While Fom causes root rot only in melon, Forc also causes severe root rot in cucumber and watermelon. This could be due to effector genes in Forc that allow cucumber and watermelon infection (van Dam et al., 2017). Here, we show that Fom strains without SIX6 do not show reduced virulence at tested conditions in melon plants. In contrast, SIX6 has been shown to contribute to virulence in cucurbit-infecting strain Forc016 at 25 °C (van Dam et al., 2017) as well as in a watermelon-infecting strain (Niu et al., 2016). Deletion of SIX6 in a tomato-infecting strain modestly compromised virulence in one study (Gawehns et al., 2014), but in another study, deletion strains lacking a large part of the Fol
pathogenicity chromosome, including SIX6, SIX9, and SIX11, did not show significantly reduced virulence (Vlaardingerbroek et al., 2016b); SIX6 of Forc016 does not contribute to virulence at 20 °C, indicating that the environment can influence the requirement of effectors. It could be that SIX6 of Fom contributes to virulence in other conditions.

Effector genes in plant-pathogenic fungi are sometimes located on conditionally dispensable chromosomes, and some of these chromosomes can be transferred from one strain to another (Friesen et al., 2006; Akagi et al., 2009; Ma et al., 2010; van Dam et al., 2017). In Fo, HCT has been previously shown in Fo and Forc, and in both cases the recipient nonpathogenic strain became pathogenic to tomato and multiple cucurbits, respectively (Ma et al., 2010; van Dam et al., 2017). Here, we show that Fom strains can also engage in HCT. Both Fom001 and Fom005, which have different mating types, MAT1-1 (Fom005) and MAT1-2 (Fom001), could transfer one or more chromosomes to the same MAT1-2 (Fo47) strain. This is the first demonstration of HCT between the same mating type. Interestingly, in two different HCT experiments involving Fom001 and Fom005, besides transfer of the SIX6-containing chromosome, another chromosome was cotransferred (Figure 4). Cotransfer of a second nonselected chromosome has been previously observed (Ma et al., 2010). Transfer of a single chromosome from Fom001 or Fom005 was not found for any of the double-resistant colonies. This supports the hypothesis that HCT happens through nuclear fusion and selective chromosome loss or retention rather than uptake of chromosomes by the recipient nucleus (Vlaardingerbroek et al., 2016a). How these chromosomes are selectively retained and replicated remains to be discovered. Following HCT, (a) large deletion(s) of the transferred chromosome was observed for HCT strain Fom001_HCT #5 (Figure 5). This strain showed no reduction in virulence compared to the other two Fom001_HCT strains, indicating that the lost region does not contribute to virulence. Transfer of genomic sequences of Fom001 was confirmed by whole-genome sequencing, but no extra bands were observed on the CHEF gel; it could be that the transferred regions or chromosomes acquired a size indistinguishable from a core chromosome in the CHEF gel.

With the development of next-generation sequencing technologies, prediction of putative (host-specific) virulence genes is relatively straightforward (Borah et al., 2018). However, functional verification of genes involved in the host range is still challenging. This can be due to the pathosystem under investigation and/or to the probability that multiple genes are collectively responsible for host specificity (Borah et al., 2018). In Alternaria alternata, host-specific toxin genes have been found in several pathotypes (Tsuge et al., 2013). Interestingly, host-selective toxin gene clusters in this fungus reside on single small chromosomes and these chromosomes can be combined by protoplast fusion, resulting in strains producing both toxins (Tsuge et al., 2013). Single chromosomes that determine the host range have also been identified through HCT (Ma et al., 2010; van Dam et al., 2017). In this way, genes involved in host specificity are narrowed down to single chromosomes. Here, too, we found chromosomes of Fom001 and Fom005 that determine virulence on melon plants through HCT. In addition, we demonstrated that differences between transferred chromosomes of Fom and chrRC determine differences in host range between Fom and Forc. Because the shared regions of transferred chromosomes between Fom001 and Fom005 are largely syntenic with chrRC (Figure 3), finding genes that are responsible for the differences in host range between Fom and Forc becomes possible.

Schulze-Lefert and Panstruga suggest that recognition of effectors by nonhosts (effector-triggered immunity) plays a predominant role in nonhost resistance in plant species closely related to a host species (Schulze-Lefert and Panstruga, 2011). SIX1 is the only SIX gene homolog that is consistently present in Fom genomes but is not found in Forc (van Dam et al., 2017), suggesting that SIX1 of Fom could be recognized by cucumber and watermelon. However, we found that Fom_HCT strains without SIX1 still could not infect cucumber and watermelon plants, indicating that SIX1 does not act as (the sole) avirulence gene in Fom for cucumber and watermelon. Of course, non-SIX homologs may also act as avirulence genes. Moreover, about 300 kb of sequence is present on chrRC but absent on the shared regions of transferred chromosomes between Fom001 and Fom005. These sequences may contain virulence genes whose products can suppress immunity in cucumber and watermelon. Our future work will include finding genes on chrRC or transferred chromosomes of Fom that determine the difference in host range between Fom and Forc.

In conclusion, we report here for the first time colonization differences between host and nonhost plants by Fom. Moreover, we show that largely homologous chromosomes determine virulence to their host plant(s) and are thus also responsible for differences in host range. This opens up the possibility of finding genes that determine differences in host range. Lastly, we demonstrate again that HCT plays an important role in environmental adaptation in Fom.

4 | EXPERIMENTAL PROCEDURES

4.1 | Cloning

Vector pRW2h_Pfem_GFP_Tsix1 was constructed by amplifying the GFP coding sequence from pPK2-HPH-GFP (Michielse and Rep, 2009) using primers FP740 (5′-AAAtctagaATGGTGAGCAAGGGCGAGGAG-3′, lowercase for ΙΙ restriction site) and FP7001 (5′-TTTagatctTTACTTGATCCGTCGCTCC-3′, lower case for ΙΙΙ restriction site) followed by Xbal-BglII digestion and inserting it into the Xbal-BglII site of pRW2h_Pfem_MCS_Tsix1 (van der Does et al., 2016). The hygromycin resistance cassette of pRW2h_Pfem_GFP_Tsix1 was replaced by the phleomycin resistance cassette of pRW1p_Pfem_MCS_Tsix1, which was modified from pRW1p (Houterman et al., 2008) using the same method as described by van der Does et al. (2016), resulting in pRW1p_Pfem_GFP_Tsix1.

To delete SIX6 in Fom001 and Fom005, two SIX6 deletion constructs were used. The first one, pPDh_SIX6, was generated previously (van Dam et al., 2017). The second SIX6 deletion construct was
modified from pPK2-HPH-GFP (Michielse et al., 2009). First, around 1 kb SIX6 flanks were amplified. One flank was amplified using primer pair FP7186 (5′-ATGATTAGAATATCTTAATTAAATGATCCGAAGACCTGAGCTGTTTGA-3′) and FP7187 (5′-CCATCACTTTGCTTGCTCATCACATGATGCTGTTTGA-3′), while another flank was amplified using primer pair FP7188 (5′-cttcatctgccgcatgcaCTATAAAGCCAATACGATTCGAA-3′) and FP7189 (5′-GCACGTGATCAGTTATTTACGCCACTGGCGTGTCGTTTTA3′). These two flanks were introduced into pPK2-HPH-GFP using the HiFi cloning kit (New England Biolabs (UK) Ltd). Then, a PmlI fragment containing the herpes simplex virus thymidine kinase (HSVtk) gene under the control of the Chobloobus heterostrophus glyceraldehyde-3-phosphate dehydrogenase (ChGPD) gene promoter and the Neurospora crassa β-tubulin gene terminator was inserted into the vector as a conditional negative selection marker against ectopic transformants (Khang et al., 2005).

4.2 | Generation of strains with green fluorescence

Agrobacterium-mediated Fusarium transformation was performed as described by (Takken et al., 2004). GFP-expressing T-DNA of pRW2h_Pfem_GFP_Tsix1 was integrated randomly into the genome as described by (Takken et al., 2004; van Dam et al., 2013). Transformants Forc016_GFP (FP4379) and Fom005_GFP (FP4374) showing wild-type phenotype with green fluorescence were confirmed by fluorescence microscopy and selected for microscopic examination of fungal colonization.

4.3 | Microscopic examination of fungal colonization

Conidia were isolated from 5-day-old cultures grown in NO3-medium (0.17% yeast nitrogen base, 3% sucrose, 100 mM KNO3) by filtering through Miracloth (pore size 22–25 μm; Merck). Spores were centrifuged, resuspended in sterile milli-Q water, counted, and brought to a final concentration of 10⁷ spores/mL. Roots of 6-day-old cucumber and 10-day-old melon and watermelon seedlings were carefully taken out of the soil and rinsed with tap water to wash away soil particles. Three plants for each treatment were inoculated with 10⁷ spores/ml of Forc016_GFP, Fom005_GFP or water as control in a Petri dish (Figure S1). Colonization was examined at 1, 2, 3, 4, 6, and 14 dpi using the AMG Evos FL digital inverted microscope. GFP was excited with a 488-nm light (emission 525–550 nm BP filter). At 14 dpi, the hypocotyls of some plants were hand-sectioned and examined for the presence of fungal hyphae.

4.4 | Fungal biomass quantification using qPCR

The relative amount of fungal DNA in plant roots was quantified using qPCR. Nine-day-old cucumber and melon seedlings were inoculated with 10⁷ spores/ml of Forc016, Fom001, or Fom005 (Schmidt et al., 2016) and roots from five plants for each treatment were randomly collected and rinsed with water 1 week after inoculation. DNA was isolated using GeneJET plant Genomic DNA purification Mini kit (Thermos Scientific). For detection and quantification of fungal DNA, primers FP8520 (5′-AGATTAGGACACCCCCCTTC-3′) and FP8521 (5′-TTTGGGGCTCTTCCACTG-3′) for amplifying the single-copy gene SIX6 were used for Forc016, Fom001, and Fom005. Primers FP8434 (5′-CAGTGAACAGGTCAGGAA-3′) and FP8435 (5′-CTGGTGTAATGACCACCGAG-3′) were used for amplifying the α-tubulin gene of cucumber plants as an endogenous gene for normalization, while primers FP8512 (5′-GGGGTCCCTAGACAAATGA-3′) and FP8513 (5′-CTGGGATCAACACCGAGTTCAG-3′) were used for amplifying the melon α-tubulin gene (Kong et al., 2014). qPCR was performed on a QuantStudio 3 system (Thermo Fisher Scientific). A total volume of 10 μl of the reaction mixture included 2 μl of 5 × HOT FIREPol EvaGreen qPCR Mix Plus (Solis BioDyne), 5 pmol of each primer, 20 ng of template, and 1 μl of sterile milli-Q water. Three technical replicates were used for each sample to confirm the reproducibility of the results, and a negative control sample with sterile milli-Q water as template was included. Standard curves for all three primer pairs were generated and assessed. The PCR programme, including melting curve analysis, was set as follows: 15 min at 95 °C; 40 cycles of 15 s at 95 °C, 20 s at 60 °C, and 30 s at 72 °C; then 15 s at 95 °C, 1 min at 60 °C, and 15 s at 95 °C. Data analysis was performed using Thermo Fisher Cloud RQ analysis tool combined with qbase.

4.5 | SIX6 replacement

To replace SIX6 in Fom001 and Fom005 with a hygromycin resistance cassette, Agrobacterium-mediated transformation was performed as previously described (Takken et al., 2004; van Dam et al., 2017). Following monosporing of hygromycin-resistant colonies, the transformants were grown in 96-well plates containing in each well 150 μl of potato dextrose broth (PDB) supplemented with hygromycin and 5 μM 5-fluoro-2-deoxyuridine (Alfa-Aesar) for preselection of in locus insertion of the construct through homologous recombination. Successful deletion of SIX6 was confirmed by PCR using primers inside the T-DNA and outside the 1 kb flanking regions in the construct. Fom001SIX6#11 and Fom005SIX6#1 were generated using the construct of pPDh_SIX6, while Fom005SIX6B7 was generated using pPK2-HPH-GFP_h_SIX6.

4.6 | Horizontal chromosome transfer

HCT experiments were performed by co-incubating Forc016ΔSIX6#46, Fom001ΔSIX6#11, Fom005ΔSIX6#1, and Fom005ΔSIX6#B7 with Fo47pGRB (Vlaardingerbroek et al., 2016a), respectively. Conidia (10⁵) from each pair of strains were mixed and co-incubated on potato dextrose agar (PDA) plates for 7 days at 25 °C. Microconidia were harvested from the co-incubation plate using 5 ml of sterile milli-Q water filtered
through sterile Miracloth and pipetted on a double-selective PDA plate containing 0.1 M Tris (pH 8) supplemented with 100 μg/ml hygromycin (Duchefa) and 100 μg/ml zeocin (InvivoGen). Double drug-resistant colonies were selected after 3 days and transferred to a new double-selective plate. Growing colonies were then mon-spored by spreading on a fresh plate supplemented with both antifungal drugs. After 2 days of growth, single-spore colonies were selected and transferred to fresh plates.

4.7 Contour-clamped homogeneous electric field electrophoresis

Preparation of protoplasts and pulsed-field gel electrophoresis were performed as described previously (van Dam et al., 2017). Fusarium strains were cultured in 100 ml NO₃ medium (0.17% yeast nitrogen base, 100 mM KNO₃, and 3% sucrose) for 5 days at 25 °C. Then, conidia were collected by filtering through a double layer of Miracloth and the concentration of spores was measured. Conidia (5 × 10⁷) were transferred to 40 ml PDB (BD Biosciences). After approximately 16 hr of growth at 25 °C, germinated spores were resuspended in 10 ml of MgSO₄ solution (1.2 M MgSO₄, 50 mM sodium citrate, pH 5.8) supplemented with 50 mg/ml Glucanex (Sigma) + 5 mg/ml Driselase (Sigma) and incubated for approximately 17 hr at 30 °C in a shaking water bath (65 rpm). The protoplasts were filtered through a double layer of Miracloth, collected by centrifugation and, cast in InCert agarose (Lonza) at a concentration of 2 × 10⁸ protoplasts per millilitre. Plugs were treated with 2 mg/ml pronase E at 50 °C. Chromosomes were separated by pulsed-field electrophoresis for 260 hr in 1% Seakem Gold agarose (Lonza) at 1.5 V/cm in a CHEF-DRII system (Biorad) in 0.5 × Tris-borate-EDTA (TBE) buffer at 4 °C, with switch times between 1,200 and 4,800 s. The gels were stained with 1 μg/ml ethidium bromide in 0.5 × TBE.

4.8 DNA isolation, genome sequencing, and assembly

DNA isolation was performed on freeze-dried mycelium ground in liquid nitrogen as starting material, using multiple rounds of phenol-chloroform extraction and precipitation, as well as the Purelink plant total DNA purification kit (Invitrogen).

SMRT sequencing was performed at Keygene N.V. (Wageningen, Netherlands). PacBio libraries were prepared and size-selected at c.20 kb using Blue Pippin prep. Sequencing of five SMRT cells was performed using the P6-C4 polymerase-chemistry combination, ≥4 hr movie time, stage start. De novo assembly was performed with the Hierarchical Genome Assembly Process v. 3 (HGAP.3, Pacific Biosciences) within the SMRT Portal environment (v. 1.87.139483). Default values were kept and the expected genome size was set to 60 Mb.

Illumina sequencing (150 bp paired-end, insert size c.500 bp) of HCT strains was performed on a HiSeq 2,500 machine at the Hartwig Medical Foundation (Amsterdam, Netherlands) at c.100 × coverage, resulting in 5.0–5.6 Mb of sequence data per sample.

Raw reads were trimmed to remove low-quality bases and adapter sequences using fastq-mcf v. 1.04.807 (~q 20). PCR duplicates were also removed using PicardTools MarkDuplicates v. 2.7.1 with standard settings. To confirm HCT, trimmed reads were first mapped against the Fo47 genome assembly with Bowtie2 v. 2.2.5 (DNAseq). Unmapped reads were selected from the bam-file that resulted from mapping trimmed reads to the assembly of Fo47 with SAMtools view v 1 1 0 4 2 6 4 2 6 4 (both mates unmapped), SAMtools view v 8 2 6 8 F 2 6 0 (mate 1 mapped, other mate unmapped), and SAMTools view v 8 2 6 8 F 2 5 6 2 5 6 (mate 2 mapped, other mate unmapped). The three resulting bamfiles were sorted with SAMtools sort –n, merged with SAMTools merge and converted to fastq format with bedtools bamtofastq. These reads were then mapped to the SMRT assembly of Fom001 or Fom005, respectively. To establish whether core chromosomes were transferred, trimmed reads were directly mapped to SMRT assembly of Fom001 or Fom005, and only reads that mapped once with 100% coverage and 100% identity were selected (with SAMtools view –q 42) when calculating read densities. For visualization of the reads counts in 10 kb nonoverlapping sliding windows, SAMtools bedcov was used. SAMtools v. 1.8 was used in all above-mentioned cases.

Whole-genome or chromosome alignments were performed using nucmer (with –maxmatch or otherwise default settings) from the MUMmer v. 3.23 package (Delcher et al., 2002).

4.9 Virulence assay

Virulence assays were performed as described previously (van Dam et al., 2017). Briefly, spores at 10⁶/m1l (SIX6 deletion assay) or 10⁷/ml (chromosome transfer) were used to inoculate seedlings of cucumber (around 6–7 days old), melon (9–10 days old), or watermelon (9–10 days old). For each treatment, six to eight seedlings were inoculated and grown at 25 °C (SIX6 deletion assay) or 20 °C (HCT assay) in a greenhouse. The following plant cultivars were used: Cucumis sativus ‘Paraïso’, Cucumis melo ‘Cha-T’, and Citrullus lanatus ‘Black Diamond’. Two weeks after inoculation, disease symptoms were scored using a disease index ranging from 0 to 4 (0, no symptoms; 1, slight root rot symptoms, only at tip of main root; 2, root rot symptoms and stem lesions visible aboveground; 3, extensive rot of the entire root system, often with a large lesion extending above the cotyledons; 4, plant either dead or very small and wilted).

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CONFLICT OF INTEREST
No conflict of interest is declared.

DATA AVAILABILITY STATEMENT
Data available on request from the authors.

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**SUPPORTING INFORMATION**

Additional Supporting Information may be found online in the Supporting Information section.

**FIGURE S1** Phenotypes of infected cucumber and melon plants in soil at 7 days post-inoculation. Nine-day-old cucumber and melon seedlings were treated with water (Mock), Forc016 (10^7 spores/ml), Fom001 (10^7 spores/ml), or Fom005 (10^7 spores/ml).

**FIGURE S2** Phenotypes of infected cucumber, melon, and watermelon plants in Petri dishes at 14 days post-inoculation. Six-day-old cucumber and 10-day-old melon and watermelon seedlings were treated with water (Mock), Forc016_GFP (10^7 spores/ml), or Fom005_GFP (10^7 spores/ml) in Petri dishes for 14 days. Forc016_GFP causes severe wilting, and root and stem rot on cucumber, melon, and watermelon plants, while Fom005_GFP causes disease on melon, but not on cucumber or watermelon. All infected roots were dark brown compared to mock-treated roots. Fom005_GFP-infected cucumber plants produced many new roots, comparable to mock-treated cucumber plants. All mock-treated plants were healthy.

**FIGURE S3** Fom005 is not able to colonize the hypocotyl of cucumber or watermelon plants. The hypocoitols of infected or mock-treated plants at 14 days post-inoculation in Petri dishes were hand-sectioned and examined for the presence of fungal hyphae inside plants using an AMG Evos FL digital inverted microscope. Forc016_GFP was found in the cross-section of the hypocotyl of both cucumber (bright green dots indicated with white arrows) and watermelon (not shown). It was not possible to visualize Forc016_GFP in the hypocotyl of melon because of rotted stems. Fom005_GFP was present in the cross-section of the melon hypocotyl (bright green dots indicated with a white arrow), but was not found in the cross-section of hypocotyls of cucumber or watermelon (not shown).

**FIGURE S4** SIX6 does not contribute to the virulence of Fom001 and Fom005. Disease index (DI) (a) and fresh weight (b) of infected melon plants were scored 2 weeks after inoculation. When 10-day-old melon seedlings were inoculated with 10^6 spores/ml at 25 °C, the SIX6 knockout strains Fom001ΔSIX6#1, #34, and Fom005ΔSIX6#1, #17 showed similar disease index and fresh weight as wild-type strains Fom001 and Fom005, respectively. As controls, disease symptoms of two ectopic transformants (T-DNA was randomly inserted in the genome) from each background were assessed, and these also showed no change in virulence compared to the wild-type strains. The Kruskal–Wallis test was performed on disease index. One-way analysis of variance was performed on fresh weight.

**FIGURE S5** Syntenic regions between transferred contigs of Fom001 and Fom005. Among all transferred contigs of Fom001 and Fom005, only contigs 127 and 13 of Fom001 are syntenic with contigs 139, 144, 129, 168, and 16 (nucmer alignment with manual adjustment). Alignments are colour-coded according to their similarity.

**FIGURE S6** Stringent selection of mapped Illumina reads of horizontal chromosome transfer (HCT) strains and Fom005 to the single molecule real-time (SMRT) sequencing assembly of Fom001 or Fom005 shows the absence of core chromosome transfer. (a) Reads of HCT strains Fom001_HCT #3, #4, and #5 were mapped to the SMRT assembly of Fom001 donor strain. (b) Reads of Fom001_HCT #3 (blue line), #4 (green line), and Fom001_HCT #5 (red line) mapped more abundantly to Fom001 contigs 124, 127, 3, and 13 than to the rest of the assembly. (c) Reads of HCT strains Fom005_HCT #2, #3, and #4 were mapped to the SMRT assembly of Fom005 donor strain. (d) Reads of Fom005_HCT#2 (blue line), #3 (green line), and #4 (red line) mapped more abundantly to Fom005 contigs 129, 139, 168, 142, 144, and 16 than to the rest of the assembly. (e) Reads of Fom005_HCT#2 (blue line), #3 (green line), and #4 (red line) and Fom005 (dark blue line) were mapped to the SMRT assembly of the Fom005 donor strain. Fom005 HCT strains showed clear read density drops at subtelomere regions, but no clear drop was observed.
for Fom005 (dark blue line). Only reads that mapped once with 100% coverage and 100% identity were selected, to differentiate between HCT strains and the donor strain Fom001 or Fom005 based on single nucleotide polymorphisms.

**TABLE S1** Assembly statistics of assemblies of Fom005 and Fo47 that were generated for this study, and of Fom001 (van Dam *et al.*, 2017)