APPENDIX

(a) Consistent order, consistent strandedness

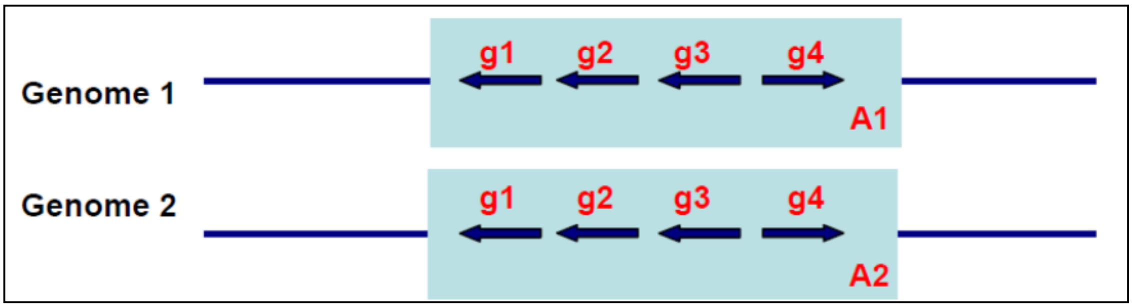

Figure 7.1: In this example, blocks A1 in genome 1 and A2in genome 2 are composed of four genes. The order of the genes in each block is the same, and each pair of genes has the same orientation.

(b) Consistent order, reversed strandedness

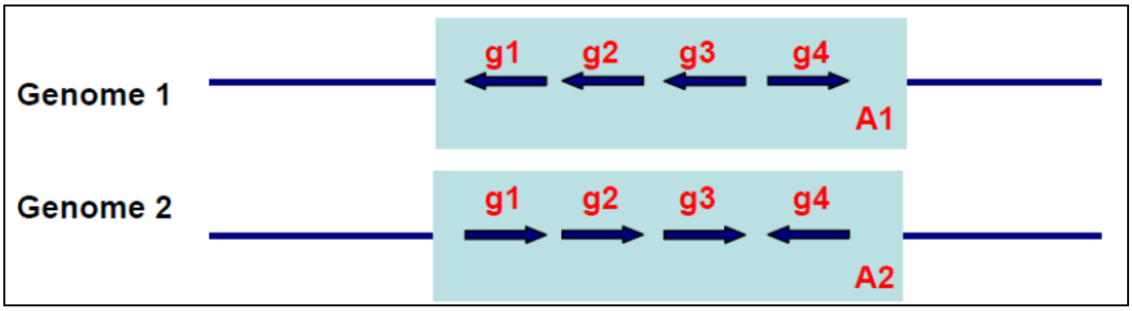

Figure 7.2: In this example, blocks A1 in genome 1 and A2 in genome 2 are composed of four genes. The order of the genes in each block is the same, but each pair of genes has different orientation.

(c) Inverted order, consistent strandedness

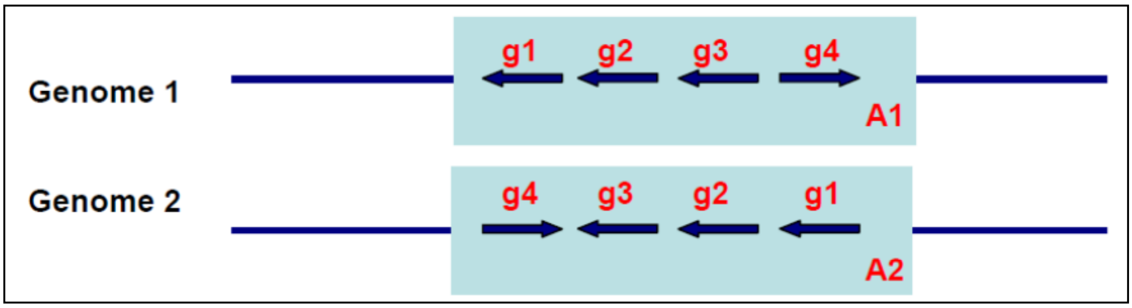

Figure 7.3: In this example, blocks A1 in genome 1 and A2 in genome 2 are composed of four genes. The order of the genes in block A1 is inverted with respect to that in block A2, and each pair of genes has the same orientation.

(d) Inverted order, reversed strandedness

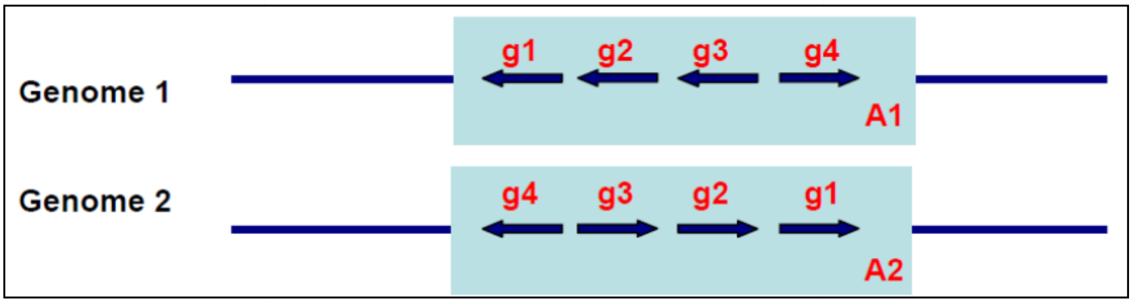

Figure 7.4: In this example, blocks A1 in genome 1 and A2 in genome 2 are composed of four genes. The order of the genes in block A1 is inverted with respect to that in block A2, and each pair of genes has different orientation.

(e) No in-map / out-map mismatch

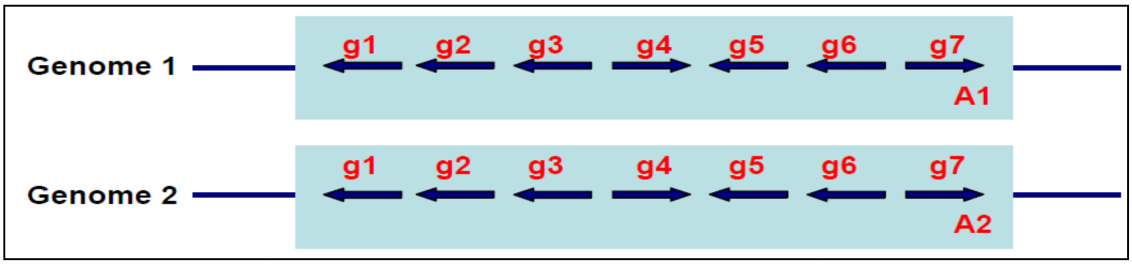

Figure 7.5: Blocks conformed of the 7 ortholog genes with no in-map mismatches and no out-map mismatches.

(f) One in-map mismatch and one out-map mismatch

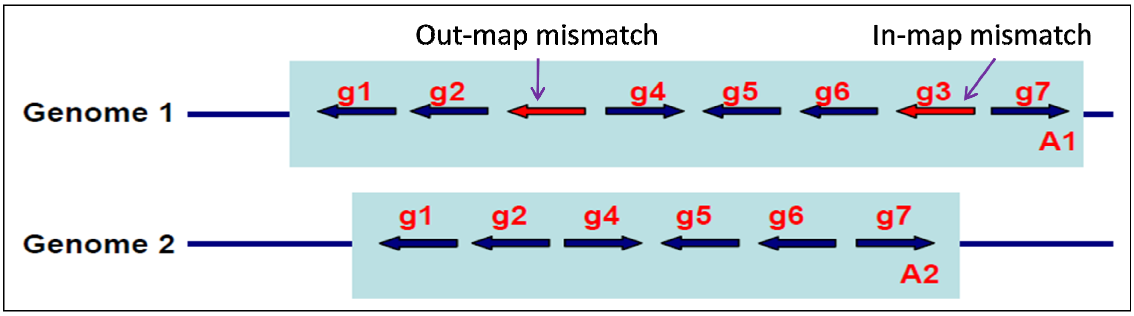

Figure 7.6: Blocks conformed of 6 ortholog genes. For block A1, one in-map mismatch (g3) and one out-map mismatch exists.

Table 7.1: One-to-one orthologous relationships between *O. sativa* (row) and *A. thaliana* (column) from InParanoid and ad hoc BLAST. Numbers in parenthesis represent one-to-one orthologous relationships result from ad hoc BLAST method.

Chromosome	**Chr I**	**Chr II**	**Chr III**	**Chr IV**	**Chr V**	**Chr C**	**Chr M**	**Total**
Chr 1	470 (202)	274 (128)	416 (180)	236 (108)	422 (189)	1 (0)	0 (0)	1,819 (807)
Chr 2	388 (177)	209 (113)	251 (124)	247 (107)	387 (175)	0 (0)	0 (0)	1,482 (696)
Chr 3	486 (242)	317 (143)	403 (179)	238 (124)	373 (184)	3 (1)	0 (0)	1,820 (873)
Chr 4	300 (132)	132 (59)	190 (84)	165 (65)	277 (102)	2 (0)	1 (0)	1,067 (442)
Chr 5	255 (122)	157 (74)	216 (109)	142 (59)	226 (91)	0 (0)	0 (0)	996 (455)
Chr 6	232 (110)	127 (71)	133 (47)	162 (78)	244 (124)	0 (0)	1 (0)	899 (430)
Chr 7	197 (102)	112 (47)	200 (99)	138 (54)	220 (108)	0 (0)	0 (0)	867 (410)
Chr 8	252 (118)	118 (61)	168 (71)	151 (61)	199 (91)	1 (0)	0 (0)	889 (402)
Chr 9	161 (63)	103 (60)	111 (60)	130 (59)	127 (67)	1 (1)	1 (0)	634 (310)
Chr 10	156 (60)	93 (43)	104 (32)	133 (46)	136 (72)	0 (0)	0 (0)	622 (253)
Chr 11	112 (49)	62 (33)	103 (54)	45 (23)	163 (60)	2 (1)	0 (0)	487 (220)
Chr 12	156 (72)	87 (33)	127 (73)	78 (33)	144 (68)	2 (1)	1 (1)	595 (281)
Total	3,165 (1,449)	1,791 (865)	2,422 (1,112)	1,865 (817)	2,918 (1,331)	12 (4)	4 (1)	12,177 (5,579)

Table 7.2: Conserved synteny blocks and their corresponding genomic coverage, size and range in *O. sativa* identified from orthologous gene datasets of InParanoid and ad hoc BLAST method. Numbers in parenthesis represent conserved synteny blocks result from ad hoc BLAST method.

Chromosome	**Genome size (bp)**	**Synteny block**	**Coverage (%)**	**Range (kb)**	**Range (gene)**
Chr 1	45,038,604	115 (41)	1.36 (0.45)	[0.4 - 35.2] ([0.8 - 15.8])	[2 – 3] ([2 – 2])
Chr 2	36,792,247	94 (42)	1.41 (0.82)	[0.5 - 44.1] ([0.8 - 44.1])	[2 – 3] ([2 – 3])
Chr 3	37,312,367	88 (40)	1.14 (0.74)	[0.4 - 27.9] ([0.8 - 54.1])	[2 – 4] ([2 – 3])
Chr 4	36,060,865	87 (34)	1.82 (0.69)	[0.7 - 68.8] ([1.2 - 40.7])	[2 – 3] ([2 – 3])
Chr 5	30,073,438	42 (18)	0.91 (0.50)	[0.7 - 43.2] ([1.8 - 26.4])	[2 – 4] ([2 – 2])
Chr 6	32,124,789	80 (28)	1.95 (0.63)	[0.6 - 149.8] ([1.1 - 33.5])	[2 – 5] ([2 – 2])
Chr 7	30,357,780	55 (24)	1.34 (0.59)	[0.6 - 52.0] ([1.6 - 52.0])	[2 – 5] ([2 – 3])
Chr 8	28,530,027	80 (15)	1.92 (0.45)	[0.4 - 39.7] ([2.1 - 38.8])	[2 – 7] ([2 – 2])
Chr 9	23,895,721	86 (18)	2.10 (0.64)	[0.5 - 46.5] ([0.8 - 46.5])	[2 – 4] ([2 – 2])
Chr 10	23,703,430	69 (20)	1.71 (0.48)	[0.5 - 26.4] ([0.6 - 16.1])	[2 – 3] ([2 – 2])
Chr 11	31,219,694	89 (15)	1.58 (0.36)	[0.3 - 61.4] ([1.7 - 43.1])	[2 – 4] ([2 – 2])
Chr 12	27,679,166	57 (19)	1.80 (0.84)	[0.4 - 116.3] ([1.7 - 116.3])	[2 – 3] ([2 – 2])
Total	382,788,128	942 (314)	1.56 (0.60)	[0.3 - 149.8] ([0.6 - 116.3])	[2 – 7] ([2 – 3])

Table 7.3: Conserved synteny blocks and their corresponding genomic coverage, size and range in *A. thaliana* identified from orthologous gene datasets of InParanoid and ad hoc BLAST method. Numbers in parenthesis represent conserved synteny blocks result from ad hoc BLAST method.

Chromosome	**Genome size (bp)**	**Synteny block**	**Coverage (%)**	**Range (kb)**	**Range (gene)**
Chr I	30,427,671	339 (74)	2.63 (0.90)	[0.5 - 26.8] ([0.9 - 20.5])	[2 – 5] ([2 – 4])
Chr II	19,698,289	125 (43)	1.91 (0.57)	[0.5 - 25.2] ([0.3 - 10.6])	[2 – 5] ([2 – 3])
Chr III	23,459,830	178 (73)	2.52 (1.01)	[0.5 - 39.9] ([1.6 - 16.3])	[2 – 7] ([2 – 3])
Chr IV	18,585,056	124 (55)	2.56 (1.10)	[0.4 - 23.3] ([0.9 - 20.2])	[2 – 6] ([2 – 4])
Chr V	26,975,502	175 (69)	1.93 (0.94)	[0.4 - 17.9] ([1.4 - 12.7])	[2 – 6] ([2 – 4])
Chr C	154,478	1 (0)	0.25 (0.00)	[0.4 - 0.4] ([0])	[2 – 2] ([0])
Chr M	366,924	0 (0)	0.00 (0.00)	[0] ([0])	[0] ([0])
Total	119,667,750	942 (314)	2.31 (0.90)	[0.4 - 39.9] ([0.3 - 20.5])	[2 – 7] ([2 – 4])

Table 7.4: Distribution of perfect synteny blocks between *O. sativa* chromosomes (rows) and *A. thaliana* chromosomes (columns) identified from orthologous gene datasets of InParanoid and ad hoc BLAST method. Numbers in parenthesis represent conserved synteny blocks result from ad hoc BLAST method. Mitochondria chromosome (ChrM) of *A. thaliana* was excluded because it doesn't have any synteny blocks with *O. sativa*.

Chromosome	**Chr I**	**Chr II**	**Chr III**	**Chr IV**	**Chr V**	**Chr C**	**Total**
Chr 1	37 (9)	11 (8)	28 (13)	13 (3)	26 (8)	0 (0)	115 (41)
Chr 2	33 (11)	11 (3)	22 (12)	11 (3)	17 (13)	0 (0)	94 (42)
Chr 3	26 (9)	22 (6)	17 (9)	15 (9)	7 (7)	1 (0)	88 (40)
Chr 4	40 (12)	5 (2)	18 (4)	8 (9)	16 (7)	0 (0)	87 (34)
Chr 5	19 (4)	3 (5)	9 (5)	4 (1)	7 (3)	0 (0)	42 (18)
Chr 6	37 (7)	8 (3)	15 (2)	5 (7)	15 (9)	0 (0)	80 (28)
Chr 7	11 (6)	8 (2)	14 (6)	11 (5)	11 (5)	0 (0)	55 (24)
Chr 8	17 (5)	17 (2)	16 (3)	9 (0)	21 (5)	0 (0)	80 (15)
Chr 9	46 (5)	8 (2)	9 (6)	11 (5)	12 (0)	0 (0)	86 (18)
Chr 10	40 (1)	8 (2)	7 (3)	7 (9)	7 (5)	0 (0)	69 (20)
Chr 11	25 (3)	12 (3)	9 (5)	19 (2)	24 (2)	0 (0)	89 (15)
Chr 12	8 (2)	12 (5)	14 (5)	11 (2)	12 (5)	0 (0)	57 (19)
Total	339 (74)	125 (43)	178 (73)	124 (55)	175 (69)	1 (0)	942 (314)

Table 7.5: Non-conserved synteny blocks for mismatches (10% / 50%) and their corresponding genomic coverage, size and range in *O. sativa* identified from orthologous gene datasets of InParanoid and ad hoc BLAST method. Numbers in parenthesis represent conserved synteny blocks result from ad hoc BLAST method. Result for 10% mismatches was excluded because it was same with the result of conserved synteny block.

Chromosome	**Genome size (bp)**	**Synteny block**	**Coverage (%)**	**Range (kb)**	**Range (gene)**
Chr 1	45,038,604	202 (84)	6.63 (1.97)	[0.4 - 134.1] ([0.8 - 67.7])	[2 - 22] ([2 - 8])
Chr 2	36,792,247	155 (81)	5.53 (3.36)	[0.5 - 90.2] ([0.8 - 209.8])	[2 - 11] ([2 - 10])
Chr 3	37,312,367	180 (82)	8.34 (3.45)	[0.4 - 150.3] ([0.8 - 150.3])	[2 - 15] ([2 - 15])
Chr 4	36,060,865	137 (56)	7.86 (1.90)	[0.7 - 193.5] ([1.2 - 48.1])	[2 - 12] ([2 - 6])
Chr 5	30,073,438	93 (43)	4.83 (1.92)	[0.7 - 78.3] ([1.4 - 90.4])	[2 - 8] ([2 - 5])
Chr 6	32,124,789	128 (39)	5.96 (2.08)	[0.6 - 307.4] ([1.1 - 77.5])	[2 - 11] ([2 - 7])
Chr 7	30,357,780	90 (49)	4.64 (1.86)	[0.6 - 136.3] ([0.8 - 60.3])	[2 - 8] ([2 - 6])
Chr 8	28,530,027	134 (35)	9.36 (2.20)	[0.4 - 110.1] ([2.1 - 120.1])	[2 - 30] ([2 - 6])
Chr 9	23,895,721	115 (31)	7.84 (1.48)	[0.6 - 104.7] ([1.6 - 46.5])	[2 - 24] ([2 - 5])
Chr 10	23,703,430	94 (33)	7.43 (1.83)	[0.7 - 152.9] ([0.6 - 57.8])	[2 - 30] ([2 - 8])

Table 7.5, continued: Non-conserved synteny blocks for mismatches (10% / 50%) and their corresponding genomic coverage, size and range in *O. sativa* identified from orthologous gene datasets of InParanoid and ad hoc BLAST method. Numbers in parenthesis represent conserved synteny blocks result from ad hoc BLAST method. Result for 10% mismatches was excluded because it was same with the result of conserved synteny block.

Chr 11	31,219,694	100 (25)	5.81 (1.32)	[0.4 - 221.2] ([1.6 - 107.1])	[2 - 11] ([2 - 7])
Chr 12	27,679,166	82 (31)	4.39 (1.77)	[0.4 - 207.6] ([1.7 - 207.6])	[2 - 13] ([2 - 7])
Total	382,788,128	1510 (589)	6.55 (2.15)	[0.4 - 307.4] ([0.6 - 209.8])	[2 - 30] ([2 - 15])

Table 7.6: Non-conserved synteny blocks for mismatches (50%) and their corresponding genomic coverage, size and range in *A. thaliana* identified from orthologous gene datasets of InParanoid and ad hoc BLAST method. Numbers in parenthesis represent conserved synteny blocks result from ad hoc BLAST method. Result for 10% mismatches was excluded because it was same with the result of conserved synteny block.

Chromosome	**Genome size (bp)**	**Synteny block**	**Coverage (%)**	**Range (kb)**	**Range (gene)**
Chr I	30,427,671	518 (149)	7.98 (2.91)	[0.5 – 103.8] ([0.9 – 33.0])	[2 - 12] ([2 - 10])
Chr II	19,698,289	197 (85)	7.14 (2.41)	[0.5 – 61.1] ([0.3 – 22.7])	[2 - 12] ([2 - 8])
Chr III	23,459,830	327 (137)	9.02 (2.89)	[0.5 – 57.8] ([1.2 – 38.6])	[2 - 21] ([2 - 10])
Chr IV	18,585,056	197 (103)	7.24 (3.05)	[0.4 – 46.4] ([1.4 – 27.1])	[2 - 14] ([2 - 8])
Chr V	26,975,502	270 (115)	6.54 (2.66)	[0.4 – 61.8] ([1.4 – 23.9])	[2 - 24] ([2 - 8])
Chr C	154,478	1 (0)	0.25 (0)	[0.4 – 0.4] ([0 - 0])	[2 - 2] ([0])
Chr M	366,924	0 (0)	0 (0)	[0 - 0] ([0 - 0])	[0] ([0])
Total	119,667,750	1510 (589)	7.57 (2.78)	[0.4 - 103.8] ([0.3 – 38.6])	[2 - 24] ([2 - 10])

Table 7.7: Distribution of non-conserved synteny blocks for mismatches (10% / 50%) between *O. sativa* chromosomes (rows) and *A. thaliana* chromosomes (columns) identified from orthologous gene datasets of InParanoid and ad hoc BLAST method. Numbers in parenthesis represent conserved synteny blocks result from ad hoc BLAST method. Mitochondria chromosome (ChrM) of *A. thaliana* was excluded because it doesn't have any synteny blocks with *O. sativa*. Result for 10% mismatches was excluded because it was similar with the result of conserved synteny block.

Chromosome	**Chr I**	**Chr II**	**Chr III**	**Chr IV**	**Chr V**	**Chr C**	**Total**
Chr 1	67 (16)	26 (20)	51 (19)	26 (13)	32 (16)	0 (0)	202 (84)
Chr 2	55 (23)	19 (8)	34 (19)	17 (10)	30 (21)	0 (0)	155 (81)
Chr 3	55 (23)	37 (10)	45 (20)	22 (15)	20 (14)	1 (0)	179 (82)
Chr 4	57 (20)	15 (4)	30 (8)	12 (16)	23 (8)	0 (0)	137 (56)
Chr 5	38 (12)	13 (12)	22 (9)	9 (5)	11 (5)	0 (0)	93 (43)
Chr 6	48 (9)	10 (6)	25 (4)	19 (8)	26 (12)	0 (0)	128 (39)
Chr 7	20 (11)	12 (4)	23 (17)	15 (7)	20 (10)	0 (0)	90 (49)
Chr 8	31 (11)	21 (4)	34 (8)	13 (4)	35 (8)	0 (0)	134 (35)
Chr 9	54 (7)	11 (4)	16 (9)	18 (7)	16 (4)	0 (0)	115 (31)
Chr 10	49 (5)	9 (3)	11 (6)	13 (10)	12 (9)	0 (0)	94 (33)
Chr 11	30 (7)	12 (3)	13 (8)	17 (3)	28 (4)	0 (0)	100 (25)
Chr 12	14 (5)	12 (7)	23 (10)	16 (5)	17 (4)	0 (0)	82 (31)
Total	518 (149)	197 (85)	327 (85)	197 (137)	270 (103)	1 (0)	1510 (589)