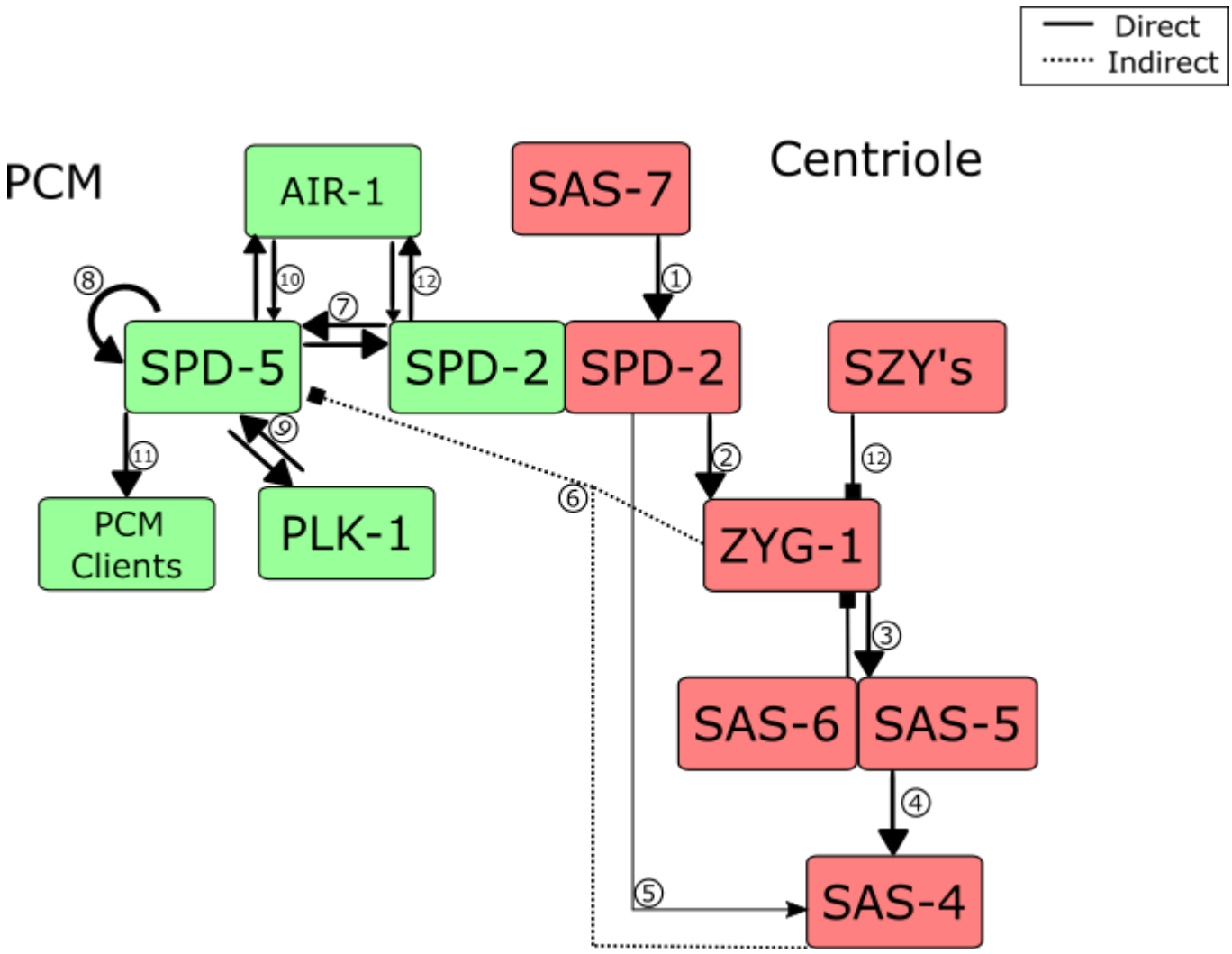

Figure 1: Interaction network.

Template document

1 Interaction Diagram

1.1 Proteins and Associated Phenotypes

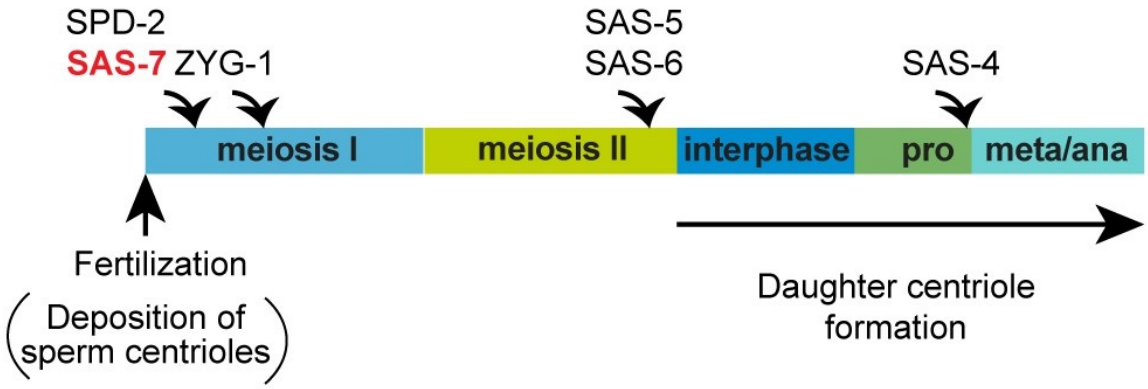

Figure 2: Schematic illustration of the timing of core protein recruitment to the centriole[1]

1. SAS-7

   (a) Localizes to centrioles independently of SPD-2, and is required for centriolar SPD-2, thus placing SAS-7 as the earliest centriole maturation factor[1].

   (b) Maternal GFP::SAS-7 can be found at the centrioles during meiosis I, just after fertilization [Fig. 2;[1]].

2. SPD-2

   (a) In spd-2(RNAi) embryos ZYG-1, GFP-SAS-5, GFP-SAS-6, and GFP-SAS-4 fail to localize to the centriole[2]. Also paternal SAS-4 is diminished compared to WT after SPD-2 RNAi[2]. RNAi knockdown of those proteins does not change SPD-2 localization[2].

   (b) Maternal GFP::SPD-2 is found at centrioles during meiosis I [Fig. 2;[2]].

   (c) A limiting factor for centrosome size[3].[4–6]

3. SPD-5

   (a) SPD-5 exists in two states,an inactive form primarily in the cytoplasm and a phosphorylated form the makes up the PCM[7].

   (b) [8] SPD-5 is able to assemble into supramolecular networks *in vitro* in the presence of simulated crowding by polyethylene glycol (PEG); however, the assemblies lack the shape and microtubule nucleation function as PCM *in vivo*[9]. Initially, SPD-5 assemblies are amorphous, labile, able to merge together, possible unstable, and experience Ostwald ripening[9]. However, once allowed to age, 18 minutes, the assemblies are more resistant, larger, and clump together instead of merging[9]. This suggests an internal change in structure called ”aging” or ”maturation” that has been observed in other biomolecular condensates[10,11].

   (c) SPD-5 contains 9 predicted coiled-coil domains that make up 40% of the protein[8,9].

4. ZYG-1

(a) ZYG-1 related Plk4 is necessary for centriole formation in human cells and in *Drosophila*[12]. Plk4 over-expression leads to excess centriole formation in human cells[13]. In *Drosophila*, overexpression leads to amplification and de novo formation of centrioles[14].

(b) ZYG-1, and more specifically the S123 phosphorylation of SAS-6, is required for centriole formation in *C. elegans*[12]. SAS-6 may be able to be recruited to the centriole without ZYG-1, however ZYG-1 is critical for SAS-6 maintenance[12].

5. SAS-6

(a) SAS-6 is not present in sperm centrioles[15].[6,15–17]

(b) Maternal GFP::SAS-6 is first observed weakly at the centriole at the end of meiosis II and its signal becomes more robust thereafter [Fig. 2;[2]].

6. SAS-5

(a) SAS-5 is present in sperm centrioles[17].[6,15–17]

(b) Maternal GFP::SAS-5 is first observed weakly at the centriole at the end of meiosis II and its signal becomes more robust thereafter [Fig. 2;[2]].

7. SAS-4

(a) SAS-4 is present in sperm centrioles[18,19].[6,18,19]

(b) Maternal GFP::SAS-4 starts to be incorporated at the time of pronuclear formation [Fig. 2;[2]].

8. PLK-1

(a) required for both assembly and maintenance of the PCM[7].

9. PCMD-1

(a) pericentriolar matrix deficient-1

(b) primarily localizes to centrioles independent of other PCM factors SPD-2, SPD-5, or PLK-1[20]. PCMD-1 organizes the PCM core of SPD-2 and SPD-5[20]. In PCMD mutants, centriolar SPD-2 is sufficient to recruit enough PLK-1 to the centrosome so that SPD-5 can form a small and disorganized PCM matrix[20].

10. PCM Clients

(a)

1.2 Interactions

1. SAS-7 & SPD-2
   (a) SAS-7 has two SPD-2 binding domains in its C-Terminus[1]. SAS-7 mutants result in a SPD-2 levels being reduced more than half[1]. Further, the timing of SPD-2 incorporation starts later and ends sooner than wild-type[1]

2. SPD-2 & ZYG-1
   (a) SPD-2 localized to the centriole is required for the recruitment of ZYG-1 to the centriole.

3. ZYG-1 & SAS-6/SAS-5
   (a) ZYG-1 directly phosphorylates SAS-6 at Serine 123 and recruits SAS-6 to the daughter centriole[12,21]
   (b) In SAS-5 mutants and in SAS-6 RNAi, ZYG-1 levels remain high throughout the cell cycle indicating that these two proteins work together to reduce centriolar ZYG-1 during interphase[2].

4. SAS-6/SAS-5 & SAS-4
   (a) Together SAS-6 and SAS-5 recruit SAS-4[6,18,19].

5. SPD-2 & SAS-4
   (a) In wild-type embryos SAS-4 remains stably associated with centrioles. However, in SPD-2 RNAi SAS-4 levels on paternal centrioles is diminished[2]; indicating a role for SPD-2 to maintain SAS-4 after its centriole incorporation.

6. SAS-4 & SPD-5 Indirect Connection
   (a) The size of the centriole correlates with the amount of PCM found. Larger centrioles have a larger PCM.

7. SPD-2 & SPD-5
   (a) *in vitro* conditions where SPD-5 condensates to not form spontaneously (3.25% PEG 100nM SPD-5) addition SPD-2 lead to condensates and addition of SPD-2 and active PLK-1 leads to higher total mass of condensates formed[9].
   (b) SPD-2 is upstream of SPD-5 in the maturation pathway and localizes to the daughter centriole before SPD-5[2]. *in vitro* SPD-2 ”seeds” are able to form large condensates composed of both SPD-2 and SPD-5 when placed in solution with PEG and SPD-5::TagRFP at conditions where SPD-5 would not form self assemblies alone[9].
   (c) In PCMD-1 mutants, some SPD-5 is able to form the PCM core when SPD-2 is present[20].

8. SPD-5 self-activation

   (a) In the absence of SPD-2 and PLK-1, a small shell of SPD-5 still forms a PCM core[7]. SPD-5 can self assemble without SPD-2 or PLK-1, but not a rate high enough to produce a fully formed PCM[7].

   (b) PCM growth rate in WT conditions was measured at 0.48 ± 0.08 /min, when SPD-5 with 4 potential phosphorylation sites mutate to alanine was examined the growth rate was 0.01 ± 0.05 /min

   (c) [4,5]

9. SPD-5 & PLK-1

   (a) PLK-1 is able to accelerate the rate of SPD-5 self-assembly[7].

   (b) Strains expressing SPD-5 with 4 residues mutated to alanine (S530,S627,S658 were likely PLK-1 target sites confirmed to be phosphorylation sites, and S653 a predicted phosphorylation site not confirmed) can form a small PCM core but the core fails to grow[7]. These results are similar to *plk-1 (RNAi)*.

   (c) *in vitro* conditions where SPD-5 condensates to not form spontaneously (3.25% PEG 100nM SPD-5) addition of kinase-dead PLK-1 does not lead to condensates forming but active PLK-1 does lead to condensates[9].

10. PCMD-1 & SPD-5

    (a) PCMD-1 mutants are unable to form the spherical PCM core, instead a highly disordered SPD-5 structures are formed[20]. This suggests that *in vivo*, PCMD-1 is able to concentrate and stabilize SPD-5 to the PCM[20].

11. SPD-5 & PCM Clients

    (a) SPD-5 serves as a scaffold in the PCM for the recruitment of downstream proteins such as PLK-1, SPD-2, TPXL-1, and ZYG-9, which are collectively referred to as ”PCM Clients”[4,5,8,22,23]

    (b) SPD-5 is not able to nucleate microtubules but SPD-5, TPXL-1, and ZYG-9 together can[9].

12. SZY's and ZYG-1

    (a) Multiple proteins are known to suppress ZYG-1[24,25]. Mutations in some of these suppressors can rescue the loss of centriole duplication seen in ZYG-1 mutants.

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